



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 04:44 pm BST

PDB ID : 5XXQ
Title : Crystal structure of RBBP4: ZNF827 and its function in telomere
Authors : Sun, A.; Shi, Y.
Deposited on : 2017-07-04
Resolution : 1.90 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

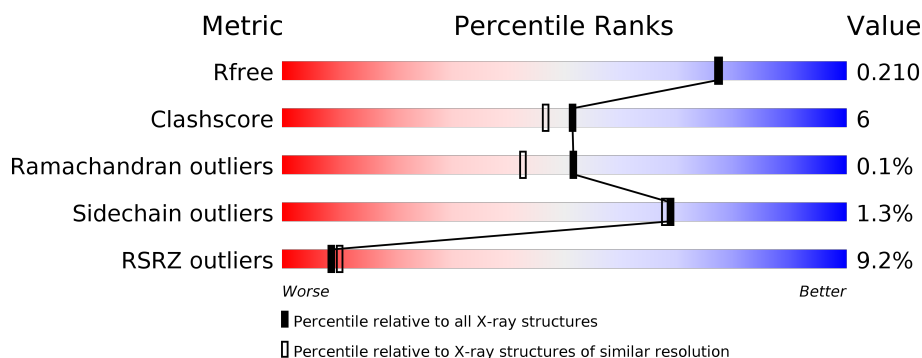
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	456	<div> <div>7%</div> <div> <div></div> <div>72%</div> <div>11%</div> <div>17%</div> </div> </div>
1	B	456	<div> <div>9%</div> <div> <div></div> <div>71%</div> <div>12%</div> <div>17%</div> </div> </div>
2	C	14	<div> <div>7%</div> <div> <div></div> <div>50%</div> <div>21%</div> <div>29%</div> </div> </div>
2	D	14	<div> <div>7%</div> <div> <div></div> <div>57%</div> <div>14%</div> <div>29%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6602 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 Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	380	Total	C	N	O	S	0	2	0
			3007	1906	517	574	10			
1	B	380	Total	C	N	O	S	0	1	0
			2993	1889	512	582	10			

There are 62 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-30	MET	-	initiating methionine	UNP Q09028
A	-29	SER	-	expression tag	UNP Q09028
A	-28	TYR	-	expression tag	UNP Q09028
A	-27	TYR	-	expression tag	UNP Q09028
A	-26	HIS	-	expression tag	UNP Q09028
A	-25	HIS	-	expression tag	UNP Q09028
A	-24	HIS	-	expression tag	UNP Q09028
A	-23	HIS	-	expression tag	UNP Q09028
A	-22	HIS	-	expression tag	UNP Q09028
A	-21	HIS	-	expression tag	UNP Q09028
A	-20	ASP	-	expression tag	UNP Q09028
A	-19	TYR	-	expression tag	UNP Q09028
A	-18	ASP	-	expression tag	UNP Q09028
A	-17	ILE	-	expression tag	UNP Q09028
A	-16	PRO	-	expression tag	UNP Q09028
A	-15	THR	-	expression tag	UNP Q09028
A	-14	THR	-	expression tag	UNP Q09028
A	-13	GLU	-	expression tag	UNP Q09028
A	-12	ASN	-	expression tag	UNP Q09028
A	-11	LEU	-	expression tag	UNP Q09028
A	-10	TYR	-	expression tag	UNP Q09028
A	-9	PHE	-	expression tag	UNP Q09028
A	-8	GLN	-	expression tag	UNP Q09028
A	-7	GLY	-	expression tag	UNP Q09028
A	-6	ALA	-	expression tag	UNP Q09028

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	expression tag	UNP Q09028
A	-4	GLY	-	expression tag	UNP Q09028
A	-3	SER	-	expression tag	UNP Q09028
A	-2	GLY	-	expression tag	UNP Q09028
A	-1	ILE	-	expression tag	UNP Q09028
A	0	GLN	-	expression tag	UNP Q09028
B	-30	MET	-	initiating methionine	UNP Q09028
B	-29	SER	-	expression tag	UNP Q09028
B	-28	TYR	-	expression tag	UNP Q09028
B	-27	TYR	-	expression tag	UNP Q09028
B	-26	HIS	-	expression tag	UNP Q09028
B	-25	HIS	-	expression tag	UNP Q09028
B	-24	HIS	-	expression tag	UNP Q09028
B	-23	HIS	-	expression tag	UNP Q09028
B	-22	HIS	-	expression tag	UNP Q09028
B	-21	HIS	-	expression tag	UNP Q09028
B	-20	ASP	-	expression tag	UNP Q09028
B	-19	TYR	-	expression tag	UNP Q09028
B	-18	ASP	-	expression tag	UNP Q09028
B	-17	ILE	-	expression tag	UNP Q09028
B	-16	PRO	-	expression tag	UNP Q09028
B	-15	THR	-	expression tag	UNP Q09028
B	-14	THR	-	expression tag	UNP Q09028
B	-13	GLU	-	expression tag	UNP Q09028
B	-12	ASN	-	expression tag	UNP Q09028
B	-11	LEU	-	expression tag	UNP Q09028
B	-10	TYR	-	expression tag	UNP Q09028
B	-9	PHE	-	expression tag	UNP Q09028
B	-8	GLN	-	expression tag	UNP Q09028
B	-7	GLY	-	expression tag	UNP Q09028
B	-6	ALA	-	expression tag	UNP Q09028
B	-5	MET	-	expression tag	UNP Q09028
B	-4	GLY	-	expression tag	UNP Q09028
B	-3	SER	-	expression tag	UNP Q09028
B	-2	GLY	-	expression tag	UNP Q09028
B	-1	ILE	-	expression tag	UNP Q09028
B	0	GLN	-	expression tag	UNP Q09028

- Molecule 2 is a protein called Zinc finger protein 827.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			87	53	20	14			

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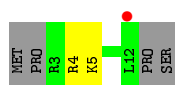
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	10	Total	C	N	O	0	0	0
			87	53	20	14			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	235	Total	O	0	0
			235	235		
3	B	178	Total	O	0	0
			178	178		
3	C	8	Total	O	0	0
			8	8		
3	D	7	Total	O	0	0
			7	7		



● Molecule 2: Zinc finger protein 827



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.96 Å 59.78 Å 102.56 Å 90.00° 95.07° 90.00°	Depositor
Resolution (Å)	40.70 – 1.90 40.70 – 1.90	Depositor EDS
% Data completeness (in resolution range)	86.0 (40.70-1.90) 86.1 (40.70-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 1.89 Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.172 , 0.212 0.171 , 0.210	Depositor DCC
R_{free} test set	3094 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	17.5	Xtriage
Anisotropy	0.956	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6602	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.96% 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

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	0.67	0/3097	0.76	3/4228 (0.1%)
1	B	0.61	0/3078	0.73	2/4203 (0.0%)
2	C	0.62	0/87	0.78	0/113
2	D	0.58	0/87	0.67	0/113
All	All	0.64	0/6349	0.74	5/8657 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	ASP	CB-CG-OD1	5.79	123.51	118.30
1	B	206	ASP	CB-CG-OD1	5.46	123.22	118.30
1	A	237	LEU	CA-CB-CG	-5.29	103.14	115.30
1	A	232	ASP	CB-CG-OD2	-5.05	113.75	118.30
1	B	296	LYS	CD-CE-NZ	-5.00	100.19	111.70

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	3007	0	2872	30	0
1	B	2993	0	2810	35	0
2	C	87	0	93	7	0
2	D	87	0	93	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	235	0	0	3	0
3	B	178	0	0	1	0
3	C	8	0	0	0	0
3	D	7	0	0	0	0
All	All	6602	0	5868	67	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 6.

All (67) 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:56:PRO:HB2	1:B:59:LYS:HG3	1.66	0.77
1:B:294:ALA:HA	1:B:319:GLU:HG3	1.75	0.69
1:A:338:THR:HG21	3:A:551:HOH:O	1.93	0.68
1:A:366:LEU:HD21	1:A:369:ILE:HD11	1.78	0.65
1:B:174:ARG:HG3	1:B:216:VAL:HG13	1.80	0.64
1:B:246:VAL:HB	1:B:276:VAL:HG13	1.79	0.64
1:B:231:GLU:OE2	2:C:4:ARG:HD3	2.02	0.60
1:B:16:VAL:O	1:B:20:GLU:HG3	2.02	0.59
1:B:321:PHE:HE1	2:C:4:ARG:HD2	1.66	0.58
1:A:65:ARG:NH2	1:A:154:TYR:OH	2.27	0.56
1:B:321:PHE:CE1	2:C:4:ARG:HD2	2.40	0.56
1:A:181:TYR:CE1	2:D:4:ARG:HD3	2.44	0.52
1:B:302:ASP:HB2	1:B:310:LEU:HD11	1.92	0.52
1:B:329:ASN:HB3	3:B:590:HOH:O	2.10	0.52
1:B:253:MET:HG2	1:B:265:PRO:HG3	1.92	0.51
1:A:333:LEU:N	1:A:333:LEU:HD23	2.26	0.51
1:B:406:GLU:HA	1:B:409:TYR:CE2	2.46	0.51
1:B:250:GLN:HG2	1:B:274:ALA:O	2.12	0.49
1:A:143:LYS:HD2	1:A:149:VAL:HG22	1.94	0.49
1:B:195:SER:HB3	1:B:205:TRP:HZ3	1.78	0.49
1:A:37:THR:HG22	1:A:400:GLN:HG2	1.95	0.48
1:B:117:ILE:HG21	1:B:120:LYS:HD3	1.95	0.48
1:B:42:TRP:CG	1:B:72:THR:HG22	2.48	0.48
1:B:181:TYR:CE2	2:C:4:ARG:HG3	2.48	0.48
1:B:174:ARG:HG3	1:B:216:VAL:CG1	2.42	0.48
1:A:278:CYS:SG	1:A:323[B]:VAL:HG23	2.54	0.48
1:A:12:VAL:O	1:A:16:VAL:HG13	2.14	0.47
1:B:143:LYS:NZ	1:B:195:SER:OG	2.32	0.47
1:B:246:VAL:HB	1:B:276:VAL:CG1	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:12:LEU:HD23	2:C:12:LEU:HA	1.52	0.47
1:B:205:TRP:CD1	1:B:219:ALA:HA	2.49	0.47
1:A:173:LEU:HB3	1:A:205:TRP:CE2	2.50	0.47
1:A:160:LYS:HA	1:A:160:LYS:HD3	1.65	0.46
1:B:186:ASN:HB2	1:B:235:TRP:CE2	2.51	0.46
1:A:123:HIS:CE1	1:A:144:THR:HG22	2.50	0.45
1:B:314:GLU:O	1:B:315:SER:HB2	2.16	0.45
1:B:80:VAL:HG11	1:B:117:ILE:HD12	1.98	0.45
1:B:330:GLU:HG2	1:B:331:THR:HG23	1.99	0.45
1:A:294:ALA:HA	1:A:319:GLU:HG3	1.98	0.45
1:A:115:ILE:HD13	1:A:399:MET:HE2	1.99	0.44
1:B:226:HIS:CE1	1:B:253:MET:SD	3.10	0.44
1:B:225:GLY:HA3	1:B:253:MET:HE1	1.98	0.44
1:A:141:ALA:HB2	1:A:185:TRP:CZ2	2.53	0.44
1:B:283:PRO:HG2	1:B:284:TYR:CD2	2.52	0.44
1:B:303:LEU:HA	1:B:303:LEU:HD23	1.84	0.44
1:A:181:TYR:OH	2:D:5:LYS:HG3	2.18	0.44
1:A:20:GLU:OE2	1:A:341:ARG:NH2	2.51	0.44
1:A:38:HIS:HE1	3:A:715:HOH:O	2.00	0.43
1:A:238:LEU:HA	1:A:238:LEU:HD23	1.90	0.43
1:B:366:LEU:HD21	1:B:369:ILE:HD11	2.00	0.43
2:C:4:ARG:HE	2:C:4:ARG:HB3	1.57	0.43
1:A:340:ARG:HG2	1:A:375:ALA:C	2.38	0.42
1:B:73:SER:OG	2:C:9:PRO:HD2	2.20	0.42
1:A:64:HIS:CE1	1:A:86:LEU:HD12	2.55	0.42
1:A:133:MET:HE3	1:A:191:GLY:N	2.35	0.42
1:A:376:LYS:HD3	1:A:395:GLU:OE2	2.20	0.42
1:A:329:ASN:HB3	3:A:632:HOH:O	2.19	0.41
1:B:38:HIS:HB3	1:B:399:MET:HE3	2.02	0.41
1:A:306:LEU:HA	1:A:306:LEU:HD23	1.90	0.41
1:A:133:MET:HE3	1:A:191:GLY:H	1.84	0.41
1:A:119:ILE:HG23	1:A:159:SER:HA	2.02	0.41
1:B:42:TRP:CE3	1:B:72:THR:HA	2.56	0.41
1:B:126:GLU:O	1:B:145:PRO:HD3	2.21	0.41
1:B:42:TRP:CD1	1:B:72:THR:HG22	2.56	0.41
1:A:298:VAL:HB	1:A:313:PHE:HB2	2.04	0.40
1:A:156:LYS:NZ	1:A:212:LYS:O	2.54	0.40
1:A:180:GLY:HA3	1:A:197:SER:HA	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	378/456 (83%)	369 (98%)	9 (2%)	0	100	100
1	B	375/456 (82%)	363 (97%)	11 (3%)	1 (0%)	41	31
2	C	8/14 (57%)	8 (100%)	0	0	100	100
2	D	8/14 (57%)	8 (100%)	0	0	100	100
All	All	769/940 (82%)	748 (97%)	20 (3%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	315	SER

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	334/402 (83%)	331 (99%)	3 (1%)	78	79
1	B	331/402 (82%)	325 (98%)	6 (2%)	59	55
2	C	9/14 (64%)	9 (100%)	0	100	100
2	D	9/14 (64%)	9 (100%)	0	100	100
All	All	683/832 (82%)	674 (99%)	9 (1%)	69	68

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASP
1	A	160	LYS
1	A	354	GLN
1	B	14	GLU
1	B	168	ASN
1	B	170	ASP
1	B	289	LEU
1	B	314	GLU
1	B	407	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	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](#)

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 [i](#)

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	380/456 (83%)	0.33	31 (8%) 11 13	11, 27, 76, 101	0
1	B	380/456 (83%)	0.45	39 (10%) 6 7	17, 34, 77, 104	0
2	C	10/14 (71%)	0.35	1 (10%) 7 8	29, 37, 55, 59	0
2	D	10/14 (71%)	0.80	1 (10%) 7 8	36, 53, 61, 64	0
All	All	780/940 (82%)	0.40	72 (9%) 9 10	11, 31, 77, 104	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	ALA	7.1
1	B	12	VAL	6.6
1	A	356	PRO	6.3
1	B	214	GLY	6.2
1	A	12	VAL	5.9
1	B	8	PHE	5.7
1	A	30	PHE	5.3
1	A	358	ASP	5.2
1	B	213	GLU	5.1
1	A	58	GLY	5.1
1	B	210	VAL	5.1
1	A	355	SER	5.0
1	B	359	ALA	4.9
1	A	360	GLU	4.9
1	A	357	GLU	4.9
1	B	7	ALA	4.8
1	B	112	SER	4.7
1	B	11	ALA	4.6
1	B	89	ASP	4.5
1	A	361	ASP	4.3
1	B	360	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	8	PHE	4.2
1	A	16	VAL	4.2
1	B	30	PHE	4.0
1	B	9	ASP	4.0
1	B	212	LYS	3.7
1	A	59	LYS	3.6
1	B	361	ASP	3.5
1	B	364	PRO	3.5
1	A	23	ILE	3.5
1	B	353	GLU	3.5
1	A	26	LYS	3.4
1	B	358	ASP	3.3
1	A	6	ALA	3.3
1	A	60	ASP	3.1
1	A	55	ARG	3.1
1	B	10	ASP	3.1
1	A	14	GLU	3.0
1	A	19	GLU	3.0
1	B	58	GLY	3.0
1	A	15	ARG	3.0
1	A	57	GLU	3.0
1	A	18	ASN	3.0
1	B	113	GLY	2.9
1	B	90	ASP	2.9
1	A	10	ASP	2.9
1	A	56	PRO	2.9
1	A	9	ASP	2.8
1	B	15	ARG	2.7
1	B	13	GLU	2.7
1	A	61	PHE	2.6
1	B	16	VAL	2.6
1	B	60	ASP	2.6
1	B	308	LEU	2.6
1	B	362	GLY	2.6
1	A	354	GLN	2.6
1	B	410	ASN	2.6
1	B	352	GLU	2.6
2	C	12	LEU	2.4
1	B	14	GLU	2.4
1	A	11	ALA	2.4
1	A	362	GLY	2.3
1	B	351	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	359	ALA	2.3
1	B	211	PRO	2.3
1	B	68	LEU	2.3
1	B	407	ASN	2.2
2	D	12	LEU	2.1
1	B	209	ALA	2.1
1	B	350	ILE	2.1
1	B	260	ASN	2.0
1	B	348	SER	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.