



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:44 am BST

PDB ID : 2QIY
Title : yeast Deubiquitinase Ubp3 and Bre5 cofactor complex
Authors : Li, K.; Liu, X.; Marmorstein, R.
Deposited on : 2007-07-05
Resolution : 1.69 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

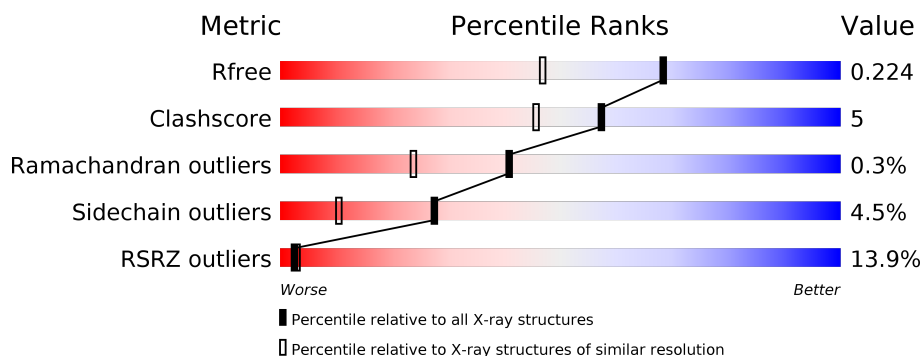
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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	154	
1	B	154	
2	C	48	
2	D	48	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2800 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 UBP3-associated protein BRE5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	134	Total	C	N	O	S	0	0	0
			1094	708	178	203	5			
1	B	133	Total	C	N	O	S	0	0	0
			1086	703	175	203	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	EXPRESSION TAG	UNP P53741
A	-4	SER	-	EXPRESSION TAG	UNP P53741
A	-3	HIS	-	EXPRESSION TAG	UNP P53741
A	-2	MET	-	EXPRESSION TAG	UNP P53741
A	-1	ALA	-	EXPRESSION TAG	UNP P53741
A	0	SER	-	EXPRESSION TAG	UNP P53741
A	147	LEU	-	EXPRESSION TAG	UNP P53741
A	148	GLU	-	EXPRESSION TAG	UNP P53741
B	-5	GLY	-	EXPRESSION TAG	UNP P53741
B	-4	SER	-	EXPRESSION TAG	UNP P53741
B	-3	HIS	-	EXPRESSION TAG	UNP P53741
B	-2	MET	-	EXPRESSION TAG	UNP P53741
B	-1	ALA	-	EXPRESSION TAG	UNP P53741
B	0	SER	-	EXPRESSION TAG	UNP P53741
B	147	LEU	-	EXPRESSION TAG	UNP P53741
B	148	GLU	-	EXPRESSION TAG	UNP P53741

- Molecule 2 is a protein called Ubiquitin carboxyl-terminal hydrolase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	25	Total	C	N	O	S	0	0	0
			200	129	32	38	1			
2	D	25	Total	C	N	O	S	0	0	0
			200	129	32	38	1			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	186	GLY	-	EXPRESSION TAG	UNP Q01477
C	187	SER	-	EXPRESSION TAG	UNP Q01477
C	188	ALA	-	EXPRESSION TAG	UNP Q01477
C	189	SER	-	EXPRESSION TAG	UNP Q01477
D	186	GLY	-	EXPRESSION TAG	UNP Q01477
D	187	SER	-	EXPRESSION TAG	UNP Q01477
D	188	ALA	-	EXPRESSION TAG	UNP Q01477
D	189	SER	-	EXPRESSION TAG	UNP Q01477

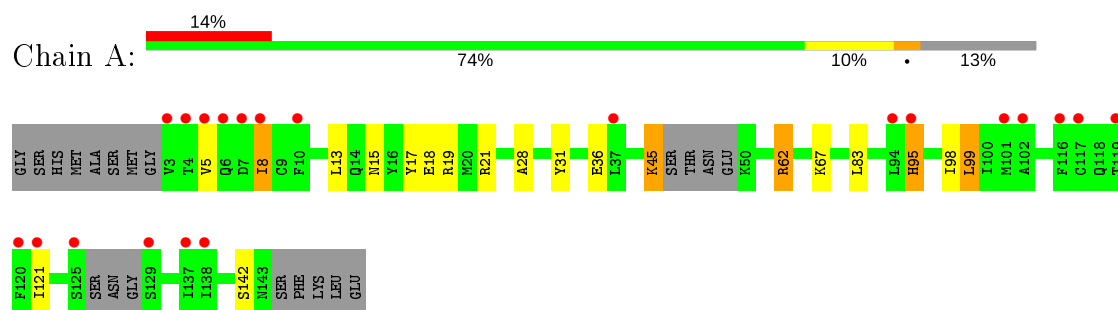
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	95	Total O 95 95	0	0
3	C	30	Total O 30 30	0	0
3	B	81	Total O 81 81	0	0
3	D	14	Total O 14 14	0	0

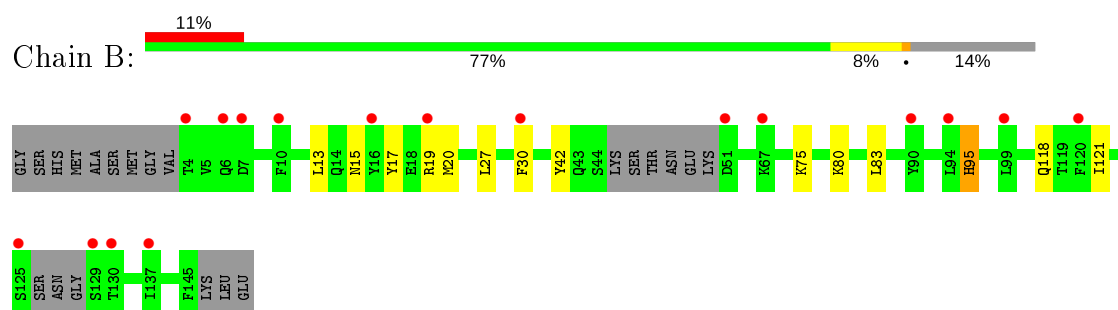
3 Residue-property plots [i](#)

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.

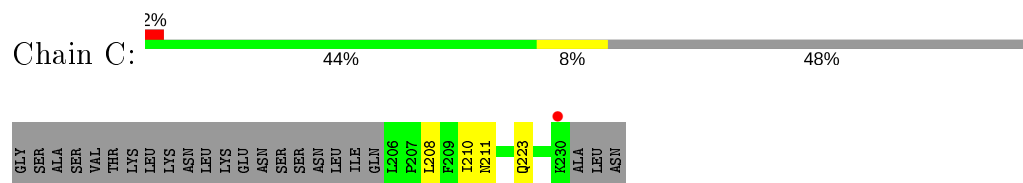
- Molecule 1: UBP3-associated protein BRE5



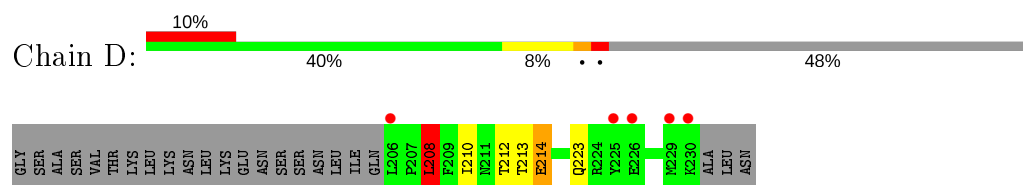
- Molecule 1: UBP3-associated protein BRE5



- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 3



- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.10Å 90.24Å 101.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.45 – 1.69 27.07 – 1.69	Depositor EDS
% Data completeness (in resolution range)	94.8 (49.45-1.69) 91.7 (27.07-1.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 1.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.207 , 0.225 0.207 , 0.224	Depositor DCC
R_{free} test set	5681 reflections (10.09%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2800	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% of the height of the origin peak. No significant pseudotranslation is detected.*

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](#)

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	0.63	0/1118	0.91	2/1511 (0.1%)
1	B	0.57	0/1111	0.70	0/1503
2	C	0.61	0/203	0.69	0/274
2	D	0.47	0/203	0.75	1/274 (0.4%)
All	All	0.59	0/2635	0.80	3/3562 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	ARG	NE-CZ-NH1	12.41	126.50	120.30
1	A	62	ARG	NE-CZ-NH2	-12.04	114.28	120.30
2	D	208	LEU	CA-CB-CG	5.07	126.95	115.30

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	1094	0	1080	14	0
1	B	1086	0	1059	8	0
2	C	200	0	198	4	0
2	D	200	0	198	5	0
3	A	95	0	0	0	0
3	B	81	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	30	0	0	1	0
3	D	14	0	0	1	0
All	All	2800	0	2535	25	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 (25) 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:8:ILE:HD11	1:A:98:ILE:HD13	1.46	0.97
1:A:36:GLU:OE2	1:B:95:HIS:NE2	2.06	0.88
1:A:28:ALA:O	1:A:62:ARG:HD2	1.78	0.82
1:B:17:TYR:OH	1:B:118:GLN:NE2	2.29	0.65
1:A:45:LYS:O	1:A:45:LYS:HG2	2.00	0.62
1:A:8:ILE:HD11	1:A:98:ILE:CD1	2.26	0.60
1:A:99:LEU:HA	1:A:121:ILE:HD13	1.87	0.56
1:A:5:VAL:O	1:A:8:ILE:HD13	2.07	0.55
2:D:213:THR:O	2:D:214:GLU:HB2	2.10	0.52
1:B:42:TYR:CD2	1:B:75:LYS:HG2	2.45	0.51
1:B:15:ASN:O	1:B:19:ARG:HG3	2.10	0.51
1:A:15:ASN:O	1:A:19:ARG:HG3	2.11	0.51
1:A:21:ARG:NH1	2:C:211:ASN:HD22	2.09	0.50
2:D:213:THR:O	2:D:214:GLU:CB	2.60	0.50
1:B:80:LYS:HB3	2:D:212:THR:HB	1.95	0.48
1:A:31:TYR:O	1:A:62:ARG:HD3	2.15	0.46
2:C:223:GLN:NE2	3:C:235:HOH:O	2.48	0.46
2:D:223:GLN:NE2	3:D:234:HOH:O	2.44	0.45
1:B:20:MET:HG3	1:B:27:LEU:HD11	1.99	0.44
2:D:208:LEU:HD13	2:D:210:ILE:HG12	1.99	0.43
1:A:121:ILE:HD11	1:B:121:ILE:HD11	2.00	0.43
1:A:95:HIS:HE1	3:B:157:HOH:O	2.02	0.43
1:B:19:ARG:HD2	1:B:30:PHE:CE1	2.54	0.42
1:A:18:GLU:HA	2:C:211:ASN:HD21	1.85	0.41
1:A:17:TYR:HB2	2:C:210:ILE:HG21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	128/154 (83%)	125 (98%)	3 (2%)	0	100	100
1	B	127/154 (82%)	125 (98%)	2 (2%)	0	100	100
2	C	23/48 (48%)	23 (100%)	0	0	100	100
2	D	23/48 (48%)	22 (96%)	0	1 (4%)	2	0
All	All	301/404 (74%)	295 (98%)	5 (2%)	1 (0%)	41	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	214	GLU

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	123/140 (88%)	115 (94%)	8 (6%)	17	4
1	B	122/140 (87%)	119 (98%)	3 (2%)	47	29
2	C	21/41 (51%)	20 (95%)	1 (5%)	25	9
2	D	21/41 (51%)	20 (95%)	1 (5%)	25	9
All	All	287/362 (79%)	274 (96%)	13 (4%)	27	10

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ILE
1	A	13	LEU
1	A	45	LYS
1	A	67	LYS
1	A	83	LEU
1	A	95	HIS
1	A	99	LEU
1	A	142	SER
2	C	208	LEU
1	B	13	LEU
1	B	83	LEU
1	B	95	HIS
2	D	208	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	HIS
1	A	118	GLN
1	A	135	ASN
2	C	211	ASN
2	C	223	GLN
1	B	14	GLN
1	B	118	GLN
1	B	135	ASN
2	D	211	ASN
2	D	223	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, 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	134/154 (87%)	0.80	21 (15%) 2 2	19, 23, 35, 43	0
1	B	133/154 (86%)	0.73	17 (12%) 3 4	23, 28, 40, 48	0
2	C	25/48 (52%)	-0.05	1 (4%) 38 42	22, 26, 30, 38	0
2	D	25/48 (52%)	1.06	5 (20%) 1 0	37, 41, 47, 49	0
All	All	317/404 (78%)	0.73	44 (13%) 2 3	19, 27, 42, 49	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	VAL	10.4
1	B	10	PHE	7.0
1	A	125	SER	6.2
1	B	129	SER	5.6
1	B	94	LEU	5.1
1	A	129	SER	4.4
1	B	125	SER	4.3
2	D	225	TYR	4.3
1	A	10	PHE	4.2
1	A	4	THR	3.9
1	A	117	CYS	3.7
1	A	138	ILE	3.6
1	B	4	THR	3.5
2	D	230	LYS	3.5
2	D	229	MET	3.4
1	B	99	LEU	3.1
1	A	7	ASP	3.0
1	A	8	ILE	2.9
1	A	137	ILE	2.9
1	B	7	ASP	2.8
1	A	6	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	19	ARG	2.7
1	B	30	PHE	2.7
1	B	137	ILE	2.6
1	A	5	VAL	2.6
1	A	120	PHE	2.5
2	D	206	LEU	2.5
2	D	226	GLU	2.5
1	A	101	MET	2.4
1	A	95	HIS	2.4
1	B	67	LYS	2.4
1	A	37	LEU	2.4
1	A	121	ILE	2.3
1	B	6	GLN	2.3
1	B	51	ASP	2.3
1	B	120	PHE	2.3
1	B	90	TYR	2.2
1	A	102	ALA	2.2
1	A	116	PHE	2.1
1	A	94	LEU	2.1
1	B	16	TYR	2.1
2	C	230	LYS	2.1
1	A	119	THR	2.0
1	B	130	THR	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.