



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:24 PM GMT

PDB ID : 1OTV
Title : PqqC, Pyrroloquinolinquinone Synthase C
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Deposited on : 2003-03-23
Resolution : 2.10 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 : 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

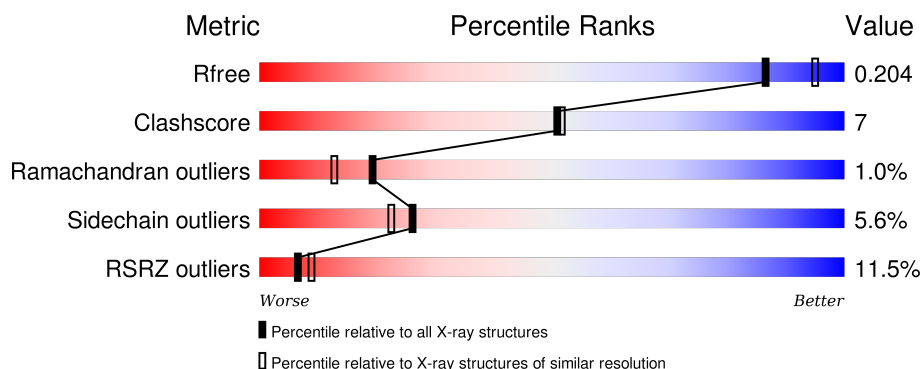
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	259	<div> <div>8%</div> <div>83%</div> <div>13%</div> <div>..</div> </div>
1	B	259	<div> <div>14%</div> <div>76%</div> <div>20%</div> <div>..</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4284 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 Coenzyme PQQ synthesis protein C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	97	0	0
			2077	1318	378	371	10			
1	B	254	Total	C	N	O	S	131	0	0
			2077	1318	378	371	10			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ASP	ALA	ENGINEERED	UNP P27505
A	252	LEU	-	EXPRESSION TAG	UNP P27505
A	253	GLU	-	EXPRESSION TAG	UNP P27505
A	254	HIS	-	EXPRESSION TAG	UNP P27505
A	255	HIS	-	EXPRESSION TAG	UNP P27505
A	256	HIS	-	EXPRESSION TAG	UNP P27505
A	257	HIS	-	EXPRESSION TAG	UNP P27505
A	258	HIS	-	EXPRESSION TAG	UNP P27505
A	259	HIS	-	EXPRESSION TAG	UNP P27505
B	21	ASP	ALA	ENGINEERED	UNP P27505
B	252	LEU	-	EXPRESSION TAG	UNP P27505
B	253	GLU	-	EXPRESSION TAG	UNP P27505
B	254	HIS	-	EXPRESSION TAG	UNP P27505
B	255	HIS	-	EXPRESSION TAG	UNP P27505
B	256	HIS	-	EXPRESSION TAG	UNP P27505
B	257	HIS	-	EXPRESSION TAG	UNP P27505
B	258	HIS	-	EXPRESSION TAG	UNP P27505
B	259	HIS	-	EXPRESSION TAG	UNP P27505

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	78	Total	O	0	0
			78	78		

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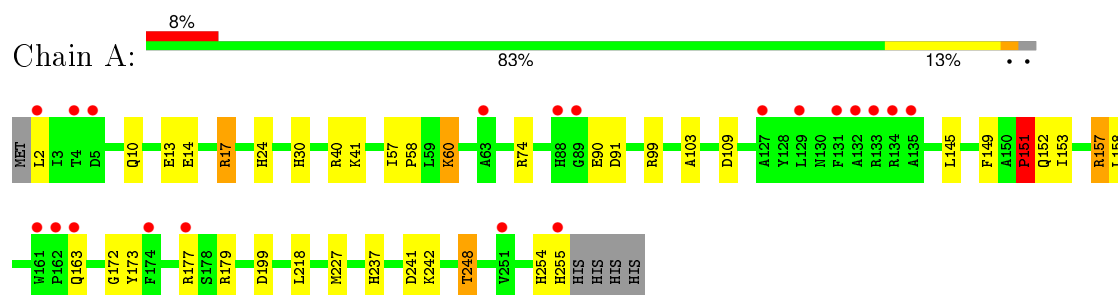
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	52	Total	O	0	0
			52	52		

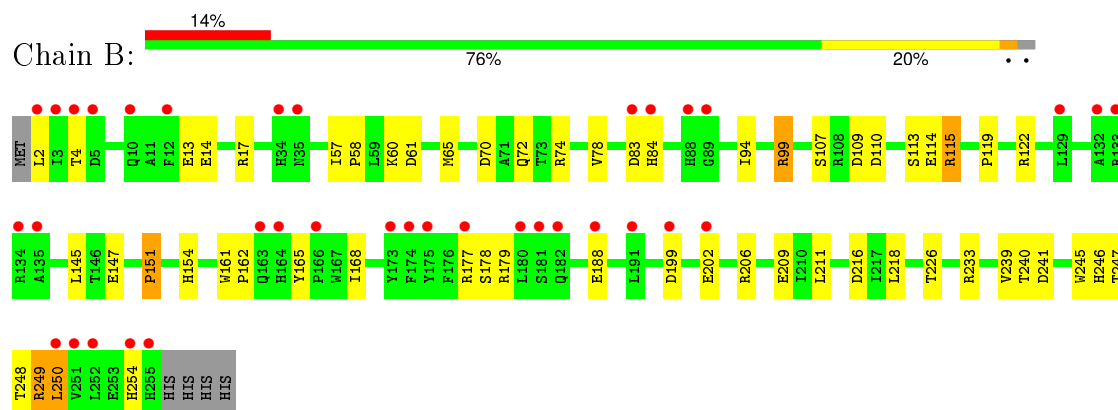
3 Residue-property plots

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: Coenzyme PQQ synthesis protein C



• Molecule 1: Coenzyme PQQ synthesis protein C



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	74.15Å 118.13Å 68.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.01 – 2.10 44.83 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (69.01-2.10) 98.9 (44.83-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.195 , 0.230 0.208 , 0.204	Depositor DCC
R_{free} test set	1784 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 35745 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4284	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% 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, 0.375 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	0.91	0/2137	1.04	12/2901 (0.4%)
1	B	0.81	0/2137	1.02	15/2901 (0.5%)
All	All	0.86	0/4274	1.03	27/5802 (0.5%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	PRO	CA-N-CD	-17.80	86.58	111.50
1	B	162	PRO	O-C-N	13.17	143.77	122.70
1	B	151	PRO	CA-N-CD	-10.97	96.14	111.50
1	B	162	PRO	C-N-CA	-10.81	94.67	121.70
1	A	17	ARG	NE-CZ-NH1	-9.80	115.40	120.30
1	B	162	PRO	CA-C-N	-9.24	96.86	117.20
1	A	17	ARG	NE-CZ-NH2	7.37	123.98	120.30
1	B	249	ARG	NE-CZ-NH2	-7.14	116.73	120.30
1	A	109	ASP	CB-CG-OD2	7.02	124.62	118.30
1	A	241	ASP	CB-CG-OD2	6.45	124.11	118.30
1	B	249	ARG	NE-CZ-NH1	6.31	123.46	120.30
1	B	216	ASP	CB-CG-OD1	6.31	123.98	118.30
1	A	99	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	A	91	ASP	CB-CG-OD2	6.14	123.83	118.30
1	B	109	ASP	CB-CG-OD2	5.99	123.69	118.30
1	A	248	THR	OG1-CB-CG2	-5.78	96.72	110.00
1	B	241	ASP	CB-CG-OD2	5.74	123.46	118.30
1	A	199	ASP	CB-CG-OD2	5.71	123.44	118.30
1	B	233	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	B	199	ASP	CB-CG-OD2	5.60	123.34	118.30
1	B	99	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	74	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	A	99	ARG	NE-CZ-NH1	5.51	123.05	120.30
1	A	157	ARG	CB-CA-C	5.47	121.34	110.40
1	B	70	ASP	CB-CG-OD2	5.27	123.05	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B	233	ARG	NE-CZ-NH1	5.17	122.89	120.30

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	2077	0	1996	27	5
1	B	2077	0	1996	34	0
2	A	78	0	0	8	0
2	B	52	0	0	6	0
All	All	4284	0	3992	53	5

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 7.

All (53) 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:72:GLN:NE2	2:B:299:HOH:O	1.64	1.22
1:A:30:HIS:HD2	2:A:317:HOH:O	1.53	0.89
1:B:254:HIS:CE1	2:B:293:HOH:O	2.26	0.88
1:B:74:ARG:O	1:B:78:VAL:HG23	1.76	0.85
1:B:84:HIS:HB2	2:B:302:HOH:O	1.83	0.79
1:B:13:GLU:OE1	1:B:17:ARG:NH1	2.16	0.77
1:B:147:GLU:OE1	2:B:307:HOH:O	2.04	0.73
1:B:145:LEU:HD12	1:B:145:LEU:C	2.08	0.72
1:A:13:GLU:OE1	1:A:17:ARG:NH1	2.23	0.71
1:A:40:ARG:HD3	2:A:316:HOH:O	1.91	0.70
1:B:65:MET:HE1	1:B:78:VAL:HG22	1.74	0.68
1:B:254:HIS:NE2	2:B:293:HOH:O	2.25	0.67
1:A:227:MET:CE	1:B:226:THR:HG21	2.25	0.66
1:A:248:THR:HG21	2:A:322:HOH:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:247:THR:O	1:B:247:THR:HG22	1.97	0.64
1:A:227:MET:HE3	1:B:226:THR:CG2	2.27	0.64
1:A:10:GLN:NE2	1:A:14:GLU:OE1	2.31	0.64
1:B:65:MET:CE	1:B:78:VAL:HG22	2.28	0.62
1:A:254:HIS:HE1	2:A:320:HOH:O	1.84	0.61
1:B:83:ASP:OD1	2:B:304:HOH:O	2.17	0.59
1:B:84:HIS:CE1	1:B:94:ILE:HB	2.38	0.58
1:A:227:MET:CE	1:B:226:THR:CG2	2.82	0.58
1:B:115:ARG:HA	1:B:247:THR:HG23	1.84	0.58
1:A:30:HIS:CD2	2:A:317:HOH:O	2.40	0.57
1:A:14:GLU:OE1	2:A:299:HOH:O	2.18	0.56
1:A:254:HIS:CE1	2:A:320:HOH:O	2.59	0.55
1:A:227:MET:HE3	1:B:226:THR:HG21	1.87	0.55
1:A:60:LYS:HD2	1:A:60:LYS:C	2.28	0.54
1:B:115:ARG:HA	1:B:247:THR:CG2	2.38	0.54
1:B:165:TYR:HB2	1:B:168:ILE:HD12	1.90	0.53
1:A:248:THR:HG23	1:B:209:GLU:OE2	2.09	0.52
1:B:202:GLU:H	1:B:202:GLU:CD	2.13	0.52
1:A:227:MET:HE3	1:B:226:THR:HG22	1.91	0.52
1:B:119:PRO:HG3	1:B:245:TRP:HB2	1.93	0.51
1:B:113:SER:O	1:B:114:GLU:HB2	2.12	0.49
1:B:114:GLU:OE2	1:B:249:ARG:HD2	2.13	0.49
1:A:254:HIS:HD2	1:A:255:HIS:HD2	1.61	0.49
1:A:145:LEU:C	1:A:145:LEU:HD12	2.33	0.49
1:B:57:ILE:N	1:B:58:PRO:HD2	2.29	0.48
1:B:145:LEU:HD12	1:B:145:LEU:O	2.13	0.47
1:A:173:TYR:CZ	1:A:177:ARG:HD2	2.50	0.47
1:A:149:PHE:O	1:A:151:PRO:HD2	2.16	0.45
1:A:237:HIS:HE1	2:A:265:HOH:O	1.98	0.45
1:A:57:ILE:N	1:A:58:PRO:CD	2.81	0.43
1:B:248:THR:HB	1:B:250:LEU:HD13	1.99	0.43
1:A:57:ILE:HB	1:A:58:PRO:HD3	1.99	0.43
1:A:227:MET:HE1	1:B:226:THR:HG21	2.01	0.43
1:B:74:ARG:O	1:B:78:VAL:CG2	2.57	0.42
1:A:254:HIS:CE1	1:B:206:ARG:HD3	2.55	0.42
1:B:107:SER:O	1:B:110:ASP:HB2	2.20	0.41
1:A:103:ALA:HB2	1:A:172:GLY:HA3	2.03	0.41
1:B:122:ARG:HD2	1:B:246:HIS:CE1	2.57	0.40
1:A:41:LYS:HZ3	1:A:41:LYS:HG3	1.79	0.40

All (5) 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)
1:A:157:ARG:CZ	1:A:242:LYS:NZ[4_555]	1.06	1.14
1:A:157:ARG:NH2	1:A:242:LYS:NZ[4_555]	1.25	0.95
1:A:157:ARG:NE	1:A:242:LYS:NZ[4_555]	1.78	0.42
1:A:157:ARG:NH1	1:A:242:LYS:NZ[4_555]	1.99	0.21
1:A:157:ARG:NH2	1:A:242:LYS:CE[4_555]	2.12	0.08

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	252/259 (97%)	244 (97%)	5 (2%)	3 (1%)	16	10
1	B	252/259 (97%)	243 (96%)	7 (3%)	2 (1%)	24	17
All	All	504/518 (97%)	487 (97%)	12 (2%)	5 (1%)	19	13

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	A	158	LEU
1	B	151	PRO
1	A	151	PRO
1	B	161	TRP

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	213/218 (98%)	205 (96%)	8 (4%)	40	40
1	B	213/218 (98%)	197 (92%)	16 (8%)	17	13
All	All	426/436 (98%)	402 (94%)	24 (6%)	26	22

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	24	HIS
1	A	60	LYS
1	A	90	GLU
1	A	153	ILE
1	A	163	GLN
1	A	179	ARG
1	A	218	LEU
1	B	2	LEU
1	B	4	THR
1	B	14	GLU
1	B	60	LYS
1	B	99	ARG
1	B	115	ARG
1	B	154	HIS
1	B	177	ARG
1	B	178	SER
1	B	179	ARG
1	B	188	GLU
1	B	211	LEU
1	B	218	LEU
1	B	239	VAL
1	B	240	THR
1	B	250	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	237	HIS
1	A	254	HIS
1	A	255	HIS
1	B	182	GLN
1	B	255	HIS

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	245/259 (94%)	0.44	20 (8%) 14 20	18, 30, 60, 81	4 (1%)
1	B	242/259 (93%)	0.73	36 (14%) 3 5	21, 39, 67, 87	5 (2%)
All	All	487/518 (94%)	0.59	56 (11%) 6 9	18, 34, 63, 87	9 (1%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	GLN	6.7
1	A	88	HIS	5.0
1	B	89	GLY	3.7
1	B	174	PHE	3.6
1	B	5	ASP	3.5
1	B	2	LEU	3.5
1	B	3	ILE	3.3
1	A	89	GLY	3.3
1	B	4	THR	3.2
1	A	174	PHE	3.2
1	B	129	LEU	3.1
1	B	164	HIS	3.0
1	B	188	GLU	3.0
1	B	35	ASN	3.0
1	B	251	VAL	3.0
1	A	161	TRP	3.0
1	B	34	HIS	3.0
1	A	5	ASP	2.9
1	A	163	GLN	2.9
1	B	88	HIS	2.8
1	A	251	VAL	2.8
1	A	4	THR	2.8
1	A	133	ARG	2.8
1	A	132	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	182	GLN	2.7
1	B	181	SER	2.7
1	B	252	LEU	2.7
1	B	255	HIS	2.6
1	A	63	ALA	2.6
1	B	177	ARG	2.6
1	A	135	ALA	2.5
1	B	202	GLU	2.5
1	A	162	PRO	2.5
1	B	180	LEU	2.4
1	B	83	ASP	2.4
1	B	191	LEU	2.4
1	B	10	GLN	2.3
1	B	175	TYR	2.3
1	B	166	PRO	2.3
1	A	134	ARG	2.3
1	B	12	PHE	2.3
1	B	133	ARG	2.3
1	B	132	ALA	2.3
1	B	250	LEU	2.2
1	A	127	ALA	2.2
1	B	134	ARG	2.2
1	A	2	LEU	2.2
1	A	255	HIS	2.2
1	A	131	PHE	2.1
1	B	135	ALA	2.1
1	A	177	ARG	2.1
1	B	199	ASP	2.1
1	A	129	LEU	2.0
1	B	84	HIS	2.0
1	B	254	HIS	2.0
1	B	173	TYR	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.