



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:51 PM GMT

PDB ID : 3PWE
Title : Crystal structure of the E. coli beta clamp mutant R103C, I305C, C260S, C333S at 2.2Å resolution
Authors : Marzahn, M.R.; Robbins, A.H.; McKenna, R.; Bloom, L.B.
Deposited on : 2010-12-08
Resolution : 2.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

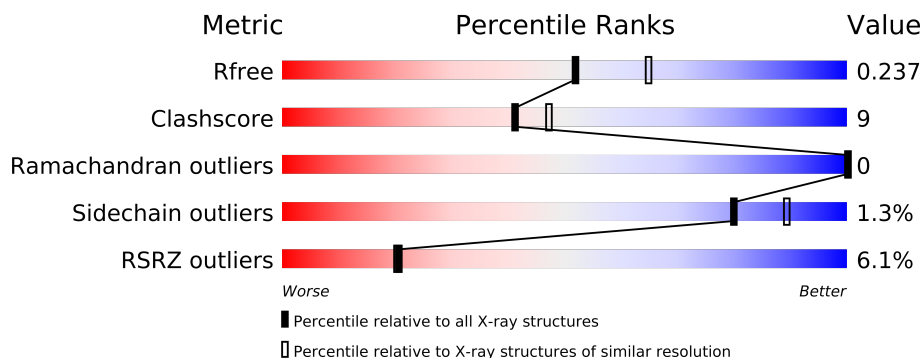
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	366	
1	B	366	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6026 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA polymerase III subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	1	0
			2844	1785	496	544	19			
1	B	366	Total	C	N	O	S	0	1	0
			2847	1786	498	544	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	CYS	ARG	ENGINEERED MUTATION	UNP P0A988
A	260	SER	CYS	ENGINEERED MUTATION	UNP P0A988
A	305	CYS	ILE	ENGINEERED MUTATION	UNP P0A988
A	333	SER	CYS	ENGINEERED MUTATION	UNP P0A988
B	103	CYS	ARG	ENGINEERED MUTATION	UNP P0A988
B	260	SER	CYS	ENGINEERED MUTATION	UNP P0A988
B	305	CYS	ILE	ENGINEERED MUTATION	UNP P0A988
B	333	SER	CYS	ENGINEERED MUTATION	UNP P0A988

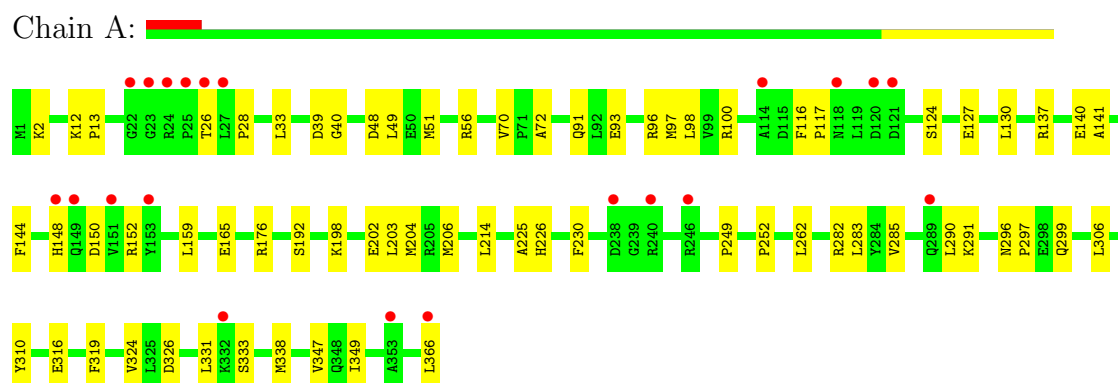
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	160	Total	O	0	0
			160	160		
2	B	175	Total	O	0	0
			175	175		

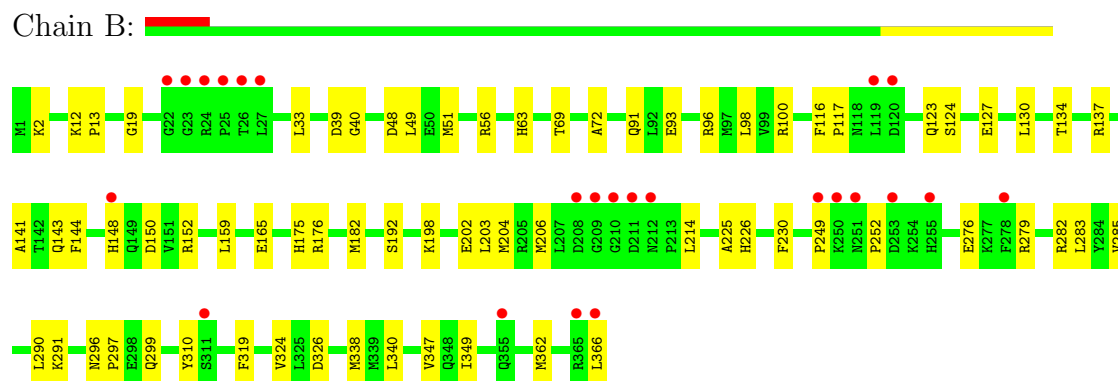
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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: DNA polymerase III subunit beta



- Molecule 1: DNA polymerase III subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.80Å 67.36Å 80.74Å 90.00° 114.16° 90.00°	Depositor
Resolution (Å)	28.50 – 2.20 28.50 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (28.50-2.20) 99.4 (28.50-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.61 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.3_467)	Depositor
R, R_{free}	0.204 , 0.245 0.197 , 0.237	Depositor DCC
R_{free} test set	2000 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 43.1	EDS
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 39772 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6026	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.35	0/2893	0.51	0/3916
1	B	0.35	0/2897	0.50	0/3920
All	All	0.35	0/5790	0.50	0/7836

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2844	0	2855	55	0
1	B	2847	0	2859	53	0
2	A	160	0	0	3	0
2	B	175	0	0	3	0
All	All	6026	0	5714	105	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (105) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:283:LEU:CD1	1:A:290:LEU:HD11	1.95	0.96

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:283:LEU:CD1	1:B:290:LEU:HD11	1.97	0.95
1:A:283:LEU:HD11	1:A:290:LEU:HD11	1.56	0.87
1:B:137:ARG:NH1	1:B:141:ALA:HB2	1.90	0.86
1:B:283:LEU:HD11	1:B:290:LEU:HD11	1.59	0.85
1:A:137:ARG:NH1	1:A:141:ALA:HB2	1.94	0.83
1:B:282:ARG:CG	1:B:282:ARG:HH11	1.93	0.82
1:A:338:MET:HE3	1:A:347:VAL:HG11	1.62	0.81
1:A:282:ARG:HH11	1:A:282:ARG:HG3	1.46	0.80
1:B:338:MET:HE3	1:B:347:VAL:HG11	1.64	0.80
1:B:282:ARG:HG3	1:B:282:ARG:HH11	1.46	0.79
1:B:214:LEU:HD11	1:B:225:ALA:HB1	1.64	0.79
1:A:282:ARG:HH11	1:A:282:ARG:CG	1.94	0.78
1:B:39:ASP:CG	1:B:40:GLY:H	1.84	0.77
1:A:39:ASP:CG	1:A:40:GLY:H	1.86	0.77
1:A:214:LEU:HD11	1:A:225:ALA:HB1	1.67	0.77
1:B:150:ASP:OD1	1:B:152:ARG:HD3	1.93	0.69
1:A:283:LEU:HD12	1:A:290:LEU:HD11	1.73	0.68
1:B:39:ASP:CG	1:B:40:GLY:N	2.47	0.68
1:B:283:LEU:HD12	1:B:290:LEU:HD11	1.76	0.67
1:A:39:ASP:CG	1:A:40:GLY:N	2.49	0.66
1:B:175:HIS:HB3	1:B:362:MET:HE2	1.79	0.65
1:A:150:ASP:OD1	1:A:152:ARG:HD3	1.98	0.64
1:A:140:GLU:HG3	1:A:204:MET:CE	2.26	0.64
1:A:51:MET:CE	1:A:202:GLU:HG3	2.28	0.63
1:A:282:ARG:HG3	1:A:282:ARG:NH1	2.13	0.63
1:B:51:MET:CE	1:B:202:GLU:HG3	2.28	0.63
1:A:319:PHE:CE2	1:A:324:VAL:HG21	2.34	0.63
1:B:51:MET:HE1	1:B:198:LYS:HG2	1.81	0.61
1:B:319:PHE:CE2	1:B:324:VAL:HG21	2.36	0.61
1:B:282:ARG:NH1	1:B:282:ARG:HG3	2.13	0.60
1:A:51:MET:HE1	1:A:198:LYS:HG2	1.85	0.58
1:A:51:MET:HE2	1:A:198:LYS:HE3	1.86	0.58
1:B:51:MET:HE2	1:B:198:LYS:HE3	1.87	0.56
1:A:159:LEU:HD11	1:A:192:SER:HB3	1.89	0.55
1:A:96:ARG:HH21	1:B:299:GLN:HB2	1.71	0.55
1:A:165:GLU:O	1:A:165:GLU:HG3	2.07	0.54
1:B:143:GLN:NE2	1:B:204:MET:SD	2.80	0.54
1:B:159:LEU:HD11	1:B:192:SER:HB3	1.89	0.53
1:B:165:GLU:O	1:B:165:GLU:HG3	2.09	0.52
1:A:2:LYS:HG3	2:A:460:HOH:O	2.10	0.52
1:A:140:GLU:HG3	1:A:204:MET:HE2	1.91	0.51
1:B:203:LEU:O	1:B:206:MET:HG2	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:282:ARG:NH1	1:B:366:LEU:HB2	2.26	0.50
1:A:140:GLU:HG3	1:A:204:MET:HE1	1.94	0.49
1:B:276:GLU:HA	1:B:279[A]:ARG:HH21	1.78	0.49
1:A:282:ARG:NH1	1:A:366:LEU:HB2	2.28	0.48
1:B:296:ASN:HB2	1:B:297:PRO:CD	2.42	0.48
1:B:51:MET:HE3	1:B:202:GLU:HG3	1.94	0.48
1:A:12:LYS:HB3	1:A:13:PRO:HD3	1.95	0.48
1:B:134:THR:HG23	1:B:182:MET:HE2	1.96	0.48
1:B:282:ARG:HH11	1:B:366:LEU:HD12	1.79	0.48
1:A:296:ASN:HB2	1:A:297:PRO:CD	2.45	0.47
1:A:130:LEU:N	1:A:130:LEU:HD23	2.29	0.47
1:B:93:GLU:OE2	1:B:98:LEU:HD22	2.13	0.47
1:B:124:SER:HG	1:B:127:GLU:HG2	1.80	0.47
1:A:93:GLU:OE2	1:A:98:LEU:HD22	2.14	0.47
1:B:63:HIS:HE1	2:B:488:HOH:O	1.98	0.47
1:B:175:HIS:O	1:B:362:MET:HG2	2.15	0.47
1:B:338:MET:HG2	1:B:349:ILE:HG12	1.97	0.46
1:A:249:PRO:HB2	1:A:252:PRO:HG3	1.97	0.46
1:B:249:PRO:HB2	1:B:252:PRO:HG3	1.98	0.46
1:A:282:ARG:HH11	1:A:366:LEU:HD12	1.81	0.46
1:A:124:SER:HG	1:A:127:GLU:HG2	1.81	0.46
1:A:51:MET:HE1	1:A:202:GLU:HG3	1.98	0.45
1:A:48:ASP:O	1:A:49:LEU:HB2	2.17	0.45
1:A:203:LEU:O	1:A:206:MET:HG2	2.17	0.45
1:A:299:GLN:HB2	1:B:96:ARG:HH21	1.82	0.44
1:A:338:MET:HG2	1:A:349:ILE:HG12	2.00	0.44
1:A:12:LYS:HE2	2:A:491:HOH:O	2.17	0.43
1:A:331:LEU:HA	1:A:331:LEU:HD23	1.86	0.43
1:B:130:LEU:HD23	1:B:130:LEU:N	2.33	0.43
1:A:96:ARG:NH2	1:B:299:GLN:HB2	2.33	0.43
1:B:33:LEU:HG	1:B:72:ALA:HB2	2.01	0.43
1:A:285:VAL:HG21	1:A:310:TYR:CD1	2.53	0.43
1:A:70:VAL:HG11	1:A:97:MET:CE	2.49	0.43
1:A:51:MET:HE3	1:A:202:GLU:HG3	2.00	0.42
1:B:285:VAL:HG21	1:B:310:TYR:CD1	2.54	0.42
1:B:19:GLY:HA3	2:B:444:HOH:O	2.19	0.42
1:A:283:LEU:O	1:A:316:GLU:HA	2.19	0.42
1:A:51:MET:CE	1:A:198:LYS:HG2	2.49	0.42
1:B:124:SER:HG	1:B:127:GLU:CG	2.32	0.42
1:A:333:SER:HB2	2:A:414:HOH:O	2.18	0.42
1:A:33:LEU:HG	1:A:72:ALA:HB2	2.02	0.42
1:B:123:GLN:NE2	2:B:468:HOH:O	2.51	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:144:PHE:CD2	1:B:326:ASP:HB3	2.54	0.42
1:B:12:LYS:HB3	1:B:13:PRO:HD3	2.02	0.42
1:B:116:PHE:HA	1:B:117:PRO:HD3	1.89	0.42
1:A:98:LEU:HD23	1:A:100:ARG:NH2	2.35	0.41
1:A:124:SER:HG	1:A:127:GLU:CG	2.33	0.41
1:A:116:PHE:HA	1:A:117:PRO:HD3	1.89	0.41
1:B:33:LEU:O	1:B:69:THR:HA	2.19	0.41
1:A:26:THR:O	1:A:28:PRO:HD3	2.21	0.41
1:B:290:LEU:HD12	1:B:291:LYS:N	2.35	0.41
1:B:13:PRO:HA	1:B:230:PHE:HE1	1.84	0.41
1:A:2:LYS:NZ	1:A:91:GLN:HE21	2.19	0.41
1:A:290:LEU:HD12	1:A:291:LYS:N	2.36	0.41
1:A:144:PHE:CD2	1:A:326:ASP:HB3	2.56	0.41
1:B:2:LYS:NZ	1:B:91:GLN:HE21	2.19	0.41
1:B:48:ASP:O	1:B:49:LEU:HB2	2.21	0.41
1:A:262:LEU:HG	1:A:306:LEU:HD11	2.02	0.41
1:B:51:MET:CE	1:B:198:LYS:HG2	2.48	0.40
1:B:98:LEU:HD23	1:B:100:ARG:NH2	2.35	0.40
1:A:13:PRO:HA	1:A:230:PHE:HE1	1.86	0.40
1:B:340:LEU:HD23	1:B:347:VAL:HG22	2.02	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	365/366 (100%)	356 (98%)	9 (2%)	0	100	100
1	B	365/366 (100%)	356 (98%)	9 (2%)	0	100	100
All	All	730/732 (100%)	712 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	314/313 (100%)	310 (99%)	4 (1%)	80	89
1	B	314/313 (100%)	310 (99%)	4 (1%)	80	89
All	All	628/626 (100%)	620 (99%)	8 (1%)	80	89

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	ARG
1	A	148	HIS
1	A	176	ARG
1	A	226	HIS
1	B	56	ARG
1	B	148	HIS
1	B	176	ARG
1	B	226	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	143	GLN
1	B	91	GLN
1	B	123	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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	366/366 (100%)	0.26	21 (5%)	23 23	16, 28, 51, 96	0
1	B	366/366 (100%)	0.32	24 (6%)	18 17	15, 28, 51, 93	0
All	All	732/732 (100%)	0.29	45 (6%)	21 20	15, 28, 51, 96	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	23	GLY	14.3
1	B	366	LEU	8.7
1	A	24	ARG	7.7
1	A	26	THR	7.0
1	B	365	ARG	5.8
1	B	251	ASN	5.7
1	A	22	GLY	5.6
1	B	23	GLY	5.5
1	A	25	PRO	5.3
1	A	240	ARG	5.2
1	B	211	ASP	5.1
1	B	22	GLY	4.9
1	B	148	HIS	4.7
1	B	208	ASP	4.3
1	B	24	ARG	4.3
1	B	210	GLY	3.9
1	B	311	SER	3.8
1	B	355	GLN	3.7
1	A	120	ASP	3.6
1	A	118	ASN	3.6
1	A	153	TYR	3.5
1	B	26	THR	3.5
1	B	25	PRO	3.4
1	B	120	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	149	GLN	3.4
1	A	366	LEU	3.2
1	B	249	PRO	3.1
1	A	27	LEU	3.1
1	A	148	HIS	3.1
1	B	119	LEU	3.1
1	B	212	ASN	3.0
1	B	253	ASP	3.0
1	A	151	VAL	3.0
1	B	209	GLY	3.0
1	A	353	ALA	2.9
1	B	27	LEU	2.7
1	A	114	ALA	2.6
1	A	332	LYS	2.6
1	B	250	LYS	2.6
1	A	121	ASP	2.4
1	A	238	ASP	2.4
1	B	255	HIS	2.2
1	A	246	ARG	2.2
1	A	289	GLN	2.1
1	B	278	PHE	2.1

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 ⓘ

There are no such residues in this entry.