



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 20, 2020 – 03:09 PM BST

PDB ID : 6IQQ
Title : Crystal structure of Prc with S452I and L252Y mutations in complex with NlpI
Authors : Chueh, C.K.; Chang, C.I.
Deposited on : 2018-11-08
Resolution : 2.80 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 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	:	2.13.1
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)	:	2.13.1

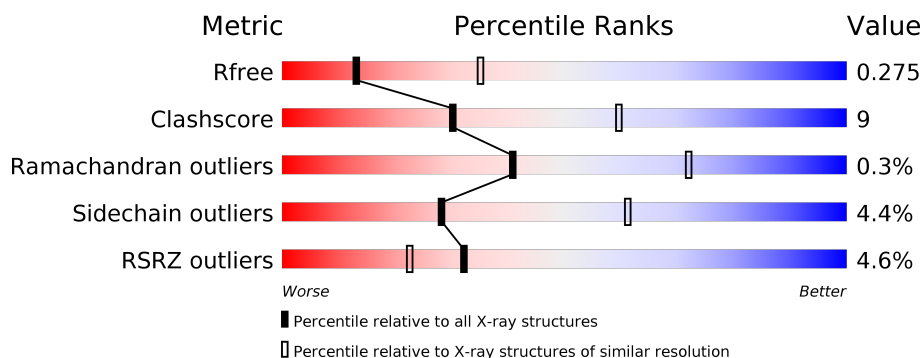
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 $\leq 5\%$. 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	296	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 5%, orange 5%, yellow 11%, green 74%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 6% 74% 11% 13% </div> </div>
1	B	296	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 79%, yellow 8%, orange 1%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 79% 8% 13% </div> </div>
2	C	688	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 6%, orange 5%, yellow 17%, green 74%, grey 6%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 6% 74% 17% 6% </div> </div>
2	D	688	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 5%, orange 5%, yellow 16%, green 74%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 5% 74% 16% 7% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14502 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 Lipoprotein NlpI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2082	1331	345	403	3			
1	B	258	Total	C	N	O	S	0	0	0
			2091	1336	346	406	3			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AFB1
A	2	GLY	-	expression tag	UNP P0AFB1
A	3	SER	-	expression tag	UNP P0AFB1
A	4	SER	-	expression tag	UNP P0AFB1
A	5	HIS	-	expression tag	UNP P0AFB1
A	6	HIS	-	expression tag	UNP P0AFB1
A	7	HIS	-	expression tag	UNP P0AFB1
A	8	HIS	-	expression tag	UNP P0AFB1
A	9	HIS	-	expression tag	UNP P0AFB1
A	10	HIS	-	expression tag	UNP P0AFB1
A	11	SER	-	expression tag	UNP P0AFB1
A	12	SER	-	expression tag	UNP P0AFB1
A	13	GLY	-	expression tag	UNP P0AFB1
A	14	LEU	-	expression tag	UNP P0AFB1
A	15	VAL	-	expression tag	UNP P0AFB1
A	16	PRO	-	expression tag	UNP P0AFB1
A	17	ARG	-	expression tag	UNP P0AFB1
A	18	GLY	-	expression tag	UNP P0AFB1
A	19	SER	-	expression tag	UNP P0AFB1
A	20	HIS	-	expression tag	UNP P0AFB1
A	21	MET	-	expression tag	UNP P0AFB1
B	1	MET	-	initiating methionine	UNP P0AFB1
B	2	GLY	-	expression tag	UNP P0AFB1
B	3	SER	-	expression tag	UNP P0AFB1
B	4	SER	-	expression tag	UNP P0AFB1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	HIS	-	expression tag	UNP P0AFB1
B	6	HIS	-	expression tag	UNP P0AFB1
B	7	HIS	-	expression tag	UNP P0AFB1
B	8	HIS	-	expression tag	UNP P0AFB1
B	9	HIS	-	expression tag	UNP P0AFB1
B	10	HIS	-	expression tag	UNP P0AFB1
B	11	SER	-	expression tag	UNP P0AFB1
B	12	SER	-	expression tag	UNP P0AFB1
B	13	GLY	-	expression tag	UNP P0AFB1
B	14	LEU	-	expression tag	UNP P0AFB1
B	15	VAL	-	expression tag	UNP P0AFB1
B	16	PRO	-	expression tag	UNP P0AFB1
B	17	ARG	-	expression tag	UNP P0AFB1
B	18	GLY	-	expression tag	UNP P0AFB1
B	19	SER	-	expression tag	UNP P0AFB1
B	20	HIS	-	expression tag	UNP P0AFB1
B	21	MET	-	expression tag	UNP P0AFB1

- Molecule 2 is a protein called Tail-specific protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	645	Total	C	N	O	S	0	0	0
			5128	3229	895	992	12			
2	D	642	Total	C	N	O	S	0	0	0
			5106	3214	891	989	12			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	252	TYR	LEU	engineered mutation	UNP P23865
C	452	ILE	SER	engineered mutation	UNP P23865
C	683	HIS	-	expression tag	UNP P23865
C	684	HIS	-	expression tag	UNP P23865
C	685	HIS	-	expression tag	UNP P23865
C	686	HIS	-	expression tag	UNP P23865
C	687	HIS	-	expression tag	UNP P23865
C	688	HIS	-	expression tag	UNP P23865
D	252	TYR	LEU	engineered mutation	UNP P23865
D	452	ILE	SER	engineered mutation	UNP P23865
D	683	HIS	-	expression tag	UNP P23865
D	684	HIS	-	expression tag	UNP P23865
D	685	HIS	-	expression tag	UNP P23865

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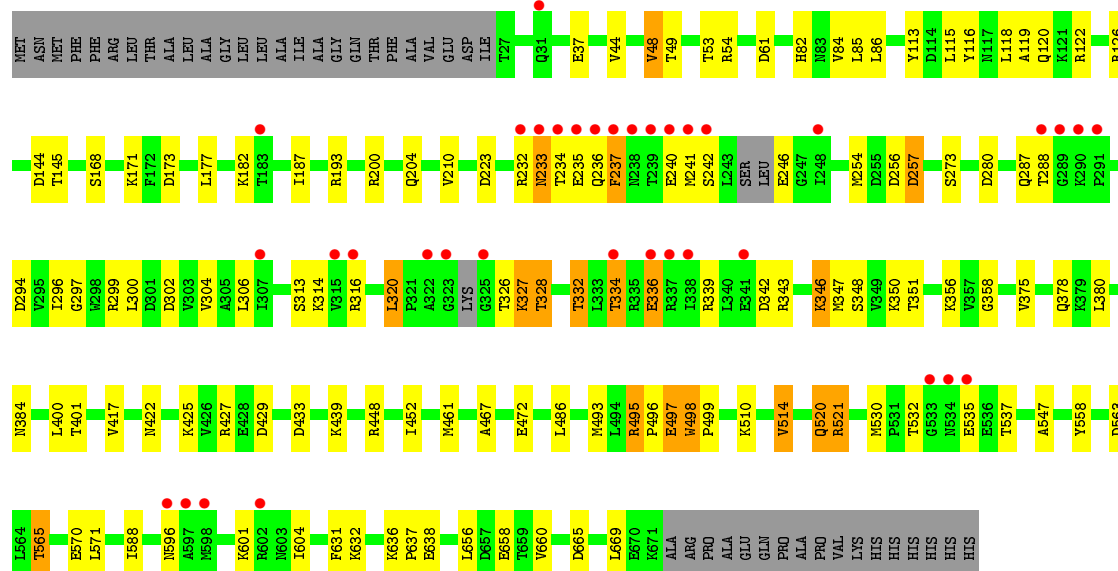
Chain	Residue	Modelled	Actual	Comment	Reference
D	686	HIS	-	expression tag	UNP P23865
D	687	HIS	-	expression tag	UNP P23865
D	688	HIS	-	expression tag	UNP P23865

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	16	Total	O	0	0
			16	16		
4	B	19	Total	O	0	0
			19	19		
4	C	23	Total	O	0	0
			23	23		
4	D	35	Total	O	0	0
			35	35		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	118.94Å 143.88Å 153.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 2.80 29.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.8 (29.98-2.80) 97.0 (29.98-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.8.0232	Depositor
R, R_{free}	0.222 , 0.278 0.224 , 0.275	Depositor DCC
R_{free} test set	3248 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	14502	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.71 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0586e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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

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	0.90	4/2126 (0.2%)	1.05	6/2886 (0.2%)
1	B	0.92	4/2135 (0.2%)	1.04	4/2898 (0.1%)
2	C	0.79	0/5215	0.99	2/7040 (0.0%)
2	D	0.79	0/5192	1.02	4/7008 (0.1%)
All	All	0.83	8/14668 (0.1%)	1.02	16/19832 (0.1%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	50	GLU	CD-OE2	-6.42	1.18	1.25
1	A	99	GLU	CD-OE2	-6.08	1.19	1.25
1	A	206	GLU	CD-OE2	6.06	1.32	1.25
1	B	38	PRO	C-O	-5.74	1.11	1.23
1	B	99	GLU	CD-OE2	-5.68	1.19	1.25

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	495	ARG	NE-CZ-NH1	8.57	124.58	120.30
1	B	275	TYR	CB-CA-C	7.24	124.87	110.40
1	A	275	TYR	CB-CA-C	7.12	124.64	110.40
1	A	85	ASN	CB-CA-C	6.77	123.95	110.40
1	B	85	ASN	CB-CA-C	6.51	123.41	110.40

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	2082	0	2016	25	0
1	B	2091	0	2022	21	0
2	C	5128	0	5142	135	0
2	D	5106	0	5112	99	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	16	0	0	0	0
4	B	19	0	0	1	0
4	C	23	0	0	1	0
4	D	35	0	0	0	0
All	All	14502	0	14292	268	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 9.

The worst 5 of 268 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:C:119:ALA:O	2:C:123:ARG:HG3	1.37	1.24
2:D:497:GLU:C	2:D:499:PRO:HD2	1.74	1.07
2:C:316:ARG:HD2	2:C:332:THR:HG22	1.33	1.05
2:C:316:ARG:CD	2:C:332:THR:HG22	1.85	1.05
2:D:601:LYS:HG2	2:D:604:ILE:HB	1.42	1.02

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	255/296 (86%)	242 (95%)	12 (5%)	1 (0%)	34	66
1	B	256/296 (86%)	244 (95%)	12 (5%)	0	100	100
2	C	641/688 (93%)	599 (93%)	40 (6%)	2 (0%)	41	72
2	D	636/688 (92%)	603 (95%)	30 (5%)	3 (0%)	29	61
All	All	1788/1968 (91%)	1688 (94%)	94 (5%)	6 (0%)	41	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	452	ILE
2	D	452	ILE
1	A	269	ASN
2	D	497	GLU
2	C	248	ILE

5.3.2 Protein sidechains ⓘ

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	218/253 (86%)	212 (97%)	6 (3%)	43	77
1	B	219/253 (87%)	218 (100%)	1 (0%)	88	96
2	C	556/590 (94%)	532 (96%)	24 (4%)	29	62
2	D	554/590 (94%)	517 (93%)	37 (7%)	16	43
All	All	1547/1686 (92%)	1479 (96%)	68 (4%)	28	61

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	554	ASP
2	D	173	ASP
2	D	439	LYS
2	D	37	GLU

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Mol	Chain	Res	Type
2	D	82	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	287	GLN
2	C	423	ASN
2	D	143	ASN
2	C	253	GLN
2	D	120	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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 [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	257/296 (86%)	-0.57	2 (0%) 86 81	18, 31, 58, 109	0
1	B	258/296 (87%)	-0.55	1 (0%) 92 91	16, 33, 61, 110	0
2	C	645/688 (93%)	0.12	44 (6%) 17 10	31, 64, 134, 197	0
2	D	642/688 (93%)	-0.04	36 (5%) 24 16	30, 59, 126, 184	0
All	All	1802/1968 (91%)	-0.13	83 (4%) 32 22	16, 53, 125, 197	0

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	323	GLY	10.0
2	D	241	MET	7.4
2	C	323	GLY	6.1
2	C	241	MET	6.0
2	C	322	ALA	5.2

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 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, 95th 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(\AA^2)	Q<0.9
3	CA	D	701	1/1	0.91	0.18	48,48,48,48	0
3	CA	C	701	1/1	0.92	0.14	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.