



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:12 AM UTC

PDB ID : 1C93 / pdb_00001c93
Title : Endo-Beta-N-Acetylglucosaminidase H, D130N/E132Q Double Mutant
Authors : Rao, V.; Cui, T.; Guan, C.; Van Roey, P.
Deposited on : 1999-07-30
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

<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

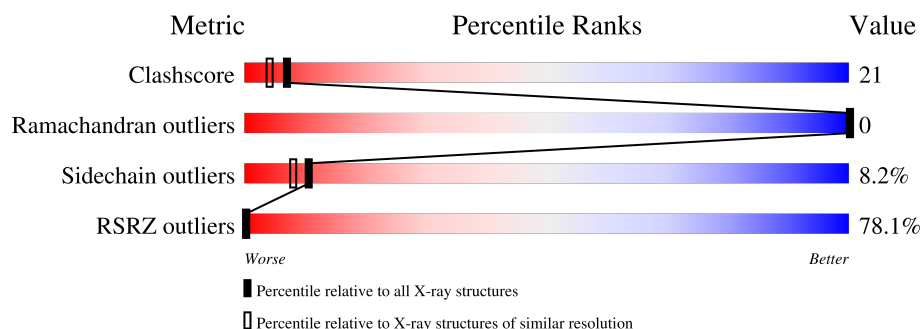
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 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	265	78% 70% 25% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2140 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 ENDO-BETA-N-ACETYLGLUCOSAMINIDASE H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			2016	1266	349	399	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	GLN	GLU	engineered mutation	UNP P04067
A	130	ASN	ASP	engineered mutation	UNP P04067

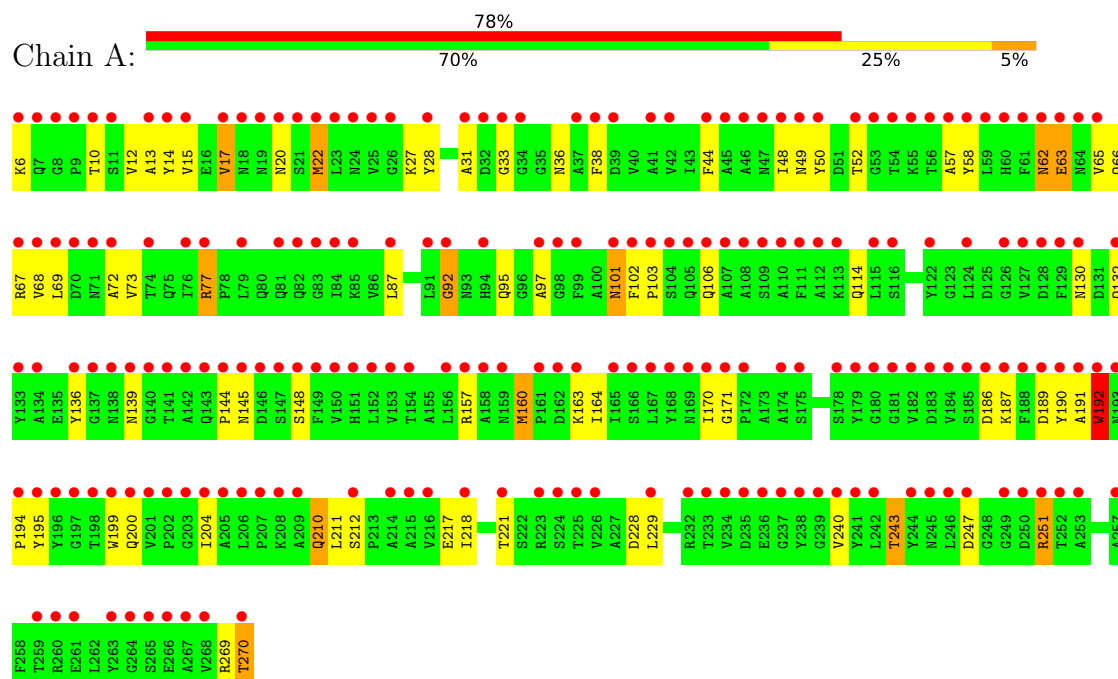
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	124	Total	O	0	0
			124	124		

3 Residue-property plots

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.

• Molecule 1: ENDO-BETA-N-ACETYLGLUCOSAMINIDASE H



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.30Å 55.50Å 46.70Å 90.00° 104.50° 90.00°	Depositor
Resolution (Å)	10.00 – 2.10 10.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.10) 95.0 (10.00-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.05 (at 2.10Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.200 , (Not available) 0.368 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	10.5	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 79.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.67	EDS
Total number of atoms	2140	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.95% 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	0.82	1/2058 (0.0%)	1.17	7/2803 (0.2%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	192	TRP	NE1-CE2	-5.28	1.31	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	171	GLY	CA-C-N	6.65	126.16	119.24
1	A	171	GLY	C-N-CA	6.65	126.16	119.24
1	A	170	ILE	N-CA-C	6.62	117.15	107.75
1	A	92	GLY	N-CA-C	-6.15	105.56	112.33
1	A	160	MET	CA-C-N	5.37	124.89	119.19
1	A	160	MET	C-N-CA	5.37	124.89	119.19
1	A	22	MET	N-CA-C	-5.09	105.73	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	77	ARG	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	2016	0	1935	83	1
2	A	124	0	0	4	2
All	All	2140	0	1935	83	2

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 21.

All (83) 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:72:ALA:HB1	1:A:77:ARG:CZ	1.90	1.01
1:A:17:VAL:HG21	1:A:65:VAL:HG22	1.47	0.97
1:A:72:ALA:HB1	1:A:77:ARG:NH2	1.83	0.93
1:A:73:VAL:HA	1:A:77:ARG:HD3	1.49	0.93
1:A:62:ASN:HD22	1:A:65:VAL:HG23	1.35	0.89
1:A:62:ASN:ND2	1:A:65:VAL:HG23	1.96	0.80
1:A:72:ALA:CB	1:A:77:ARG:NH1	2.49	0.76
1:A:17:VAL:HG13	1:A:22:MET:HE3	1.71	0.73
1:A:17:VAL:HG12	1:A:68:VAL:HG21	1.71	0.71
1:A:72:ALA:HB1	1:A:77:ARG:NH1	2.05	0.71
1:A:73:VAL:CA	1:A:77:ARG:HD3	2.21	0.70
1:A:72:ALA:CB	1:A:77:ARG:CZ	2.69	0.70
1:A:17:VAL:HG22	1:A:44:PHE:O	1.92	0.70
1:A:101:ASN:ND2	1:A:136:TYR:HD2	1.91	0.69
1:A:77:ARG:N	1:A:77:ARG:HD2	2.09	0.67
1:A:221:THR:HG22	2:A:388:HOH:O	1.94	0.66
1:A:77:ARG:HD2	1:A:77:ARG:H	1.61	0.65
1:A:72:ALA:O	1:A:77:ARG:HD2	1.97	0.64
1:A:101:ASN:ND2	1:A:136:TYR:CD2	2.67	0.62
1:A:12:VAL:O	1:A:243:THR:HB	2.01	0.61
1:A:52:THR:HG22	1:A:139:ASN:HB3	1.82	0.60
1:A:212:SER:HB2	1:A:240:VAL:HB	1.84	0.60
1:A:72:ALA:HB3	1:A:77:ARG:NH1	2.16	0.59
1:A:101:ASN:CG	1:A:136:TYR:HD2	2.10	0.59
1:A:72:ALA:O	1:A:77:ARG:CD	2.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:TYR:HA	1:A:114:GLN:HE22	1.68	0.58
1:A:72:ALA:C	1:A:77:ARG:HD3	2.29	0.57
1:A:62:ASN:ND2	1:A:65:VAL:H	2.02	0.57
1:A:191:ALA:HB3	1:A:211:LEU:CD2	2.35	0.57
1:A:15:VAL:HB	1:A:22:MET:SD	2.45	0.56
1:A:66:GLN:HG3	1:A:67:ARG:HH11	1.71	0.55
1:A:73:VAL:HA	1:A:77:ARG:CD	2.32	0.55
1:A:17:VAL:HG13	1:A:22:MET:CE	2.36	0.55
1:A:145:ASN:OD1	1:A:148:SER:HB2	2.06	0.54
1:A:218:ILE:CG2	1:A:251:ARG:HG2	2.39	0.52
1:A:73:VAL:O	1:A:77:ARG:HB2	2.09	0.52
1:A:218:ILE:HG12	1:A:243:THR:HG23	1.91	0.52
1:A:28:TYR:CE2	1:A:269:ARG:HB2	2.45	0.51
1:A:189:ASP:O	1:A:210:GLN:HB2	2.09	0.51
1:A:217:GLU:H	1:A:221:THR:CG2	2.24	0.51
1:A:50:TYR:H	1:A:95:GLN:NE2	2.09	0.50
1:A:194:PRO:HG2	1:A:195:TYR:CE1	2.46	0.50
1:A:87:LEU:HD21	1:A:164:ILE:CG2	2.41	0.50
1:A:48:ILE:O	1:A:48:ILE:HG23	2.11	0.49
1:A:157:ARG:NH1	1:A:163:LYS:O	2.39	0.49
1:A:31:ALA:C	1:A:33:GLY:H	2.20	0.48
1:A:63:GLU:O	1:A:67:ARG:HG2	2.13	0.48
1:A:190:TYR:HA	1:A:210:GLN:O	2.14	0.48
1:A:12:VAL:HG21	1:A:192:TRP:CZ3	2.49	0.48
1:A:73:VAL:HG23	2:A:293:HOH:O	2.13	0.48
1:A:73:VAL:N	1:A:77:ARG:HD3	2.27	0.48
1:A:17:VAL:CG2	1:A:65:VAL:HG22	2.34	0.48
1:A:48:ILE:HG22	1:A:92:GLY:HA2	1.96	0.47
1:A:199:TRP:HB2	1:A:229:LEU:CD2	2.45	0.47
1:A:17:VAL:CG1	1:A:22:MET:HE3	2.41	0.46
1:A:62:ASN:HD22	1:A:65:VAL:CG2	2.19	0.46
1:A:101:ASN:CG	1:A:136:TYR:CD2	2.91	0.45
1:A:14:TYR:HD1	1:A:44:PHE:HD1	1.63	0.45
1:A:15:VAL:HB	1:A:22:MET:CE	2.47	0.45
1:A:13:ALA:HB2	1:A:38:PHE:CD1	2.53	0.45
1:A:15:VAL:HB	1:A:22:MET:HE1	1.99	0.45
1:A:49:ASN:O	1:A:57:ALA:HA	2.17	0.44
1:A:160:MET:HB2	1:A:163:LYS:HB2	2.00	0.44
1:A:72:ALA:C	1:A:77:ARG:CD	2.91	0.43
1:A:27:LYS:O	1:A:269:ARG:HA	2.18	0.43
1:A:17:VAL:CG1	1:A:68:VAL:HG21	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:PHE:N	1:A:148:SER:OG	2.51	0.43
1:A:50:TYR:CD1	1:A:97:ALA:HB2	2.54	0.43
1:A:102:PHE:HA	1:A:103:PRO:HD3	1.86	0.43
1:A:157:ARG:NH2	1:A:187:LYS:O	2.48	0.42
1:A:57:ALA:HB2	1:A:97:ALA:HB1	2.01	0.42
1:A:36:ASN:HB3	2:A:275:HOH:O	2.18	0.42
1:A:221:THR:CG2	2:A:388:HOH:O	2.62	0.42
1:A:87:LEU:HD21	1:A:164:ILE:HG22	2.01	0.42
1:A:130:ASN:OD1	1:A:132:GLN:HG3	2.20	0.42
1:A:191:ALA:HB3	1:A:211:LEU:HD23	2.02	0.41
1:A:269:ARG:HG2	1:A:270:THR:N	2.34	0.41
1:A:217:GLU:H	1:A:221:THR:HG23	1.85	0.41
1:A:20:ASN:ND2	1:A:247:ASP:CB	2.84	0.41
1:A:87:LEU:HD21	1:A:164:ILE:HG21	2.03	0.41
1:A:218:ILE:CG1	1:A:243:THR:HG23	2.52	0.40
1:A:163:LYS:HA	1:A:163:LYS:HD2	1.87	0.40
1:A:192:TRP:HB3	1:A:212:SER:HB3	2.03	0.40

All (2) 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:228:ASP:OD1	2:A:353:HOH:O[2_748]	2.13	0.07
2:A:334:HOH:O	2:A:370:HOH:O[2_858]	2.16	0.04

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	263/265 (99%)	251 (95%)	12 (5%)	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	208/208 (100%)	191 (92%)	17 (8%)	10 8

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

Mol	Chain	Res	Type
1	A	6	LYS
1	A	10	THR
1	A	17	VAL
1	A	62	ASN
1	A	63	GLU
1	A	69	LEU
1	A	101	ASN
1	A	106	GLN
1	A	144	PRO
1	A	186	ASP
1	A	192	TRP
1	A	200	GLN
1	A	204	ILE
1	A	210	GLN
1	A	243	THR
1	A	251	ARG
1	A	270	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	20	ASN
1	A	36	ASN
1	A	49	ASN
1	A	60	HIS
1	A	66	GLN
1	A	71	ASN
1	A	82	GLN

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Mol	Chain	Res	Type
1	A	95	GLN
1	A	101	ASN
1	A	105	GLN
1	A	114	GLN
1	A	139	ASN
1	A	159	ASN
1	A	200	GLN
1	A	210	GLN

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 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	265/265 (100%)	2.94	207 (78%) 0 0	9, 16, 28, 55	0

All (207) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	34	GLY	7.8
1	A	97	ALA	7.5
1	A	203	GLY	7.4
1	A	77	ARG	7.3
1	A	205	ALA	7.0
1	A	252	THR	6.3
1	A	7	GLN	5.8
1	A	31	ALA	5.5
1	A	204	ILE	5.5
1	A	170	ILE	5.4
1	A	264	GLY	5.4
1	A	181	GLY	5.4
1	A	179	TYR	5.0
1	A	207	PRO	4.9
1	A	84	ILE	4.9
1	A	189	ASP	4.9
1	A	109	SER	4.8
1	A	257	ALA	4.7
1	A	103	PRO	4.7
1	A	148	SER	4.7
1	A	11	SER	4.6
1	A	178	SER	4.6
1	A	53	GLY	4.6
1	A	259	THR	4.5
1	A	249	GLY	4.5
1	A	62	ASN	4.5
1	A	200	GLN	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	215	ALA	4.5
1	A	182	VAL	4.4
1	A	209	ALA	4.4
1	A	74	THR	4.3
1	A	270	THR	4.3
1	A	162	ASP	4.3
1	A	58	TYR	4.2
1	A	33	GLY	4.2
1	A	101	ASN	4.2
1	A	149	PHE	4.1
1	A	18	ASN	4.1
1	A	187	LYS	4.1
1	A	13	ALA	4.1
1	A	106	GLN	4.1
1	A	6	LYS	4.0
1	A	79	LEU	4.0
1	A	195	TYR	4.0
1	A	141	THR	3.9
1	A	196	TYR	3.9
1	A	8	GLY	3.9
1	A	229	LEU	3.9
1	A	116	SER	3.9
1	A	161	PRO	3.9
1	A	55	LYS	3.8
1	A	199	TRP	3.8
1	A	169	ASN	3.8
1	A	59	LEU	3.8
1	A	91	LEU	3.7
1	A	185	SER	3.7
1	A	150	VAL	3.7
1	A	175	SER	3.7
1	A	46	ALA	3.7
1	A	190	TYR	3.7
1	A	44	PHE	3.6
1	A	32	ASP	3.6
1	A	39	ASP	3.6
1	A	138	ASN	3.6
1	A	147	SER	3.6
1	A	83	GLY	3.5
1	A	268	VAL	3.5
1	A	225	THR	3.5
1	A	253	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	206	LEU	3.5
1	A	212	SER	3.5
1	A	19	ASN	3.5
1	A	188	PHE	3.5
1	A	50	TYR	3.5
1	A	241	TYR	3.5
1	A	54	THR	3.5
1	A	192	TRP	3.4
1	A	238	TYR	3.4
1	A	167	LEU	3.4
1	A	49	ASN	3.4
1	A	134	ALA	3.4
1	A	250	ASP	3.4
1	A	20	ASN	3.3
1	A	159	ASN	3.3
1	A	136	TYR	3.3
1	A	146	ASP	3.3
1	A	171	GLY	3.3
1	A	265	SER	3.3
1	A	25	VAL	3.3
1	A	110	ALA	3.3
1	A	165	ILE	3.3
1	A	172	PRO	3.2
1	A	174	ALA	3.2
1	A	111	PHE	3.2
1	A	142	ALA	3.2
1	A	244	TYR	3.2
1	A	234	VAL	3.2
1	A	137	GLY	3.1
1	A	237	GLY	3.1
1	A	17	VAL	3.1
1	A	263	TYR	3.1
1	A	140	GLY	3.1
1	A	202	PRO	3.1
1	A	63	GLU	3.1
1	A	57	ALA	3.1
1	A	158	ALA	3.1
1	A	65	VAL	3.1
1	A	236	GLU	3.0
1	A	107	ALA	3.0
1	A	216	VAL	3.0
1	A	186	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	71	ASN	3.0
1	A	24	ASN	3.0
1	A	197	GLY	3.0
1	A	10	THR	3.0
1	A	38	PHE	3.0
1	A	223	ARG	2.9
1	A	47	ASN	2.9
1	A	105	GLN	2.9
1	A	67	ARG	2.9
1	A	232	ARG	2.9
1	A	60	HIS	2.9
1	A	208	LYS	2.8
1	A	72	ALA	2.8
1	A	180	GLY	2.8
1	A	266	GLU	2.8
1	A	48	ILE	2.8
1	A	28	TYR	2.8
1	A	133	TYR	2.8
1	A	42	VAL	2.8
1	A	201	VAL	2.8
1	A	21	SER	2.7
1	A	191	ALA	2.7
1	A	139	ASN	2.7
1	A	224	SER	2.7
1	A	92	GLY	2.7
1	A	239	GLY	2.7
1	A	41	ALA	2.7
1	A	9	PRO	2.7
1	A	240	VAL	2.7
1	A	235	ASP	2.7
1	A	115	LEU	2.7
1	A	221	THR	2.7
1	A	14	TYR	2.7
1	A	126	GLY	2.7
1	A	267	ALA	2.6
1	A	23	LEU	2.6
1	A	56	THR	2.6
1	A	102	PHE	2.6
1	A	184	VAL	2.6
1	A	163	LYS	2.5
1	A	245	ASN	2.5
1	A	144	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	129	PHE	2.5
1	A	68	VAL	2.5
1	A	104	SER	2.5
1	A	124	LEU	2.5
1	A	152	LEU	2.5
1	A	85	LYS	2.5
1	A	226	VAL	2.4
1	A	52	THR	2.4
1	A	69	LEU	2.4
1	A	94	HIS	2.4
1	A	251	ARG	2.4
1	A	130	ASN	2.4
1	A	132	GLN	2.4
1	A	194	PRO	2.4
1	A	156	LEU	2.4
1	A	218	ILE	2.4
1	A	45	ALA	2.4
1	A	193	ASN	2.4
1	A	198	THR	2.4
1	A	122	TYR	2.3
1	A	108	ALA	2.3
1	A	246	LEU	2.3
1	A	61	PHE	2.3
1	A	260	ARG	2.3
1	A	166	SER	2.3
1	A	143	GLN	2.3
1	A	247	ASP	2.3
1	A	99	PHE	2.3
1	A	15	VAL	2.3
1	A	183	ASP	2.3
1	A	151	HIS	2.2
1	A	22	MET	2.2
1	A	145	ASN	2.2
1	A	128	ASP	2.2
1	A	81	GLN	2.2
1	A	112	ALA	2.2
1	A	242	LEU	2.2
1	A	157	ARG	2.2
1	A	70	ASP	2.2
1	A	233	THR	2.2
1	A	26	GLY	2.1
1	A	98	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	87	LEU	2.1
1	A	76	ILE	2.1
1	A	153	VAL	2.1
1	A	82	GLN	2.1
1	A	214	ALA	2.1
1	A	261	GLU	2.1
1	A	64	ASN	2.1
1	A	168	TYR	2.1
1	A	37	ALA	2.1
1	A	113	LYS	2.0
1	A	127	VAL	2.0
1	A	154	THR	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.