Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:33 AM GMT

PDB ID	:	3PBH
Title	:	REFINED CRYSTAL STRUCTURE OF HUMAN PROCATHEPSIN B AT 2.5 ANGSTROM RESOLUTION
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Deposited on	:	1997-02-13
Resolution	:	2.50 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

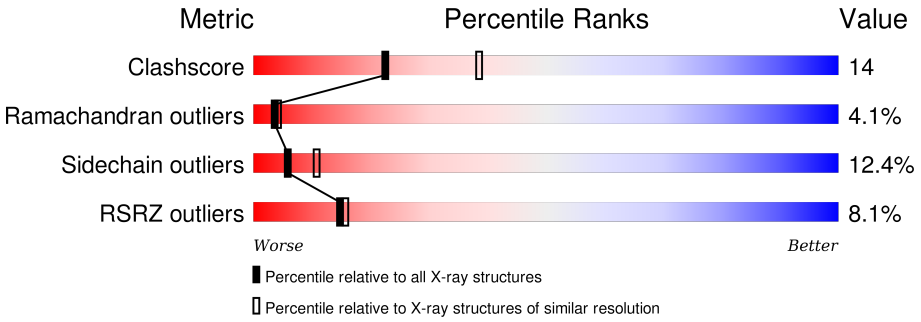
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	317	8%, 65%, 29%, 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3360 atoms, of which 775 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 PROCATHEPSIN B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	317	3015	1552	545	428	468	22	745	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9P	LEU	VAL	CONFLICT	UNP P07858

- Molecule 2 is water.

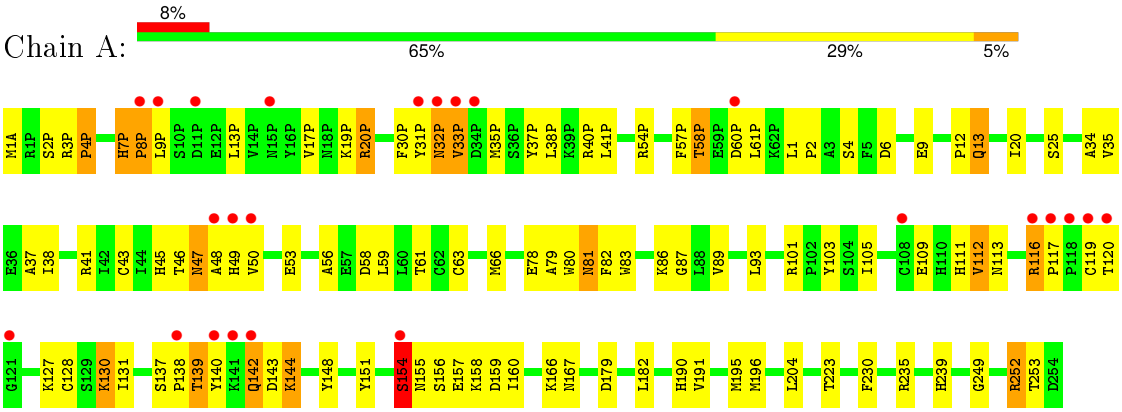
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	H	O			
2	A	115	345	230	115		230	0

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 errors 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: PROCATHEPSIN B

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	77.55Å 77.55Å 153.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.50 33.26 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.50) 92.7 (33.26-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.22 (at 2.39Å)	Xtriage
Refinement program	MAIN	Depositor
R, R_{free}	0.179 , 0.234 0.191 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	25.1	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 74.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 10488 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3360	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.52	0/2545	0.74	1/3457 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	154	SER	N-CA-C	7.30	130.72	111.00

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	2470	545	2305	60	8
2	A	115	230	0	2	4
All	All	2585	775	2305	60	8

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 14.

All (60) 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:A:139:THR:HG23	1:A:142:GLN:HB2	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35(P):MET:HA	1:A:38(P):LEU:HD12	1.70	0.74
1:A:6:ASP:HB3	1:A:9:GLU:HG3	1.70	0.72
1:A:137:SER:HA	2:A:353:HOH:O	1.94	0.68
1:A:58:ASP:HA	1:A:101:ARG:NH1	2.11	0.66
1:A:9:GLU:O	1:A:12:PRO:HD3	1.95	0.65
1:A:8(P):PRO:HD2	1:A:30(P):PHE:O	1.96	0.64
1:A:130:LYS:HG3	1:A:140:TYR:CE1	2.34	0.62
1:A:57(P):PHE:HE2	1:A:166:LYS:HE3	1.64	0.61
1:A:138:PRO:HB2	1:A:142:GLN:HB3	1.83	0.61
1:A:59:LEU:HD21	1:A:79:ALA:HB1	1.83	0.60
1:A:33(P):VAL:HG12	1:A:119:CYS:HB2	1.83	0.60
1:A:25:SER:HB3	1:A:120:THR:O	2.01	0.59
1:A:190:HIS:H	1:A:239:HIS:CE1	2.22	0.57
1:A:156:SER:O	1:A:160:ILE:HG13	2.04	0.57
1:A:30(P):PHE:HB3	1:A:33(P):VAL:HG21	1.88	0.55
1:A:37:ALA:O	1:A:41:ARG:HG3	2.06	0.55
1:A:78:GLU:HA	1:A:81:ASN:HB2	1.90	0.54
1:A:20:ILE:HB	1:A:223:THR:HG22	1.88	0.54
1:A:190:HIS:H	1:A:239:HIS:HE1	1.57	0.51
1:A:45:HIS:HE1	1:A:167:ASN:HD22	1.57	0.50
1:A:103:TYR:CE2	1:A:105:ILE:HB	2.47	0.50
1:A:34:ALA:O	1:A:38:ILE:HG13	2.11	0.49
1:A:17(P):VAL:O	1:A:20(P):ARG:HB2	2.12	0.49
1:A:156:SER:HB3	1:A:159:ASP:HB2	1.94	0.49
1:A:89:VAL:HG13	1:A:144:LYS:HE3	1.94	0.49
1:A:2:PRO:HB2	1:A:4:SER:O	2.13	0.48
1:A:35:VAL:HG11	1:A:56:ALA:HA	1.96	0.48
1:A:80:TRP:O	1:A:83:TRP:HB3	2.13	0.48
1:A:139:THR:CG2	1:A:142:GLN:HB2	2.40	0.48
1:A:130:LYS:HG3	1:A:140:TYR:CZ	2.48	0.48
1:A:157:GLU:OE2	1:A:235:ARG:NH1	2.47	0.48
1:A:116:ARG:O	1:A:117:PRO:C	2.49	0.48
1:A:20:ILE:HD11	1:A:230:PHE:CZ	2.49	0.47
1:A:37(P):TYR:CD1	1:A:119:CYS:HB3	2.49	0.47
1:A:179:ASP:O	1:A:182:LEU:HB2	2.15	0.47
1:A:116:ARG:HG2	1:A:117:PRO:HD3	1.97	0.46
1:A:128:CYS:SG	1:A:130:LYS:HD2	2.56	0.46
1:A:57(P):PHE:CE2	1:A:166:LYS:HE3	2.47	0.45
1:A:32(P):ASN:CG	1:A:33(P):VAL:N	2.69	0.45
1:A:37(P):TYR:CG	1:A:119:CYS:HB3	2.51	0.45
1:A:13:GLN:CD	1:A:13:GLN:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:THR:O	1:A:49:HIS:CD2	2.70	0.44
1:A:87:GLY:O	1:A:144:LYS:HE2	2.17	0.44
1:A:130:LYS:NZ	2:A:310:HOH:O	2.50	0.44
1:A:63:CYS:HA	1:A:82:PHE:CD1	2.53	0.43
1:A:9(P):LEU:N	1:A:9(P):LEU:HD22	2.33	0.43
1:A:61:THR:O	1:A:128:CYS:HB2	2.19	0.43
1:A:8(P):PRO:HG2	1:A:9(P):LEU:H	1.84	0.43
1:A:151:TYR:CE2	1:A:249:GLY:HA2	2.55	0.42
1:A:32(P):ASN:O	1:A:33(P):VAL:O	2.36	0.42
1:A:37(P):TYR:CZ	1:A:41(P):LEU:HD11	2.54	0.42
1:A:89:VAL:HA	1:A:143:ASP:O	2.19	0.42
1:A:40(P):ARG:HG3	1:A:40(P):ARG:HH11	1.85	0.42
1:A:8(P):PRO:HB2	1:A:9(P):LEU:HD22	2.02	0.42
1:A:43:CYS:HA	1:A:50:VAL:O	2.20	0.42
1:A:9(P):LEU:HA	1:A:9(P):LEU:HD13	1.84	0.41
1:A:35:VAL:HG21	1:A:56:ALA:HB2	2.02	0.41
1:A:32(P):ASN:O	1:A:33(P):VAL:C	2.59	0.40
1:A:63:CYS:HA	1:A:82:PHE:CE1	2.56	0.40

All (8) 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)
1:A:54(P):ARG:CD	1:A:109:GLU:OE2[5_555]	1.77	0.43
1:A:54(P):ARG:CB	1:A:109:GLU:OE2[5_555]	1.79	0.41
1:A:3(P):ARG:N	2:A:328:HOH:O[8_565]	1.89	0.31
1:A:4(P):PRO:O	1:A:31(P):TYR:OH[12_564]	1.89	0.31
1:A:195:MET:CE	2:A:327:HOH:O[10_665]	2.03	0.17
1:A:3(P):ARG:CB	2:A:328:HOH:O[8_565]	2.10	0.10
1:A:54(P):ARG:CG	1:A:109:GLU:OE2[5_555]	2.16	0.04
1:A:58(P):THR:O	2:A:314:HOH:O[5_555]	2.18	0.02

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	315/317 (99%)	274 (87%)	28 (9%)	13 (4%)	3 4

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4(P)	PRO
1	A	8(P)	PRO
1	A	111	HIS
1	A	113	ASN
1	A	2(P)	SER
1	A	33(P)	VAL
1	A	47	ASN
1	A	112	VAL
1	A	154	SER
1	A	48	ALA
1	A	148	TYR
1	A	7(P)	HIS
1	A	252	ARG

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	267/267 (100%)	234 (88%)	33 (12%)	6 11

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1(A)	MET
1	A	7(P)	HIS
1	A	13(P)	LEU
1	A	19(P)	LYS
1	A	20(P)	ARG
1	A	32(P)	ASN

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Mol	Chain	Res	Type
1	A	58(P)	THR
1	A	60(P)	ASP
1	A	61(P)	LEU
1	A	1	LEU
1	A	13	GLN
1	A	47	ASN
1	A	53	GLU
1	A	66	MET
1	A	81	ASN
1	A	86	LYS
1	A	93	LEU
1	A	112	VAL
1	A	116	ARG
1	A	127	LYS
1	A	130	LYS
1	A	131	ILE
1	A	139	THR
1	A	142	GLN
1	A	144	LYS
1	A	154	SER
1	A	155	ASN
1	A	158	LYS
1	A	191	VAL
1	A	196	MET
1	A	204	LEU
1	A	252	ARG
1	A	253	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53(P)	GLN
1	A	10	GLN
1	A	49	HIS
1	A	145	HIS
1	A	167	ASN
1	A	190	HIS
1	A	237	GLN
1	A	239	HIS

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	297/317 (93%)	0.21	24 (8%) 15 16	7, 15, 49, 63	10 (3%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	48	ALA	7.2
1	A	8(P)	PRO	6.6
1	A	60(P)	ASP	6.3
1	A	118	PRO	5.5
1	A	108	CYS	4.8
1	A	33(P)	VAL	4.8
1	A	117	PRO	4.6
1	A	116	ARG	4.4
1	A	34(P)	ASP	4.2
1	A	32(P)	ASN	4.1
1	A	49	HIS	4.0
1	A	31(P)	TYR	3.9
1	A	138	PRO	3.5
1	A	11(P)	ASP	3.1
1	A	142	GLN	3.0
1	A	9(P)	LEU	3.0
1	A	154	SER	2.8
1	A	141	LYS	2.8
1	A	119	CYS	2.6
1	A	50	VAL	2.3
1	A	120	THR	2.3
1	A	121	GLY	2.3
1	A	140	TYR	2.3
1	A	15(P)	ASN	2.2

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 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.