wwPDB X-ray Structure Validation Summary Report (i)

Dec 23, 2024 – 04:21 PM JST

PDB ID	:	8XO2
Title	:	Crystal structure of measles virus fusion inhibitor M1 complexed with F protein HR1 (HR1-42) (P21212 space group)
Authors	:	Oishi, S.; Takahara, A.; Nakatsu, T.
Deposited on	:	2023-12-31
Resolution	:	1.31 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 (1)) were used in the production of this report:

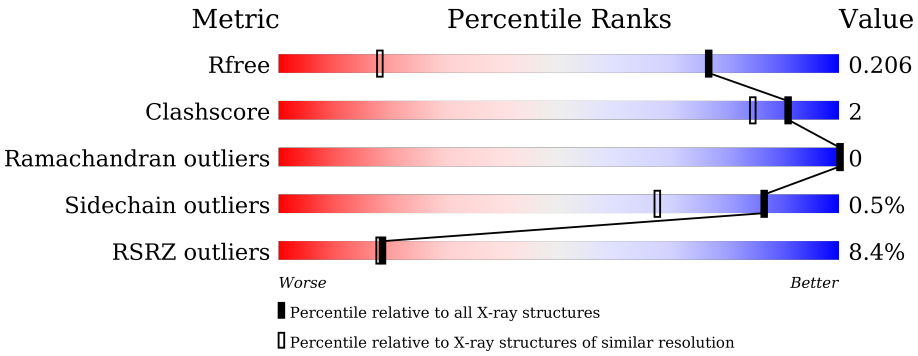
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 1.31 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}	164625	1387 (1.30-1.30)
Clashscore	180529	1497 (1.30-1.30)
Ramachandran outliers	177936	1455 (1.30-1.30)
Sidechain outliers	177891	1455 (1.30-1.30)
RSRZ outliers	164620	1384 (1.30-1.30)

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	44	2% 93% 7%
1	C	44	11% 93% 7%
1	E	44	14% 98%
2	B	37	8% 95% 5%
2	D	37	3% 95%
2	F	37	8% 84% 5% 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2231 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 Fusion glycoprotein F1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	44	Total	C	N	O	S	0	9	1
			367	221	67	77	2			
1	C	44	Total	C	N	O	S	0	3	1
			345	208	62	73	2			
1	E	44	Total	C	N	O	S	0	5	1
			351	212	63	75	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	142	ACE	-	acetylation	UNP P69353
A	185	NH2	-	amidation	UNP P69353
C	142	ACE	-	acetylation	UNP P69353
C	185	NH2	-	amidation	UNP P69353
E	142	ACE	-	acetylation	UNP P69353
E	185	NH2	-	amidation	UNP P69353

- Molecule 2 is a protein called Fusion glycoprotein F1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	35	Total	C	N	O	0	4	1
			277	169	47	61			
2	D	37	Total	C	N	O	0	4	1
			292	182	49	61			
2	F	33	Total	C	N	O	0	3	1
			253	154	44	55			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	451	ACE	-	acetylation	UNP P69353
B	487	NH2	-	amidation	UNP P69353

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Chain	Residue	Modelled	Actual	Comment	Reference
D	451	ACE	-	acetylation	UNP P69353
D	487	NH2	-	amidation	UNP P69353
F	451	ACE	-	acetylation	UNP P69353
F	487	NH2	-	amidation	UNP P69353

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	1
3	F	2	Total Mg 2 2	0	0

- Molecule 4 is water.

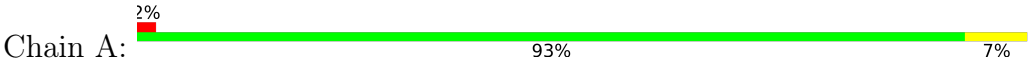
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	49	Total O 49 49	0	2
4	B	70	Total O 70 70	0	3
4	C	60	Total O 60 60	0	2
4	D	63	Total O 63 63	0	1
4	E	49	Total O 49 49	0	4
4	F	51	Total O 51 51	0	1

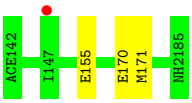
3 Residue-property plots

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: Fusion glycoprotein F1

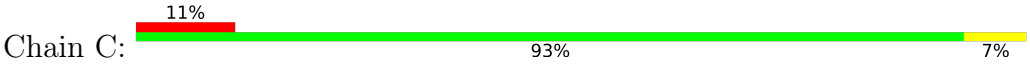
Chain A:

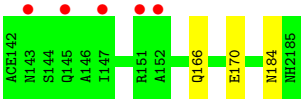




• Molecule 1: Fusion glycoprotein F1

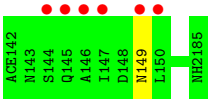
Chain C:





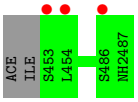
• Molecule 1: Fusion glycoprotein F1

Chain E:



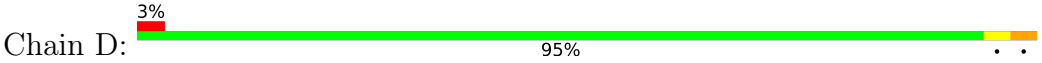
• Molecule 2: Fusion glycoprotein F1

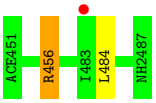
Chain B:



• Molecule 2: Fusion glycoprotein F1

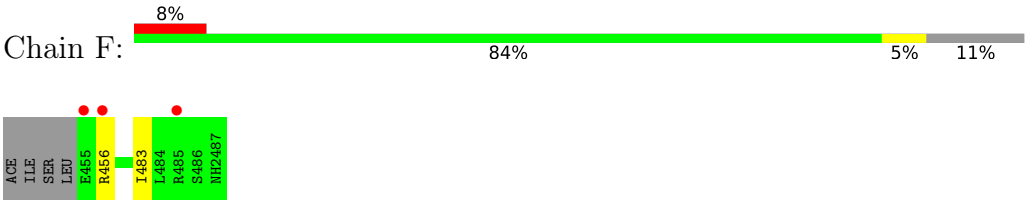
Chain D:





• Molecule 2: Fusion glycoprotein F1

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	54.04Å 54.78Å 64.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.80 – 1.31 41.80 – 1.31	Depositor EDS
% Data completeness (in resolution range)	99.9 (41.80-1.31) 99.9 (41.80-1.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.57 (at 1.31Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.179 , 0.205 0.180 , 0.206	Depositor DCC
R_{free} test set	2363 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	14.0	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 38.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	2231	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.51% 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: ACE, MG, NH2

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	0.93	1/383 (0.3%)	0.80	0/516
1	C	0.86	1/348 (0.3%)	0.77	0/470
1	E	0.81	0/363	0.85	0/491
2	B	0.84	0/287	0.82	0/383
2	D	0.89	0/300	1.02	1/402 (0.2%)
2	F	0.85	0/259	0.82	0/345
All	All	0.87	2/1940 (0.1%)	0.85	1/2607 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	170	GLU	CD-OE1	-9.23	1.15	1.25
1	C	170	GLU	CD-OE1	-5.33	1.19	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	456	ARG	NE-CZ-NH1	-5.80	117.40	120.30

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	367	0	370	2	0
1	C	345	0	339	2	0
1	E	351	0	350	1	0
2	B	277	0	284	0	0
2	D	292	0	314	2	0
2	F	253	0	259	1	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	F	2	0	0	0	0
4	A	49	0	0	0	0
4	B	70	0	0	0	0
4	C	60	0	0	2	0
4	D	63	0	0	1	0
4	E	49	0	0	0	0
4	F	51	0	0	0	0
All	All	2231	0	1916	6	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 2.

The worst 5 of 6 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:E:149[A]:ASN:ND2	2:F:483:ILE:O	2.32	0.54
1:A:155:GLU:HG3	2:D:484:LEU:HD13	1.97	0.46
1:C:184:ASN:ND2	4:C:301:HOH:O	2.49	0.44
2:D:456:ARG:HG3	4:D:525:HOH:O	2.19	0.42
1:C:166[B]:GLN:NE2	4:C:304:HOH:O	2.53	0.41

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	50/44 (114%)	50 (100%)	0	0	100	100
1	C	45/44 (102%)	45 (100%)	0	0	100	100
1	E	47/44 (107%)	47 (100%)	0	0	100	100
2	B	37/37 (100%)	37 (100%)	0	0	100	100
2	D	39/37 (105%)	39 (100%)	0	0	100	100
2	F	34/37 (92%)	34 (100%)	0	0	100	100
All	All	252/243 (104%)	252 (100%)	0	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	42/34 (124%)	42 (100%)	0	100	100
1	C	37/34 (109%)	37 (100%)	0	100	100
1	E	39/34 (115%)	39 (100%)	0	100	100
2	B	32/30 (107%)	32 (100%)	0	100	100
2	D	34/30 (113%)	34 (100%)	0	100	100
2	F	29/30 (97%)	28 (97%)	1 (3%)	32	4
All	All	213/192 (111%)	212 (100%)	1 (0%)	86	67

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	456	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	184	ASN

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Mol	Chain	Res	Type
2	D	462	ASN
2	D	465	ASN
2	F	462	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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

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	42/44 (95%)	0.28	1 (2%) 59 63	7, 14, 23, 29	8 (19%)
1	C	42/44 (95%)	0.60	5 (11%) 10 9	8, 14, 42, 47	3 (7%)
1	E	42/44 (95%)	0.52	6 (14%) 7 6	6, 13, 34, 50	5 (11%)
2	B	34/37 (91%)	0.72	3 (8%) 17 16	8, 15, 45, 60	4 (11%)
2	D	35/37 (94%)	0.44	1 (2%) 54 58	7, 14, 29, 42	4 (11%)
2	F	32/37 (86%)	0.56	3 (9%) 15 14	8, 15, 40, 45	3 (9%)
All	All	227/243 (93%)	0.51	19 (8%) 18 18	6, 14, 40, 60	27 (11%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	454	LEU	4.9
1	E	146	ALA	3.4
2	F	455	GLU	3.3
2	B	453	SER	3.3
1	C	147	ILE	3.2

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

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
3	MG	B	501	1/1	0.82	0.29	37,37,37,37	0
3	MG	F	502	1/1	0.82	0.26	43,43,43,43	0
3	MG	C	201[B]	1/1	0.94	0.08	23,23,23,23	1
3	MG	F	501	1/1	0.96	0.20	21,21,21,21	0

6.5 Other polymers

There are no such residues in this entry.