Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:43 AM GMT

PDB ID	:	3BWB
Title	:	Crystal structure of the apo form of spermidine synthase from Trypanosoma cruzi at 2.5 A resolution
Authors	:	Bosch, J.; Hol, W.G.J.; Structural Genomics of Pathogenic Protozoa Consortium (SGPP)
Deposited on	:	2008-01-08
Resolution	:	2.50 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 (i) symbol.

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

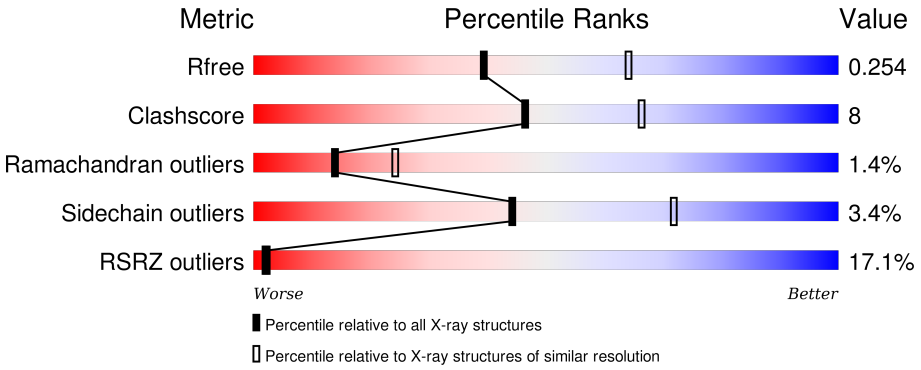
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 <=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	304	13% 79% 13% •• 5%
1	B	304	18% 76% 16% • 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4671 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 Spermidine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	Se	4	8	0
			2310	1468	393	431	10	8			
1	B	283	Total	C	N	O	S	Se	0	5	0
			2261	1438	384	421	8	10			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q4DA73
A	2	ALA	-	EXPRESSION TAG	UNP Q4DA73
A	3	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	4	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	5	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	6	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	7	HIS	-	EXPRESSION TAG	UNP Q4DA73
A	8	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	1	MSE	-	EXPRESSION TAG	UNP Q4DA73
B	2	ALA	-	EXPRESSION TAG	UNP Q4DA73
B	3	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	4	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	5	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	6	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	7	HIS	-	EXPRESSION TAG	UNP Q4DA73
B	8	HIS	-	EXPRESSION TAG	UNP Q4DA73

- Molecule 2 is water.

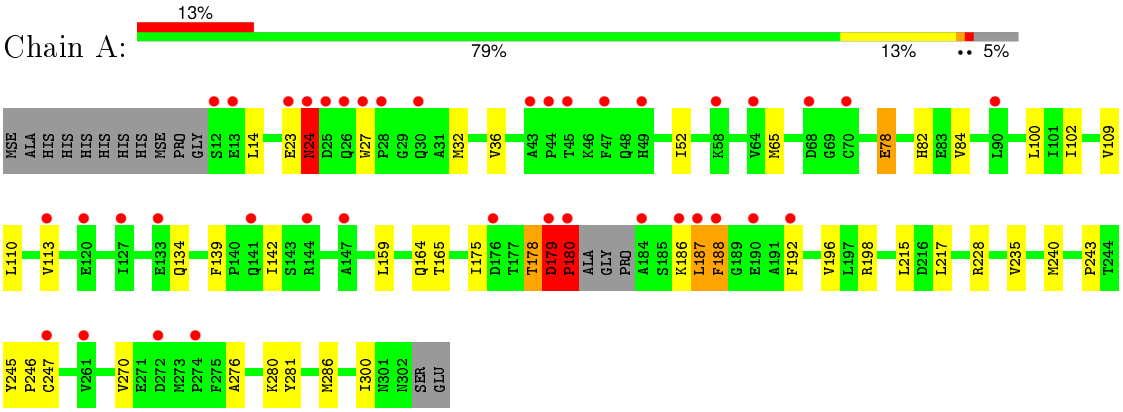
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	48	Total	O	0	0
			48	48		
2	B	52	Total	O	0	0
			52	52		

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 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.

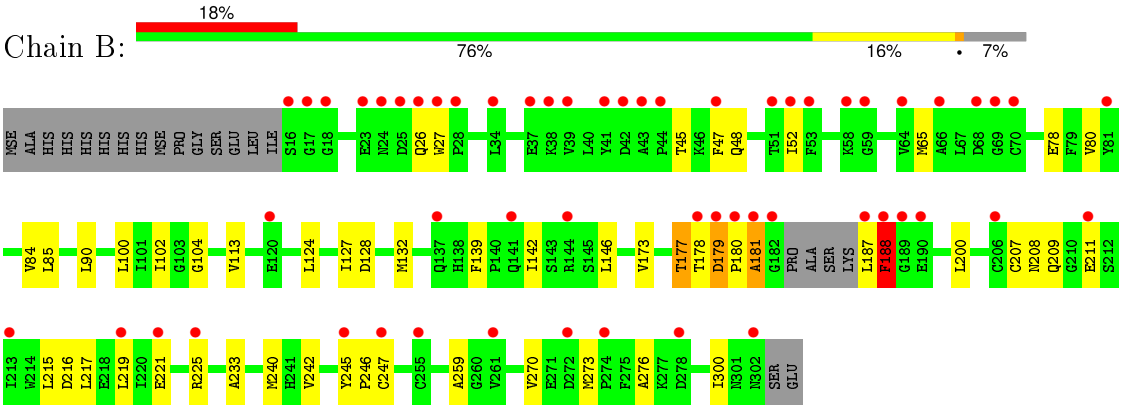
- Molecule 1: Spermidine synthase

Chain A:



- Molecule 1: Spermidine synthase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	43.67Å 97.00Å 69.65Å 90.00° 106.33° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	89.1 (20.00-2.50) 89.1 (19.90-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.57 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.198 , 0.248 0.204 , 0.254	Depositor DCC
R_{free} test set	895 reflections (5.49%)	DCC
Wilson B-factor (Å^2)	45.1	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 57.8	EDS
Estimated twinning fraction	0.045 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 17201 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4671	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	2.46	5/2382 (0.2%)	1.48	7/3214 (0.2%)
1	B	0.38	0/2327	0.56	0/3142
All	All	1.77	5/4709 (0.1%)	1.12	7/6356 (0.1%)

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	A	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	ASP	CG-OD1	79.64	3.08	1.25
1	A	179	ASP	CG-OD2	69.71	2.85	1.25
1	A	180	PRO	CG-CD	47.37	3.06	1.50
1	A	179	ASP	CB-CG	20.02	1.93	1.51
1	A	178	THR	CB-OG1	16.28	1.75	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	179	ASP	CB-CG-OD2	-46.76	76.22	118.30
1	A	180	PRO	N-CD-CG	-39.50	43.95	103.20
1	A	179	ASP	CB-CG-OD1	32.43	147.49	118.30
1	A	180	PRO	CA-CB-CG	-31.39	44.36	104.00
1	A	180	PRO	CB-CG-CD	-13.76	52.83	106.50
1	A	178	THR	OG1-CB-CG2	-6.94	94.04	110.00
1	A	178	THR	CA-CB-CG2	6.10	120.94	112.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	179	ASP	Sidechain

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	2310	0	2280	30	0
1	B	2261	0	2222	40	0
2	A	48	0	0	1	0
2	B	52	0	0	1	0
All	All	4671	0	4502	69	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 8.

All (69) 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:14:LEU:HD12	1:A:36:VAL:HG21	1.41	1.01
1:A:178:THR:O	1:A:179:ASP:HB3	1.65	0.93
1:A:180:PRO:HB3	2:A:351:HOH:O	1.67	0.93
1:B:132:MSE:HE3	1:B:146:LEU:HD13	1.51	0.90
1:B:221[A]:GLU:CD	1:B:225[A]:ARG:HH21	1.85	0.80
1:A:228:ARG:HG3	1:A:235:VAL:HG12	1.72	0.71
1:B:45:THR:HG22	1:B:48:GLN:O	1.91	0.71
1:A:159:LEU:HD11	1:A:188:PHE:HD1	1.56	0.69
1:B:221[A]:GLU:CG	1:B:225[A]:ARG:HH21	2.07	0.67
1:B:65:MSE:HE3	1:B:139:PHE:CE2	2.31	0.66
1:B:84:VAL:HG11	1:B:240:MSE:HE2	1.80	0.63
1:B:221[A]:GLU:OE1	1:B:225[A]:ARG:NH2	2.32	0.61
1:A:159:LEU:HD11	1:A:188:PHE:CD1	2.36	0.61
1:B:173:VAL:HG23	1:B:200:LEU:HD21	1.82	0.60
1:B:211:GLU:HG3	1:B:219:LEU:HD23	1.85	0.58
1:B:177:THR:HG23	1:B:179:ASP:H	1.69	0.57
1:A:281:TYR:CE2	1:A:286:MSE:HE2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:LEU:HD21	1:A:102:ILE:HD11	1.87	0.55
1:B:139:PHE:HB3	1:B:142:ILE:HD12	1.88	0.54
1:B:45:THR:HG21	1:B:128:ASP:OD2	2.09	0.53
1:B:102:ILE:HD12	1:B:102:ILE:N	2.23	0.53
1:B:85:LEU:HD22	1:B:207:CYS:SG	2.49	0.52
1:B:45:THR:HG23	1:B:47:PHE:H	1.75	0.52
1:B:270:VAL:O	1:B:276:ALA:HB2	2.10	0.51
1:B:221[A]:GLU:HG2	1:B:225[A]:ARG:HE	1.75	0.51
1:B:80:VAL:O	1:B:84:VAL:HG23	2.11	0.51
1:B:187:LEU:O	1:B:188:PHE:CD1	2.64	0.50
1:A:139:PHE:HB3	1:A:142:ILE:HD12	1.93	0.50
1:A:23:GLU:O	1:A:24:ASN:ND2	2.44	0.50
1:A:78:GLU:HG2	1:A:82:HIS:CE1	2.47	0.50
1:B:127:ILE:CD1	1:B:181:ALA:HB1	2.42	0.50
1:A:281:TYR:CZ	1:A:286:MSE:HE2	2.47	0.49
1:B:104:GLY:O	1:B:124:LEU:HD11	2.13	0.49
1:B:178:THR:O	1:B:178:THR:HG22	2.13	0.49
1:B:221[A]:GLU:CG	1:B:225[A]:ARG:NH2	2.75	0.48
1:A:109:VAL:O	1:A:113:VAL:HG13	2.13	0.48
1:B:177:THR:OG1	1:B:180:PRO:HD2	2.13	0.48
1:A:27:TRP:CZ2	1:A:247[B]:CYS:SG	3.04	0.48
1:B:127:ILE:HD12	1:B:181:ALA:HB1	1.95	0.47
1:A:84:VAL:HG11	1:A:240:MSE:HE2	1.96	0.47
1:B:52:ILE:HD11	1:B:65:MSE:HE2	1.96	0.47
1:A:14:LEU:CD1	1:A:36:VAL:HG21	2.29	0.47
1:A:192:PHE:O	1:A:196:VAL:HG23	2.15	0.47
1:B:233:ALA:HB1	1:B:259:ALA:HA	1.97	0.46
1:A:228:ARG:HG3	1:A:235:VAL:CG1	2.41	0.45
1:A:245:TYR:CG	1:A:246:PRO:HD2	2.51	0.45
1:A:165:THR:O	1:A:198:ARG:NH2	2.48	0.45
1:B:52:ILE:CD1	1:B:65:MSE:HE2	2.47	0.45
1:B:90:LEU:HD21	1:B:113:VAL:HG13	1.97	0.44
1:A:100:LEU:CD2	1:A:102:ILE:HD11	2.46	0.44
1:B:245:TYR:CG	1:B:246:PRO:HD2	2.52	0.44
1:A:270:VAL:O	1:A:276:ALA:HB2	2.17	0.44
1:B:65:MSE:HE3	1:B:139:PHE:CD2	2.53	0.44
1:A:65:MSE:HE3	1:A:139:PHE:CE2	2.53	0.44
1:B:273[B]:MSE:HE2	1:B:273[B]:MSE:HA	1.99	0.44
1:B:100:LEU:CD2	1:B:102:ILE:HD11	2.48	0.43
1:B:173:VAL:HG23	1:B:200:LEU:CD2	2.47	0.43
1:A:110:LEU:O	1:A:113:VAL:HG22	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:GLU:C	1:A:24:ASN:HD22	2.22	0.42
1:B:217:LEU:CD1	1:B:300:ILE:HD11	2.50	0.42
1:A:217:LEU:HD12	1:A:300:ILE:HD11	2.01	0.41
1:B:221[A]:GLU:HG2	1:B:225[A]:ARG:NE	2.35	0.41
1:B:240:MSE:HG3	1:B:242:VAL:HG23	2.02	0.41
1:B:179:ASP:OD2	1:B:187:LEU:HD23	2.21	0.41
1:B:124:LEU:HD23	1:B:124:LEU:C	2.41	0.41
1:A:243:PRO:HA	1:B:247:CYS:O	2.21	0.41
1:A:32:MSE:HE2	2:B:377:HOH:O	2.20	0.41
1:A:52:ILE:CD1	1:A:134:GLN:HB3	2.51	0.40
1:A:175:ILE:HD13	1:A:192:PHE:CE2	2.57	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	292/304 (96%)	274 (94%)	14 (5%)	4 (1%)	14	24
1	B	285/304 (94%)	268 (94%)	13 (5%)	4 (1%)	14	24
All	All	577/608 (95%)	542 (94%)	27 (5%)	8 (1%)	14	24

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	179	ASP
1	B	179	ASP
1	B	181	ALA
1	B	188	PHE
1	A	187	LEU
1	A	188	PHE

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Mol	Chain	Res	Type
1	B	27	TRP

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	258/253 (102%)	249 (96%)	9 (4%)	43	70
1	B	250/253 (99%)	242 (97%)	8 (3%)	46	74
All	All	508/506 (100%)	491 (97%)	17 (3%)	44	73

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	78	GLU
1	A	164	GLN
1	A	179	ASP
1	A	180	PRO
1	A	186	LYS
1	A	187	LEU
1	A	215	LEU
1	A	280	LYS
1	B	26	GLN
1	B	78	GLU
1	B	177	THR
1	B	188	PHE
1	B	208	ASN
1	B	209	GLN
1	B	215	LEU
1	B	216	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	209	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, 95^{th} 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	281/304 (92%)	0.82	39 (13%)	4	4	19, 35, 61, 72	3 (1%)
1	B	276/304 (90%)	1.10	56 (20%)	1	1	19, 35, 63, 79	0
All	All	557/608 (91%)	0.96	95 (17%)	2	2	19, 35, 63, 79	3 (0%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	16	SER	11.9
1	A	180	PRO	9.2
1	B	24	ASN	7.5
1	A	187	LEU	7.2
1	B	188	PHE	7.1
1	B	187	LEU	6.9
1	A	179	ASP	6.9
1	A	12	SER	6.8
1	B	17	GLY	6.6
1	B	178	THR	6.3
1	B	27	TRP	6.1
1	B	25	ASP	5.9
1	B	179	ASP	5.8
1	B	64	VAL	5.7
1	A	27	TRP	5.6
1	A	25	ASP	5.2
1	B	302	ASN	4.5
1	B	18	GLY	4.5
1	A	186	LYS	4.1
1	B	181	ALA	4.1
1	B	245	TYR	4.1
1	A	188	PHE	4.0
1	A	43	ALA	3.8
1	A	24	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	58	LYS	3.8
1	A	13	GLU	3.7
1	A	44	PRO	3.7
1	A	192	PHE	3.6
1	A	147	ALA	3.6
1	B	26	GLN	3.5
1	B	69	GLY	3.4
1	A	141	GLN	3.4
1	B	23	GLU	3.4
1	B	58	LYS	3.3
1	A	127	ILE	3.3
1	B	39	VAL	3.3
1	B	180	PRO	3.2
1	B	44	PRO	3.2
1	B	182	GLY	3.2
1	A	272	ASP	3.2
1	A	113	VAL	3.1
1	A	144[A]	ARG	3.1
1	B	247	CYS	3.1
1	B	120	GLU	2.9
1	B	137	GLN	2.9
1	B	219	LEU	2.9
1	B	34	LEU	2.8
1	A	23	GLU	2.8
1	B	274	PRO	2.8
1	A	90	LEU	2.7
1	B	81	TYR	2.7
1	B	42	ASP	2.7
1	A	47	PHE	2.7
1	B	70[A]	CYS	2.7
1	A	64	VAL	2.7
1	A	184	ALA	2.7
1	B	141	GLN	2.7
1	B	52	ILE	2.6
1	B	225[A]	ARG	2.6
1	A	120	GLU	2.6
1	A	26	GLN	2.5
1	B	261	VAL	2.5
1	A	176	ASP	2.4
1	B	37	GLU	2.4
1	A	133	GLU	2.4
1	A	68	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	190	GLU	2.4
1	A	49	HIS	2.3
1	B	59	GLY	2.3
1	A	28	PRO	2.3
1	B	68	ASP	2.3
1	A	30	GLN	2.3
1	A	45	THR	2.3
1	A	261	VAL	2.3
1	A	274	PRO	2.2
1	B	47	PHE	2.2
1	B	190	GLU	2.2
1	B	53	PHE	2.2
1	B	221[A]	GLU	2.1
1	B	255	CYS	2.1
1	A	247[A]	CYS	2.1
1	B	66	ALA	2.1
1	B	272	ASP	2.1
1	B	278	ASP	2.1
1	B	189	GLY	2.1
1	A	70[A]	CYS	2.1
1	B	211	GLU	2.1
1	B	144	ARG	2.1
1	B	38	LYS	2.1
1	B	28	PRO	2.0
1	B	41	TYR	2.0
1	B	206	CYS	2.0
1	B	43	ALA	2.0
1	B	213	ILE	2.0
1	B	51	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.