wwPDB X-ray Structure Validation Summary Report (i)

May 29, 2020 – 02:54 am BST

PDB ID	:	3HNM
Title	:	Crystal Structure of Protein BT_411 (putative chitobiase, fragment 298-461) from Bacteroides thetaiotaomicron, Northeast Structural Genomics Consortium Target BtR319D
Authors	:	Kuzin, A.; Abashidze, M.; Seetharaman, J.; Sahdev, S.; Xiao, R.; Ciccosanti, C.; Foote, E.L.; Lee, D.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-05-31
Resolution	:	3.00 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 (i) symbol.

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

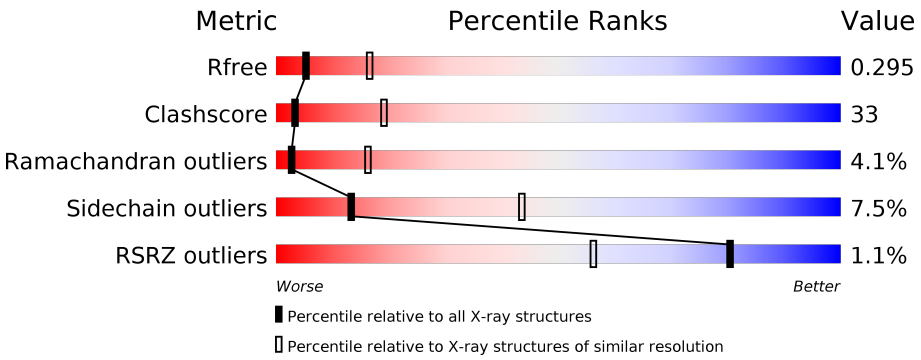
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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	172	% 45% 48% • • •
1	B	172	44% 46% 8% •
1	C	172	3% 41% 48% 7% • •
1	D	172	40% 52% 6% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5448 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 Putative chitobiase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	167	1361	884	224	247	3	3	0	0	0
1	B	167	1361	884	224	247	3	3	0	0	0
1	C	167	1361	884	224	247	3	3	0	0	0
1	D	167	1361	884	224	247	3	3	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	LEU	-	EXPRESSION TAG	UNP Q8AAM3
A	166	GLU	-	EXPRESSION TAG	UNP Q8AAM3
A	167	HIS	-	EXPRESSION TAG	UNP Q8AAM3
A	168	HIS	-	EXPRESSION TAG	UNP Q8AAM3
A	169	HIS	-	EXPRESSION TAG	UNP Q8AAM3
A	170	HIS	-	EXPRESSION TAG	UNP Q8AAM3
A	171	HIS	-	EXPRESSION TAG	UNP Q8AAM3
A	172	HIS	-	EXPRESSION TAG	UNP Q8AAM3
B	165	LEU	-	EXPRESSION TAG	UNP Q8AAM3
B	166	GLU	-	EXPRESSION TAG	UNP Q8AAM3
B	167	HIS	-	EXPRESSION TAG	UNP Q8AAM3
B	168	HIS	-	EXPRESSION TAG	UNP Q8AAM3
B	169	HIS	-	EXPRESSION TAG	UNP Q8AAM3
B	170	HIS	-	EXPRESSION TAG	UNP Q8AAM3
B	171	HIS	-	EXPRESSION TAG	UNP Q8AAM3
B	172	HIS	-	EXPRESSION TAG	UNP Q8AAM3
C	165	LEU	-	EXPRESSION TAG	UNP Q8AAM3
C	166	GLU	-	EXPRESSION TAG	UNP Q8AAM3
C	167	HIS	-	EXPRESSION TAG	UNP Q8AAM3
C	168	HIS	-	EXPRESSION TAG	UNP Q8AAM3
C	169	HIS	-	EXPRESSION TAG	UNP Q8AAM3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	170	HIS	-	EXPRESSION TAG	UNP Q8AAM3
C	171	HIS	-	EXPRESSION TAG	UNP Q8AAM3
C	172	HIS	-	EXPRESSION TAG	UNP Q8AAM3
D	165	LEU	-	EXPRESSION TAG	UNP Q8AAM3
D	166	GLU	-	EXPRESSION TAG	UNP Q8AAM3
D	167	HIS	-	EXPRESSION TAG	UNP Q8AAM3
D	168	HIS	-	EXPRESSION TAG	UNP Q8AAM3
D	169	HIS	-	EXPRESSION TAG	UNP Q8AAM3
D	170	HIS	-	EXPRESSION TAG	UNP Q8AAM3
D	171	HIS	-	EXPRESSION TAG	UNP Q8AAM3
D	172	HIS	-	EXPRESSION TAG	UNP Q8AAM3

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

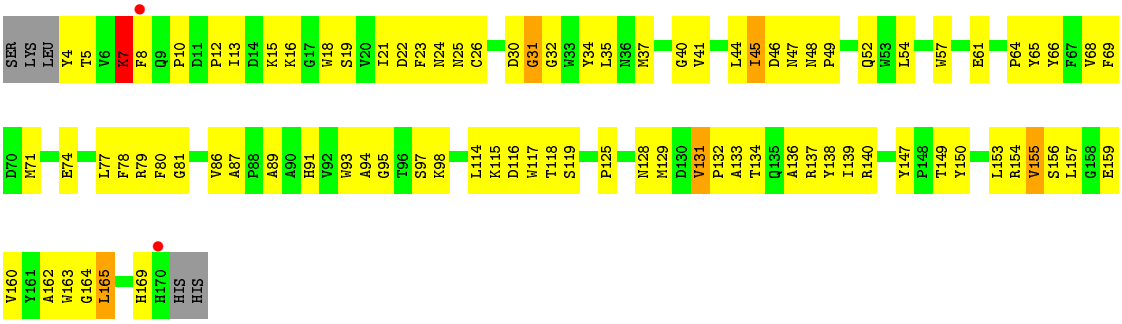
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0

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.

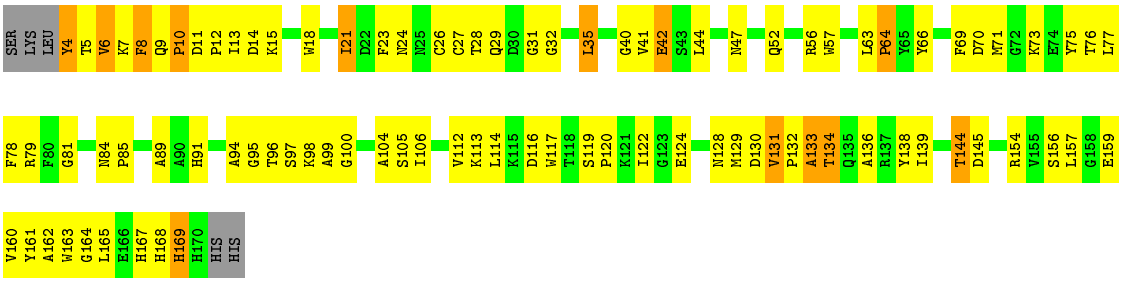
- Molecule 1: Putative chitobiase

Chain A:



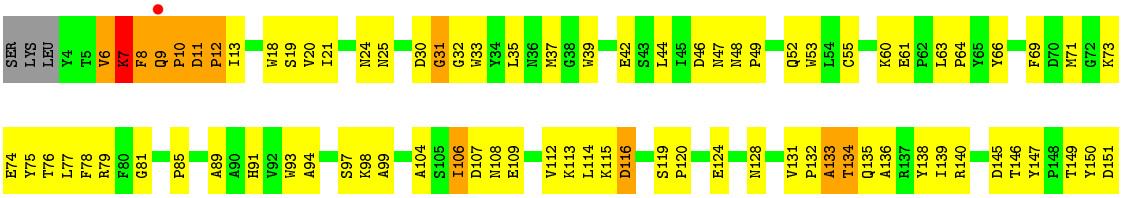
- Molecule 1: Putative chitobiase

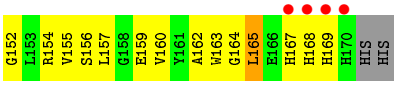
Chain B:



- Molecule 1: Putative chitobiase

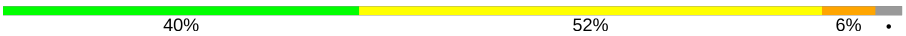
Chain C:

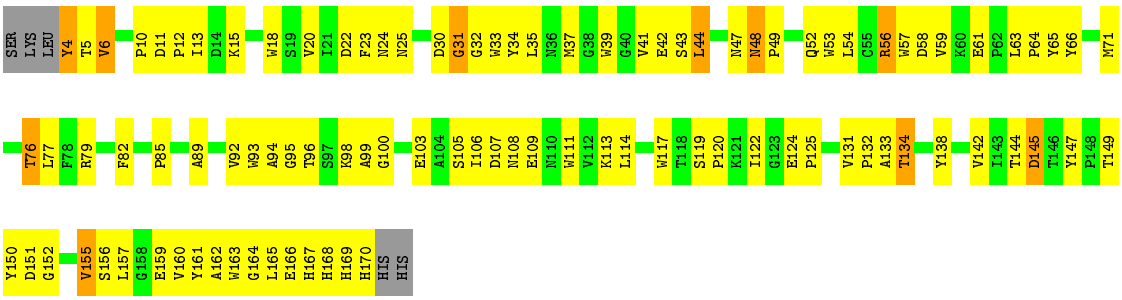




- Molecule 1: Putative chitobiase

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	141.52Å 141.52Å 232.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 29.99 – 3.00	Depositor EDS
% Data completeness (in resolution range)	86.9 (20.00-3.00) 97.6 (29.99-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.42	Depositor
$< I/\sigma(I) >$ [1]	4.59 (at 3.00Å)	Xtriage
Refinement program	CNS 1.2, REFMAC	Depositor
R, R_{free}	0.235 , 0.281 0.255 , 0.295	Depositor DCC
R_{free} test set	2264 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	43.6	Xtriage
Anisotropy	0.678	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 42.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	5448	wwPDB-VP
Average B, all atoms (Å^2)	42.0	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 31.66 % 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 1.0673e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (i)

5.1 Standard geometry (i)

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

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	0.48	0/1409	0.64	0/1923
1	B	0.47	0/1409	0.63	0/1923
1	C	0.50	0/1409	0.67	1/1923 (0.1%)
1	D	0.50	0/1409	0.64	0/1923
All	All	0.49	0/5636	0.64	1/7692 (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	1

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	C	10	PRO	N-CA-C	-5.64	97.42	112.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	65	TYR	Sidechain

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	1361	0	1269	68	0
1	B	1361	0	1269	92	0
1	C	1361	0	1269	93	0
1	D	1361	0	1269	100	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	5448	0	5076	344	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 33.

The worst 5 of 344 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:C:149:THR:HG22	1:C:151:ASP:H	1.16	1.09
1:D:13:ILE:HD11	1:D:164:GLY:H	1.24	1.01
1:D:149:THR:HG22	1:D:151:ASP:H	1.25	1.00
1:C:77:LEU:H	1:C:77:LEU:HD22	1.30	0.96
1:B:114:LEU:HD11	1:B:134:THR:HG21	1.48	0.96

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	165/172 (96%)	141 (86%)	17 (10%)	7 (4%)	3	16
1	B	165/172 (96%)	128 (78%)	31 (19%)	6 (4%)	3	19
1	C	165/172 (96%)	138 (84%)	20 (12%)	7 (4%)	3	16
1	D	165/172 (96%)	139 (84%)	19 (12%)	7 (4%)	3	16
All	All	660/688 (96%)	546 (83%)	87 (13%)	27 (4%)	3	16

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	133	ALA
1	C	9	GLN
1	C	12	PRO
1	B	8	PHE
1	B	95	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	143/145 (99%)	132 (92%)	11 (8%)	13	42
1	B	143/145 (99%)	132 (92%)	11 (8%)	13	42
1	C	143/145 (99%)	133 (93%)	10 (7%)	15	47
1	D	143/145 (99%)	132 (92%)	11 (8%)	13	42
All	All	572/580 (99%)	529 (92%)	43 (8%)	13	43

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	134	THR
1	C	11	ASP
1	D	144	THR
1	B	144	THR
1	B	169	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	128	ASN
1	C	52	GLN
1	D	48	ASN
1	B	91	HIS
1	D	128	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 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	164/172 (95%)	-0.29	2 (1%) 79 54	19, 41, 58, 72	0
1	B	164/172 (95%)	-0.22	0 100 100	21, 42, 62, 71	0
1	C	164/172 (95%)	-0.08	5 (3%) 50 22	16, 43, 64, 79	0
1	D	164/172 (95%)	-0.29	0 100 100	15, 39, 61, 72	0
All	All	656/688 (95%)	-0.22	7 (1%) 80 56	15, 41, 63, 79	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	168	HIS	3.7
1	C	169	HIS	2.8
1	C	170	HIS	2.5
1	A	8	PHE	2.3
1	C	167	HIS	2.2

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 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, 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(Å^2)	Q<0.9
2	MG	D	173	1/1	0.85	0.11	26,26,26,26	0
2	MG	A	173	1/1	0.92	0.10	26,26,26,26	0
2	MG	C	173	1/1	0.96	0.13	42,42,42,42	0
2	MG	B	173	1/1	0.98	0.10	43,43,43,43	0

6.5 Other polymers (i)

There are no such residues in this entry.