Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 10:20 PM EDT

PDB ID	:	3RA2
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	:	2011-03-26
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

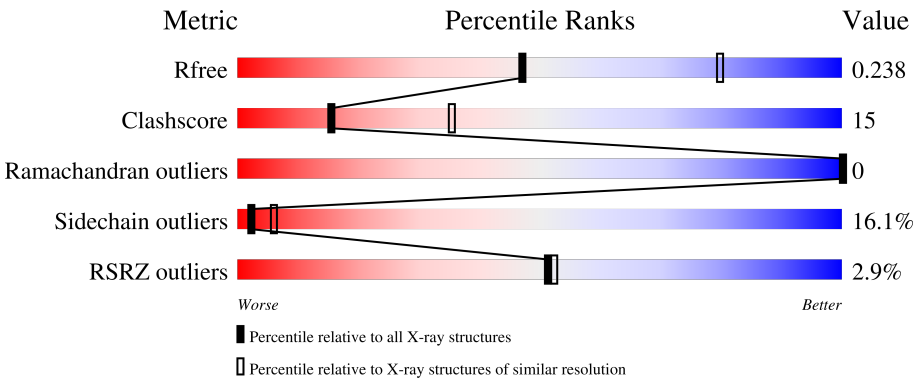
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

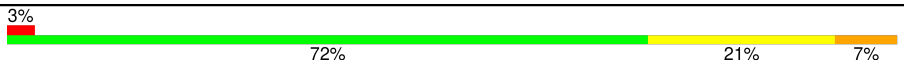
The reported resolution of this entry is 2.70 Å.

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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 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 <=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	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4223 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
			Total	C	N	O	S			
1	A	519	4136	2609	716	798	13	0	0	0

- Molecule 2 is water.

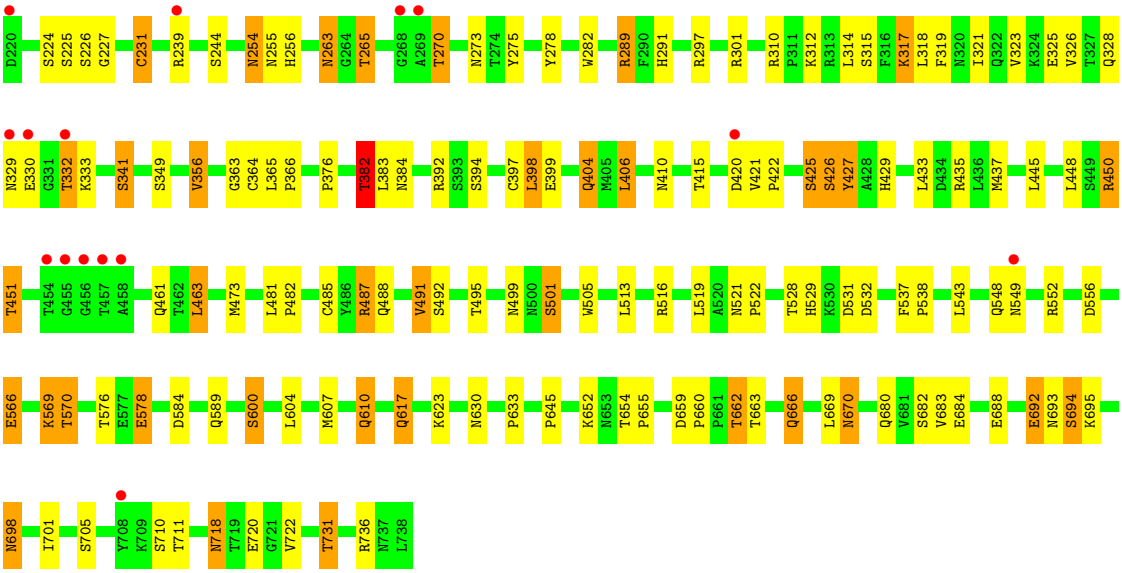
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	87	87	87	0	0

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: Capsid protein

Chain A:



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 39.96 – 2.60	Depositor EDS
% Data completeness (in resolution range)	86.8 (40.00-2.70) 82.8 (39.96-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.244 , 0.244 0.239 , 0.238	Depositor DCC
R_{free} test set	11064 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	33.7	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	4223	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.68% 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, 0.333 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	1.67	4/4259 (0.1%)	0.74	1/5811 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	364	CYS	CB-SG	-5.86	1.72	1.81
1	A	397	CYS	CB-SG	-5.76	1.72	1.81
1	A	278	TYR	CD2-CE2	-5.20	1.31	1.39
1	A	427	TYR	CD2-CE2	-5.08	1.31	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	382	THR	CB-CA-C	-5.03	98.03	111.60

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	4136	0	3893	119	0
2	A	87	0	0	1	0
All	All	4223	0	3893	119	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 15.

All (119) 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:289:ARG:HG2	1:A:289:ARG:HH11	1.05	1.17
1:A:426:SER:HB3	1:A:731:THR:HG23	1.31	1.08
1:A:289:ARG:HG2	1:A:289:ARG:NH1	1.69	0.96
1:A:666:GLN:O	1:A:666:GLN:HG3	1.62	0.96
1:A:289:ARG:HH11	1:A:289:ARG:CG	1.82	0.93
1:A:718:ASN:HB3	1:A:720:GLU:H	1.35	0.92
1:A:566:GLU:O	1:A:569:LYS:HG2	1.72	0.90
1:A:426:SER:HB3	1:A:731:THR:CG2	2.02	0.89
1:A:329:ASN:O	1:A:332:THR:HG23	1.74	0.87
1:A:426:SER:HA	1:A:731:THR:HG22	1.59	0.84
1:A:382:THR:HG21	1:A:394:SER:H	1.42	0.84
1:A:435:ARG:CD	1:A:473:MET:CE	2.58	0.82
1:A:698:ASN:HD22	1:A:698:ASN:H	1.23	0.81
1:A:255:ASN:O	1:A:256:HIS:HB2	1.79	0.79
1:A:566:GLU:HA	1:A:566:GLU:OE2	1.82	0.78
1:A:731:THR:CG2	1:A:731:THR:O	2.30	0.78
1:A:329:ASN:HB3	1:A:330:GLU:OE1	1.83	0.77
1:A:265:THR:O	1:A:265:THR:HG23	1.83	0.77
1:A:435:ARG:CD	1:A:473:MET:HE1	2.14	0.76
1:A:426:SER:HA	1:A:731:THR:CG2	2.15	0.76
1:A:718:ASN:HB2	1:A:722:VAL:H	1.49	0.75
1:A:566:GLU:OE2	1:A:566:GLU:CA	2.36	0.72
1:A:435:ARG:NE	1:A:473:MET:HE3	2.06	0.71
1:A:450:ARG:NH1	1:A:450:ARG:HG3	2.05	0.69
1:A:227:GLY:HA3	1:A:319:PHE:CD1	2.28	0.69
1:A:435:ARG:HD3	1:A:473:MET:CE	2.22	0.68
1:A:698:ASN:H	1:A:698:ASN:ND2	1.92	0.68
1:A:254:ASN:O	1:A:255:ASN:HB2	1.94	0.67
1:A:450:ARG:HG3	1:A:450:ARG:HH11	1.59	0.67
1:A:429:HIS:HB2	1:A:570:THR:HG21	1.76	0.67
1:A:566:GLU:O	1:A:569:LYS:CG	2.43	0.66
1:A:610:GLN:HE21	1:A:610:GLN:CA	2.09	0.65
1:A:426:SER:CB	1:A:731:THR:CG2	2.75	0.65
1:A:330:GLU:OE1	1:A:330:GLU:N	2.30	0.65
1:A:662:THR:CG2	1:A:662:THR:O	2.46	0.64
1:A:435:ARG:CD	1:A:473:MET:HE3	2.26	0.64
1:A:435:ARG:NE	1:A:473:MET:CE	2.60	0.64
1:A:450:ARG:HH11	1:A:450:ARG:CG	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:LEU:N	1:A:398:LEU:HD23	2.13	0.63
1:A:531:ASP:O	1:A:532:ASP:HB2	1.97	0.63
1:A:451:THR:CG2	1:A:451:THR:O	2.46	0.63
1:A:297:ARG:HG3	1:A:301:ARG:CZ	2.30	0.62
1:A:265:THR:O	1:A:265:THR:CG2	2.48	0.61
1:A:718:ASN:HB3	1:A:720:GLU:N	2.12	0.61
1:A:731:THR:HG23	1:A:731:THR:O	1.99	0.61
1:A:731:THR:HG22	1:A:731:THR:O	2.01	0.61
1:A:421:VAL:HG22	1:A:422:PRO:HD2	1.82	0.60
1:A:662:THR:O	1:A:662:THR:HG23	2.01	0.60
1:A:485:CYS:O	1:A:600:SER:HA	2.03	0.59
1:A:426:SER:CA	1:A:731:THR:CG2	2.82	0.58
1:A:435:ARG:HD3	1:A:473:MET:HE3	1.85	0.58
1:A:670:ASN:H	1:A:670:ASN:HD22	1.50	0.58
1:A:321:ILE:CD1	1:A:406:LEU:HD12	2.34	0.58
1:A:312:LYS:HD3	1:A:688:GLU:OE2	2.04	0.58
1:A:255:ASN:O	1:A:256:HIS:CB	2.50	0.57
1:A:356:VAL:O	1:A:356:VAL:HG13	2.06	0.56
1:A:399:GLU:OE2	1:A:652:LYS:NZ	2.37	0.55
1:A:451:THR:O	1:A:451:THR:HG23	2.07	0.55
1:A:487:ARG:HG3	1:A:488:GLN:N	2.22	0.55
1:A:659:ASP:OD2	1:A:659:ASP:N	2.34	0.55
1:A:289:ARG:NH1	1:A:617:GLN:O	2.40	0.55
1:A:610:GLN:CA	1:A:610:GLN:NE2	2.71	0.54
1:A:610:GLN:NE2	1:A:610:GLN:HA	2.23	0.54
1:A:231:CYS:SG	1:A:244:SER:HA	2.48	0.53
1:A:382:THR:HG22	1:A:383:LEU:H	1.72	0.53
1:A:435:ARG:HD3	1:A:473:MET:HE1	1.83	0.53
1:A:435:ARG:CZ	1:A:473:MET:CE	2.87	0.53
1:A:435:ARG:HD2	1:A:473:MET:HE1	1.88	0.52
1:A:310:ARG:NH1	1:A:421:VAL:O	2.36	0.52
1:A:263:ASN:HB2	1:A:275:TYR:CE2	2.44	0.52
1:A:323:VAL:HG11	1:A:341:SER:HB3	1.92	0.52
1:A:670:ASN:H	1:A:670:ASN:ND2	2.08	0.52
1:A:491:VAL:HG22	1:A:537:PHE:CE2	2.45	0.52
1:A:317:LYS:HD3	1:A:319:PHE:CD2	2.46	0.51
1:A:329:ASN:C	1:A:330:GLU:OE1	2.50	0.51
1:A:529:HIS:CD2	1:A:566:GLU:OE1	2.64	0.51
1:A:297:ARG:HG3	1:A:301:ARG:NH1	2.26	0.50
1:A:404:GLN:NE2	1:A:406:LEU:CD2	2.75	0.50
1:A:692:GLU:HG2	1:A:693:ASN:N	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:VAL:HG22	1:A:422:PRO:CD	2.42	0.49
1:A:363:GLY:HA3	1:A:376:PRO:HG3	1.94	0.48
1:A:482:PRO:O	1:A:607:MET:HG2	2.15	0.47
1:A:382:THR:HG21	1:A:394:SER:N	2.21	0.47
1:A:425:SER:HB3	1:A:427:TYR:CE2	2.51	0.46
1:A:670:ASN:HD22	1:A:670:ASN:N	2.06	0.46
1:A:695:LYS:HA	1:A:695:LYS:HD2	1.61	0.46
1:A:384:ASN:OD1	1:A:516:ARG:NH2	2.49	0.46
1:A:670:ASN:ND2	1:A:670:ASN:N	2.63	0.46
1:A:578:GLU:H	1:A:578:GLU:HG3	1.45	0.45
1:A:314:LEU:C	1:A:314:LEU:HD12	2.37	0.45
1:A:328:GLN:OE1	1:A:333:LYS:HB2	2.15	0.45
1:A:319:PHE:CD2	1:A:319:PHE:N	2.84	0.45
1:A:521:ASN:HA	1:A:522:PRO:HA	1.82	0.45
1:A:623:LYS:HB2	1:A:645:PRO:HG3	1.99	0.44
1:A:263:ASN:HD22	1:A:263:ASN:HA	1.49	0.44
1:A:630:ASN:CG	1:A:633:PRO:HG3	2.38	0.43
1:A:692:GLU:HG2	1:A:694:SER:H	1.83	0.43
1:A:491:VAL:HG23	1:A:492:SER:N	2.34	0.43
1:A:406:LEU:HB3	1:A:410:ASN:HB2	2.01	0.42
1:A:398:LEU:N	1:A:398:LEU:CD2	2.82	0.42
1:A:435:ARG:CZ	1:A:473:MET:HE2	2.49	0.42
1:A:528:THR:HG23	1:A:538:PRO:HD3	2.02	0.42
1:A:718:ASN:HD22	1:A:718:ASN:HA	1.53	0.42
1:A:529:HIS:O	1:A:566:GLU:OE1	2.37	0.42
1:A:383:LEU:HD12	1:A:392:ARG:HB2	2.02	0.42
1:A:499:ASN:ND2	1:A:501:SER:OG	2.51	0.42
1:A:282:TRP:CE2	1:A:652:LYS:HD3	2.55	0.42
1:A:365:LEU:HA	1:A:366:PRO:HD3	1.92	0.41
1:A:654:THR:HA	1:A:655:PRO:HD3	1.93	0.41
1:A:610:GLN:HE21	1:A:610:GLN:HA	1.80	0.41
1:A:318:LEU:HD23	1:A:318:LEU:HA	1.88	0.41
1:A:543:LEU:HA	2:A:13:HOH:O	2.20	0.41
1:A:659:ASP:HA	1:A:660:PRO:HD2	1.86	0.41
1:A:463:LEU:HD12	1:A:463:LEU:HA	1.84	0.41
1:A:329:ASN:CB	1:A:330:GLU:OE1	2.62	0.40
1:A:487:ARG:NH1	1:A:576:THR:O	2.52	0.40
1:A:270:THR:HG23	1:A:273:ASN:HD22	1.85	0.40
1:A:314:LEU:HA	1:A:684:GLU:O	2.21	0.40
1:A:548:GLN:O	1:A:549:ASN:HB3	2.21	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%)	508 (98%)	9 (2%)	0	100 100

There are no Ramachandran outliers to report.

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%)	380 (84%)	73 (16%)	2 6

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	SER
1	A	225	SER
1	A	226	SER
1	A	231	CYS
1	A	239	ARG
1	A	254	ASN
1	A	263	ASN
1	A	265	THR
1	A	270	THR
1	A	289	ARG
1	A	291	HIS
1	A	315	SER
1	A	317	LYS

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Mol	Chain	Res	Type
1	A	325	GLU
1	A	326	VAL
1	A	332	THR
1	A	341	SER
1	A	349	SER
1	A	356	VAL
1	A	382	THR
1	A	398	LEU
1	A	404	GLN
1	A	406	LEU
1	A	415	THR
1	A	420	ASP
1	A	425	SER
1	A	426	SER
1	A	433	LEU
1	A	437	MET
1	A	445	LEU
1	A	448	LEU
1	A	450	ARG
1	A	451	THR
1	A	461	GLN
1	A	463	LEU
1	A	481	LEU
1	A	487	ARG
1	A	491	VAL
1	A	495	THR
1	A	501	SER
1	A	505	TRP
1	A	513	LEU
1	A	519	LEU
1	A	552	ARG
1	A	556	ASP
1	A	566	GLU
1	A	569	LYS
1	A	570	THR
1	A	578	GLU
1	A	584	ASP
1	A	589	GLN
1	A	600	SER
1	A	604	LEU
1	A	610	GLN
1	A	617	GLN

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Mol	Chain	Res	Type
1	A	662	THR
1	A	663	THR
1	A	666	GLN
1	A	669	LEU
1	A	670	ASN
1	A	680	GLN
1	A	682	SER
1	A	683	VAL
1	A	692	GLU
1	A	694	SER
1	A	698	ASN
1	A	701	ILE
1	A	705	SER
1	A	710	SER
1	A	711	THR
1	A	718	ASN
1	A	731	THR
1	A	736	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	GLN
1	A	263	ASN
1	A	273	ASN
1	A	404	GLN
1	A	467	GLN
1	A	499	ASN
1	A	529	HIS
1	A	549	ASN
1	A	601	GLN
1	A	610	GLN
1	A	653	ASN
1	A	670	ASN
1	A	698	ASN
1	A	718	ASN
1	A	737	ASN

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 monosaccharides 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 (i)

6.1 Protein, DNA and RNA chains (i)

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	519/519 (100%)	-0.11	15 (2%) 51 52	25, 34, 59, 91	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	457	THR	5.2
1	A	329	ASN	4.8
1	A	458	ALA	4.7
1	A	549	ASN	4.1
1	A	220	ASP	3.7
1	A	269	ALA	3.6
1	A	456	GLY	3.4
1	A	268	GLY	3.3
1	A	455	GLY	3.2
1	A	330	GLU	3.0
1	A	454	THR	2.7
1	A	239	ARG	2.2
1	A	420	ASP	2.2
1	A	708	TYR	2.1
1	A	332	THR	2.1

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 monosaccharides 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.