



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 19, 2017 – 07:35 AM EST

PDB ID : 5M52
Title : Crystal structure of yeast Brr2 full-length in complex with Prp8 Jab1 domain
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Deposited on : 2016-10-20
Resolution : 3.40 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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)	:	rb-20028442

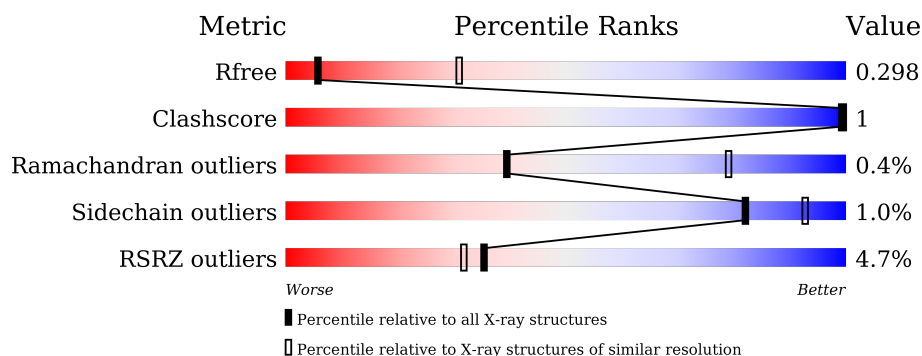
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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 $\leq 5\%$. 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	2163	<div> <div>4%</div> <div>86%</div> <div>12%</div> </div>
1	B	2163	<div> <div>5%</div> <div>83%</div> <div>14%</div> </div>
2	C	270	<div> <div>3%</div> <div>97%</div> <div>..</div> </div>
2	D	270	<div> <div>%</div> <div>96%</div> <div>...</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34522 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 Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1910	Total	C	N	O	S	0	0	0
			15320	9818	2546	2898	58			
1	B	1862	Total	C	N	O	S	0	0	0
			14927	9563	2476	2832	56			

- Molecule 2 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	266	Total	C	N	O	S	0	0	0
			2127	1368	341	412	6			
2	D	268	Total	C	N	O	S	0	0	0
			2138	1374	343	415	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2144	GLY	-	expression tag	UNP P33334
C	2145	ALA	-	expression tag	UNP P33334
C	2146	MET	-	expression tag	UNP P33334
D	2144	GLY	-	expression tag	UNP P33334
D	2145	ALA	-	expression tag	UNP P33334
D	2146	MET	-	expression tag	UNP P33334

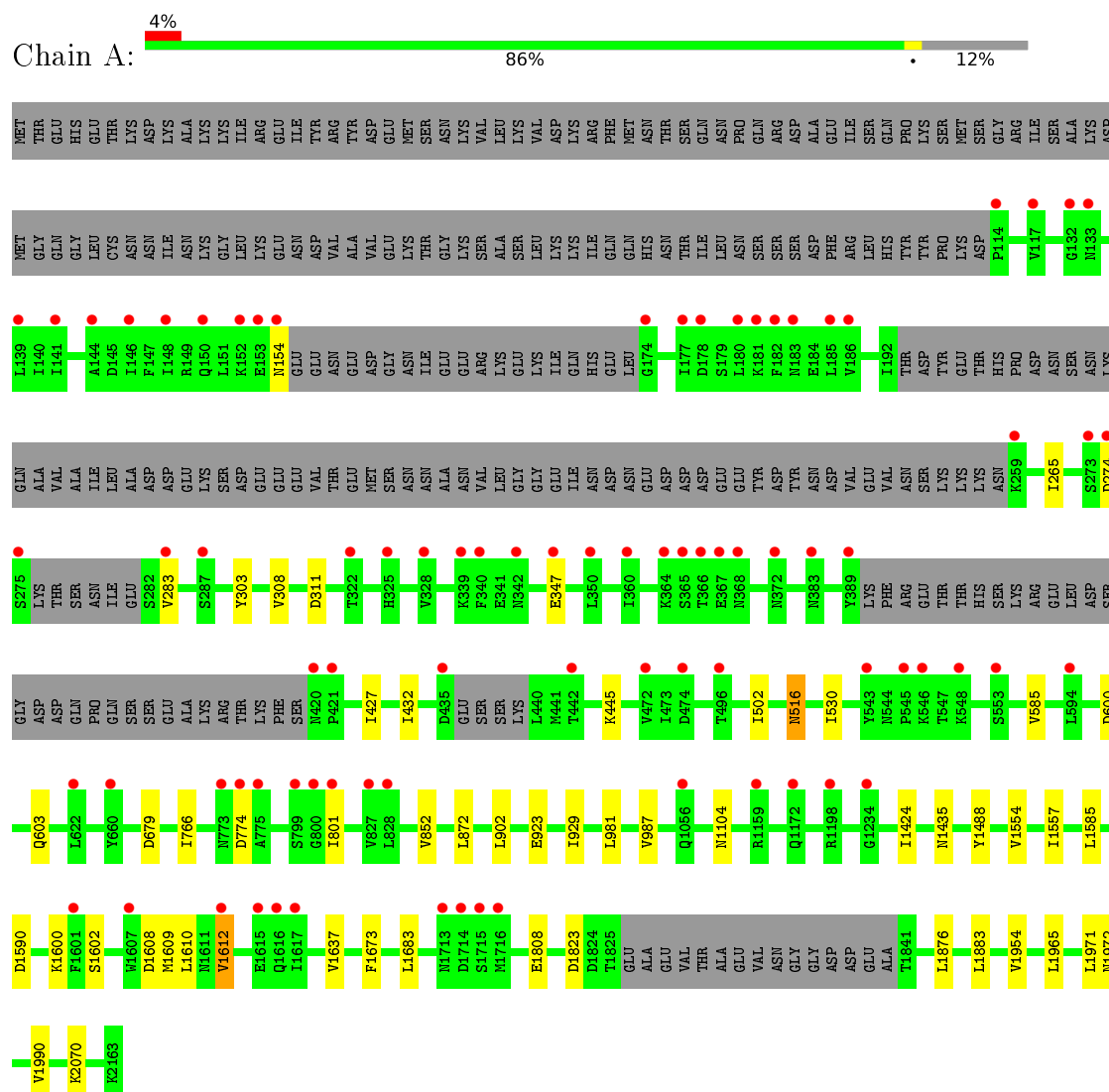
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	4	Total	O	0	0
			4	4		

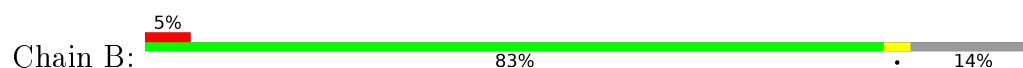
3 Residue-property plots

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: Pre-mRNA-splicing helicase BRR2



• Molecule 1: Pre-mRNA-splicing helicase BRR2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	179.34Å 181.16Å 210.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.72 – 3.40 48.72 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.72-3.40) 99.7 (48.72-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.33	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.8.0124	Depositor
R, R_{free}	0.252 , 0.296 0.252 , 0.298	Depositor DCC
R_{free} test set	2100 reflections (2.27%)	DCC
Wilson B-factor (Å ²)	78.0	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	34522	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.17% 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	0.36	0/15638	0.50	0/21190
1	B	0.36	0/15238	0.50	0/20653
2	C	0.35	0/2177	0.47	0/2952
2	D	0.35	0/2188	0.48	1/2966 (0.0%)
All	All	0.36	0/35241	0.49	1/47761 (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	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	2398	LEU	CA-CB-CG	5.11	127.05	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	2133	PRO	Peptide

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	15320	0	15372	13	0
1	B	14927	0	14939	25	0
2	C	2127	0	2071	2	0
2	D	2138	0	2075	2	0
3	A	6	0	0	0	0
3	B	4	0	0	0	0
All	All	34522	0	34457	41	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 1.

All (41) 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:B:1554:VAL:HG23	1:B:1557:ILE:HD11	1.73	0.70
2:C:2194:ILE:HD11	2:C:2293:ILE:HG21	1.74	0.69
1:B:557:ILE:HD11	1:B:604:VAL:HG22	1.81	0.62
1:A:1554:VAL:HG23	1:A:1557:ILE:HD11	1.84	0.59
1:A:1965:LEU:HD22	1:A:1972:ASN:HD22	1.68	0.59
1:B:1971:LEU:HD11	1:B:2143:TRP:CZ3	2.41	0.54
1:B:427:ILE:HD12	1:B:432:ILE:HD11	1.89	0.54
1:B:2063:LEU:HD23	1:B:2162:VAL:HG22	1.89	0.54
1:B:1160:LEU:HD11	1:B:1183:ILE:HG22	1.91	0.53
1:B:1224:ALA:HB1	1:B:1226:TRP:CZ3	2.45	0.52
1:B:1057:LEU:HD11	1:B:1087:LEU:HD11	1.92	0.51
1:B:1883:LEU:HD21	1:B:1954:VAL:HG23	1.94	0.49
1:A:981:LEU:HB3	1:A:987:VAL:HG22	1.94	0.48
2:C:2323:ASN:O	2:C:2324:VAL:HG22	2.13	0.48
1:B:707:PHE:CZ	1:B:902:LEU:HD12	2.49	0.48
1:B:923:GLU:HB2	1:B:929:ILE:HD12	1.96	0.47
1:B:850:THR:HG21	1:B:898:TYR:CE2	2.50	0.47
1:B:1409:LEU:HD22	1:B:1426:ASN:HB3	1.98	0.46
1:A:427:ILE:HD12	1:A:432:ILE:HD11	1.98	0.46
1:B:1479:ILE:HG22	1:B:1488:TYR:HB3	1.98	0.45
1:B:539:LEU:HD11	1:B:583:ILE:HD11	1.98	0.45
1:B:1425:ILE:HG21	1:B:1438:LEU:HD22	1.98	0.45
1:A:502:ILE:HD11	1:A:530:ILE:HD11	1.99	0.44
1:B:981:LEU:HB3	1:B:987:VAL:HG22	1.98	0.44
1:A:516:ASN:N	1:A:516:ASN:HD22	2.16	0.44
1:B:463:ILE:HD12	1:B:895:VAL:HG11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:872:LEU:CD1	1:A:902:LEU:HD21	2.48	0.43
1:A:303:TYR:CD1	1:A:308:VAL:HG11	2.54	0.43
1:A:923:GLU:HB2	1:A:929:ILE:HD12	2.01	0.43
1:B:872:LEU:HD22	1:B:902:LEU:HD21	2.02	0.42
1:B:895:VAL:HG12	1:B:899:LEU:HD13	2.01	0.42
1:A:1435:ASN:HD22	1:A:1435:ASN:N	2.18	0.42
1:B:539:LEU:CD1	1:B:583:ILE:HD11	2.50	0.41
1:A:1585:LEU:HD21	1:A:1683:LEU:HD23	2.01	0.41
1:A:1883:LEU:HD21	1:A:1954:VAL:HG23	2.01	0.41
2:D:2398:LEU:O	2:D:2399:ALA:HB3	2.20	0.41
1:B:563:LEU:HD11	2:D:2407:GLU:HG2	2.02	0.41
1:A:1600:LYS:O	1:A:1602:SER:N	2.53	0.41
1:B:1750:ILE:HD11	1:B:1773:PHE:CZ	2.56	0.41
1:B:1005:ALA:HB2	1:B:1015:MET:HG3	2.03	0.40
1:B:567:VAL:HG13	1:B:606:VAL:HG12	2.02	0.40

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	1896/2163 (88%)	1780 (94%)	105 (6%)	11 (1%)	30	72
1	B	1846/2163 (85%)	1740 (94%)	101 (6%)	5 (0%)	46	82
2	C	264/270 (98%)	246 (93%)	17 (6%)	1 (0%)	39	79
2	D	266/270 (98%)	243 (91%)	21 (8%)	2 (1%)	24	67
All	All	4272/4866 (88%)	4009 (94%)	244 (6%)	19 (0%)	39	79

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1612	VAL
2	C	2324	VAL
2	D	2401	ASP
1	A	1424	ILE
1	A	1609	MET
1	B	862	GLN
1	A	603	GLN
1	A	766	ILE
1	A	801	ILE
1	A	283	VAL
1	B	343	ILE
2	D	2399	ALA
1	A	445	LYS
1	A	1673	PHE
1	A	265	ILE
1	B	1636	GLY
1	A	1637	VAL
1	B	1910	PRO
1	B	327	PRO

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	1726/1955 (88%)	1704 (99%)	22 (1%)	76	91
1	B	1681/1955 (86%)	1669 (99%)	12 (1%)	88	95
2	C	235/237 (99%)	234 (100%)	1 (0%)	93	97
2	D	235/237 (99%)	230 (98%)	5 (2%)	61	86
All	All	3877/4384 (88%)	3837 (99%)	40 (1%)	82	93

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	ASN
1	A	274	ASP
1	A	311	ASP

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Mol	Chain	Res	Type
1	A	347	GLU
1	A	516	ASN
1	A	585	VAL
1	A	600	ASP
1	A	679	ASP
1	A	774	ASP
1	A	852	VAL
1	A	1104	ASN
1	A	1488	TYR
1	A	1590	ASP
1	A	1608	ASP
1	A	1610	LEU
1	A	1612	VAL
1	A	1808	GLU
1	A	1823	ASP
1	A	1876	LEU
1	A	1971	LEU
1	A	1990	VAL
1	A	2070	LYS
2	C	2296	THR
1	B	311	ASP
1	B	420	ASN
1	B	539	LEU
1	B	747	ARG
1	B	933	ASN
1	B	1086	GLN
1	B	1130	ASN
1	B	1435	ASN
1	B	1488	TYR
1	B	1544	LEU
1	B	1678	ASP
1	B	2124	GLN
2	D	2246	ASP
2	D	2296	THR
2	D	2309	ASP
2	D	2316	GLU
2	D	2401	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	ASN

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Mol	Chain	Res	Type
1	A	183	ASN
1	A	500	ASN
1	A	516	ASN
1	A	529	ASN
1	A	1104	ASN
1	A	1426	ASN
1	A	1435	ASN
1	A	1972	ASN
1	A	2002	ASN
2	C	2358	ASN
1	B	368	ASN
1	B	676	ASN
1	B	1130	ASN
1	B	1701	ASN
1	B	1755	ASN
1	B	1864	GLN
2	D	2408	GLN

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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	1910/2163 (88%)	0.27	83 (4%) 39 34	50, 91, 156, 200	0
1	B	1862/2163 (86%)	0.30	108 (5%) 26 24	48, 85, 158, 200	0
2	C	266/270 (98%)	0.25	8 (3%) 54 49	61, 93, 158, 170	0
2	D	268/270 (99%)	0.28	3 (1%) 82 77	63, 95, 137, 162	0
All	All	4306/4866 (88%)	0.28	202 (4%) 35 32	48, 89, 156, 200	0

All (202) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	146	ILE	6.9
1	B	121	GLU	6.4
1	A	366	THR	6.4
1	B	117	VAL	6.4
1	B	327	PRO	5.9
1	B	325	HIS	5.8
1	B	294	GLN	5.5
1	B	1826	GLU	5.5
1	B	289	ASP	5.3
1	B	326	ASN	5.2
1	A	367	GLU	5.0
1	B	371	PRO	4.9
1	B	338	LEU	4.9
1	B	328	VAL	4.8
1	B	1827	ALA	4.8
1	A	775	ALA	4.8
1	B	370	ILE	4.7
1	A	273	SER	4.7
1	B	271	LYS	4.6
1	B	125	GLN	4.6
1	B	341	GLU	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	774	ASP	4.5
1	B	141	ILE	4.4
1	B	378	VAL	4.3
1	A	177	ILE	4.3
1	B	186	VAL	4.3
1	A	372	ASN	4.2
2	C	2398	LEU	4.2
1	B	1611	ASN	4.2
1	A	365	SER	4.2
1	A	1615	GLU	4.2
1	B	337	LEU	4.1
2	D	2321	ILE	4.0
1	B	148	ILE	4.0
1	A	368	ASN	3.9
1	A	420	ASN	3.9
1	B	142	GLY	3.9
1	A	117	VAL	3.9
2	C	2397	GLU	3.8
1	B	145	ASP	3.8
1	B	144	ALA	3.8
2	C	2334	SER	3.8
1	B	1715	SER	3.8
1	B	182	PHE	3.7
1	A	186	VAL	3.6
1	A	174	GLY	3.6
1	A	1714	ASP	3.6
1	B	118	GLU	3.6
1	A	347	GLU	3.6
1	B	335	VAL	3.5
1	B	545	PRO	3.5
1	B	372	ASN	3.5
1	B	175	ILE	3.5
1	B	375	GLU	3.5
1	B	368	ASN	3.5
1	A	178	ASP	3.4
1	A	472	VAL	3.4
1	B	273	SER	3.4
1	B	283	VAL	3.4
1	B	298	ARG	3.3
1	B	282	SER	3.3
1	B	1658	TYR	3.3
1	A	185	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	182	PHE	3.3
1	B	344	SER	3.2
1	A	141	ILE	3.2
2	C	2148	SER	3.2
1	B	258	ASN	3.2
1	A	144	ALA	3.2
1	A	180	LEU	3.2
1	B	285	ILE	3.2
1	B	377	MET	3.2
1	A	114	PRO	3.2
1	B	138	ASP	3.1
1	A	181	LYS	3.1
1	A	148	ILE	3.1
1	B	287	SER	3.1
1	B	286	TYR	3.1
1	B	1167	TRP	3.0
1	A	1617	ILE	3.0
1	B	133	ASN	3.0
1	A	132	GLY	3.0
1	B	274	ASP	3.0
1	A	660	TYR	3.0
1	A	340	PHE	3.0
1	A	342	ASN	3.0
1	A	442	THR	3.0
1	A	259	LYS	3.0
1	A	274	ASP	3.0
1	A	275	SER	2.9
1	B	259	LYS	2.9
1	B	340	PHE	2.9
1	B	185	LEU	2.9
2	C	2399	ALA	2.9
1	A	133	ASN	2.9
1	B	183	ASN	2.9
1	A	1612	VAL	2.9
1	A	800	GLY	2.9
1	B	270	ILE	2.8
1	B	300	GLU	2.8
1	B	373	LEU	2.8
1	B	284	PRO	2.8
1	B	120	TYR	2.8
2	C	2396	SER	2.8
1	B	1717	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	325	HIS	2.8
1	B	336	ASP	2.8
1	B	1325	GLU	2.8
1	B	303	TYR	2.8
1	A	548	LYS	2.7
1	B	320	ILE	2.7
2	D	2322	MET	2.7
1	A	1713	ASN	2.7
1	A	799	SER	2.7
1	A	183	ASN	2.7
1	B	139	LEU	2.7
1	A	435	ASP	2.6
1	A	828	LEU	2.6
1	B	184	GLU	2.6
1	B	379	ALA	2.6
1	A	287	SER	2.6
1	A	146	ILE	2.6
1	B	178	ASP	2.6
1	B	329	ALA	2.6
1	B	128	THR	2.6
1	A	1716	MET	2.6
1	B	310	GLN	2.6
1	B	435	ASP	2.6
1	B	1825	THR	2.6
1	B	309	ILE	2.6
1	B	1190	LYS	2.5
1	B	331	GLU	2.5
1	A	1715	SER	2.5
1	A	389	TYR	2.5
1	A	1172	GLN	2.5
1	B	317	LEU	2.5
1	A	553	SER	2.5
1	A	139	LEU	2.5
1	B	1716	MET	2.5
1	A	328	VAL	2.5
1	A	150	GLN	2.5
1	A	545	PRO	2.5
1	A	546	LYS	2.5
1	B	123	ILE	2.5
1	B	126	TRP	2.5
1	B	318	ASN	2.5
1	A	1056	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	775	ALA	2.4
1	A	1616	GLN	2.4
1	B	119	THR	2.4
1	B	367	GLU	2.4
1	A	1159	ARG	2.4
2	D	2274	VAL	2.4
1	B	316	ILE	2.4
1	A	350	LEU	2.4
1	A	622	LEU	2.4
1	B	319	ASP	2.4
1	A	474	ASP	2.4
1	B	1181	ARG	2.4
1	A	283	VAL	2.4
1	B	376	LYS	2.4
1	A	152	LYS	2.3
1	B	314	GLU	2.3
1	A	496	THR	2.3
1	A	1601	PHE	2.3
1	B	1388	TRP	2.3
1	A	801	ILE	2.3
1	B	485	ASP	2.3
2	C	2402	GLU	2.3
1	A	383	ASN	2.3
1	B	304	LYS	2.3
1	B	1535	PHE	2.3
2	C	2331	PRO	2.3
1	B	302	GLY	2.3
1	B	291	PHE	2.3
1	A	827	VAL	2.2
1	B	124	LEU	2.2
1	A	773	ASN	2.2
1	B	288	ILE	2.2
1	A	153	GLU	2.2
1	B	313	SER	2.2
1	A	594	LEU	2.2
1	A	360	ILE	2.2
1	A	1234	GLY	2.2
1	B	330	LEU	2.1
1	A	421	PRO	2.1
1	A	1198	ARG	2.1
1	B	1828	GLU	2.1
1	B	176	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	272	LEU	2.1
1	B	1418	HIS	2.1
1	B	323	LEU	2.1
1	B	1177	ALA	2.1
1	A	364	LYS	2.1
1	A	543	TYR	2.1
1	B	312	LEU	2.1
1	B	339	LYS	2.1
1	B	1547	ASN	2.1
1	A	1607	TRP	2.0
1	A	322	THR	2.0
1	A	154	ASN	2.0
1	A	339	LYS	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.