



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:31 AM UTC

PDB ID : 8EN0 / pdb_00008en0
Title : Structure of GII.17 norovirus in complex with Nanobody 7
Authors : Kher, G.; Sabin, C.; Koromyslova, A.; Pancera, M.; Hansman, G.
Deposited on : 2022-09-28
Resolution : 2.99 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

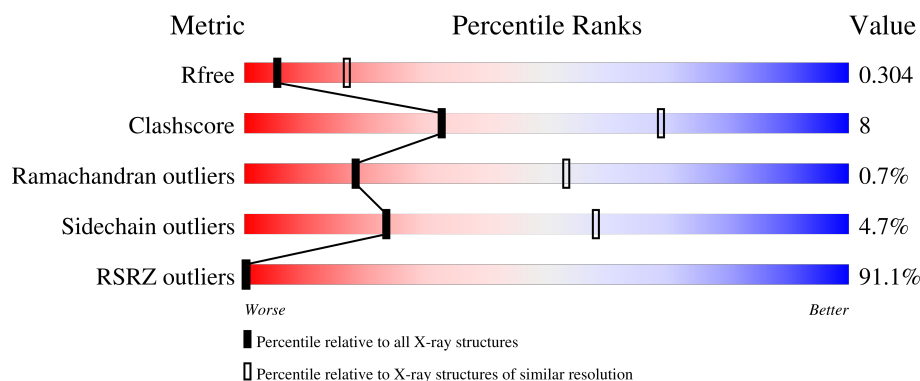
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	D	136	83% 60% 24% 13%
2	A	308	89% 80% 18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3317 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 Nanobody 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	118	Total	C	N	O	S	0	0	0
			878	541	160	173	4			

- Molecule 2 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	307	Total	C	N	O	S	0	0	0
			2418	1534	418	457	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	223	GLY	-	expression tag	UNP A0A0S1Z370
A	224	SER	-	expression tag	UNP A0A0S1Z370

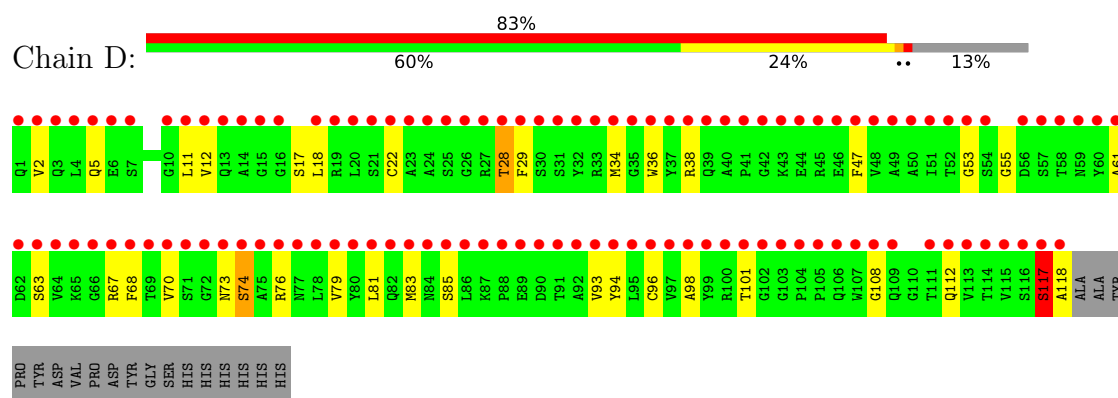
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	6	Total	O	0	0
			6	6		
3	A	15	Total	O	0	0
			15	15		

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: Nanobody 7



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	74.82Å 85.46Å 223.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.96 – 2.99 70.96 – 2.99	Depositor EDS
% Data completeness (in resolution range)	94.5 (70.96-2.99) 95.5 (70.96-2.99)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.249 , 0.306 0.248 , 0.304	Depositor DCC
R_{free} test set	714 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	61.8	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 14.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.65	EDS
Total number of atoms	3317	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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	D	0.51	2/894 (0.2%)	0.61	1/1209 (0.1%)
2	A	0.28	1/2489 (0.0%)	0.46	0/3403
All	All	0.36	3/3383 (0.1%)	0.50	1/4612 (0.0%)

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	D	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	117	SER	C-O	-10.77	1.10	1.23
2	A	321	PRO	C-O	-6.94	1.15	1.24
1	D	117	SER	C-N	6.09	1.41	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	117	SER	O-C-N	-13.27	105.74	122.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	117	SER	Mainchain

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	D	878	0	850	20	0
2	A	2418	0	2307	31	0
3	A	15	0	0	0	0
3	D	6	0	0	0	0
All	All	3317	0	3157	51	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 8.

All (51) 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:A:339:ASN:HA	2:A:382:GLN:HG2	1.54	0.88
2:A:288:GLY:HA2	2:A:305:GLN:HG3	1.70	0.73
1:D:93:VAL:HG22	1:D:112:GLN:HG2	1.72	0.71
2:A:382:GLN:HG3	2:A:383:PRO:HD2	1.75	0.68
2:A:277:GLN:HG2	2:A:279:LEU:H	1.60	0.65
2:A:394:ASP:HB3	2:A:398:HIS:HB2	1.80	0.63
1:D:12:VAL:HG11	1:D:18:LEU:HD21	1.81	0.63
2:A:473:ALA:HB2	2:A:520:TRP:CZ3	2.36	0.61
2:A:254:ASN:HD21	2:A:424:PRO:HD2	1.64	0.60
2:A:433:PHE:HB3	2:A:450:ASP:HB3	1.84	0.59
1:D:2:VAL:HG21	1:D:28:THR:HB	1.86	0.56
1:D:11:LEU:HD12	1:D:12:VAL:H	1.72	0.53
2:A:241:ARG:NH1	2:A:326:ASP:OD1	2.42	0.51
1:D:67:ARG:HD2	1:D:85:SER:HB2	1.92	0.51
1:D:22:CYS:HB3	1:D:79:VAL:HG13	1.93	0.51
1:D:34:MET:HE2	1:D:98:ALA:HB2	1.93	0.51
1:D:117:SER:O	1:D:118:ALA:C	2.52	0.50
2:A:262:GLN:HE21	2:A:405:LEU:HD21	1.75	0.50
2:A:321:PRO:O	2:A:324:THR:OG1	2.29	0.49
2:A:354:TRP:HB2	2:A:372:ARG:HB2	1.95	0.49
2:A:234:LEU:HA	2:A:237:LEU:HD12	1.96	0.48
2:A:250:PHE:HD2	2:A:435:ARG:CZ	2.26	0.48
2:A:422:VAL:HG23	2:A:431:LEU:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:335:VAL:HG21	2:A:373:ILE:HD11	1.95	0.47
2:A:472:VAL:CG1	2:A:490:LYS:HG2	2.44	0.47
2:A:431:LEU:HD23	2:A:498:THR:HG22	1.97	0.46
2:A:250:PHE:CD2	2:A:435:ARG:CZ	2.98	0.46
2:A:280:PRO:HG3	2:A:455:GLN:HG2	1.96	0.46
1:D:34:MET:HG3	1:D:74:SER:HB3	1.97	0.46
2:A:237:LEU:HB3	2:A:246:ILE:HD13	1.96	0.46
2:A:328:LYS:HB3	2:A:358:TYR:CE1	2.50	0.46
2:A:246:ILE:HG12	2:A:434:PHE:HB3	1.99	0.45
1:D:28:THR:OG1	1:D:29:PHE:N	2.50	0.45
1:D:36:TRP:NE1	1:D:81:LEU:HB2	2.32	0.45
1:D:70:VAL:HG22	1:D:81:LEU:HD12	1.99	0.45
2:A:334:MET:HE3	2:A:334:MET:HB3	1.84	0.45
1:D:47:PHE:HD2	1:D:61:ALA:HB2	1.82	0.44
2:A:471:ASP:OD1	2:A:471:ASP:N	2.41	0.44
1:D:53:GLY:O	1:D:73:ASN:HA	2.18	0.43
2:A:358:TYR:OH	2:A:399:PRO:O	2.33	0.43
1:D:17:SER:O	1:D:18:LEU:HD13	2.19	0.42
2:A:238:THR:HG21	2:A:280:PRO:HB3	2.01	0.42
1:D:36:TRP:CD1	1:D:81:LEU:HB2	2.54	0.42
1:D:96:CYS:O	1:D:108:GLY:N	2.52	0.41
2:A:335:VAL:HG22	2:A:353:ALA:HB2	2.03	0.41
1:D:5:GLN:O	1:D:22:CYS:HA	2.20	0.41
1:D:68:PHE:CZ	1:D:83:MET:HG2	2.55	0.41
1:D:38:ARG:HD3	1:D:94:TYR:CZ	2.55	0.41
2:A:262:GLN:HB3	2:A:275:THR:HG23	2.01	0.41
2:A:269:ASP:O	2:A:465:SER:HA	2.21	0.41
2:A:302:MET:HE3	2:A:384:THR:HB	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	D	116/136 (85%)	108 (93%)	5 (4%)	3 (3%)	4	23
2	A	305/308 (99%)	293 (96%)	12 (4%)	0	100	100
All	All	421/444 (95%)	401 (95%)	17 (4%)	3 (1%)	18	53

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	63	SER
1	D	28	THR
1	D	55	GLY

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	D	91/106 (86%)	88 (97%)	3 (3%)	33	67
2	A	269/269 (100%)	255 (95%)	14 (5%)	21	55
All	All	360/375 (96%)	343 (95%)	17 (5%)	23	58

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

Mol	Chain	Res	Type
1	D	74	SER
1	D	76	ARG
1	D	101	THR
2	A	256	VAL
2	A	261	CYS
2	A	277	GLN
2	A	279	LEU
2	A	281	THR
2	A	311	THR
2	A	316	ASP
2	A	374	SER
2	A	382	GLN
2	A	391	VAL

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Mol	Chain	Res	Type
2	A	438	VAL
2	A	471	ASP
2	A	494	SER
2	A	526	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	D	5	GLN
1	D	39	GLN
1	D	109	GLN
2	A	254	ASN
2	A	263	ASN
2	A	370	ASN
2	A	382	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 ⓘ

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	D	118/136 (86%)	3.60	113 (95%) 0 0	68, 77, 87, 95	0
2	A	307/308 (99%)	3.37	274 (89%) 0 0	55, 63, 75, 86	0
All	All	425/444 (95%)	3.44	387 (91%) 0 0	55, 66, 80, 95	0

All (387) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	118	ALA	7.1
2	A	396	ASP	6.9
2	A	256	VAL	6.3
2	A	523	GLN	6.3
2	A	414	LEU	6.1
2	A	257	LEU	6.1
1	D	107	TRP	6.1
1	D	41	PRO	6.0
2	A	258	GLN	5.9
1	D	25	SER	5.9
2	A	368	SER	5.7
2	A	378	ASP	5.7
1	D	46	GLU	5.7
1	D	117	SER	5.6
2	A	481	ASP	5.6
2	A	516	ARG	5.6
2	A	379	PHE	5.6
1	D	52	THR	5.6
2	A	225	LYS	5.5
2	A	512	ASN	5.5
2	A	425	ASN	5.3
2	A	421	PRO	5.3
2	A	423	ALA	5.3
2	A	377	ASP	5.3

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Mol	Chain	Res	Type	RSRZ
2	A	300	TRP	5.3
2	A	255	ASN	5.2
2	A	434	PHE	5.2
2	A	375	ASP	5.2
2	A	426	PHE	5.1
2	A	250	PHE	5.1
1	D	62	ASP	5.1
2	A	252	ALA	5.1
2	A	530	MET	5.1
1	D	1	GLN	5.1
2	A	231	ILE	5.1
2	A	303	GLN	5.0
2	A	508	VAL	5.0
1	D	28	THR	5.0
1	D	101	THR	5.0
1	D	95	LEU	5.0
2	A	504	ASP	5.0
2	A	524	PHE	4.9
2	A	337	GLN	4.9
2	A	528	ALA	4.9
2	A	253	GLN	4.9
2	A	476	ARG	4.9
2	A	527	LEU	4.9
1	D	87	LYS	4.8
2	A	422	VAL	4.8
2	A	404	GLU	4.8
2	A	249	LEU	4.8
1	D	51	ILE	4.7
2	A	297	ARG	4.7
2	A	260	GLN	4.7
2	A	511	ALA	4.7
2	A	486	LEU	4.6
2	A	522	ASN	4.6
2	A	444	TYR	4.5
1	D	73	ASN	4.5
2	A	338	ARG	4.5
1	D	99	TYR	4.5
2	A	515	PHE	4.5
1	D	7	SER	4.5
1	D	27	ARG	4.5
2	A	437	PHE	4.5
2	A	294	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	65	LYS	4.4
2	A	424	PRO	4.4
2	A	485	THR	4.4
1	D	66	GLY	4.4
2	A	391	VAL	4.4
2	A	395	ASP	4.4
1	D	21	SER	4.4
2	A	254	ASN	4.4
1	D	32	TYR	4.4
2	A	499	VAL	4.4
2	A	458	ILE	4.4
2	A	514	HIS	4.4
1	D	108	GLY	4.3
2	A	228	SER	4.3
2	A	385	LYS	4.3
2	A	500	ALA	4.3
1	D	43	LYS	4.3
2	A	351	GLN	4.3
1	D	89	GLU	4.3
2	A	279	LEU	4.3
2	A	295	ASN	4.3
2	A	283	ILE	4.3
2	A	428	GLY	4.3
1	D	44	GLU	4.3
2	A	477	TYR	4.2
2	A	417	ASN	4.2
1	D	63	SER	4.2
1	D	64	VAL	4.2
1	D	79	VAL	4.2
2	A	371	LEU	4.2
2	A	507	LEU	4.2
2	A	497	ILE	4.2
1	D	88	PRO	4.2
2	A	464	GLU	4.2
2	A	393	ASP	4.2
1	D	60	TYR	4.1
1	D	35	GLY	4.1
2	A	313	ASP	4.1
1	D	36	TRP	4.1
2	A	494	SER	4.1
1	D	93	VAL	4.1
1	D	115	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
2	A	509	VAL	4.1
2	A	358	TYR	4.1
1	D	45	ARG	4.1
2	A	433	PHE	4.1
2	A	352	GLN	4.1
2	A	471	ASP	4.0
1	D	76	ARG	4.0
2	A	291	THR	4.0
2	A	247	ASP	4.0
2	A	298	ASP	4.0
2	A	299	ARG	4.0
1	D	78	LEU	4.0
1	D	71	SER	4.0
2	A	235	SER	4.0
2	A	343	ASP	3.9
1	D	70	VAL	3.9
2	A	236	GLU	3.9
2	A	489	ALA	3.9
2	A	432	LEU	3.9
2	A	226	PRO	3.9
1	D	116	SER	3.9
2	A	251	THR	3.9
2	A	457	TRP	3.9
1	D	109	GLN	3.9
1	D	100	ARG	3.9
2	A	482	THR	3.9
1	D	34	MET	3.8
1	D	48	VAL	3.8
2	A	505	TYR	3.8
2	A	364	PRO	3.8
2	A	336	SER	3.8
2	A	438	VAL	3.8
2	A	296	GLN	3.8
2	A	285	ALA	3.8
1	D	12	VAL	3.8
1	D	24	ALA	3.8
1	D	18	LEU	3.8
1	D	26	GLY	3.8
2	A	317	ASP	3.8
2	A	280	PRO	3.8
2	A	301	HIS	3.8
1	D	85	SER	3.7

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Mol	Chain	Res	Type	RSRZ
2	A	450	ASP	3.7
1	D	22	CYS	3.7
2	A	430	GLN	3.7
1	D	23	ALA	3.7
2	A	365	LYS	3.7
1	D	3	GLN	3.7
2	A	459	GLN	3.7
1	D	39	GLN	3.7
2	A	242	PHE	3.7
2	A	449	ILE	3.7
2	A	467	PRO	3.6
2	A	293	GLN	3.6
2	A	312	TYR	3.6
2	A	462	TYR	3.6
2	A	448	ILE	3.6
1	D	69	THR	3.6
2	A	348	THR	3.6
2	A	455	GLN	3.6
1	D	72	GLY	3.6
2	A	355	VAL	3.6
1	D	114	THR	3.6
1	D	40	ALA	3.6
1	D	30	SER	3.6
1	D	97	VAL	3.6
2	A	259	VAL	3.6
2	A	389	VAL	3.6
2	A	472	VAL	3.6
2	A	521	VAL	3.6
2	A	308	ASN	3.6
2	A	333	GLY	3.6
2	A	246	ILE	3.6
2	A	392	ASN	3.6
2	A	407	ASN	3.6
1	D	75	ALA	3.5
1	D	112	GLN	3.5
2	A	445	ASN	3.5
2	A	292	ALA	3.5
2	A	394	ASP	3.5
1	D	61	ALA	3.5
1	D	102	GLY	3.5
2	A	307	LEU	3.5
2	A	326	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	59	ASN	3.5
2	A	451	CYS	3.5
2	A	374	SER	3.5
2	A	327	PHE	3.4
2	A	475	ILE	3.4
2	A	363	VAL	3.4
2	A	234	LEU	3.4
2	A	359	SER	3.4
2	A	427	PRO	3.4
1	D	49	ALA	3.4
1	D	54	SER	3.4
2	A	526	SER	3.4
2	A	334	MET	3.4
2	A	240	SER	3.4
2	A	403	TRP	3.4
1	D	47	PHE	3.4
1	D	4	LEU	3.4
2	A	318	VAL	3.4
2	A	369	VAL	3.4
2	A	488	GLU	3.4
2	A	248	SER	3.4
1	D	11	LEU	3.3
1	D	86	LEU	3.3
2	A	366	LEU	3.3
2	A	412	LEU	3.3
2	A	397	GLY	3.3
1	D	113	VAL	3.3
1	D	38	ARG	3.3
2	A	306	ASN	3.3
2	A	493	ARG	3.3
2	A	473	ALA	3.3
2	A	431	LEU	3.3
1	D	90	ASP	3.3
1	D	94	TYR	3.3
2	A	461	PHE	3.3
2	A	289	ARG	3.3
2	A	520	TRP	3.3
1	D	98	ALA	3.3
2	A	478	VAL	3.3
2	A	328	LYS	3.2
2	A	415	ASN	3.2
2	A	446	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	53	GLY	3.2
1	D	67	ARG	3.2
2	A	456	GLU	3.2
2	A	510	PRO	3.2
2	A	381	PHE	3.2
2	A	443	GLY	3.2
1	D	37	TYR	3.2
2	A	468	SER	3.2
1	D	77	ASN	3.2
2	A	278	LEU	3.2
2	A	227	PHE	3.2
2	A	286	PHE	3.2
2	A	416	MET	3.2
2	A	429	GLU	3.2
1	D	20	LEU	3.1
2	A	460	HIS	3.1
2	A	277	GLN	3.1
2	A	380	GLN	3.1
1	D	104	PRO	3.1
2	A	241	ARG	3.1
2	A	386	PHE	3.1
2	A	305	GLN	3.1
1	D	74	SER	3.1
2	A	370	ASN	3.1
2	A	243	PRO	3.1
2	A	276	THR	3.1
2	A	354	TRP	3.1
1	D	19	ARG	3.1
2	A	268	LEU	3.1
2	A	271	GLU	3.1
2	A	492	HIS	3.0
2	A	331	VAL	3.0
2	A	496	TYR	3.0
1	D	57	SER	3.0
2	A	447	GLY	3.0
2	A	474	LEU	3.0
2	A	340	VAL	3.0
2	A	376	ASN	3.0
2	A	302	MET	3.0
2	A	525	TYR	3.0
1	D	82	GLN	3.0
2	A	470	SER	3.0

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Mol	Chain	Res	Type	RSRZ
2	A	519	SER	3.0
2	A	284	CYS	3.0
2	A	399	PRO	3.0
2	A	408	TYR	3.0
1	D	5	GLN	3.0
2	A	329	GLY	3.0
2	A	316	ASP	3.0
2	A	506	PRO	3.0
2	A	320	ALA	3.0
1	D	33	ARG	2.9
1	D	80	TYR	2.9
2	A	272	LEU	2.9
2	A	405	LEU	2.9
2	A	440	CYS	2.9
1	D	14	ALA	2.9
2	A	357	THR	2.9
1	D	42	GLY	2.9
2	A	382	GLN	2.9
2	A	466	ALA	2.9
2	A	281	THR	2.9
2	A	490	LYS	2.9
2	A	330	VAL	2.9
2	A	484	ARG	2.9
2	A	367	GLY	2.9
1	D	68	PHE	2.9
2	A	418	LEU	2.9
1	D	105	PRO	2.8
2	A	349	ARG	2.8
2	A	435	ARG	2.8
2	A	356	SER	2.8
1	D	13	GLN	2.8
2	A	400	PHE	2.8
2	A	232	LEU	2.8
1	D	103	GLY	2.8
2	A	282	GLY	2.8
1	D	106	GLN	2.8
2	A	463	GLN	2.8
1	D	6	GLU	2.8
1	D	92	ALA	2.8
2	A	517	PHE	2.8
2	A	398	HIS	2.8
2	A	452	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
2	A	311	THR	2.8
2	A	309	GLY	2.8
2	A	245	PRO	2.8
2	A	315	THR	2.8
1	D	31	SER	2.8
2	A	264	GLY	2.8
2	A	362	PHE	2.7
2	A	237	LEU	2.7
2	A	373	ILE	2.7
1	D	111	THR	2.7
2	A	224	SER	2.7
2	A	288	GLY	2.7
2	A	361	GLN	2.7
1	D	2	VAL	2.7
2	A	402	GLN	2.7
2	A	239	ASN	2.7
2	A	383	PRO	2.7
2	A	487	PHE	2.7
2	A	342	ASN	2.6
2	A	411	GLU	2.6
2	A	410	GLY	2.6
1	D	58	THR	2.6
2	A	409	SER	2.6
2	A	436	SER	2.6
2	A	420	PRO	2.6
2	A	229	LEU	2.6
2	A	238	THR	2.5
2	A	319	PRO	2.5
2	A	441	SER	2.5
2	A	265	ARG	2.5
2	A	384	THR	2.5
2	A	483	GLY	2.4
1	D	29	PHE	2.4
2	A	401	ARG	2.4
2	A	491	LEU	2.4
2	A	325	PRO	2.4
2	A	304	LEU	2.4
2	A	263	ASN	2.4
2	A	406	PRO	2.4
1	D	10	GLY	2.4
1	D	16	GLY	2.4
2	A	439	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
2	A	372	ARG	2.3
1	D	96	CYS	2.3
1	D	50	ALA	2.3
2	A	290	VAL	2.3
2	A	503	GLY	2.3
2	A	350	ALA	2.3
2	A	346	GLY	2.3
1	D	56	ASP	2.3
2	A	287	ARG	2.2
2	A	267	THR	2.2
1	D	15	GLY	2.2
2	A	341	GLY	2.2
2	A	453	ILE	2.2
1	D	91	THR	2.2
2	A	335	VAL	2.2
2	A	332	PHE	2.2
2	A	353	ALA	2.2
1	D	84	ASN	2.2
2	A	339	ASN	2.2
2	A	501	HIS	2.1
2	A	244	VAL	2.1
1	D	83	MET	2.1
1	D	81	LEU	2.1
2	A	518	ASP	2.1
2	A	390	GLY	2.1
2	A	513	GLY	2.1
2	A	266	CYS	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.