Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:25 PM GMT

PDB ID	:	3RA9
Title	:	Structural studies of AAV8 capsid transitions associated with endosomal trafficking
Authors	:	Nam, H.-J.; Gurda, B.; McKenna, R.; Porter, M.; Byrne, B.; Salganik, M.; Muzyczka, N.; Agbandje-McKenna, M.
Deposited on	:	2011-03-27
Resolution	:	2.70 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ⓘ) were used in the production of this report:

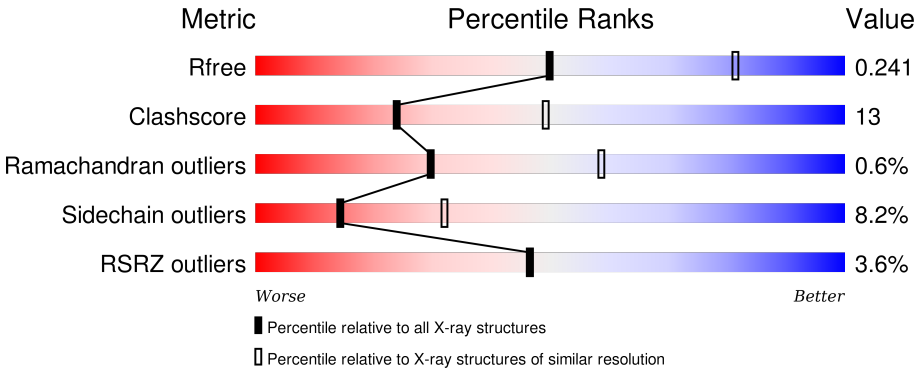
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=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	519	3%, 74%, 22%, ·
2	D	2	50%, 50%, 50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4231 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 Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			4136	2609	716	798	13			

- Molecule 2 is a DNA chain called DNA (5'-D(P*CP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	2	Total	C	N	O	P	0	0	0
			41	19	8	12	2			

- Molecule 3 is water.

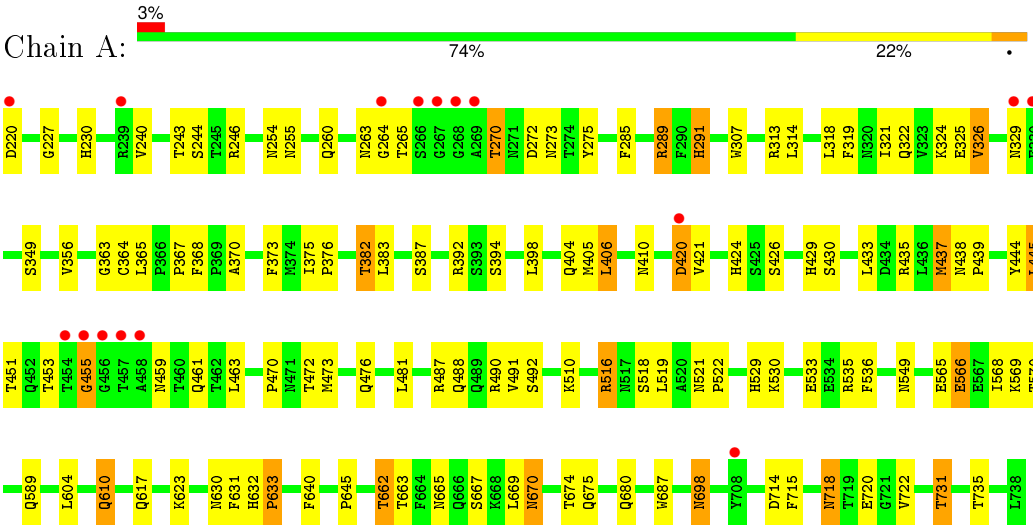
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	54	Total	O	0	0
			54	54		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Capsid protein

Chain A:



- Molecule 2: DNA (5'-D(P*CP*A)-3')

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α, β, γ	257.94Å 257.94Å 448.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 2.70 39.51 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.70) 73.5 (39.51-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.76 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.248 0.240 , 0.241	Depositor DCC
R_{free} test set	8780 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	31.2	Xtriage
Anisotropy	0.512	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Outliers	3 of 175411 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	4231	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.46	0/4259	0.71	1/5811 (0.0%)
2	D	1.81	1/45 (2.2%)	1.22	0/65
All	All	0.49	1/4304 (0.0%)	0.71	1/5876 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	DC	OP3-P	-7.27	1.52	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	455	GLY	N-CA-C	5.33	126.41	113.10

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	4136	0	3893	106	0
2	D	41	0	23	7	0
3	A	54	0	0	1	0
All	All	4231	0	3916	106	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 13.

All (106) 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:420:ASP:HB3	2:D:1:DC:N4	1.61	1.14
1:A:382:THR:HG21	1:A:394:SER:H	1.25	0.99
1:A:289:ARG:HG2	1:A:289:ARG:HH11	1.26	0.95
1:A:632:HIS:N	1:A:633:PRO:HD3	1.82	0.93
1:A:698:ASN:H	1:A:698:ASN:HD22	1.15	0.93
1:A:718:ASN:HB3	1:A:720:GLU:H	1.32	0.91
1:A:632:HIS:N	1:A:633:PRO:CD	2.36	0.87
1:A:566:GLU:O	1:A:569:LYS:HG3	1.78	0.84
1:A:420:ASP:HB3	2:D:1:DC:H41	1.40	0.81
1:A:529:HIS:CG	1:A:533:GLU:O	2.34	0.80
1:A:289:ARG:HG2	1:A:289:ARG:NH1	1.93	0.75
1:A:420:ASP:HB3	2:D:1:DC:H42	1.51	0.73
1:A:698:ASN:ND2	1:A:698:ASN:H	1.84	0.72
1:A:321:ILE:HD13	1:A:343:ILE:HD11	1.73	0.71
1:A:270:THR:HG23	1:A:273:ASN:HD22	1.58	0.69
1:A:429:HIS:HB2	1:A:570:THR:HG21	1.75	0.68
1:A:529:HIS:CD2	1:A:533:GLU:O	2.48	0.67
1:A:420:ASP:CB	2:D:1:DC:H41	2.09	0.66
1:A:420:ASP:CB	2:D:1:DC:N4	2.51	0.66
1:A:289:ARG:CG	1:A:289:ARG:HH11	2.06	0.65
1:A:426:SER:HA	1:A:731:THR:CG2	2.26	0.65
1:A:383:LEU:HD12	1:A:392:ARG:HB2	1.80	0.64
1:A:670:ASN:HD22	1:A:670:ASN:H	1.45	0.64
1:A:363:GLY:HA3	1:A:376:PRO:HG3	1.81	0.63
1:A:631:PHE:C	1:A:633:PRO:HD3	2.19	0.63
1:A:630:ASN:OD1	1:A:633:PRO:HG3	1.99	0.63
1:A:420:ASP:C	2:D:1:DC:N4	2.52	0.62
1:A:382:THR:HG22	1:A:383:LEU:H	1.64	0.62
1:A:718:ASN:HB2	1:A:722:VAL:H	1.65	0.61
1:A:220:ASP:HA	3:A:42:HOH:O	2.00	0.61
1:A:404:GLN:HE21	1:A:406:LEU:HD22	1.66	0.61
1:A:264:GLY:CA	1:A:387:SER:HB3	2.31	0.60
1:A:435:ARG:NE	1:A:473:MET:HE3	2.17	0.59
1:A:382:THR:HG21	1:A:394:SER:N	2.09	0.59
1:A:314:LEU:HD12	1:A:314:LEU:C	2.23	0.58
1:A:321:ILE:HD13	1:A:343:ILE:CD1	2.34	0.58
1:A:623:LYS:HB2	1:A:645:PRO:HG3	1.86	0.58
1:A:321:ILE:CD1	1:A:406:LEU:HD12	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:SER:HA	1:A:731:THR:HG23	1.86	0.57
1:A:321:ILE:HD12	1:A:406:LEU:HD12	1.87	0.57
1:A:490:ARG:HD2	1:A:536:PHE:CG	2.40	0.56
1:A:264:GLY:HA3	1:A:387:SER:HB3	1.89	0.55
1:A:510:LYS:HB3	1:A:518:SER:O	2.07	0.54
1:A:437:MET:HG2	1:A:476:GLN:OE1	2.08	0.54
1:A:326:VAL:HG13	1:A:674:THR:HG22	1.89	0.53
1:A:313:ARG:HB3	1:A:313:ARG:NH1	2.25	0.52
1:A:406:LEU:N	1:A:406:LEU:HD23	2.25	0.51
1:A:665:ASN:HD21	1:A:667:SER:HB2	1.74	0.51
1:A:492:SER:HB2	1:A:536:PHE:CE2	2.45	0.51
1:A:670:ASN:HD22	1:A:670:ASN:N	2.04	0.51
1:A:329:ASN:O	1:A:332:THR:CG2	2.59	0.51
1:A:289:ARG:HD2	1:A:364:CYS:SG	2.51	0.50
1:A:244:SER:HB2	1:A:246:ARG:HH12	1.75	0.50
1:A:285:PHE:CZ	1:A:318:LEU:HD21	2.46	0.50
1:A:632:HIS:N	1:A:633:PRO:HD2	2.26	0.50
1:A:289:ARG:NH1	1:A:617:GLN:O	2.45	0.49
1:A:405:MET:C	1:A:406:LEU:HD23	2.34	0.48
1:A:492:SER:HB2	1:A:536:PHE:HE2	1.78	0.48
1:A:487:ARG:HG3	1:A:488:GLN:N	2.28	0.48
1:A:444:TYR:CD2	1:A:445:LEU:HD13	2.49	0.48
1:A:324:LYS:O	1:A:675:GLN:HB2	2.14	0.48
1:A:326:VAL:HG13	1:A:674:THR:CG2	2.43	0.48
1:A:535:ARG:HG2	1:A:535:ARG:HH11	1.79	0.47
1:A:451:THR:O	1:A:451:THR:HG22	2.12	0.47
1:A:633:PRO:HD2	2:D:2:DA:H2"	1.96	0.47
1:A:270:THR:CG2	1:A:273:ASN:HD22	2.26	0.47
1:A:424:HIS:CD2	1:A:731:THR:HG21	2.49	0.47
1:A:450:ARG:HH11	1:A:450:ARG:HG3	1.79	0.47
1:A:329:ASN:O	1:A:332:THR:HG22	2.15	0.47
1:A:669:LEU:H	1:A:669:LEU:HD22	1.80	0.46
1:A:529:HIS:HD2	1:A:530:LYS:O	1.99	0.46
1:A:698:ASN:HD22	1:A:698:ASN:N	1.97	0.45
1:A:662:THR:HG22	1:A:663:THR:HG23	1.98	0.45
1:A:254:ASN:O	1:A:255:ASN:HB2	2.16	0.45
1:A:439:PRO:O	1:A:470:PRO:HB3	2.17	0.45
1:A:246:ARG:HG3	1:A:365:LEU:HB3	1.99	0.45
1:A:670:ASN:ND2	1:A:670:ASN:C	2.70	0.45
1:A:230:HIS:O	1:A:243:THR:HG22	2.17	0.45
1:A:272:ASP:HA	1:A:516:ARG:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:THR:O	1:A:662:THR:HG23	2.16	0.44
1:A:610:GLN:CA	1:A:610:GLN:HE21	2.28	0.44
1:A:368:PHE:CE2	1:A:370:ALA:HB3	2.52	0.44
1:A:435:ARG:CZ	1:A:473:MET:HE3	2.47	0.43
1:A:529:HIS:CB	1:A:533:GLU:O	2.66	0.43
1:A:421:VAL:HG21	1:A:640:PHE:HB3	2.01	0.43
1:A:714:ASP:O	1:A:715:PHE:HB2	2.19	0.43
1:A:430:SER:HB3	1:A:735:THR:HB	2.01	0.42
1:A:698:ASN:ND2	1:A:698:ASN:N	2.58	0.42
1:A:438:ASN:HA	1:A:439:PRO:HD3	1.88	0.42
1:A:670:ASN:ND2	1:A:670:ASN:N	2.68	0.42
1:A:453:THR:OG1	1:A:459:ASN:HA	2.20	0.42
1:A:227:GLY:HA3	1:A:319:PHE:CD1	2.54	0.42
1:A:490:ARG:HB2	1:A:576:THR:HB	2.01	0.42
1:A:240:VAL:CG1	1:A:687:TRP:HB2	2.50	0.42
1:A:307:TRP:C	1:A:426:SER:OG	2.58	0.42
1:A:291:HIS:CE1	1:A:367:PRO:HG3	2.55	0.41
1:A:718:ASN:HB3	1:A:720:GLU:N	2.16	0.41
1:A:451:THR:O	1:A:451:THR:CG2	2.69	0.41
1:A:406:LEU:HB3	1:A:410:ASN:CB	2.50	0.41
1:A:275:TYR:C	1:A:275:TYR:CD1	2.94	0.41
1:A:365:LEU:HD22	1:A:373:PHE:CZ	2.56	0.41
1:A:662:THR:HG22	1:A:663:THR:CG2	2.50	0.41
1:A:398:LEU:HD23	1:A:398:LEU:N	2.36	0.41
1:A:375:ILE:HA	1:A:376:PRO:HD3	1.80	0.40
1:A:565:GLU:O	1:A:568:ILE:HG12	2.22	0.40
1:A:521:ASN:HA	1:A:522:PRO:HA	1.82	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	517/519 (100%)	493 (95%)	21 (4%)	3 (1%)	30 59

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	455	GLY
1	A	633	PRO
1	A	331	GLY

5.3.2 Protein sidechains (i)

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	453/453 (100%)	416 (92%)	37 (8%)	14 32

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	260	GLN
1	A	263	ASN
1	A	265	THR
1	A	270	THR
1	A	289	ARG
1	A	291	HIS
1	A	322	GLN
1	A	325	GLU
1	A	326	VAL
1	A	349	SER
1	A	356	VAL
1	A	382	THR
1	A	406	LEU
1	A	420	ASP
1	A	433	LEU
1	A	437	MET
1	A	445	LEU
1	A	448	LEU

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Mol	Chain	Res	Type
1	A	461	GLN
1	A	463	LEU
1	A	472	THR
1	A	481	LEU
1	A	491	VAL
1	A	516	ARG
1	A	519	LEU
1	A	549	ASN
1	A	566	GLU
1	A	578	GLU
1	A	589	GLN
1	A	604	LEU
1	A	610	GLN
1	A	662	THR
1	A	670	ASN
1	A	680	GLN
1	A	698	ASN
1	A	718	ASN
1	A	731	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	GLN
1	A	263	ASN
1	A	273	ASN
1	A	322	GLN
1	A	404	GLN
1	A	429	HIS
1	A	467	GLN
1	A	499	ASN
1	A	529	HIS
1	A	549	ASN
1	A	610	GLN
1	A	611	ASN
1	A	653	ASN
1	A	665	ASN
1	A	666	GLN
1	A	670	ASN
1	A	698	ASN
1	A	718	ASN
1	A	737	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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, 95^{th} 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	519/519 (100%)	-0.01	18 (3%) 48 48	20, 30, 50, 84	0
2	D	2/2 (100%)	3.60	1 (50%) 0 0	54, 54, 54, 103	2 (100%)
All	All	521/521 (100%)	-0.00	19 (3%) 46 46	20, 30, 50, 103	2 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	1	DC	6.2
1	A	458	ALA	5.2
1	A	457	THR	4.8
1	A	267	GLY	4.1
1	A	330	GLU	4.0
1	A	332	THR	3.9
1	A	456	GLY	3.6
1	A	266	SER	3.2
1	A	331	GLY	2.9
1	A	264	GLY	2.5
1	A	420	ASP	2.5
1	A	269	ALA	2.4
1	A	220	ASP	2.4
1	A	455	GLY	2.4
1	A	329	ASN	2.2
1	A	708	TYR	2.2
1	A	454	THR	2.1
1	A	268	GLY	2.1
1	A	239	ARG	2.1

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 carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.