wwPDB X-ray Structure Validation Summary Report (i)

Jan 14, 2024 – 01:07 pm GMT

PDB ID	:	6T2N
Title	:	Prominent members of the human gut microbiota express endo-acting O-glycanases to initiate mucin breakdown
Authors	:	Crouch, L.I.; Liberato, M.V.; Ubranowicz, P.A.; Basle, A.; Lamb, C.A.; Cooke, K.; Doona, M.; Needham, S.; Brady, R.R.; Berrington, J.E.; Madubic, K.; Chater, P.; Zhang, F.; Linhardt, R.J.; Spence, D.I.R.; Bolam, D.N.
Deposited on	:	2019-10-09
Resolution	:	2.70 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

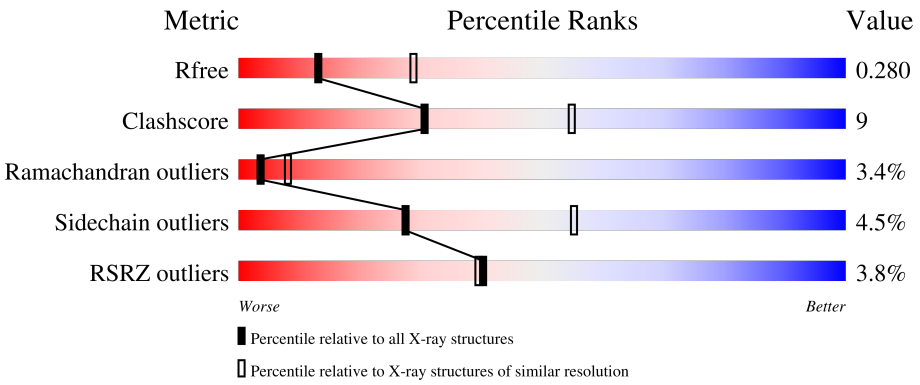
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 of 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	AAA	324	3% 58% 23% • • 14%
1	BBB	324	3% 63% 21% • • 14%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4472 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 Glycoside hydrolase family 16 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	278	2235	1434	381	412	8	0	0	0
1	BBB	278	2235	1434	381	412	8	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-33	MET	-	initiating methionine	UNP A0A2N8IRP0
AAA	-32	GLY	-	expression tag	UNP A0A2N8IRP0
AAA	-31	SER	-	expression tag	UNP A0A2N8IRP0
AAA	-30	SER	-	expression tag	UNP A0A2N8IRP0
AAA	-29	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	-28	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	-27	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	-26	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	-25	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	-24	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	-23	SER	-	expression tag	UNP A0A2N8IRP0
AAA	-22	SER	-	expression tag	UNP A0A2N8IRP0
AAA	-21	GLY	-	expression tag	UNP A0A2N8IRP0
AAA	-20	LEU	-	expression tag	UNP A0A2N8IRP0
AAA	-19	VAL	-	expression tag	UNP A0A2N8IRP0
AAA	-18	PRO	-	expression tag	UNP A0A2N8IRP0
AAA	-17	ARG	-	expression tag	UNP A0A2N8IRP0
AAA	-16	GLY	-	expression tag	UNP A0A2N8IRP0
AAA	-15	SER	-	expression tag	UNP A0A2N8IRP0
AAA	-14	HIS	-	expression tag	UNP A0A2N8IRP0
AAA	172	THR	LYS	conflict	UNP A0A2N8IRP0
BBB	-33	MET	-	initiating methionine	UNP A0A2N8IRP0
BBB	-32	GLY	-	expression tag	UNP A0A2N8IRP0
BBB	-31	SER	-	expression tag	UNP A0A2N8IRP0
BBB	-30	SER	-	expression tag	UNP A0A2N8IRP0

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Chain	Residue	Modelled	Actual	Comment	Reference
BBB	-29	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	-28	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	-27	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	-26	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	-25	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	-24	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	-23	SER	-	expression tag	UNP A0A2N8IRP0
BBB	-22	SER	-	expression tag	UNP A0A2N8IRP0
BBB	-21	GLY	-	expression tag	UNP A0A2N8IRP0
BBB	-20	LEU	-	expression tag	UNP A0A2N8IRP0
BBB	-19	VAL	-	expression tag	UNP A0A2N8IRP0
BBB	-18	PRO	-	expression tag	UNP A0A2N8IRP0
BBB	-17	ARG	-	expression tag	UNP A0A2N8IRP0
BBB	-16	GLY	-	expression tag	UNP A0A2N8IRP0
BBB	-15	SER	-	expression tag	UNP A0A2N8IRP0
BBB	-14	HIS	-	expression tag	UNP A0A2N8IRP0
BBB	172	THR	LYS	conflict	UNP A0A2N8IRP0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

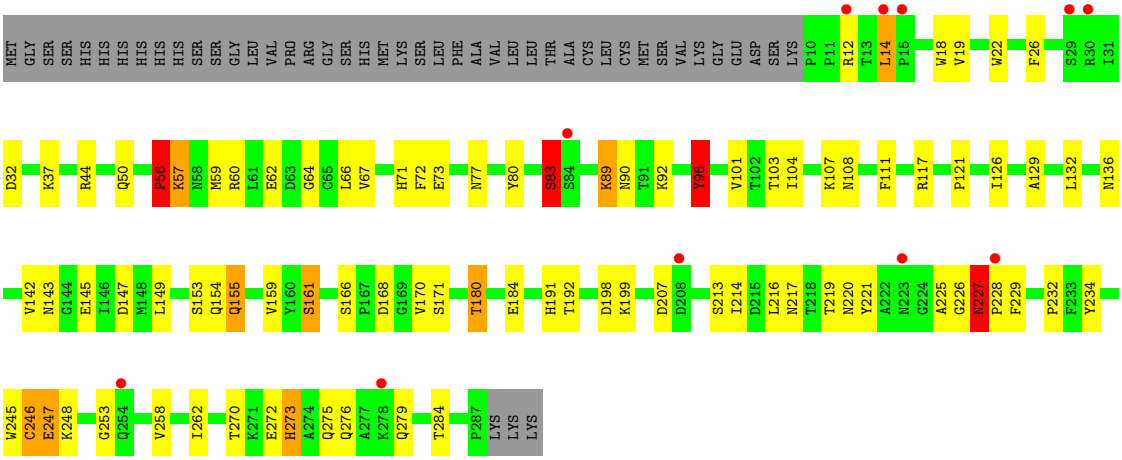
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	AAA	1	1	1	0	0
			Total	Ca		
2	BBB	1	1	1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

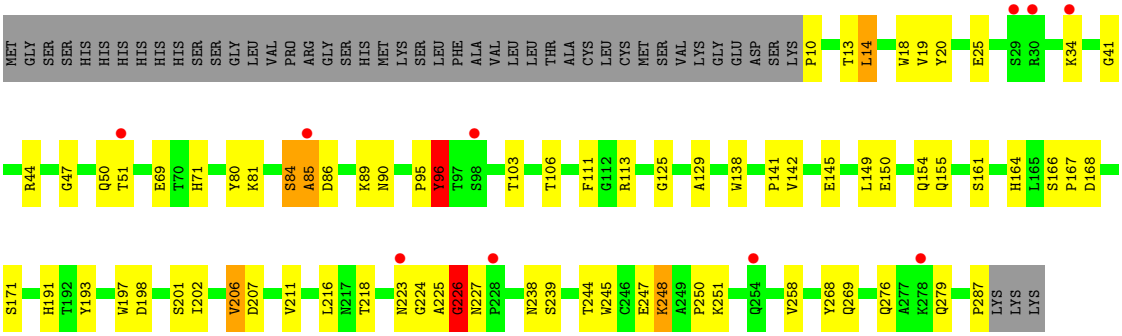
• Molecule 1: Glycoside hydrolase family 16 protein

Chain AAA:



• Molecule 1: Glycoside hydrolase family 16 protein

Chain BBB:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	87.47Å 96.13Å 128.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.72 – 2.70 19.71 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.72-2.70) 99.9 (19.71-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.35 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.233 , 0.281 0.237 , 0.280	Depositor DCC
R_{free} test set	1464 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å^2)	66.7	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.0	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	0.93	EDS
Total number of atoms	4472	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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 (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	AAA	1.01	9/2299 (0.4%)	1.22	11/3117 (0.4%)
1	BBB	0.82	1/2299 (0.0%)	1.07	1/3117 (0.0%)
All	All	0.92	10/4598 (0.2%)	1.15	12/6234 (0.2%)

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	AAA	0	2
1	BBB	0	3
All	All	0	5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	220	ASN	C-O	8.25	1.39	1.23
1	AAA	32	ASP	CB-CG	8.08	1.68	1.51
1	AAA	217	ASN	CB-CG	7.43	1.68	1.51
1	AAA	273	HIS	CB-CG	5.83	1.60	1.50
1	AAA	273	HIS	CG-CD2	5.81	1.45	1.35

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AAA	44	ARG	CG-CD-NE	-8.27	94.44	111.80
1	AAA	32	ASP	CB-CG-OD1	-7.70	111.37	118.30
1	AAA	56	PRO	O-C-N	-7.22	111.15	122.70
1	AAA	198	ASP	CB-CA-C	-7.05	96.30	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AAA	44	ARG	CB-CA-C	-6.61	97.18	110.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	143	ASN	Mainchain
1	AAA	56	PRO	Mainchain
1	BBB	226	GLY	Peptide
1	BBB	84	SER	Peptide
1	BBB	96	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	AAA	2235	0	2192	42	0
1	BBB	2235	0	2193	40	0
2	AAA	1	0	0	0	0
2	BBB	1	0	0	0	0
All	All	4472	0	4385	81	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 81 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:BBB:80:TYR:O	1:BBB:89:LYS:O	1.82	0.96
1:AAA:226:GLY:O	1:AAA:284:THR:O	1.84	0.93
1:BBB:250:PRO:O	1:BBB:251:LYS:HB2	1.78	0.82
1:BBB:71:HIS:O	1:BBB:96:TYR:HA	1.86	0.76
1:AAA:80:TYR:O	1:AAA:89:LYS:O	2.07	0.72

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	AAA	276/324 (85%)	243 (88%)	24 (9%)	9 (3%)	4 8
1	BBB	276/324 (85%)	240 (87%)	26 (9%)	10 (4%)	3 7
All	All	552/648 (85%)	483 (88%)	50 (9%)	19 (3%)	3 8

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	83	SER
1	AAA	225	ALA
1	AAA	246	CYS
1	AAA	247	GLU
1	BBB	81	LYS

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	AAA	242/282 (86%)	230 (95%)	12 (5%)	24 51
1	BBB	242/282 (86%)	232 (96%)	10 (4%)	30 59
All	All	484/564 (86%)	462 (96%)	22 (4%)	27 55

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	141	PRO

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Mol	Chain	Res	Type
1	BBB	239	SER
1	BBB	206	VAL
1	BBB	244	THR
1	AAA	184	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

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	AAA	278/324 (85%)	0.14	11 (3%)	38	37	47, 70, 98, 127	0
1	BBB	278/324 (85%)	0.18	10 (3%)	42	42	52, 75, 100, 119	0
All	All	556/648 (85%)	0.16	21 (3%)	40	39	47, 73, 100, 127	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	278	LYS	3.9
1	BBB	228	PRO	3.7
1	AAA	12	ARG	3.4
1	BBB	30	ARG	3.1
1	AAA	84	SER	2.9

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(Å^2)	Q<0.9
2	CA	AAA	401	1/1	0.82	0.14	113,113,113,113	0
2	CA	BBB	401	1/1	0.95	0.25	106,106,106,106	0

6.5 Other polymers (i)

There are no such residues in this entry.