



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 02:23 am GMT

PDB ID : 4BQQ
Title : Protein crystal structure of the N-terminal and recombinase domains of the Streptomyces temperate phage serine recombinase, fC31 integrase.
Authors : McMahon, S.A.; McEwan, A.R.; Smith, M.C.M.; Naismith, J.H.
Deposited on : 2013-05-31
Resolution : 2.15 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

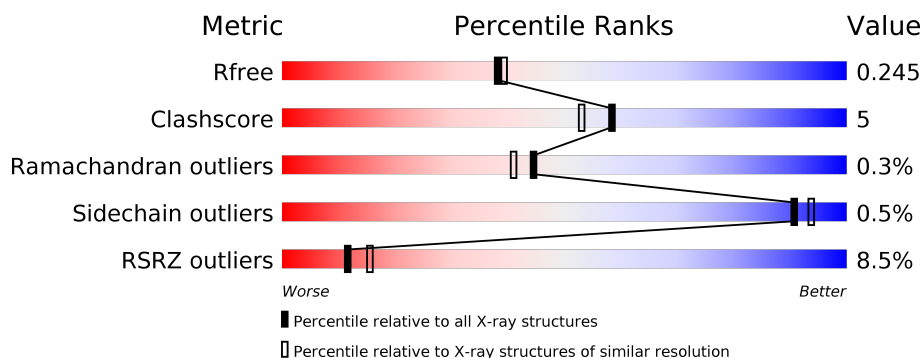
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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	396	<div> <div>10%</div> <div> <div></div> <div>74%</div> <div>11%</div> <div>15%</div> </div> </div>
1	B	396	<div> <div>5%</div> <div> <div></div> <div>74%</div> <div>9%</div> <div>16%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5480 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 INTEGRASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	3	1
			2671	1679	486	492	14			
1	B	333	Total	C	N	O	S	0	3	1
			2624	1645	478	487	14			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	EXPRESSION TAG	UNP Q9T221
A	-23	SER	-	EXPRESSION TAG	UNP Q9T221
A	-22	TYR	-	EXPRESSION TAG	UNP Q9T221
A	-21	TYR	-	EXPRESSION TAG	UNP Q9T221
A	-20	HIS	-	EXPRESSION TAG	UNP Q9T221
A	-19	HIS	-	EXPRESSION TAG	UNP Q9T221
A	-18	HIS	-	EXPRESSION TAG	UNP Q9T221
A	-17	HIS	-	EXPRESSION TAG	UNP Q9T221
A	-16	HIS	-	EXPRESSION TAG	UNP Q9T221
A	-15	HIS	-	EXPRESSION TAG	UNP Q9T221
A	-14	ASP	-	EXPRESSION TAG	UNP Q9T221
A	-13	TYR	-	EXPRESSION TAG	UNP Q9T221
A	-12	ASP	-	EXPRESSION TAG	UNP Q9T221
A	-11	ILE	-	EXPRESSION TAG	UNP Q9T221
A	-10	PRO	-	EXPRESSION TAG	UNP Q9T221
A	-9	THR	-	EXPRESSION TAG	UNP Q9T221
A	-8	THR	-	EXPRESSION TAG	UNP Q9T221
A	-7	GLU	-	EXPRESSION TAG	UNP Q9T221
A	-6	ASN	-	EXPRESSION TAG	UNP Q9T221
A	-5	LEU	-	EXPRESSION TAG	UNP Q9T221
A	-4	TYR	-	EXPRESSION TAG	UNP Q9T221
A	-3	PHE	-	EXPRESSION TAG	UNP Q9T221
A	-2	GLN	-	EXPRESSION TAG	UNP Q9T221
A	-1	GLY	-	EXPRESSION TAG	UNP Q9T221
A	0	ALA	-	EXPRESSION TAG	UNP Q9T221

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-24	MET	-	EXPRESSION TAG	UNP Q9T221
B	-23	SER	-	EXPRESSION TAG	UNP Q9T221
B	-22	TYR	-	EXPRESSION TAG	UNP Q9T221
B	-21	TYR	-	EXPRESSION TAG	UNP Q9T221
B	-20	HIS	-	EXPRESSION TAG	UNP Q9T221
B	-19	HIS	-	EXPRESSION TAG	UNP Q9T221
B	-18	HIS	-	EXPRESSION TAG	UNP Q9T221
B	-17	HIS	-	EXPRESSION TAG	UNP Q9T221
B	-16	HIS	-	EXPRESSION TAG	UNP Q9T221
B	-15	HIS	-	EXPRESSION TAG	UNP Q9T221
B	-14	ASP	-	EXPRESSION TAG	UNP Q9T221
B	-13	TYR	-	EXPRESSION TAG	UNP Q9T221
B	-12	ASP	-	EXPRESSION TAG	UNP Q9T221
B	-11	ILE	-	EXPRESSION TAG	UNP Q9T221
B	-10	PRO	-	EXPRESSION TAG	UNP Q9T221
B	-9	THR	-	EXPRESSION TAG	UNP Q9T221
B	-8	THR	-	EXPRESSION TAG	UNP Q9T221
B	-7	GLU	-	EXPRESSION TAG	UNP Q9T221
B	-6	ASN	-	EXPRESSION TAG	UNP Q9T221
B	-5	LEU	-	EXPRESSION TAG	UNP Q9T221
B	-4	TYR	-	EXPRESSION TAG	UNP Q9T221
B	-3	PHE	-	EXPRESSION TAG	UNP Q9T221
B	-2	GLN	-	EXPRESSION TAG	UNP Q9T221
B	-1	GLY	-	EXPRESSION TAG	UNP Q9T221
B	0	ALA	-	EXPRESSION TAG	UNP Q9T221

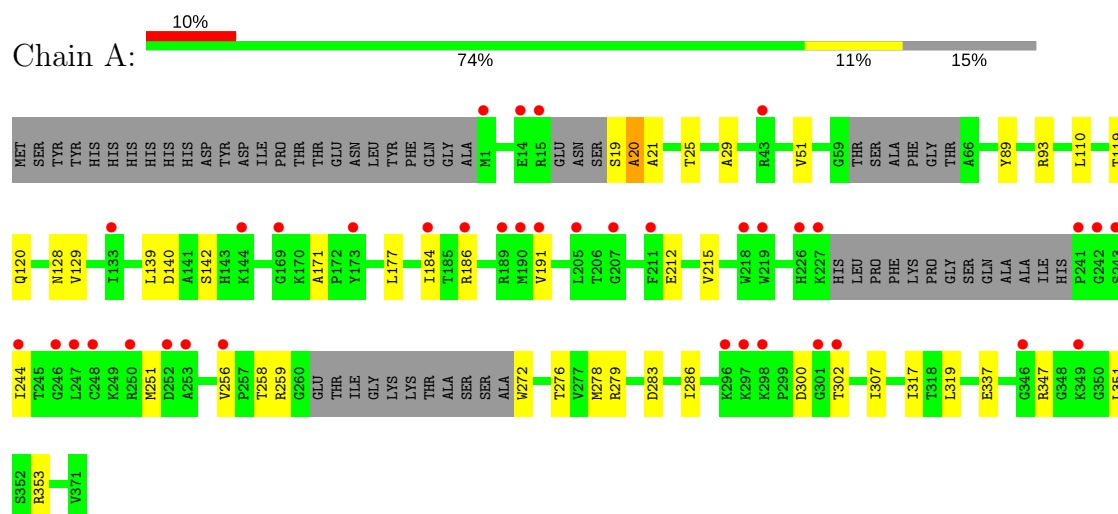
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	83	Total O 83 83	0	0
2	B	102	Total O 102 102	0	0

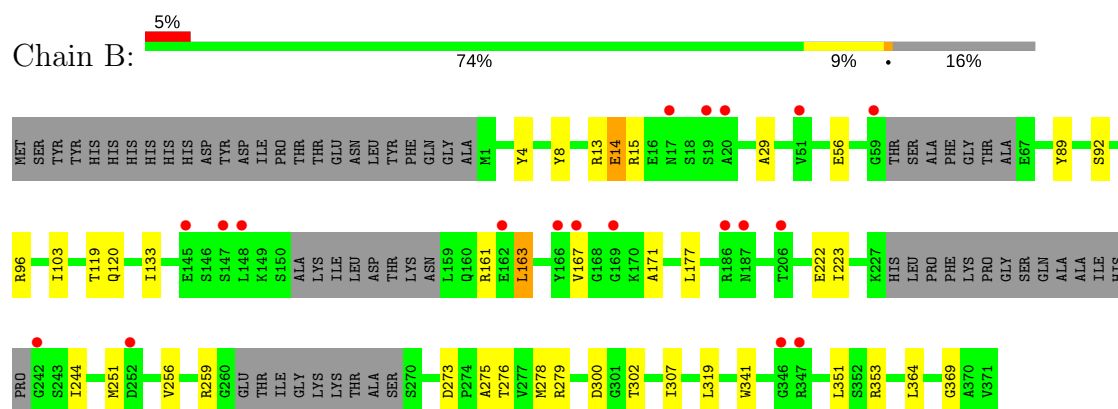
3 Residue-property plots [i](#)

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: INTEGRASE



• Molecule 1: INTEGRASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	96.04Å 96.04Å 117.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	96.04 – 2.15 96.04 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.3 (96.04-2.15) 98.3 (96.04-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.6.0111	Depositor
R, R_{free}	0.218 , 0.244 0.221 , 0.245	Depositor DCC
R_{free} test set	2865 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5480	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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	0.49	0/2729	0.64	0/3678
1	B	0.50	0/2681	0.64	0/3614
All	All	0.49	0/5410	0.64	0/7292

There are no bond length outliers.

There are no bond angle outliers.

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	2671	0	2693	35	0
1	B	2624	0	2622	29	1
2	A	83	0	0	4	0
2	B	102	0	0	0	1
All	All	5480	0	5315	58	2

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 (58) 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:258:THR:HG22	1:A:272:TRP:CD1	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ARG:HD2	1:A:307:ILE:HD12	1.68	0.75
1:A:337:GLU:OE1	2:A:2076:HOH:O	2.05	0.72
1:B:223[A]:ILE:HG23	1:B:341:TRP:CZ2	2.26	0.71
1:A:258:THR:HG22	1:A:272:TRP:NE1	2.08	0.69
1:B:13:ARG:O	1:B:14:GLU:HB3	1.93	0.68
1:B:13:ARG:O	1:B:14:GLU:CB	2.41	0.68
1:A:29:ALA:HB1	1:A:119:THR:HG21	1.75	0.68
1:B:279:ARG:HD2	1:B:307:ILE:HD12	1.76	0.67
1:A:351:LEU:O	1:B:353:ARG:NH2	2.25	0.66
1:B:244:ILE:HD13	1:B:278:MET:CG	2.26	0.66
1:A:171:ALA:HB2	1:A:177:LEU:HG	1.80	0.64
1:A:20:ALA:HB1	1:A:93:ARG:HH22	1.62	0.64
1:A:244:ILE:HD13	1:A:278:MET:CG	2.28	0.63
1:B:29:ALA:HB1	1:B:119:THR:HG21	1.81	0.62
1:A:128:ASN:ND2	2:A:2041:HOH:O	2.17	0.59
1:A:283:ASP:HB3	1:A:286[A]:ILE:HD13	1.84	0.59
1:B:273:ASP:OD2	1:B:275:ALA:HB3	2.02	0.59
1:A:140:ASP:O	1:A:142:SER:O	2.19	0.59
1:B:223[A]:ILE:HG23	1:B:341:TRP:CE2	2.37	0.58
1:B:251:MET:HE3	1:B:256:VAL:HG11	1.85	0.57
1:A:258:THR:CG2	1:A:272:TRP:CD1	2.86	0.57
1:A:110:LEU:HD12	1:A:129:VAL:HG23	1.87	0.57
1:B:171:ALA:O	1:B:259:ARG:NH1	2.35	0.56
1:B:15:ARG:NH2	1:B:92:SER:OG	2.39	0.55
1:A:258:THR:HG22	1:A:272:TRP:CE2	2.41	0.55
1:A:319:LEU:HD12	1:B:319:LEU:CD1	2.39	0.53
1:B:96:ARG:NH1	1:B:302:THR:HG22	2.24	0.53
1:B:171:ALA:HB2	1:B:177:LEU:HG	1.92	0.52
1:B:103:ILE:HG23	1:B:133:ILE:HD12	1.92	0.52
1:A:276:THR:HG23	1:A:279:ARG:NH2	2.25	0.52
1:B:251:MET:CE	1:B:256:VAL:HG11	2.42	0.50
1:B:276:THR:HG23	1:B:279:ARG:NH2	2.26	0.50
1:B:300:ASP:OD2	1:B:302:THR:HG23	2.12	0.50
1:B:223[A]:ILE:CG2	1:B:341:TRP:CE2	2.95	0.49
1:A:353:ARG:NH2	1:B:351:LEU:O	2.45	0.48
1:A:212:GLU:OE2	1:A:259:ARG:NH1	2.47	0.47
1:A:244:ILE:HD13	1:A:278:MET:HG2	1.96	0.47
1:A:300:ASP:OD2	1:A:302:THR:HG23	2.15	0.46
1:A:19:SER:O	1:A:20:ALA:HB2	2.15	0.46
1:A:215:VAL:HG11	2:A:2050:HOH:O	2.15	0.46
1:A:319:LEU:CD1	1:B:319:LEU:HD11	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:ILE:HG22	1:A:191:VAL:O	2.17	0.44
1:A:251:MET:CE	1:A:256:VAL:HG11	2.48	0.44
1:A:89:TYR:O	1:A:120:GLN:HG2	2.17	0.43
1:A:139:LEU:HD23	1:A:317:ILE:HD12	2.00	0.43
1:A:21:ALA:HB1	1:A:25:THR:HB	1.99	0.43
1:B:364:LEU:O	1:B:364:LEU:HD12	2.19	0.43
1:A:319:LEU:HD12	1:B:319:LEU:HD11	2.01	0.43
1:B:8:TYR:OH	1:B:56:GLU:HG3	2.19	0.42
1:A:347:ARG:HH21	1:A:351:LEU:HD23	1.84	0.42
1:B:89:TYR:O	1:B:120:GLN:HG2	2.20	0.42
1:B:161:ARG:C	1:B:163:LEU:HD23	2.40	0.42
2:A:2035:HOH:O	1:B:369:GLY:HA3	2.20	0.41
1:A:319:LEU:HD12	1:B:319:LEU:HD12	2.03	0.41
1:A:251:MET:HE3	1:A:256:VAL:HG11	2.03	0.41
1:A:139:LEU:O	1:A:142:SER:O	2.39	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2024:HOH:O	2:B:2091:HOH:O[2_564]	1.96	0.24
1:B:4:TYR:OH	1:B:222:GLU:OE2[2_564]	2.15	0.05

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	331/396 (84%)	321 (97%)	9 (3%)	1 (0%)	44	41
1	B	326/396 (82%)	315 (97%)	10 (3%)	1 (0%)	44	41
All	All	657/792 (83%)	636 (97%)	19 (3%)	2 (0%)	44	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	14	GLU
1	A	20	ALA

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	283/329 (86%)	282 (100%)	1 (0%)	93	95
1	B	277/329 (84%)	275 (99%)	2 (1%)	87	91
All	All	560/658 (85%)	557 (100%)	3 (0%)	91	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	186	ARG
1	B	163	LEU
1	B	167	VAL

Some 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 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 [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	338/396 (85%)	0.82	38 (11%) 6 8	37, 75, 138, 176	0
1	B	333/396 (84%)	0.60	19 (5%) 24 32	39, 65, 116, 145	0
All	All	671/792 (84%)	0.71	57 (8%) 11 15	37, 70, 129, 176	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	20	ALA	8.8
1	A	242	GLY	6.8
1	A	256	VAL	6.2
1	A	227	LYS	4.8
1	A	247	LEU	4.6
1	B	59	GLY	4.5
1	A	169	GLY	4.2
1	B	242	GLY	3.9
1	A	189	ARG	3.9
1	B	169	GLY	3.8
1	B	19	SER	3.8
1	A	349	LYS	3.6
1	B	187	ASN	3.4
1	A	241	PRO	3.4
1	A	248	CYS	3.4
1	B	252	ASP	3.2
1	B	145	GLU	3.2
1	A	298	LYS	3.2
1	A	14	GLU	3.1
1	B	186	ARG	3.1
1	A	346	GLY	3.0
1	B	51[A]	VAL	3.0
1	B	347	ARG	2.9
1	A	219	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	244	ILE	2.8
1	B	148	LEU	2.7
1	A	250	ARG	2.7
1	A	1	MET	2.6
1	A	205	LEU	2.6
1	A	302	THR	2.6
1	A	133	ILE	2.6
1	A	297	LYS	2.6
1	A	246	GLY	2.6
1	A	226	HIS	2.4
1	B	166	TYR	2.4
1	B	162	GLU	2.3
1	B	147	SER	2.3
1	B	346	GLY	2.3
1	A	43	ARG	2.3
1	B	206	THR	2.2
1	A	186	ARG	2.2
1	A	144	LYS	2.2
1	A	301	GLY	2.2
1	A	253	ALA	2.2
1	A	218	TRP	2.2
1	A	191	VAL	2.2
1	A	173	TYR	2.2
1	A	296	LYS	2.1
1	A	184	ILE	2.1
1	A	243	SER	2.1
1	A	207	GLY	2.1
1	A	190	MET	2.1
1	B	17	ASN	2.0
1	A	211	PHE	2.0
1	A	15	ARG	2.0
1	A	252	ASP	2.0
1	B	167	VAL	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.