



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:36 AM UTC

PDB ID : 7NT8 / pdb_00007nt8
Title : Influenza virus H3N2 nucleoprotein - R416A mutant
Authors : Keown, J.R.; Knight, M.L.; Grimes, J.M.; Fodor, E.
Deposited on : 2021-03-09
Resolution : 2.22 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

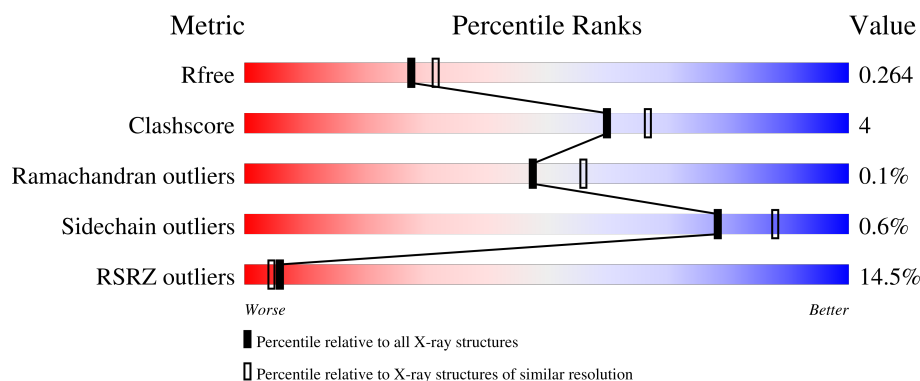
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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 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	729	10% 54% 6% 40%
1	B	729	7% 52% 6% 43%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13527 atoms, of which 6714 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 Glutathione S-transferase class-mu 26 kDa isozyme,Nucleoprotein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	439	Total	C	H	N	O	S	0	0	0
			6870	2144	3421	629	647	29			
1	B	419	Total	C	H	N	O	S	0	0	0
			6606	2056	3293	611	618	28			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	SER	-	linker	UNP P08515
A	-11	ASP	-	linker	UNP P08515
A	-10	LEU	-	linker	UNP P08515
A	-9	GLU	-	linker	UNP P08515
A	-8	VAL	-	linker	UNP P08515
A	-7	LEU	-	linker	UNP P08515
A	-6	PHE	-	linker	UNP P08515
A	-5	GLN	-	linker	UNP P08515
A	-4	GLY	-	linker	UNP P08515
A	-3	PRO	-	linker	UNP P08515
A	-2	LEU	-	linker	UNP P08515
A	-1	GLY	-	linker	UNP P08515
A	0	SER	-	linker	UNP P08515
B	-12	SER	-	linker	UNP P08515
B	-11	ASP	-	linker	UNP P08515
B	-10	LEU	-	linker	UNP P08515
B	-9	GLU	-	linker	UNP P08515
B	-8	VAL	-	linker	UNP P08515
B	-7	LEU	-	linker	UNP P08515
B	-6	PHE	-	linker	UNP P08515
B	-5	GLN	-	linker	UNP P08515
B	-4	GLY	-	linker	UNP P08515
B	-3	PRO	-	linker	UNP P08515
B	-2	LEU	-	linker	UNP P08515

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	linker	UNP P08515
B	0	SER	-	linker	UNP P08515

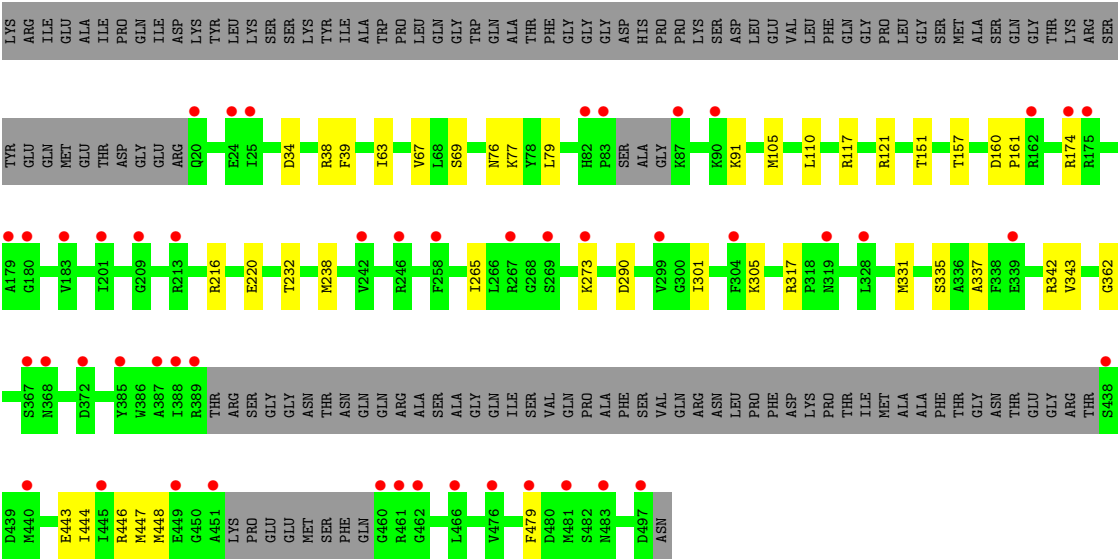
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	26	Total	O	0	0
			26	26		
2	B	25	Total	O	0	0
			25	25		

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

- Chain A:**
-
- The sequence logo displays the following amino acids from position 1 to 60: G450, A451, LYS, PRO, GLU, MET, SER, PHE, GLN, ARG, G462, V463, F464, E465, L466, S467, A471, A472, M473, Y476, F477, S478, F479, D480, H481, E484, Y487, H492, E495, Y496, D497, ASN.
- Conservation scale: 10%, 54%, 6%, 40%.

- Chain B:
-
- | Amino Acid | Frequency (%) |
|------------|---------------|
| ASP | 7% |
| PHE | 52% |
| LEU | 52% |
| SER | 52% |
| LYS | 52% |
| LEU | 52% |
| PRO | 52% |
| GLU | 52% |
| MET | 52% |
| LEU | 52% |
| ALA | 52% |
| ILE | 52% |
| LYS | 52% |
| MET | 52% |
| PHE | 52% |
| GLU | 52% |
| ASP | 52% |
| ARG | 52% |
| LEU | 52% |
| CYS | 52% |
| HIS | 52% |
| LYS | 52% |
| THR | 52% |
| TYR | 52% |
| LEU | 52% |
| ASN | 52% |
| GLY | 52% |
| ASP | 52% |
| HIS | 52% |
| VAL | 52% |
| THR | 52% |
| HIS | 52% |
| PRO | 52% |
| ASP | 52% |
| PHE | 52% |
| MET | 52% |
| LEU | 52% |
| TYR | 52% |
| ASP | 52% |
| VAL | 52% |
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| LEU | 52% |
| TYR | 52% |
| MET | 52% |
| ASP | 52% |
| VAL | 52% |
| VAL | 52% |
| LEU | 52% |
| TYR | 52% |
| MET | 52% |
| CYS | 52% |
| LEU | 52% |
| ASP | 52% |
| ALA | 52% |
| LYS | 52% |
| PHE | 52% |
| PRO | 52% |
| ASP | 52% |
| GLY | 52% |
| THR | 52% |
| VAL | 52% |
| LYS | 52% |
| VAL | 52% |
| GLY | 52% |
| ILE | 52% |
| ARG | 52% |
| ILE | 52% |
| ASP | 52% |
| GLY | 52% |
| GLU | 52% |
| LEU | 52% |
| ARG | 52% |
| TRP | 52% |
| LYS | 52% |
| ASP | 52% |
| ARG | 52% |
| ASN | 52% |
| LYS | 52% |
| PHE | 52% |
| GLU | 52% |
| LEU | 52% |
| GLY | 52% |
| LEU | 52% |
| PHE | 52% |
| PRO | 52% |
| ASN | 52% |
| PRO | 52% |
| TYR | 52% |
| TYR | 52% |
| ILE | 52% |
| ASP | 52% |



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.78Å 63.38Å 105.95Å 90.00° 98.32° 90.00°	Depositor
Resolution (Å)	86.85 – 2.22 86.85 – 2.22	Depositor EDS
% Data completeness (in resolution range)	66.6 (86.85-2.22) 62.6 (86.85-2.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.18rc2_3794	Depositor
R, R_{free}	0.212 , 0.265 0.213 , 0.264	Depositor DCC
R_{free} test set	1830 reflections (3.20%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13527	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.16	0/3508	0.37	0/4714
1	B	0.15	0/3367	0.31	0/4518
All	All	0.16	0/6875	0.34	0/9232

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 [i](#)

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	3449	3421	3421	28	0
1	B	3313	3293	3293	32	0
2	A	26	0	0	0	0
2	B	25	0	0	2	0
All	All	6813	6714	6714	58	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 4.

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:307:LEU:O	1:A:310:SER:OG	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:ARG:NH2	1:B:362:GLY:O	2.27	0.67
1:A:449:GLU:OE2	1:A:449:GLU:HA	1.95	0.67
1:B:77:LYS:NZ	2:B:501:HOH:O	2.29	0.65
1:B:343:VAL:HG22	1:B:479:PHE:CZ	2.38	0.58
1:B:34:ASP:OD2	1:B:38:ARG:NH2	2.36	0.58
1:B:91:LYS:HB3	1:B:110:LEU:HD22	1.85	0.58
1:B:335:SER:O	1:B:335:SER:OG	2.18	0.58
1:B:174:ARG:HG3	1:B:174:ARG:HH11	1.70	0.56
1:A:449:GLU:OE2	1:A:449:GLU:CA	2.52	0.56
1:A:426:MET:O	1:A:430:THR:HG23	2.04	0.56
1:B:69:SER:HA	1:B:79:LEU:HD22	1.89	0.54
1:B:39:PHE:CZ	1:B:67:VAL:HG22	2.43	0.54
1:B:216:ARG:HG3	1:B:216:ARG:HH11	1.72	0.54
1:B:157:THR:HG22	1:B:157:THR:O	2.08	0.53
1:A:73:GLU:OE2	1:B:117:ARG:NH1	2.41	0.53
1:A:196:MET:HE1	1:A:219:TYR:HA	1.90	0.53
1:A:348:ARG:NH2	1:A:380:GLU:O	2.42	0.52
1:B:273:LYS:NZ	2:B:502:HOH:O	2.42	0.52
1:A:157:THR:HG21	1:A:191:MET:HG3	1.91	0.51
1:B:174:ARG:HG3	1:B:174:ARG:NH1	2.26	0.51
1:A:255:ASP:OD2	1:A:441:ARG:NH1	2.44	0.50
1:A:317:ARG:NH2	1:A:362:GLY:O	2.45	0.50
1:B:238:MET:CE	1:B:444:ILE:HD12	2.41	0.50
1:B:238:MET:HE1	1:B:444:ILE:HD12	1.95	0.49
1:A:67:VAL:HG11	1:A:136:MET:HE1	1.95	0.49
1:A:341:LEU:HD11	1:A:487:TYR:HA	1.95	0.48
1:B:69:SER:CA	1:B:79:LEU:HD22	2.43	0.47
1:A:72:ASP:O	1:A:75:ARG:HD3	2.14	0.47
1:B:151:THR:HG23	1:B:161:PRO:HB3	1.95	0.47
1:A:216:ARG:NH2	1:A:243:ARG:O	2.48	0.47
1:B:216:ARG:NH1	1:B:220:GLU:OE2	2.48	0.47
1:A:157:THR:O	1:A:157:THR:HG22	2.15	0.46
1:A:252:GLU:OE1	1:A:252:GLU:N	2.46	0.46
1:B:63:ILE:O	1:B:67:VAL:HG23	2.15	0.46
1:B:265:ILE:HD12	1:B:448:MET:HE3	1.98	0.46
1:A:47:LEU:O	1:A:98:LYS:NZ	2.44	0.45
1:A:21:ASN:N	1:A:24:GLU:OE1	2.50	0.45
1:B:160:ASP:OD2	1:B:161:PRO:HD2	2.18	0.44
1:A:210:GLU:O	1:A:210:GLU:HG3	2.17	0.44
1:B:76:ASN:HA	1:B:79:LEU:O	2.18	0.44
1:B:105:MET:HA	1:B:105:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ARG:HD2	1:B:121:ARG:HD3	2.01	0.43
1:B:443:GLU:OE2	1:B:446:ARG:NH2	2.50	0.43
1:B:301:ILE:HG12	1:B:305:LYS:HG3	2.00	0.43
1:A:384:ARG:HD2	1:A:384:ARG:N	2.35	0.42
1:B:290:ASP:OD1	1:B:290:ASP:C	2.62	0.42
1:A:196:MET:HE2	1:A:222:MET:CE	2.49	0.42
1:A:208:ARG:O	1:A:211:ASN:OD1	2.37	0.42
1:A:372:ASP:OD1	1:A:372:ASP:N	2.53	0.42
1:B:273:LYS:HE3	1:B:273:LYS:HB3	1.79	0.42
1:A:418:LEU:HD23	1:A:481:MET:HE1	2.02	0.42
1:A:198:LYS:O	1:A:201:ILE:HG13	2.20	0.41
1:B:331:MET:CE	1:B:337:ALA:HA	2.50	0.41
1:B:216:ARG:HH11	1:B:216:ARG:CG	2.32	0.41
1:A:93:GLY:HA3	1:A:109:VAL:O	2.21	0.41
1:A:67:VAL:CG1	1:A:136:MET:HE1	2.51	0.41
1:B:232:THR:HB	1:B:447:MET:HE1	2.03	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	433/729 (59%)	420 (97%)	12 (3%)	1 (0%)	43	50
1	B	411/729 (56%)	400 (97%)	11 (3%)	0	100	100
All	All	844/1458 (58%)	820 (97%)	23 (3%)	1 (0%)	48	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	439	ASP

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	365/620 (59%)	362 (99%)	3 (1%)	73	84
1	B	351/620 (57%)	350 (100%)	1 (0%)	86	93
All	All	716/1240 (58%)	712 (99%)	4 (1%)	78	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	GLU
1	A	202	ASN
1	A	214	LYS
1	B	342	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	GLN
1	A	202	ASN
1	A	211	ASN
1	A	311	GLN
1	B	21	ASN
1	B	76	ASN
1	B	122	GLN
1	B	334	ASN

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 [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	439/729 (60%)	1.12	76 (17%) 4 3	37, 67, 108, 125	0
1	B	419/729 (57%)	0.88	48 (11%) 9 8	35, 60, 96, 116	0
All	All	858/1458 (58%)	1.00	124 (14%) 6 4	35, 64, 103, 125	0

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	83	PRO	5.0
1	A	85	ALA	4.8
1	B	179	ALA	4.3
1	A	479	PHE	4.3
1	B	451	ALA	4.1
1	A	451	ALA	4.1
1	A	82	HIS	4.0
1	B	82	HIS	4.0
1	B	461	ARG	4.0
1	A	431	GLY	3.9
1	A	477	PRO	3.7
1	A	388	ILE	3.6
1	A	86	GLY	3.6
1	B	481	MET	3.5
1	B	462	GLY	3.5
1	B	273	LYS	3.5
1	B	479	PHE	3.5
1	B	460	GLY	3.4
1	B	299	VAL	3.4
1	A	195	ARG	3.3
1	A	433	THR	3.2
1	A	462	GLY	3.1
1	A	83	PRO	3.1
1	A	440	MET	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	495	GLU	3.1
1	A	418	LEU	3.1
1	A	204	ARG	3.0
1	A	389	ARG	3.0
1	A	179	ALA	2.9
1	A	352	VAL	2.9
1	A	384	ARG	2.9
1	B	389	ARG	2.9
1	A	289	TYR	2.9
1	A	102	GLY	2.9
1	A	476	VAL	2.9
1	A	84	SER	2.8
1	B	476	VAL	2.8
1	A	344	LEU	2.8
1	A	368	ASN	2.8
1	A	206	PHE	2.8
1	A	270	VAL	2.8
1	B	242	VAL	2.8
1	B	368	ASN	2.7
1	A	450	GLY	2.7
1	A	100	VAL	2.7
1	B	497	ASP	2.7
1	B	466	LEU	2.7
1	A	471	ALA	2.7
1	A	210	GLU	2.7
1	B	388	ILE	2.7
1	A	466	LEU	2.7
1	A	387	ALA	2.6
1	A	439	ASP	2.6
1	A	449	GLU	2.6
1	A	152	ARG	2.6
1	B	269	SER	2.6
1	A	22	ALA	2.6
1	A	472	ALA	2.6
1	A	31	LYS	2.6
1	A	467	SER	2.6
1	A	178	ALA	2.6
1	A	434	GLU	2.5
1	B	319	ASN	2.5
1	A	307	LEU	2.5
1	A	346	PHE	2.5
1	A	213	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	162	ARG	2.5
1	A	105	MET	2.5
1	A	211	ASN	2.5
1	B	175	ARG	2.4
1	A	464	PHE	2.4
1	B	20	GLN	2.4
1	A	383	SER	2.4
1	B	87	LYS	2.4
1	A	47	LEU	2.4
1	A	437	THR	2.4
1	A	155	VAL	2.4
1	B	25	ILE	2.4
1	B	201	ILE	2.4
1	B	328	LEU	2.4
1	A	473	ASN	2.4
1	B	440	MET	2.3
1	B	183	VAL	2.3
1	B	90	LYS	2.3
1	A	435	GLY	2.3
1	A	438	SER	2.3
1	A	436	ARG	2.3
1	B	267	ARG	2.3
1	B	385	TYR	2.3
1	A	156	ARG	2.3
1	A	305	LYS	2.3
1	B	180	GLY	2.2
1	B	209	GLY	2.2
1	B	438	SER	2.2
1	B	304	PHE	2.2
1	B	483	ASN	2.2
1	A	209	GLY	2.2
1	A	201	ILE	2.2
1	A	299	VAL	2.2
1	B	449	GLU	2.2
1	A	207	TRP	2.2
1	B	213	ARG	2.2
1	A	101	ASP	2.2
1	A	202	ASN	2.1
1	A	492	ASN	2.1
1	A	246	ARG	2.1
1	A	23	THR	2.1
1	B	367	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	191	MET	2.1
1	A	24	GLU	2.1
1	A	432	ASN	2.1
1	B	246	ARG	2.1
1	A	81	GLU	2.1
1	B	24	GLU	2.1
1	B	372	ASP	2.1
1	B	445	ILE	2.1
1	A	463	VAL	2.1
1	B	387	ALA	2.0
1	A	328	LEU	2.0
1	A	304	PHE	2.0
1	B	258	PHE	2.0
1	A	484	GLU	2.0
1	B	339	GLU	2.0
1	B	174	ARG	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.