



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:37 AM UTC

PDB ID : 2PUS / pdb_00002pus
Title : Unprecedented activation mechanism of a non-canonical RNA-dependent RNA polymerase
Authors : Garriga, D.; Navarro, A.; Querol-Audi, J.; Abaitua, F.; Rodriguez, J.F.; Verdaguier, N.
Deposited on : 2007-05-09
Resolution : 2.40 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

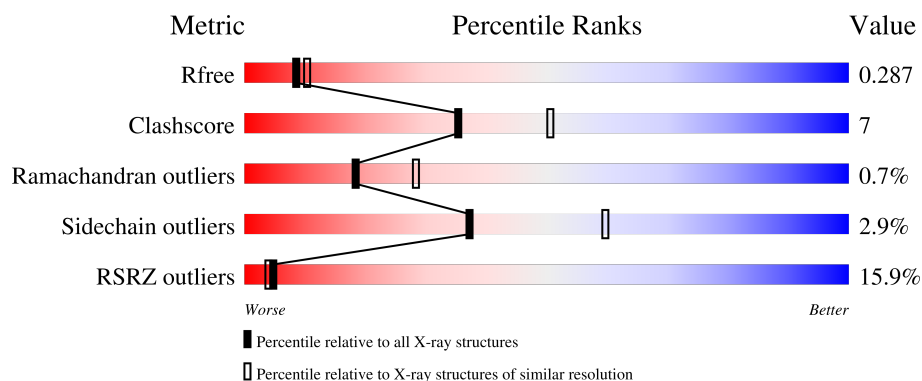
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of 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	852	14% 75% 13% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6185 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 IBDV VP1 RNA-dependant RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	765	Total	C	N	O	S	0	0	0
			5917	3786	1008	1101	22			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	268	Total	O	0	0
			268	268		

- Molecule 1: IBDV VP1 RNA-dependant RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	123.17Å 123.17Å 362.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.89 – 2.40 19.89 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.4 (19.89-2.40) 95.2 (19.89-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.41Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.234 , 0.263 (Not available) , 0.287	Depositor DCC
R_{free} test set	3094 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.0	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	0.91	EDS
Total number of atoms	6185	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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	0.45	1/6055 (0.0%)	1.01	32/8233 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	767	ALA	N-CA	-8.92	1.29	1.46

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	607	SER	CB-CA-C	-18.60	79.70	110.77
1	A	567	GLU	N-CA-C	18.24	133.63	110.65
1	A	607	SER	N-CA-CB	-17.43	82.06	109.94
1	A	604	GLU	CB-CA-C	15.34	134.16	110.08
1	A	606	LYS	CB-CA-C	-15.23	80.12	110.42
1	A	603	VAL	N-CA-C	-14.54	79.11	109.34
1	A	605	ASN	N-CA-C	-13.98	88.19	108.60
1	A	608	LEU	N-CA-C	10.38	127.99	113.56
1	A	769	TRP	N-CA-C	-10.24	90.78	108.08
1	A	567	GLU	CB-CA-C	-9.77	98.36	111.74
1	A	604	GLU	N-CA-CB	-9.42	93.95	110.34
1	A	468	SER	N-CA-C	-8.63	97.12	109.29
1	A	568	LEU	CA-C-N	-8.24	110.89	122.34
1	A	568	LEU	C-N-CA	-8.24	110.89	122.34
1	A	767	ALA	N-CA-CB	7.88	122.22	110.40
1	A	634	TYR	CA-C-N	7.21	126.74	119.24
1	A	634	TYR	C-N-CA	7.21	126.74	119.24
1	A	770	PHE	N-CA-CB	7.00	122.33	110.49
1	A	762	PRO	N-CA-CB	6.93	110.62	103.00
1	A	469	SER	N-CA-CB	-6.89	100.33	111.22
1	A	468	SER	CB-CA-C	-6.64	106.10	114.40
1	A	609	LYS	N-CA-C	-6.14	102.38	110.43
1	A	605	ASN	N-CA-CB	-5.96	102.28	111.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	608	LEU	N-CA-CB	-5.92	103.49	113.15
1	A	469	SER	N-CA-C	5.78	117.39	109.18
1	A	568	LEU	N-CA-C	5.73	119.37	112.38
1	A	771	GLU	N-CA-C	-5.66	105.10	112.23
1	A	473	MET	CB-CA-C	-5.60	108.50	115.89
1	A	145	ASN	N-CA-C	5.53	117.31	108.41
1	A	604	GLU	N-CA-C	5.39	120.10	112.93
1	A	605	ASN	CB-CA-C	-5.25	100.88	111.17
1	A	401	ALA	CB-CA-C	-5.21	110.58	116.63

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	5917	0	5868	87	0
2	A	268	0	0	6	0
All	All	6185	0	5868	87	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 7.

All (87) 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:138:PHE:CE1	1:A:144:ALA:HB1	1.80	1.16
1:A:138:PHE:CZ	1:A:144:ALA:HB1	1.95	1.01
1:A:138:PHE:CZ	1:A:144:ALA:CB	2.55	0.89
1:A:544:LEU:HD21	1:A:566:VAL:HG23	1.62	0.81
1:A:609:LYS:CB	1:A:614:ILE:HG13	2.10	0.80
1:A:401:ALA:H	1:A:494:HIS:HD2	1.34	0.75
1:A:459:ASN:O	1:A:797:THR:HG21	1.86	0.74
1:A:145:ASN:ND2	1:A:146:GLU:OE2	2.21	0.73
1:A:576:THR:HG22	1:A:585:VAL:HG23	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:576:THR:CG2	1:A:585:VAL:HG23	2.22	0.68
1:A:145:ASN:O	1:A:147:GLY:N	2.27	0.68
1:A:364:LEU:HD21	1:A:385:ILE:HD12	1.77	0.67
1:A:144:ALA:HB3	2:A:988:HOH:O	1.94	0.66
1:A:412:TRP:CE2	1:A:568:LEU:HB3	2.30	0.66
1:A:347:MET:HA	1:A:350:MET:HE3	1.77	0.66
1:A:769:TRP:O	1:A:771:GLU:N	2.28	0.66
1:A:553:LEU:HD13	1:A:585:VAL:HG11	1.77	0.65
1:A:401:ALA:H	1:A:494:HIS:CD2	2.14	0.64
1:A:768:ASP:O	2:A:931:HOH:O	2.15	0.63
1:A:144:ALA:CB	2:A:988:HOH:O	2.45	0.63
1:A:146:GLU:OE2	1:A:146:GLU:N	2.31	0.62
1:A:144:ALA:N	2:A:988:HOH:O	2.32	0.62
1:A:229:PRO:HG3	1:A:350:MET:HE1	1.81	0.61
1:A:425:THR:H	1:A:428:HIS:HD2	1.49	0.61
1:A:412:TRP:NE1	1:A:568:LEU:HB3	2.16	0.60
1:A:65:ARG:H	1:A:476:GLN:HE22	1.50	0.60
1:A:610:SER:HB3	1:A:613:GLY:H	1.66	0.59
1:A:600:PRO:HB3	1:A:622:ARG:HD2	1.85	0.59
1:A:145:ASN:O	1:A:146:GLU:C	2.45	0.59
1:A:138:PHE:HB2	1:A:636:LEU:HD11	1.85	0.57
1:A:200:GLU:HB2	1:A:769:TRP:NE1	2.21	0.55
1:A:421:GLU:HG2	1:A:489:THR:HG21	1.88	0.55
1:A:175:ARG:HE	1:A:179:MET:HE3	1.72	0.54
1:A:462:PRO:HB2	1:A:794:LEU:HD21	1.91	0.53
1:A:136:TYR:O	1:A:140:GLN:HG2	2.09	0.52
1:A:190:LYS:HD3	1:A:195:LEU:HD21	1.91	0.52
1:A:472:ILE:HG23	1:A:472:ILE:O	2.09	0.52
1:A:427:GLN:HA	1:A:430:GLN:HG2	1.92	0.51
1:A:41:GLU:HG3	1:A:118:LYS:HD2	1.92	0.51
1:A:145:ASN:C	1:A:147:GLY:N	2.69	0.50
1:A:99:LEU:HB3	1:A:101:ILE:HD13	1.93	0.50
1:A:145:ASN:O	1:A:148:LEU:N	2.44	0.50
1:A:768:ASP:O	1:A:768:ASP:CG	2.54	0.50
1:A:200:GLU:HG2	1:A:769:TRP:CD1	2.46	0.50
1:A:769:TRP:HE3	1:A:770:PHE:H	1.59	0.49
1:A:209:THR:O	1:A:371:SER:HB2	2.14	0.48
1:A:576:THR:HG23	1:A:585:VAL:HG23	1.94	0.48
1:A:346:LEU:HG	1:A:350:MET:HE2	1.94	0.48
1:A:609:LYS:C	1:A:611:LYS:N	2.68	0.48
1:A:706:ARG:HH12	1:A:728:GLU:HB3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:GLU:CB	1:A:769:TRP:NE1	2.77	0.48
1:A:385:ILE:HG21	1:A:570:LEU:HD22	1.95	0.47
1:A:314:SER:O	1:A:468:SER:HB2	2.14	0.47
1:A:472:ILE:O	1:A:473:MET:HB2	2.15	0.47
1:A:692:GLU:HA	1:A:695:LYS:HD2	1.95	0.47
1:A:200:GLU:HB2	1:A:769:TRP:HE1	1.79	0.47
1:A:588:LEU:HD22	1:A:629:VAL:CG2	2.45	0.46
1:A:133:GLN:HE21	1:A:643:ASN:HD22	1.63	0.45
1:A:576:THR:HG23	1:A:585:VAL:CG2	2.46	0.45
1:A:512:PRO:HA	1:A:517:PHE:CG	2.52	0.45
1:A:698:PRO:HA	1:A:699:PRO:HD3	1.91	0.45
1:A:44:LEU:HG	1:A:170:MET:SD	2.57	0.45
1:A:347:MET:HA	1:A:350:MET:CE	2.44	0.44
1:A:425:THR:H	1:A:428:HIS:CD2	2.31	0.44
1:A:716:VAL:O	1:A:720:LEU:HB2	2.17	0.44
1:A:170:MET:HG3	1:A:331:LEU:O	2.18	0.44
1:A:568:LEU:O	1:A:569:ASP:C	2.58	0.43
1:A:789:VAL:O	1:A:790:ALA:HB3	2.18	0.43
1:A:588:LEU:O	1:A:589:ASP:C	2.61	0.43
1:A:568:LEU:H	1:A:568:LEU:HG	1.38	0.43
1:A:609:LYS:O	1:A:611:LYS:N	2.52	0.43
1:A:382:LEU:HD13	1:A:586:PRO:HA	2.01	0.43
1:A:231:ARG:HH12	1:A:283:ARG:HH21	1.67	0.42
1:A:599:TYR:HA	1:A:600:PRO:HD2	1.93	0.42
1:A:695:LYS:HA	1:A:696:PRO:HD3	1.94	0.42
1:A:609:LYS:O	1:A:610:SER:C	2.63	0.41
1:A:146:GLU:HG2	2:A:1081:HOH:O	2.20	0.41
1:A:421:GLU:HB3	1:A:482:GLN:O	2.20	0.41
1:A:518:LYS:O	1:A:521:GLU:HG2	2.20	0.41
1:A:701:PRO:HA	1:A:702:PRO:HD3	1.97	0.41
1:A:375:PHE:CE1	1:A:385:ILE:HD13	2.55	0.41
1:A:446:ASP:HA	1:A:447:PRO:HD3	1.90	0.41
1:A:41:GLU:CG	1:A:118:LYS:HD2	2.50	0.41
1:A:57:ASN:O	1:A:180:LYS:NZ	2.53	0.41
1:A:467:ASP:OD2	2:A:879:HOH:O	2.22	0.40
1:A:667:SER:O	1:A:673:GLY:HA3	2.22	0.40
1:A:588:LEU:HD22	1:A:629:VAL:HG21	2.02	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	757/852 (89%)	721 (95%)	31 (4%)	5 (1%)	18 28

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	146	GLU
1	A	770	PHE
1	A	216	GLY
1	A	242	ASP
1	A	612	VAL

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	627/730 (86%)	609 (97%)	18 (3%)	37 60

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ARG
1	A	78	ILE
1	A	101	ILE
1	A	161	ASP
1	A	166	SER
1	A	233	LEU

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Mol	Chain	Res	Type
1	A	296	LYS
1	A	385	ILE
1	A	398	LEU
1	A	407	VAL
1	A	439	ARG
1	A	501	LEU
1	A	568	LEU
1	A	610	SER
1	A	757	LEU
1	A	768	ASP
1	A	776	LEU
1	A	794	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	GLN
1	A	145	ASN
1	A	172	GLN
1	A	174	ASN
1	A	204	GLN
1	A	280	GLN
1	A	299	ASN
1	A	336	ASN
1	A	376	ASN
1	A	428	HIS
1	A	430	GLN
1	A	476	GLN
1	A	482	GLN
1	A	494	HIS
1	A	503	GLN
1	A	561	GLN
1	A	727	ASN

5.3.3 RNA ⓘ

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 oligosaccharides 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	765/852 (89%)	1.00	122 (15%) 5 4	20, 38, 53, 59	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	ASP	11.2
1	A	216	GLY	10.9
1	A	144	ALA	10.4
1	A	607	SER	9.0
1	A	604	GLU	8.3
1	A	611	LYS	8.2
1	A	73	TYR	8.1
1	A	605	ASN	8.0
1	A	161	ASP	7.8
1	A	767	ALA	7.0
1	A	612	VAL	6.9
1	A	88	ILE	6.6
1	A	240	ASP	6.0
1	A	145	ASN	5.9
1	A	87	GLN	5.9
1	A	86	ARG	5.9
1	A	217	GLU	5.9
1	A	608	LEU	5.6
1	A	768	ASP	5.5
1	A	595	CYS	5.3
1	A	179	MET	5.3
1	A	603	VAL	5.2
1	A	236	THR	5.1
1	A	606	LYS	5.0
1	A	28	VAL	5.0
1	A	762	PRO	5.0
1	A	238	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	653	GLU	4.8
1	A	27	ASP	4.8
1	A	239	VAL	4.8
1	A	609	LYS	4.7
1	A	241	GLY	4.6
1	A	602	GLY	4.6
1	A	309	ASP	4.5
1	A	772	ARG	4.5
1	A	610	SER	4.5
1	A	76	ASP	4.3
1	A	769	TRP	4.2
1	A	790	ALA	4.2
1	A	77	GLN	4.0
1	A	531	GLU	3.9
1	A	789	VAL	3.9
1	A	181	GLU	3.9
1	A	243	PHE	3.9
1	A	174	ASN	3.8
1	A	668	GLU	3.8
1	A	235	LEU	3.7
1	A	146	GLU	3.7
1	A	486	ASN	3.7
1	A	485	GLY	3.6
1	A	244	GLU	3.5
1	A	468	SER	3.5
1	A	101	ILE	3.5
1	A	803	ALA	3.4
1	A	143	GLU	3.4
1	A	804	VAL	3.3
1	A	665	GLU	3.2
1	A	771	GLU	3.1
1	A	565	THR	3.0
1	A	674	GLU	3.0
1	A	692	GLU	3.0
1	A	660	ASP	3.0
1	A	147	GLY	3.0
1	A	567	GLU	2.9
1	A	191	ASP	2.9
1	A	237	GLY	2.9
1	A	770	PHE	2.8
1	A	488	ALA	2.8
1	A	746	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	587	VAL	2.8
1	A	251	LYS	2.7
1	A	55	ARG	2.7
1	A	515	GLU	2.7
1	A	651	HIS	2.7
1	A	680	ASN	2.7
1	A	84	TRP	2.7
1	A	487	ALA	2.6
1	A	679	PHE	2.6
1	A	379	ARG	2.6
1	A	63	GLN	2.6
1	A	797	THR	2.6
1	A	85	MET	2.6
1	A	83	ALA	2.6
1	A	119	GLU	2.6
1	A	104	GLN	2.6
1	A	323	GLU	2.5
1	A	560	GLU	2.5
1	A	655	LYS	2.5
1	A	678	GLY	2.5
1	A	568	LEU	2.4
1	A	543	GLN	2.4
1	A	56	GLU	2.4
1	A	778	ASP	2.4
1	A	677	GLU	2.4
1	A	711	GLY	2.4
1	A	301	LYS	2.4
1	A	139	LEU	2.3
1	A	296	LYS	2.3
1	A	705	ASN	2.3
1	A	150	ASP	2.3
1	A	448	MET	2.3
1	A	78	ILE	2.3
1	A	522	ASP	2.3
1	A	222	TRP	2.2
1	A	335	ARG	2.2
1	A	35	LYS	2.2
1	A	81	ASP	2.2
1	A	712	GLY	2.2
1	A	446	ASP	2.2
1	A	726	ARG	2.2
1	A	29	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	467	ASP	2.2
1	A	661	GLU	2.2
1	A	566	VAL	2.1
1	A	616	GLN	2.1
1	A	695	LYS	2.1
1	A	585	VAL	2.1
1	A	591	GLU	2.1
1	A	613	GLY	2.0
1	A	658	PRO	2.0
1	A	32	LEU	2.0
1	A	442	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 oligosaccharides 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.