



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 6X07 / pdb_00006x07
Title : Nic96 from *S. cerevisiae* bound by VHH-SAN12
Authors : Andersen, K.; Nordeen, S.A.; Schwartz, T.U.
Deposited on : 2020-05-15
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

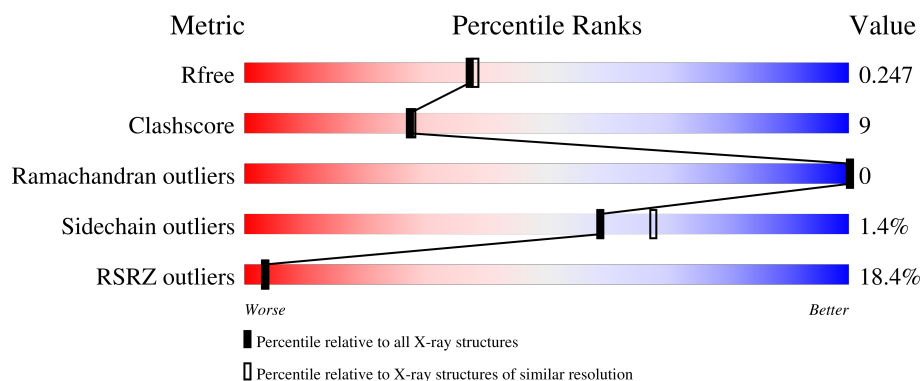
1 Overall quality at a glance

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))
R_{free}	180053	6658 (2.10-2.10)
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	669	16% 72% 19% • 8%
2	B	133	21% 68% 17% • 12%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5802 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 Nucleoporin NIC96.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	613	Total	C	N	O	S	0	4	0
			4844	3099	810	919	16			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	GLY	-	expression tag	UNP P34077
A	172	PRO	-	expression tag	UNP P34077
A	173	GLY	-	expression tag	UNP P34077
A	174	SER	-	expression tag	UNP P34077
A	175	GLU	-	expression tag	UNP P34077
A	176	PHE	-	expression tag	UNP P34077
A	177	GLU	-	expression tag	UNP P34077
A	178	LEU	-	expression tag	UNP P34077
A	179	GLY	-	expression tag	UNP P34077
A	180	ALA	-	expression tag	UNP P34077
A	181	PRO	-	expression tag	UNP P34077
A	182	ALA	-	expression tag	UNP P34077
A	183	GLY	-	expression tag	UNP P34077
A	184	ARG	-	expression tag	UNP P34077
A	185	GLN	-	expression tag	UNP P34077

- Molecule 2 is a protein called VHH-SAN12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	117	Total	C	N	O	S	0	0	0
			830	510	147	169	4			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	118	Total 118	O 118	0	0
3	B	10	Total 10	O 10	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.13Å 79.65Å 283.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.91 – 2.10 60.91 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (60.91-2.10) 99.4 (60.91-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.227 , 0.245 0.228 , 0.247	Depositor DCC
R_{free} test set	2000 reflections (3.09%)	wwPDB-VP
Wilson B-factor (Å ²)	44.4	Xtriage
Anisotropy	0.452	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 61.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5802	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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	0.62	3/4928 (0.1%)	0.69	8/6692 (0.1%)
2	B	0.82	1/845 (0.1%)	0.87	6/1153 (0.5%)
All	All	0.65	4/5773 (0.1%)	0.72	14/7845 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	746	PRO	C-O	-6.63	1.15	1.24
1	A	749	ASP	C-O	-6.13	1.18	1.24
2	B	30	ARG	C-O	-5.73	1.17	1.24
1	A	680	ASN	C-O	-5.11	1.17	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	268	ILE	N-CA-C	13.28	126.22	107.37
1	A	748	SER	N-CA-C	12.54	124.48	111.07
1	A	268	ILE	CB-CA-C	-7.11	104.26	111.80
1	A	267	ASP	N-CA-C	-6.94	99.55	109.96
1	A	613	VAL	N-CA-C	6.70	117.74	108.89
1	A	360	ILE	N-CA-C	6.45	118.71	111.88
2	B	108	TRP	N-CA-C	5.62	118.05	109.95
2	B	105	ILE	N-CA-C	5.41	115.55	110.30
2	B	29	PHE	N-CA-C	5.24	116.99	111.28
2	B	102	THR	N-CA-C	5.20	118.41	111.75
1	A	562	LEU	N-CA-C	-5.17	105.27	112.45
2	B	99	ALA	CA-C-N	5.08	124.69	119.05
2	B	99	ALA	C-N-CA	5.08	124.69	119.05
1	A	683	THR	N-CA-C	5.01	120.23	113.72

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	4844	0	4729	85	0
2	B	830	0	738	17	0
3	A	118	0	0	4	0
3	B	10	0	0	1	0
All	All	5802	0	5467	101	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 9.

All (101) 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)
2:B:9:GLY:HA2	2:B:18:LEU:CD2	1.69	1.20
2:B:9:GLY:CA	2:B:18:LEU:HD21	1.70	1.19
1:A:432:ILE:HD12	1:A:433:GLU:H	1.28	0.99
1:A:532:ILE:HG22	1:A:537:ILE:CD1	1.94	0.96
1:A:532:ILE:HG22	1:A:537:ILE:HD11	1.46	0.96
1:A:432:ILE:HD12	1:A:433:GLU:N	1.83	0.93
1:A:615:ASP:HB2	1:A:617:LYS:N	1.89	0.87
1:A:736:LEU:HD22	1:A:785:MET:HE1	1.62	0.81
1:A:615:ASP:CB	1:A:617:LYS:N	2.46	0.79
1:A:539:ALA:O	1:A:542:THR:HG22	1.86	0.76
1:A:549:ASP:HB3	1:A:552:VAL:HG12	1.74	0.69
1:A:475:SER:OG	1:A:476:ASN:N	2.27	0.68
1:A:615:ASP:HB3	1:A:618:GLU:H	1.58	0.67
1:A:532:ILE:HG22	1:A:537:ILE:HD13	1.77	0.66
2:B:66:ARG:NH2	2:B:89:ASP:OD2	2.28	0.65
1:A:543:LYS:HD2	1:A:546:ARG:HD2	1.77	0.65
1:A:272:GLU:O	1:A:276:GLN:HG3	1.98	0.64
1:A:605:GLU:HA	1:A:608:GLN:HG3	1.82	0.62
2:B:32:ARG:HA	3:B:202:HOH:O	2.02	0.60
1:A:362:LYS:HA	1:A:365:GLN:HB2	1.84	0.59
1:A:580:VAL:HB	1:A:623:ILE:HD11	1.83	0.59
1:A:215:TYR:HA	1:A:218:ILE:HD12	1.86	0.58
1:A:551:ARG:HG3	1:A:603:VAL:HG11	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:LYS:HE2	1:A:457:TYR:CD1	2.38	0.58
1:A:492:ILE:HD11	1:A:510:LEU:HD12	1.86	0.58
1:A:413:LYS:HD2	1:A:425:ILE:HD11	1.86	0.58
1:A:665:LEU:HD21	1:A:721[A]:SER:OG	2.04	0.57
1:A:808[A]:ASN:O	1:A:812[A]:GLN:HG2	2.04	0.57
2:B:90:THR:HG23	2:B:115:THR:HA	1.89	0.55
1:A:315:LYS:HG3	1:A:321:LYS:HG2	1.89	0.55
1:A:555:GLU:OE2	1:A:607:ARG:NH2	2.39	0.55
1:A:549:ASP:HB3	1:A:552:VAL:CG1	2.37	0.55
1:A:201:ASN:ND2	1:A:204:GLU:HB3	2.22	0.54
1:A:213:GLU:HG3	3:A:918:HOH:O	2.08	0.54
1:A:703:SER:OG	1:A:711:LYS:NZ	2.22	0.54
2:B:9:GLY:HA2	2:B:18:LEU:HD21	0.76	0.54
1:A:615:ASP:HB3	1:A:617:LYS:N	2.22	0.54
1:A:504:VAL:HG21	1:A:541:TYR:HB2	1.90	0.53
1:A:557:LEU:O	1:A:560:ILE:HG13	2.09	0.53
1:A:704:ARG:HH12	2:B:101:THR:CG2	2.21	0.53
1:A:488:TYR:CZ	1:A:515:LEU:HD13	2.43	0.53
2:B:39:GLN:HB2	2:B:45:ARG:HG3	1.90	0.53
2:B:12:VAL:O	2:B:116:VAL:HA	2.09	0.52
1:A:323:SER:HA	3:A:911:HOH:O	2.09	0.52
1:A:202:VAL:HG11	1:A:212:PHE:CG	2.45	0.52
1:A:548:SER:HB3	3:A:925:HOH:O	2.10	0.51
1:A:218:ILE:HD11	1:A:241:ILE:HD13	1.92	0.51
1:A:227:GLN:HE21	1:A:609:PRO:HG2	1.74	0.51
1:A:539:ALA:O	1:A:543:LYS:HD3	2.11	0.50
2:B:34:MET:SD	2:B:97:ILE:HD13	2.51	0.50
2:B:29:PHE:HE2	2:B:73:ASN:OD1	1.95	0.50
1:A:432:ILE:CD1	1:A:433:GLU:N	2.65	0.49
1:A:317:ASP:HB2	1:A:319:SER:HB3	1.93	0.49
1:A:351:GLN:O	1:A:355:GLU:HG3	2.11	0.49
2:B:45:ARG:HD3	2:B:108:TRP:CZ3	2.46	0.49
1:A:830:SER:O	1:A:834:ASN:ND2	2.45	0.49
1:A:657:VAL:HG21	1:A:692:MET:HG3	1.94	0.48
1:A:203:ASN:OD1	1:A:209:ARG:NH1	2.39	0.48
1:A:317:ASP:HB2	1:A:319:SER:H	1.79	0.47
2:B:32:ARG:HD3	2:B:97:ILE:HD12	1.97	0.47
1:A:496:TYR:OH	1:A:537:ILE:HD12	2.15	0.47
1:A:533:ARG:O	1:A:537:ILE:HG12	2.14	0.47
1:A:471:PRO:HB3	1:A:478:TYR:CD2	2.50	0.46
1:A:501:MET:HG2	1:A:541:TYR:HE1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:GLN:CD	1:A:224:ASN:HD22	2.24	0.45
1:A:763:LEU:HB2	1:A:768:VAL:HG13	1.99	0.45
1:A:588:VAL:HG12	3:A:904:HOH:O	2.17	0.45
1:A:305:ILE:HD13	1:A:340:LEU:HD23	2.00	0.44
1:A:620:LEU:HD23	1:A:620:LEU:HA	1.52	0.44
1:A:356:ASN:O	1:A:360:ILE:HG23	2.18	0.44
1:A:562:LEU:HD23	1:A:562:LEU:HA	1.57	0.44
1:A:592:LYS:HG2	1:A:593:ILE:H	1.82	0.44
1:A:578:GLU:O	1:A:582:GLU:HB2	2.17	0.44
1:A:681:SER:HB2	1:A:691:ARG:HD3	1.99	0.44
2:B:99:ALA:HB1	2:B:100:PRO:HD2	1.99	0.44
1:A:460:GLU:H	1:A:460:GLU:CD	2.27	0.43
1:A:246:ASN:HB3	1:A:247:GLY:H	1.63	0.43
1:A:473:ARG:HB3	1:A:473:ARG:NH1	2.34	0.43
1:A:577:ARG:HA	1:A:623:ILE:CD1	2.49	0.43
1:A:289:LEU:HD23	1:A:289:LEU:HA	1.84	0.42
1:A:238:PHE:O	1:A:242:LEU:HB2	2.19	0.42
1:A:577:ARG:HA	1:A:623:ILE:HD12	2.02	0.42
1:A:615:ASP:OD1	1:A:615:ASP:N	2.48	0.42
1:A:636:ARG:HB3	1:A:639:ASP:HB2	2.02	0.42
1:A:695:ILE:HG13	1:A:696:TYR:CD1	2.55	0.42
1:A:821:GLN:HG3	1:A:822:TYR:CD1	2.54	0.42
1:A:204:GLU:HG2	1:A:208:LEU:HD23	2.02	0.42
1:A:587:THR:HG22	1:A:592:LYS:HG3	2.02	0.42
1:A:360:ILE:O	1:A:360:ILE:HG13	2.20	0.41
1:A:662:SER:OG	1:A:769:LYS:HD2	2.20	0.41
1:A:268:ILE:O	1:A:268:ILE:HG22	2.15	0.41
1:A:750:GLU:HA	1:A:812[A]:GLN:OE1	2.20	0.41
1:A:237:GLU:O	1:A:241:ILE:HD12	2.20	0.41
1:A:383:PRO:HG2	1:A:386:TYR:CD2	2.55	0.41
2:B:108:TRP:CD1	2:B:108:TRP:N	2.89	0.41
1:A:543:LYS:HD2	1:A:543:LYS:HA	1.67	0.41
1:A:275:LYS:HE3	1:A:441:MET:SD	2.61	0.41
2:B:51:ILE:HD11	2:B:55:GLY:HA2	2.03	0.40
1:A:348:GLU:O	1:A:351:GLN:HB3	2.22	0.40
1:A:465:ILE:HD12	1:A:465:ILE:HA	1.93	0.40
2:B:48:VAL:HG13	2:B:63:VAL:HG21	2.04	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	607/669 (91%)	593 (98%)	14 (2%)	0	100	100
2	B	115/133 (86%)	112 (97%)	3 (3%)	0	100	100
All	All	722/802 (90%)	705 (98%)	17 (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	517/601 (86%)	511 (99%)	6 (1%)	63	72
2	B	78/108 (72%)	76 (97%)	2 (3%)	40	46
All	All	595/709 (84%)	587 (99%)	8 (1%)	59	69

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

Mol	Chain	Res	Type
1	A	360	ILE
1	A	532	ILE
1	A	615	ASP
1	A	620	LEU
1	A	632	ASP
1	A	798	THR
2	B	12	VAL
2	B	118	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	ASN
1	A	224	ASN
1	A	380	HIS
1	A	536	ASN
1	A	608	GLN
1	A	621	HIS
2	B	113	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	613/669 (91%)	1.15	106 (17%) 4 4	18, 71, 114, 142	4 (0%)
2	B	117/133 (87%)	1.58	28 (23%) 2 2	48, 87, 113, 144	0
All	All	730/802 (91%)	1.22	134 (18%) 3 3	18, 73, 114, 144	4 (0%)

All (134) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	311	THR	6.9
1	A	300	THR	6.0
1	A	239	ILE	5.0
1	A	532	ILE	5.0
2	B	107	ASN	4.9
1	A	241	ILE	4.8
1	A	565	GLY	4.7
2	B	2	VAL	4.7
1	A	363	VAL	4.5
1	A	379	ASP	4.5
1	A	380	HIS	4.3
1	A	267	ASP	4.2
1	A	617	LYS	4.1
1	A	382	LEU	4.0
1	A	516	PHE	3.9
2	B	85	LEU	3.8
2	B	9	GLY	3.7
2	B	102	THR	3.7
1	A	304	LYS	3.7
1	A	597	GLY	3.6
1	A	489	GLY	3.6
1	A	207	ILE	3.5
1	A	791	GLU	3.5
1	A	245	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	213	GLU	3.5
2	B	14	ALA	3.4
2	B	103	ALA	3.4
2	B	4	LEU	3.4
2	B	101	THR	3.4
1	A	384	VAL	3.4
1	A	795	GLN	3.4
1	A	450	ASN	3.4
1	A	796	SER	3.4
1	A	564	GLU	3.3
1	A	750	GLU	3.3
1	A	238	PHE	3.3
2	B	118	SER	3.3
2	B	10	GLY	3.3
1	A	612	HIS	3.3
1	A	210	GLU	3.2
2	B	15	GLY	3.2
2	B	108	TRP	3.1
1	A	453	VAL	3.1
1	A	307	SER	3.1
1	A	797	SER	3.1
1	A	212	PHE	3.1
1	A	228	ALA	3.1
1	A	563	ASN	3.0
1	A	561	THR	3.0
1	A	244	SER	3.0
1	A	378	LYS	3.0
1	A	402	LEU	2.9
1	A	302	VAL	2.9
1	A	290	TYR	2.9
1	A	787	HIS	2.9
1	A	632	ASP	2.8
1	A	361	LYS	2.8
2	B	78	ILE	2.8
1	A	366	SER	2.8
1	A	264	LYS	2.8
1	A	376	SER	2.7
1	A	216	ALA	2.7
1	A	268	ILE	2.7
1	A	360	ILE	2.7
1	A	699	ASN	2.7
2	B	26	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	263	MET	2.6
2	B	87	PRO	2.6
1	A	204	GLU	2.6
1	A	251	ALA	2.6
1	A	199	ARG	2.6
2	B	116	VAL	2.6
1	A	568	ASP	2.6
2	B	88	ASP	2.6
1	A	748	SER	2.6
1	A	381	GLY	2.5
2	B	64	LYS	2.5
1	A	375	ALA	2.5
1	A	289	LEU	2.5
2	B	114	VAL	2.5
1	A	254	LEU	2.5
1	A	802	GLN	2.5
1	A	594	GLY	2.5
1	A	569	VAL	2.4
1	A	312	LYS	2.4
1	A	789	LEU	2.4
1	A	432	ILE	2.4
1	A	599	ARG	2.4
1	A	383	PRO	2.4
1	A	566	PRO	2.4
2	B	13	GLN	2.4
1	A	798	THR	2.4
1	A	220	PHE	2.3
2	B	25	SER	2.3
1	A	567	THR	2.3
1	A	258	LYS	2.3
2	B	29	PHE	2.3
1	A	613	VAL	2.3
1	A	248	THR	2.3
1	A	200	LEU	2.3
1	A	362	LYS	2.3
1	A	236	ASN	2.3
1	A	470	GLY	2.3
1	A	631	ALA	2.2
1	A	562	LEU	2.2
1	A	214	ASN	2.2
1	A	615	ASP	2.2
1	A	217	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	259	ILE	2.2
1	A	593	ILE	2.2
1	A	611	LEU	2.2
1	A	377	SER	2.2
1	A	595	ARG	2.2
1	A	822	TYR	2.2
2	B	109	GLY	2.1
1	A	700	ALA	2.1
1	A	240	SER	2.1
1	A	221	GLN	2.1
1	A	232	PHE	2.1
2	B	92	VAL	2.1
2	B	40	ALA	2.1
1	A	208	LEU	2.1
1	A	265	SER	2.1
1	A	226	ARG	2.1
1	A	387	SER	2.1
1	A	385	GLU	2.1
1	A	425	ILE	2.1
1	A	695	ILE	2.1
1	A	242	LEU	2.0
2	B	31	LEU	2.0
1	A	701	GLY	2.0
1	A	623	ILE	2.0
2	B	11	LEU	2.0
1	A	711	LYS	2.0

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.