Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 04:56 am BST

PDB ID	:	4H88
Title	:	Structure of POM1 FAB fragment complexed with mouse PrPc Fragment 120-230
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Deposited on	:	2012-09-21
Resolution	:	1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see references ⓘ) were used in the production of this report:

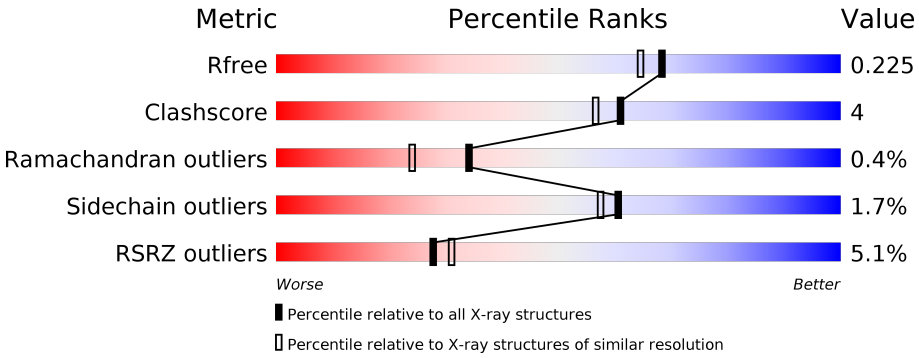
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.90 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))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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	111	7% 80% 11% • 8%
2	H	218	4% 90% 9% •
3	L	213	5% 89% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4513 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 prion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	102	Total	C	N	O	S	0	0	0
			859	538	147	165	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	189	VAL	THR	CONFLICT	UNP P04925

- Molecule 2 is a protein called POM1 FAB CHAIN H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	218	Total	C	N	O	S	4	0	0
			1642	1037	265	330	10			

- Molecule 3 is a protein called POM1 FAB CHAIN L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	0	0
			1652	1022	280	345	5			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	1	Total	Na	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	72	Total	O	0	0
			72	72		

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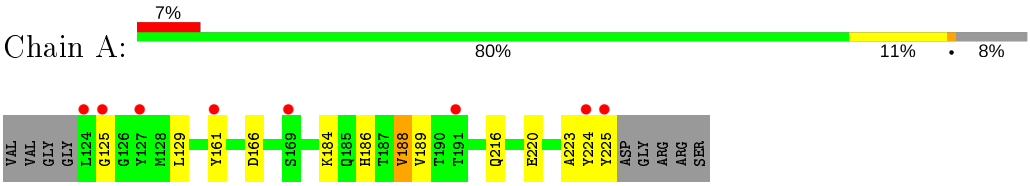
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	164	Total O 164 164	0	0
5	L	123	Total O 123 123	0	0

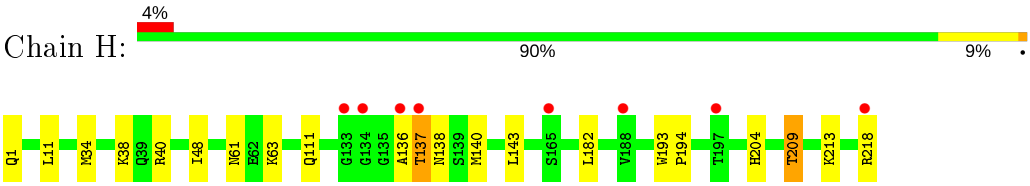
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

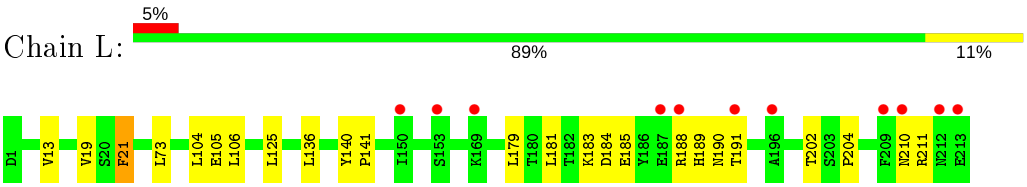
- Molecule 1: Major prion protein



- Molecule 2: POM1 FAB CHAIN H



- Molecule 3: POM1 FAB CHAIN L



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	83.41Å 107.33Å 75.44Å 90.00° 95.27° 90.00°	Depositor
Resolution (Å)	35.01 – 1.90 35.01 – 1.90	Depositor EDS
% Data completeness (in resolution range)	95.9 (35.01-1.90) 95.9 (35.01-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.71 (at 1.89Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.199 , 0.234 0.194 , 0.225	Depositor DCC
R_{free} test set	2526 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	33.3	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 55.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4513	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.03% 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: 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	0.40	0/880	0.48	0/1190
2	H	0.36	0/1688	0.53	0/2306
3	L	0.32	0/1687	0.50	0/2291
All	All	0.35	0/4255	0.51	0/5787

There are no bond length outliers.

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	859	0	798	6	0
2	H	1642	0	1578	15	0
3	L	1652	0	1573	15	0
4	L	1	0	0	0	0
5	A	72	0	0	0	2
5	H	164	0	0	3	0
5	L	123	0	0	2	1
All	All	4513	0	3949	36	2

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 4.

All (36) 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:H:111:GLN:OE1	5:H:462:HOH:O	1.90	0.86
2:H:218:ARG:NH2	5:H:433:HOH:O	2.26	0.68
2:H:1:GLN:CD	2:H:1:GLN:N	2.56	0.59
3:L:185:GLU:HA	3:L:188:ARG:HD3	1.87	0.56
3:L:136:LEU:HD12	3:L:136:LEU:N	2.22	0.55
1:A:129:LEU:HD13	1:A:161:TYR:CZ	2.42	0.54
3:L:106:LEU:HD12	5:L:430:HOH:O	2.07	0.54
1:A:129:LEU:HD13	1:A:161:TYR:CE2	2.43	0.53
2:H:40:ARG:NE	5:H:453:HOH:O	2.43	0.52
3:L:190:ASN:HD21	3:L:210:ASN:HB3	1.75	0.52
3:L:21:PHE:CE1	3:L:73:LEU:HD23	2.45	0.52
3:L:13:VAL:HG11	3:L:19:VAL:HG11	1.91	0.51
1:A:184:LYS:O	1:A:188:VAL:HG13	2.14	0.48
1:A:223:ALA:O	1:A:224:TYR:HB3	2.14	0.48
1:A:216:GLN:O	1:A:220:GLU:HG2	2.13	0.48
2:H:138:ASN:C	2:H:140:MET:H	2.15	0.48
3:L:13:VAL:CG1	3:L:19:VAL:HG11	2.44	0.47
3:L:189:HIS:O	3:L:211:ARG:NH1	2.47	0.46
2:H:143:LEU:HD22	2:H:143:LEU:N	2.31	0.46
2:H:11:LEU:HD13	2:H:11:LEU:C	2.37	0.45
1:A:186:HIS:O	1:A:189:VAL:HG22	2.16	0.45
3:L:191:THR:HG22	3:L:210:ASN:OD1	2.17	0.45
2:H:136:ALA:O	2:H:137:THR:O	2.35	0.44
3:L:140:TYR:CG	3:L:141:PRO:HA	2.53	0.44
2:H:204:HIS:HB3	2:H:209:THR:HB	2.01	0.43
3:L:189:HIS:O	3:L:211:ARG:HD3	2.18	0.43
2:H:193:TRP:CG	2:H:194:PRO:HA	2.54	0.43
2:H:182:LEU:C	2:H:182:LEU:HD12	2.39	0.43
2:H:1:GLN:H1	2:H:1:GLN:CD	2.20	0.42
3:L:184:ASP:OD2	5:L:512:HOH:O	2.21	0.42
2:H:213:LYS:HD3	2:H:213:LYS:HA	1.79	0.41
3:L:179:LEU:HG	3:L:181:LEU:HD13	2.02	0.41
2:H:61:ASN:OD1	2:H:63:LYS:HG2	2.20	0.41
3:L:125:LEU:O	3:L:183:LYS:HD2	2.21	0.41
3:L:202:THR:O	3:L:204:PRO:HD3	2.21	0.41
2:H:38:LYS:HB2	2:H:48:ILE:HD11	2.03	0.40

All (2) 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)
5:A:352:HOH:O	5:A:354:HOH:O[2_554]	2.09	0.11
5:A:355:HOH:O	5:L:512:HOH:O[2_555]	2.16	0.04

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	100/111 (90%)	97 (97%)	2 (2%)	1 (1%)	15 6
2	H	216/218 (99%)	208 (96%)	7 (3%)	1 (0%)	29 18
3	L	211/213 (99%)	205 (97%)	6 (3%)	0	100 100
All	All	527/542 (97%)	510 (97%)	15 (3%)	2 (0%)	34 24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	137	THR
1	A	125	GLY

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	95/101 (94%)	92 (97%)	3 (3%)	39 30
2	H	187/187 (100%)	185 (99%)	2 (1%)	73 73
3	L	191/191 (100%)	188 (98%)	3 (2%)	62 60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	473/479 (99%)	465 (98%)	8 (2%)	60 57

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ASP
1	A	188	VAL
1	A	225	TYR
2	H	34	MET
2	H	209	THR
3	L	21	PHE
3	L	104	LEU
3	L	105	GLU

Some 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 carbohydrates in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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	102/111 (91%)	0.40	8 (7%)	13	14	25, 37, 62, 90	0
2	H	217/218 (99%)	0.22	8 (3%)	41	44	23, 40, 60, 84	0
3	L	213/213 (100%)	0.25	11 (5%)	27	30	25, 44, 69, 80	0
All	All	532/542 (98%)	0.27	27 (5%)	28	31	23, 41, 66, 90	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	LEU	14.4
1	A	224	TYR	4.9
2	H	137	THR	4.2
3	L	196	ALA	3.9
3	L	187	GLU	3.6
1	A	127	TYR	3.6
3	L	188	ARG	3.2
3	L	209	PHE	3.2
1	A	225	TYR	2.8
1	A	169	SER	2.8
3	L	213	GLU	2.7
3	L	150	ILE	2.7
2	H	133	GLY	2.7
1	A	191	THR	2.6
2	H	134	GLY	2.6
3	L	153	SER	2.5
2	H	218	ARG	2.5
2	H	165	SER	2.5
3	L	212	ASN	2.4
1	A	125	GLY	2.4
3	L	210	ASN	2.4
2	H	136	ALA	2.2
2	H	197	THR	2.2

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Mol	Chain	Res	Type	RSRZ
3	L	191	THR	2.1
2	H	188	VAL	2.1
3	L	169	LYS	2.1
1	A	161	TYR	2.0

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)

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	301	1/1	0.96	0.46	12,12,12,12	0

6.5 Other polymers (i)

There are no such residues in this entry.