



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:45 PM UTC

PDB ID : 6N81 / pdb_00006n81
Title : Crystal structure of GII.4 2002 norovirus P domain in complex with cross-reactive human antibody A1227
Authors : Changela, A.; Verardi, R.; Kwong, P.D.
Deposited on : 2018-11-28
Resolution : 2.58 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

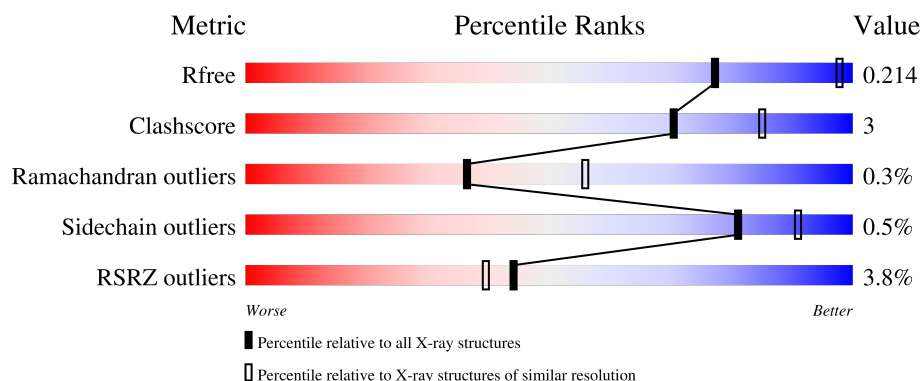
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

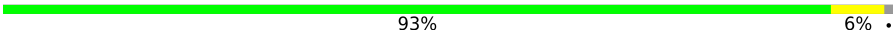
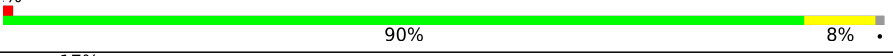
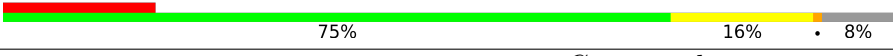
The reported resolution of this entry is 2.58 Å.

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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	309	
1	B	309	
2	D	214	
2	L	214	
3	C	236	

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Mol	Chain	Length	Quality of chain
3	H	236	2% 88% 8% 5%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11539 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 Major capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	0	0
			2375	1503	411	450	11			
1	B	306	Total	C	N	O	S	0	0	0
			2375	1503	411	450	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	GLY	-	expression tag	UNP R4I4P2
A	223	PRO	-	expression tag	UNP R4I4P2
A	224	SER	-	expression tag	UNP R4I4P2
B	222	GLY	-	expression tag	UNP R4I4P2
B	223	PRO	-	expression tag	UNP R4I4P2
B	224	SER	-	expression tag	UNP R4I4P2

- Molecule 2 is a protein called A1227 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	211	Total	C	N	O	S	0	0	0
			1619	1009	275	331	4			
2	L	211	Total	C	N	O	S	0	0	0
			1619	1009	275	331	4			

- Molecule 3 is a protein called A1227 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	217	Total	C	N	O	S	0	0	0
			1598	1004	270	315	9			
3	H	225	Total	C	N	O	S	0	0	0
			1646	1030	279	328	9			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	75	Total 75	O 75	0	0
4	B	109	Total 109	O 109	0	0
4	D	13	Total 13	O 13	0	0
4	C	18	Total 18	O 18	0	0
4	H	46	Total 46	O 46	0	0
4	L	46	Total 46	O 46	0	0

3 Residue-property plots [i](#)

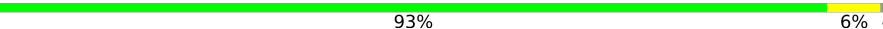
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Major capsid protein

Chain A: 



- Molecule 1: Major capsid protein

Chain B: 



- Molecule 2: A1227 Fab light chain

Chain D: 



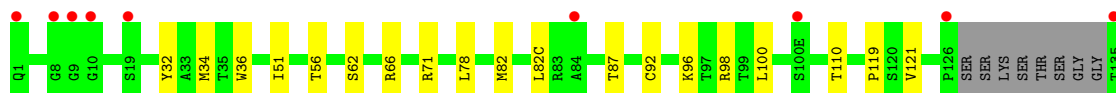
- Molecule 2: A1227 Fab light chain

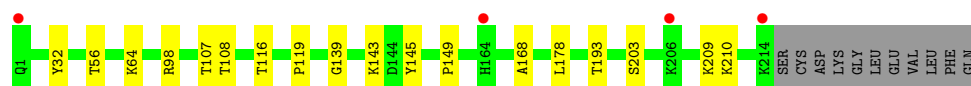
Chain L: 



- Molecule 3: A1227 Fab heavy chain

Chain C: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.60Å 150.10Å 117.25Å 90.00° 95.06° 90.00°	Depositor
Resolution (Å)	46.09 – 2.58 46.09 – 2.58	Depositor EDS
% Data completeness (in resolution range)	94.7 (46.09-2.58) 94.7 (46.09-2.58)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.173 , 0.211 0.178 , 0.214	Depositor DCC
R_{free} test set	4108 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	1.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.4	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	0.94	EDS
Total number of atoms	11539	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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	0.29	0/2446	0.67	0/3347
1	B	0.29	0/2446	0.68	0/3347
2	D	0.26	0/1653	0.68	0/2243
2	L	0.29	0/1653	0.67	0/2243
3	C	0.32	0/1632	0.74	1/2220 (0.0%)
3	H	0.29	0/1681	0.69	1/2286 (0.0%)
All	All	0.29	0/11511	0.69	2/15686 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	188	SER	N-CA-C	-6.23	105.25	112.92
3	H	139	GLY	N-CA-C	5.43	117.91	110.69

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	2375	0	2265	14	0
1	B	2375	0	2265	12	0
2	D	1619	0	1573	13	0
2	L	1619	0	1573	12	0
3	C	1598	0	1582	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1646	0	1629	11	0
4	A	75	0	0	0	0
4	B	109	0	0	2	0
4	C	18	0	0	0	0
4	D	13	0	0	0	0
4	H	46	0	0	1	0
4	L	46	0	0	1	0
All	All	11539	0	10887	76	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 3.

All (76) 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:B:507:LEU:O	4:B:601:HOH:O	2.13	0.67
3:H:143:LYS:NZ	2:L:129:THR:HG21	2.09	0.66
3:C:151:THR:HB	3:C:199:ASN:HB3	1.80	0.63
3:C:121:VAL:O	3:C:209:LYS:NZ	2.32	0.63
2:D:6:GLN:O	2:D:100:GLN:NE2	2.35	0.60
2:L:163:VAL:HG22	2:L:175:LEU:HD12	1.83	0.60
3:C:121:VAL:HG21	3:C:198:VAL:HG21	1.84	0.59
3:H:143:LYS:HZ2	2:L:129:THR:HG21	1.67	0.59
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.85	0.58
1:A:282:ASN:ND2	1:A:306:GLN:OE1	2.39	0.56
3:H:209:LYS:HZ1	2:L:123:GLU:CD	2.15	0.55
2:L:39:LYS:NZ	2:L:81:GLU:O	2.27	0.54
2:D:18:ARG:HG2	2:D:76:SER:O	2.07	0.54
2:L:159:SER:OG	4:L:301:HOH:O	2.19	0.53
1:B:282:ASN:ND2	1:B:306:GLN:OE1	2.41	0.53
3:C:193:THR:HG23	3:C:210:LYS:HE3	1.91	0.53
2:D:118:PHE:HB2	2:D:133:VAL:HG13	1.91	0.52
3:H:108:THR:HG21	3:H:149:PRO:HD3	1.91	0.52
2:D:81:GLU:N	2:D:81:GLU:OE1	2.42	0.52
2:D:167:ASP:HB3	2:D:170:ASP:OD1	2.10	0.52
2:D:83:PHE:HZ	2:D:165:GLU:HB3	1.75	0.51
3:C:138:LEU:HB2	3:C:211:VAL:HG11	1.93	0.50
1:B:315:GLU:HG2	1:B:317:ILE:HG12	1.93	0.50
1:A:287:ARG:HD2	1:A:306:GLN:HA	1.94	0.50
2:D:37:GLN:HB3	2:D:47:LEU:HD11	1.93	0.49
1:A:348:LYS:HB2	1:A:370:ASP:OD1	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:SER:HB3	1:A:520:TRP:HB3	1.93	0.49
3:C:119:PRO:HB3	3:C:145:TYR:HB3	1.94	0.49
3:H:56:THR:N	4:H:302:HOH:O	2.28	0.49
3:H:193:THR:HG23	3:H:210:LYS:HE3	1.96	0.48
3:H:119:PRO:HB3	3:H:145:TYR:HB3	1.95	0.48
3:C:36:TRP:CZ3	3:C:92:CYS:HB3	2.48	0.47
1:B:366:GLN:HB2	4:B:613:HOH:O	2.15	0.47
3:H:168:ALA:HB2	3:H:178:LEU:HD23	1.97	0.47
3:C:62:SER:O	3:C:66:ARG:NH1	2.41	0.47
3:H:32:TYR:CE2	3:H:98:ARG:HG3	2.50	0.47
1:A:225:LYS:HA	1:A:226:PRO:HD3	1.71	0.47
1:A:424:PRO:HD3	1:A:431:LEU:HG	1.97	0.47
1:A:433:PHE:HB3	1:A:450:ASP:HB3	1.97	0.46
1:A:231:ILE:HB	3:C:100:LEU:HD21	1.97	0.46
1:A:311:TYR:CE1	1:A:320:PRO:HG3	2.50	0.46
3:C:148:GLU:HB3	3:C:149:PRO:HA	1.97	0.46
2:L:80:PRO:HA	2:L:106:LEU:HD22	1.97	0.46
1:A:470:SER:OG	1:A:471:ASP:N	2.49	0.45
2:L:107:LYS:HA	2:L:140:TYR:OH	2.16	0.45
3:C:34:MET:HB3	3:C:78:LEU:HD22	1.99	0.45
2:D:120:PRO:HD3	2:D:132:VAL:HG22	1.99	0.45
1:A:440:GLY:HA3	1:B:344:THR:HG21	1.99	0.45
1:B:348:LYS:HB2	1:B:370:ASP:OD2	2.17	0.45
3:C:82:MET:HB3	3:C:82(C):LEU:HD21	1.98	0.45
1:B:371:THR:OG1	1:B:372:ASN:N	2.50	0.44
1:B:490:LYS:HG3	1:B:527:LEU:HD21	1.99	0.44
3:C:184:VAL:HG11	3:C:194:TYR:CZ	2.53	0.44
3:C:87:THR:HG23	3:C:110:THR:HA	2.00	0.43
1:A:490:LYS:HG3	1:A:527:LEU:HD21	2.00	0.43
3:H:64:LYS:HB2	3:H:64:LYS:HE3	1.81	0.43
2:D:125:LEU:O	2:D:183:LYS:HD2	2.19	0.43
3:C:32:TYR:CE2	3:C:98:ARG:HG3	2.54	0.42
2:D:49:TYR:CE1	3:C:96:LYS:HE3	2.54	0.42
1:B:475:LEU:HB2	1:B:489:CYS:SG	2.60	0.42
2:L:33:LEU:HD22	2:L:71:PHE:CG	2.55	0.42
3:C:212:GLU:HA	3:C:213:PRO:HD3	1.85	0.42
3:H:116:THR:HG22	3:H:203:SER:HB3	2.02	0.42
3:C:51:ILE:HD13	3:C:71:ARG:HD3	2.00	0.42
3:C:146:PHE:HA	3:C:147:PRO:HA	1.75	0.42
3:C:200:HIS:CD2	3:C:202:PRO:HD2	2.54	0.42
1:A:328:GLY:HA3	1:A:400:PRO:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:PRO:HB3	1:B:455:GLN:HG2	2.02	0.41
2:D:122:ASP:OD1	2:D:123:GLU:N	2.53	0.41
1:B:333:MET:HE2	1:B:333:MET:HB3	1.94	0.41
2:L:158:ASN:OD1	2:L:158:ASN:N	2.53	0.41
1:A:472:VAL:HG11	1:A:490:LYS:HE3	2.03	0.41
2:L:140:TYR:CG	2:L:141:PRO:HA	2.55	0.41
1:B:424:PRO:HD3	1:B:431:LEU:HG	2.03	0.41
2:D:83:PHE:CZ	2:D:165:GLU:HB3	2.54	0.40
2:D:80:PRO:HA	2:D:106:LEU:HG	2.02	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	304/309 (98%)	294 (97%)	10 (3%)	0	100	100
1	B	304/309 (98%)	295 (97%)	9 (3%)	0	100	100
2	D	209/214 (98%)	203 (97%)	6 (3%)	0	100	100
2	L	209/214 (98%)	205 (98%)	4 (2%)	0	100	100
3	C	213/236 (90%)	189 (89%)	20 (9%)	4 (2%)	6	12
3	H	223/236 (94%)	218 (98%)	5 (2%)	0	100	100
All	All	1462/1518 (96%)	1404 (96%)	54 (4%)	4 (0%)	36	56

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	213	PRO
3	C	56	THR
3	C	193	THR
3	C	201	LYS

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	263/265 (99%)	263 (100%)	0	100	100
1	B	263/265 (99%)	263 (100%)	0	100	100
2	D	187/189 (99%)	185 (99%)	2 (1%)	65	83
2	L	187/189 (99%)	186 (100%)	1 (0%)	81	91
3	C	179/195 (92%)	177 (99%)	2 (1%)	65	83
3	H	185/195 (95%)	184 (100%)	1 (0%)	81	91
All	All	1264/1298 (97%)	1258 (100%)	6 (0%)	81	91

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	18	ARG
2	D	94	THR
3	C	206	LYS
3	C	209	LYS
3	H	107	THR
2	L	190	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	282	ASN
1	A	309	ASN
1	A	357	HIS
1	A	368	ASN
1	B	368	ASN
1	B	505	HIS
2	D	160	GLN
3	H	39	GLN
3	H	81	GLN
2	L	38	GLN
2	L	79	GLN

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Mol	Chain	Res	Type
2	L	199	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	306/309 (99%)	-0.06	1 (0%) 90 89	24, 38, 59, 66	0
1	B	306/309 (99%)	-0.22	1 (0%) 90 89	19, 34, 54, 67	0
2	D	211/214 (98%)	0.50	8 (3%) 44 39	37, 63, 82, 98	0
2	L	211/214 (98%)	-0.07	2 (0%) 81 79	23, 37, 54, 73	0
3	C	217/236 (91%)	0.99	40 (18%) 3 3	32, 72, 120, 133	0
3	H	225/236 (95%)	-0.03	4 (1%) 67 64	25, 39, 57, 71	0
All	All	1476/1518 (97%)	0.14	56 (3%) 44 39	19, 42, 89, 133	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	159	LEU	5.5
3	C	189	LEU	5.1
3	C	191	THR	5.0
3	C	135	THR	4.5
3	C	214	LYS	4.3
3	C	185	PRO	3.9
3	H	214	LYS	3.8
1	B	451	CYS	3.7
3	C	126	PRO	3.6
3	C	188	SER	3.5
3	C	190	GLY	3.4
3	C	213	PRO	3.2
2	D	169	LYS	3.2
3	C	207	VAL	3.1
3	C	156	SER	2.9
3	C	19	SER	2.9
1	A	316	GLU	2.9
3	C	150	VAL	2.8
3	H	164	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
2	D	122	ASP	2.8
3	C	201	LYS	2.8
3	C	161	SER	2.8
3	C	136	ALA	2.8
3	H	206	LYS	2.8
3	H	1	GLN	2.8
3	C	138	LEU	2.7
3	C	198	VAL	2.7
3	C	205	THR	2.6
3	C	158	ALA	2.6
3	C	206	LYS	2.6
3	C	151	THR	2.6
2	D	127	SER	2.5
3	C	186	SER	2.5
2	D	1	ASP	2.4
3	C	9	GLY	2.4
2	L	194	CYS	2.4
3	C	194	TYR	2.4
3	C	199	ASN	2.4
3	C	195	ILE	2.3
3	C	1	GLN	2.3
3	C	149	PRO	2.3
2	L	1	ASP	2.3
2	D	194	CYS	2.3
3	C	211	VAL	2.2
3	C	183	THR	2.2
3	C	209	LYS	2.2
2	D	170	ASP	2.2
3	C	84	ALA	2.2
3	C	8	GLY	2.2
2	D	24	ARG	2.2
3	C	154	TRP	2.1
3	C	204	ASN	2.1
3	C	10	GLY	2.1
3	C	100(E)	SER	2.1
2	D	143	GLU	2.0
3	C	187	SER	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 [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.