



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 7PHU / pdb_00007phu
Title : PfrH5 bound to monoclonal antibody R5.015 and R5.016 Fab fragments
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Deposited on : 2021-08-18
Resolution : 2.53 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

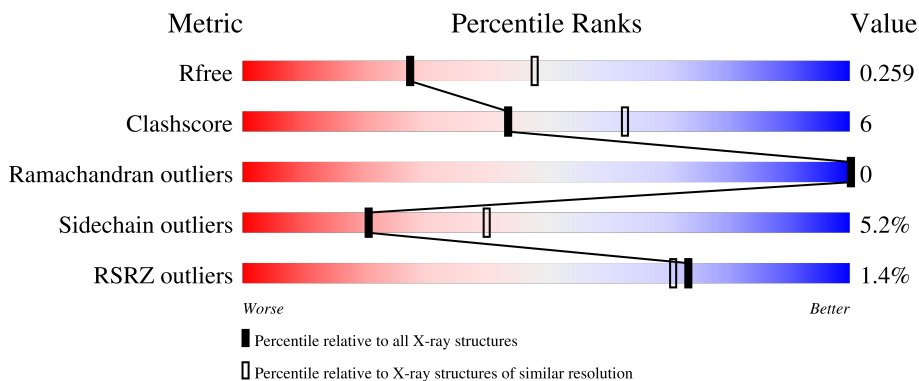
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 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}	180053	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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 $\leq 5\%$. 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	501	
2	B	236	
3	C	217	
4	D	464	
5	E	219	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9294 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 Reticulocyte-binding protein homolog 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	295	2511	1620	422	453	16	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	38	GLN	ASN	conflict	UNP Q8IFM5
A	203	TYR	CYS	conflict	UNP Q8IFM5
A	216	ALA	THR	conflict	UNP Q8IFM5

- Molecule 2 is a protein called Monoclonal antibody R5.015 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	222	1683	1069	278	327	9	0	0	0

- Molecule 3 is a protein called Monoclonal antibody R5.015 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	212	1599	1004	266	324	5	0	0	0

- Molecule 4 is a protein called Monoclonal antibody R5.016 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	232	1746	1098	290	349	9	0	0	0

- Molecule 5 is a protein called Monoclonal antibody R5.016 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	211	1628	1019	276	328	5	0	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	31	Total 31	O 31	0	0
6	B	8	Total 8	O 8	0	0
6	C	36	Total 36	O 36	0	0
6	D	27	Total 27	O 27	0	0
6	E	25	Total 25	O 25	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	97.74Å 163.30Å 176.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.79 – 2.53 47.79 – 2.53	Depositor EDS
% Data completeness (in resolution range)	99.5 (47.79-2.53) 99.5 (47.79-2.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.54Å)	Xtrriage
Refinement program	BUSTER 2.10.4 (24-FEB-2021)	Depositor
R, R_{free}	0.236 , 0.276 0.223 , 0.259	Depositor DCC
R_{free} test set	2354 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	59.9	Xtrriage
Anisotropy	0.622	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.001 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9294	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.78	1/2564 (0.0%)	1.22	4/3437 (0.1%)
2	B	0.77	0/1730	1.08	5/2362 (0.2%)
3	C	0.76	0/1641	1.09	2/2246 (0.1%)
4	D	0.70	0/1790	1.06	4/2442 (0.2%)
5	E	0.73	0/1663	1.01	0/2258
All	All	0.75	1/9388 (0.0%)	1.11	15/12745 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	332	MET	SD-CE	-8.21	1.59	1.79

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	50	ASP	CA-CB-CG	6.96	119.56	112.60
1	A	324	ASP	CA-CB-CG	6.96	119.56	112.60
4	D	146	ALA	N-CA-C	5.97	117.17	109.65
4	D	151	SER	CA-C-N	5.90	130.80	121.72
4	D	151	SER	C-N-CA	5.90	130.80	121.72

There are no chirality outliers.

There are no planarity outliers.

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	2511	0	2531	32	0
2	B	1683	0	1624	25	0
3	C	1599	0	1535	10	0
4	D	1746	0	1682	23	0
5	E	1628	0	1584	26	0
6	A	31	0	0	0	0
6	B	8	0	0	0	0
6	C	36	0	0	0	0
6	D	27	0	0	0	0
6	E	25	0	0	0	0
All	All	9294	0	8956	111	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 6.

The worst 5 of 111 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)
4:D:184:VAL:HG22	4:D:203:VAL:CG1	1.82	1.09
4:D:184:VAL:HG22	4:D:203:VAL:HG12	1.08	1.06
2:B:161:TYR:CE2	2:B:166:VAL:HG23	2.01	0.96
4:D:184:VAL:CG2	4:D:203:VAL:HG12	1.94	0.96
1:A:195:HIS:CD2	1:A:343:LEU:HD11	2.07	0.88

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	291/501 (58%)	284 (98%)	7 (2%)	0	100 100
2	B	218/236 (92%)	211 (97%)	7 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	210/217 (97%)	201 (96%)	9 (4%)	0	100	100
4	D	230/464 (50%)	218 (95%)	12 (5%)	0	100	100
5	E	209/219 (95%)	199 (95%)	10 (5%)	0	100	100
All	All	1158/1637 (71%)	1113 (96%)	45 (4%)	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	286/486 (59%)	272 (95%)	14 (5%)	22	43
2	B	188/202 (93%)	180 (96%)	8 (4%)	26	49
3	C	180/185 (97%)	173 (96%)	7 (4%)	28	52
4	D	195/409 (48%)	181 (93%)	14 (7%)	13	26
5	E	186/192 (97%)	175 (94%)	11 (6%)	18	35
All	All	1035/1474 (70%)	981 (95%)	54 (5%)	21	40

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	182	LEU
4	D	112	ASP
5	E	105	GLN
4	D	15	GLU
4	D	48	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	43	GLN
5	E	204	GLN

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Mol	Chain	Res	Type
5	E	143	ASN
2	B	57	ASN
5	E	35	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 [i](#)

There are no oligosaccharides 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	295/501 (58%)	0.05	5 (1%) 69 66	43, 60, 81, 104	0
2	B	222/236 (94%)	-0.12	4 (1%) 67 64	35, 54, 77, 90	0
3	C	212/217 (97%)	-0.17	1 (0%) 87 85	36, 57, 78, 92	0
4	D	232/464 (50%)	0.19	3 (1%) 75 72	47, 70, 97, 111	0
5	E	211/219 (96%)	0.08	3 (1%) 73 71	47, 71, 93, 106	0
All	All	1172/1637 (71%)	0.01	16 (1%) 73 71	35, 62, 90, 111	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	153	SER	4.1
5	E	7	ILE	3.9
4	D	111	PHE	3.3
2	B	149	GLY	3.2
5	E	217	GLY	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 oligosaccharides 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.