Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 11:06 pm BST

PDB ID	:	5K22
Title	:	Crystal structure of the complex between human PRL-2 phosphatase in reduced state and Bateman domain of human CNNM3
Authors	:	Kozlov, G.; Wu, H.; Gehring, K.
Deposited on	:	2016-05-18
Resolution	:	3.00 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:

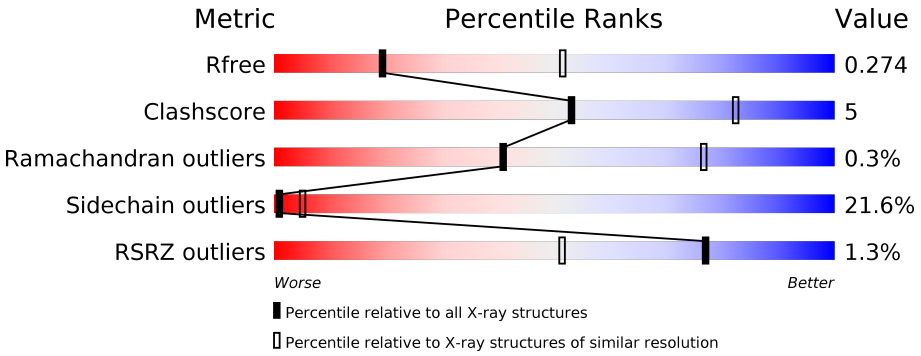
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 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	183	% 54% 28% . 15%
2	B	155	% 66% 26% . . .

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2425 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 Protein tyrosine phosphatase type IVA 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1239	793	218	222	6			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q12974
A	-18	GLY	-	expression tag	UNP Q12974
A	-17	SER	-	expression tag	UNP Q12974
A	-16	SER	-	expression tag	UNP Q12974
A	-15	HIS	-	expression tag	UNP Q12974
A	-14	HIS	-	expression tag	UNP Q12974
A	-13	HIS	-	expression tag	UNP Q12974
A	-12	HIS	-	expression tag	UNP Q12974
A	-11	HIS	-	expression tag	UNP Q12974
A	-10	HIS	-	expression tag	UNP Q12974
A	-9	SER	-	expression tag	UNP Q12974
A	-8	SER	-	expression tag	UNP Q12974
A	-7	GLY	-	expression tag	UNP Q12974
A	-6	LEU	-	expression tag	UNP Q12974
A	-5	VAL	-	expression tag	UNP Q12974
A	-4	PRO	-	expression tag	UNP Q12974
A	-3	ARG	-	expression tag	UNP Q12974
A	-2	GLY	-	expression tag	UNP Q12974
A	-1	SER	-	expression tag	UNP Q12974
A	0	HIS	-	expression tag	UNP Q12974
A	95	ALA	CYS	engineered mutation	UNP Q12974
A	96	ALA	CYS	engineered mutation	UNP Q12974
A	119	ALA	CYS	engineered mutation	UNP Q12974

- Molecule 2 is a protein called Metal transporter CNNM3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	149	Total	C	N	O	S	0	0	0
			1180	754	192	227	7			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	298	GLY	-	expression tag	UNP Q8NE01
B	299	PRO	-	expression tag	UNP Q8NE01
B	300	LEU	-	expression tag	UNP Q8NE01
B	301	ASN	-	expression tag	UNP Q8NE01
B	302	MET	-	expression tag	UNP Q8NE01
B	303	ILE	-	expression tag	UNP Q8NE01
B	304	GLN	-	expression tag	UNP Q8NE01
B	305	GLY	-	expression tag	UNP Q8NE01
B	306	VAL	-	expression tag	UNP Q8NE01
B	307	LEU	-	expression tag	UNP Q8NE01
B	308	GLU	-	expression tag	UNP Q8NE01

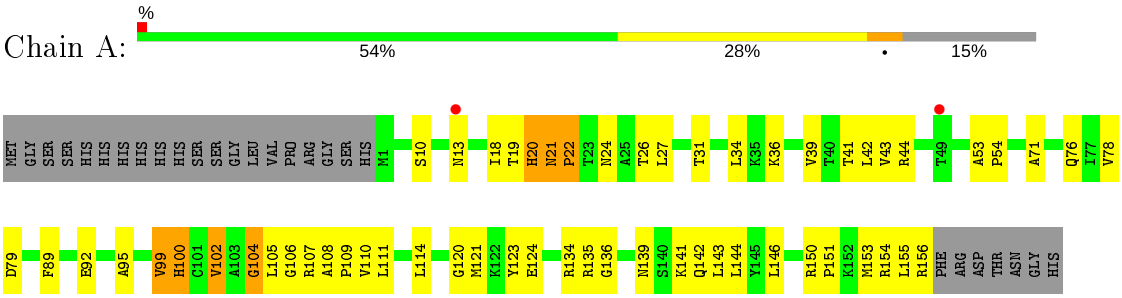
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	O	0	0
			3	3		
3	B	3	Total	O	0	0
			3	3		

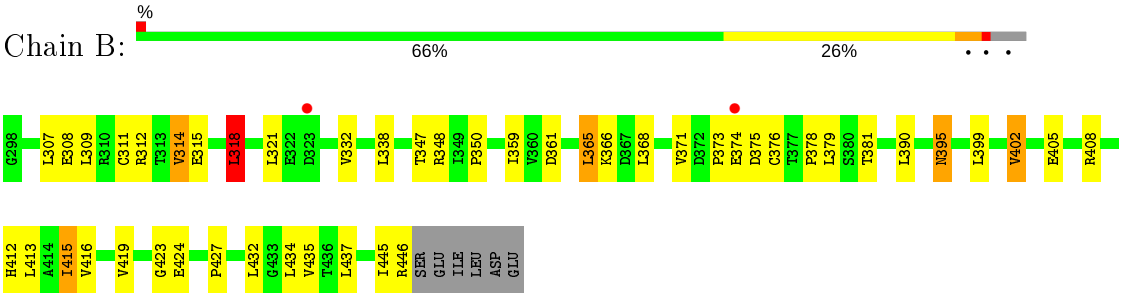
3 Residue-property plots (i)

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: Protein tyrosine phosphatase type IVA 2



- Molecule 2: Metal transporter CNNM3



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	54.45Å 126.72Å 152.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 18.36 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.9 (50.00-3.00) 99.5 (18.36-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.00 (at 3.03Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.231 , 0.274 0.231 , 0.274	Depositor DCC
R_{free} test set	601 reflections (5.56%)	wwPDB-VP
Wilson B-factor (Å^2)	91.2	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 50.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2425	wwPDB-VP
Average B, all atoms (Å^2)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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

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	0.27	0/1268	0.45	0/1723
2	B	0.27	0/1202	0.48	1/1633 (0.1%)
All	All	0.27	0/2470	0.47	1/3356 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	11
2	B	0	6
All	All	0	17

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	318	LEU	CA-CB-CG	5.79	128.62	115.30

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	100	HIS	Peptide
1	A	102	VAL	Peptide
1	A	104	GLY	Peptide
1	A	105	LEU	Peptide
1	A	120	GLY	Peptide
1	A	151	PRO	Peptide
1	A	20	HIS	Peptide
1	A	22	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	A	26	THR	Peptide
1	A	71	ALA	Peptide
1	A	89	PHE	Peptide
2	B	371	VAL	Peptide
2	B	375	ASP	Peptide
2	B	412	HIS	Peptide
2	B	423	GLY	Peptide
2	B	432	LEU	Peptide
2	B	445	ILE	Peptide

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	1239	0	1242	13	0
2	B	1180	0	1166	15	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
All	All	2425	0	2408	26	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.

All (26) 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:B:314:VAL:HG23	2:B:402:VAL:HG21	1.83	0.60
2:B:359:ILE:HD12	2:B:415:ILE:HD13	1.86	0.57
2:B:315:GLU:HA	2:B:318:LEU:HD13	1.86	0.57
2:B:347:THR:HA	2:B:365:LEU:HG	1.87	0.56
2:B:314:VAL:HG22	2:B:435:VAL:HG11	1.87	0.55
1:A:53:ALA:N	1:A:54:PRO:HD2	2.24	0.51
1:A:43:VAL:HB	1:A:99:VAL:HG13	1.92	0.50
2:B:395:ASN:H	2:B:395:ASN:HD22	1.60	0.50
2:B:332:VAL:HA	2:B:378:PRO:HA	1.93	0.50
1:A:139:ASN:HB3	2:B:427:PRO:HD3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:GLY:HA3	2:B:419:VAL:HG11	1.95	0.49
1:A:106:GLY:O	1:A:110:VAL:HG23	2.13	0.48
2:B:338:LEU:HD12	2:B:373:PRO:HB3	1.97	0.47
1:A:20:HIS:CD2	1:A:20:HIS:H	2.33	0.45
1:A:108:ALA:HB3	1:A:109:PRO:HD3	1.97	0.45
1:A:92:GLU:HB3	1:A:95:ALA:HB2	1.99	0.44
1:A:44:ARG:HG2	1:A:100:HIS:NE2	2.33	0.43
1:A:104:GLY:H	1:A:134:ARG:HH21	1.66	0.42
2:B:318:LEU:HD12	2:B:416:VAL:HG11	2.02	0.42
1:A:99:VAL:HB	1:A:108:ALA:HB1	2.02	0.41
1:A:34:LEU:HB3	1:A:39:VAL:HG22	2.02	0.41
2:B:308:GLU:HB3	2:B:312:ARG:HG3	2.03	0.41
2:B:378:PRO:HG2	2:B:381:THR:HG23	2.03	0.41
2:B:314:VAL:CG2	2:B:402:VAL:HG21	2.51	0.40
1:A:21:ASN:HD22	1:A:22:PRO:HD2	1.87	0.40
2:B:350:PRO:HG2	2:B:434:LEU:HD11	2.04	0.40

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	154/183 (84%)	145 (94%)	8 (5%)	1 (1%)	25 64
2	B	147/155 (95%)	143 (97%)	4 (3%)	0	100 100
All	All	301/338 (89%)	288 (96%)	12 (4%)	1 (0%)	41 76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	ASN

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	130/156 (83%)	98 (75%)	32 (25%)	0 3
2	B	134/142 (94%)	109 (81%)	25 (19%)	1 8
All	All	264/298 (89%)	207 (78%)	57 (22%)	1 5

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	18	ILE
1	A	19	THR
1	A	21	ASN
1	A	24	ASN
1	A	27	LEU
1	A	31	THR
1	A	36	LYS
1	A	41	THR
1	A	42	LEU
1	A	76	GLN
1	A	78	VAL
1	A	79	ASP
1	A	99	VAL
1	A	102	VAL
1	A	107	ARG
1	A	111	LEU
1	A	114	LEU
1	A	121	MET
1	A	123	TYR
1	A	124	GLU
1	A	135	ARG
1	A	141	LYS
1	A	142	GLN
1	A	143	LEU
1	A	144	LEU
1	A	146	LEU

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Mol	Chain	Res	Type
1	A	150	ARG
1	A	153	MET
1	A	154	ARG
1	A	155	LEU
1	A	156	ARG
2	B	307	LEU
2	B	309	LEU
2	B	311	CYS
2	B	314	VAL
2	B	318	LEU
2	B	321	LEU
2	B	348	ARG
2	B	361	ASP
2	B	365	LEU
2	B	366	LYS
2	B	368	LEU
2	B	374	GLU
2	B	376	CYS
2	B	379	LEU
2	B	390	LEU
2	B	395	ASN
2	B	399	LEU
2	B	402	VAL
2	B	405	GLU
2	B	408	ARG
2	B	413	LEU
2	B	415	ILE
2	B	424	GLU
2	B	437	LEU
2	B	446	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	HIS
1	A	21	ASN
2	B	343	GLN
2	B	395	ASN
2	B	417	GLN

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

There are no ligands in this entry.

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	156/183 (85%)	0.08	2 (1%)	77	51	76, 101, 130, 143	0
2	B	149/155 (96%)	-0.03	2 (1%)	77	51	68, 85, 110, 123	0
All	All	305/338 (90%)	0.03	4 (1%)	77	51	68, 92, 127, 143	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	49	THR	2.9
2	B	323	ASP	2.3
1	A	13	ASN	2.2
2	B	374	GLU	2.1

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 carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.