



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 28, 2026 – 05:23 AM UTC

PDB ID : 3RA9 / pdb_00003ra9
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

<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

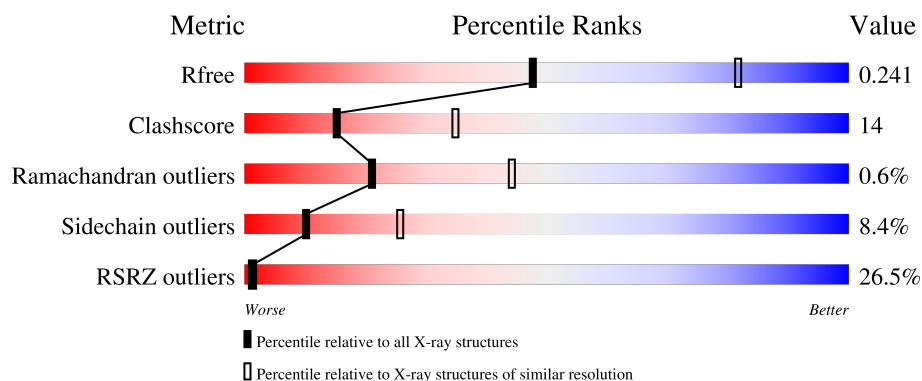
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (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 $\leq 5\%$. 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	519	26% 72% 22% 6%
2	D	2	100% 100%

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			

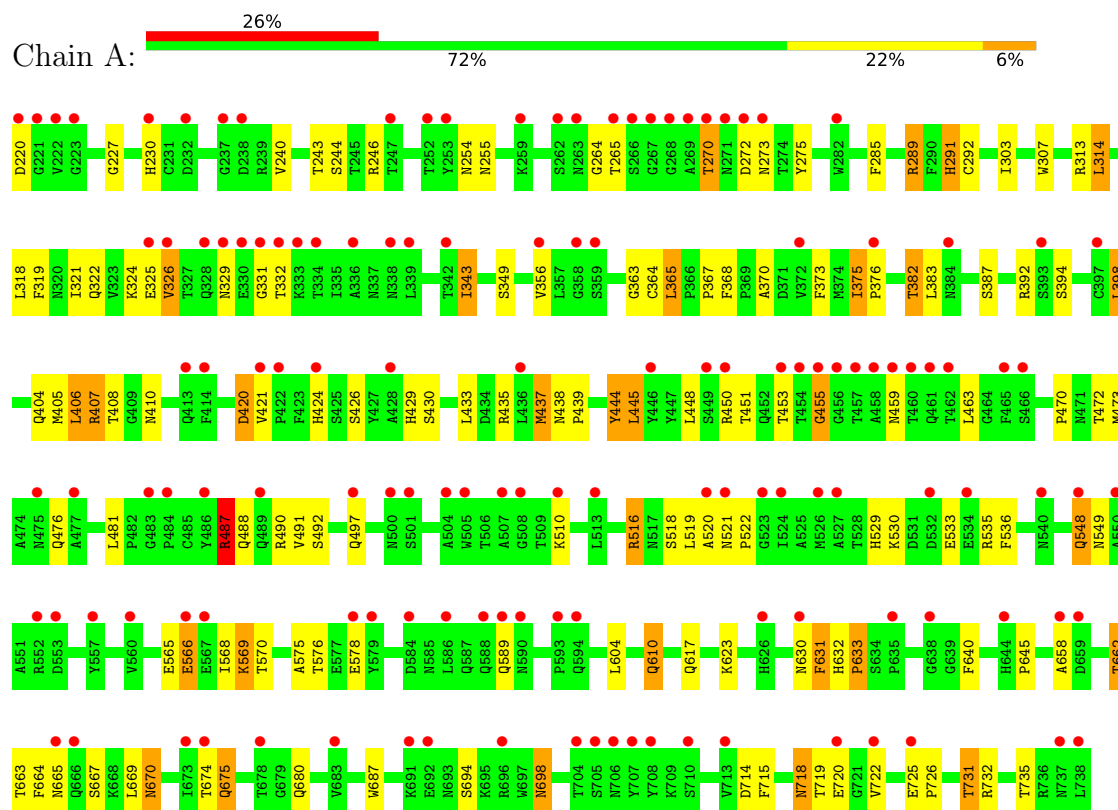
- Molecule 3 is water.

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, 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



• Molecule 2: DNA (5'-D(P*CP*A)-3')



4 Data and refinement statistics

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 40.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.70) 73.4 (40.00-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ 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 (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.512	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.28	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.*

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	0.58	5/4259 (0.1%)	1.05	24/5811 (0.4%)
2	D	0.89	0/45	0.94	0/65
All	All	0.59	5/4304 (0.1%)	1.05	24/5876 (0.4%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	725	GLU	CA-C	-7.31	1.43	1.52
1	A	726	PRO	C-N	-6.16	1.25	1.33
1	A	694	SER	C-N	5.89	1.41	1.33
1	A	497	GLN	C-N	-5.66	1.25	1.33
1	A	631	PHE	C-N	5.10	1.44	1.33

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	719	THR	N-CA-C	-11.59	99.14	113.28
1	A	548	GLN	OE1-CD-NE2	-9.35	113.25	122.60
1	A	303	ILE	N-CA-C	7.51	120.44	111.05
1	A	658	ALA	N-CA-C	-7.46	99.77	110.59
1	A	487	ARG	N-CA-C	6.86	120.44	110.42
1	A	732	ARG	N-CA-C	6.71	120.24	108.56
1	A	725	GLU	CA-C-N	6.66	126.25	119.19
1	A	725	GLU	C-N-CA	6.66	126.25	119.19
1	A	292	CYS	N-CA-C	-6.37	105.34	113.23
1	A	548	GLN	CG-CD-NE2	6.36	125.94	116.40
1	A	675	GLN	N-CA-C	6.19	117.96	108.42
1	A	375	ILE	CA-C-N	6.18	126.15	119.78
1	A	375	ILE	C-N-CA	6.18	126.15	119.78
1	A	365	LEU	CA-C-N	6.16	124.16	119.66
1	A	365	LEU	C-N-CA	6.16	124.16	119.66
1	A	575	ALA	N-CA-C	5.97	119.40	111.75
1	A	694	SER	N-CA-C	5.97	118.92	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	664	PHE	N-CA-C	5.74	118.38	110.35
1	A	455	GLY	N-CA-C	5.58	126.41	113.18
1	A	569	LYS	N-CA-C	-5.57	105.59	112.38
1	A	343	ILE	N-CA-C	-5.52	100.64	109.20
1	A	444	TYR	N-CA-C	-5.30	106.86	113.38
1	A	407	ARG	N-CA-C	-5.23	102.45	110.14
1	A	520	ALA	N-CA-C	-5.21	99.46	108.52

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	110	0
2	D	41	0	23	7	0
3	A	54	0	0	1	0
All	All	4231	0	3916	110	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 14.

All (110) 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:HD22	1:A:698:ASN:H	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:H	1:A:698:ASN:ND2	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:631:PHE:C	1:A:633:PRO:HD3	2.19	0.67
1:A:420:ASP:C	2:D:1:DC:N4	2.52	0.67
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:HH11	1:A:289:ARG:CG	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:H	1:A:670:ASN:HD22	1.45	0.64
1:A:314:LEU:C	1:A:314:LEU:HD12	2.23	0.64
1:A:363:GLY:HA3	1:A:376:PRO:HG3	1.81	0.63
1:A:435:ARG:NE	1:A:473:MET:HE3	2.13	0.63
1:A:630:ASN:OD1	1:A:633:PRO:HG3	1.99	0.63
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:382:THR:HG21	1:A:394:SER:N	2.09	0.59
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
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:405:MET:C	1:A:406:LEU:HD23	2.34	0.53
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:HD23	1:A:406:LEU:N	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:329:ASN:O	1:A:332:THR:CG2	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:670:ASN:HD22	1:A:670:ASN:N	2.04	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:492:SER:HB2	1:A:536:PHE:HE2	1.78	0.48
1:A:670:ASN:ND2	1:A:670:ASN:C	2.70	0.48
1:A:487:ARG:HG3	1:A:488:GLN:N	2.28	0.48
1:A:324:LYS:O	1:A:675:GLN:HB2	2.14	0.48
1:A:444:TYR:CD2	1:A:445:LEU:HD13	2.49	0.48
1:A:326:VAL:HG13	1:A:674:THR:CG2	2.43	0.48
1:A:535:ARG:HH11	1:A:535:ARG:HG2	1.79	0.47
1:A:451:THR:HG22	1:A:451:THR:O	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:HD22	1:A:669:LEU:H	1.80	0.46
1:A:307:TRP:C	1:A:426:SER:OG	2.58	0.46
1:A:529:HIS:HD2	1:A:530:LYS:O	1.99	0.46
1:A:275:TYR:C	1:A:275:TYR:CD1	2.94	0.46
1:A:662:THR:HG22	1:A:663:THR:HG23	1.98	0.45
1:A:698:ASN:HD22	1:A:698:ASN:N	1.97	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: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
1:A:662:THR:HG23	1:A:662:THR:O	2.16	0.44
1:A:435:ARG:CZ	1:A:473:MET:HE3	2.47	0.44
1:A:610:GLN:HE21	1:A:610:GLN:CA	2.28	0.44
1:A:568:ILE:C	1:A:570:THR:N	2.75	0.44
1:A:368:PHE:CE2	1:A:370:ALA:HB3	2.52	0.44
1:A:529:HIS:CB	1:A:533:GLU:O	2.66	0.43
1:A:630:ASN:CG	1:A:633:PRO:HG3	2.44	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:670:ASN:HD22	1:A:670:ASN:C	2.25	0.42
1:A:430:SER:HB3	1:A:735:THR:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:N	1:A:670:ASN:ND2	2.68	0.42
1:A:227:GLY:HA3	1:A:319:PHE:CD1	2.54	0.42
1:A:453:THR:OG1	1:A:459:ASN:HA	2.20	0.42
1:A:240:VAL:CG1	1:A:687:TRP:HB2	2.50	0.42
1:A:490:ARG:HB2	1:A:576:THR:HB	2.01	0.42
1:A:291:HIS:CE1	1:A:367:PRO:HG3	2.55	0.41
1:A:407:ARG:O	1:A:408:THR:C	2.62	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:365:LEU:HD22	1:A:373:PHE:CZ	2.56	0.41
1:A:398:LEU:N	1:A:398:LEU:HD23	2.36	0.41
1:A:662:THR:HG22	1:A:663:THR:CG2	2.50	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

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	517/519 (100%)	493 (95%)	21 (4%)	3 (1%)	21	44

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 ⓘ

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%)	415 (92%)	38 (8%)	10	26

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	THR
1	A	270	THR
1	A	289	ARG
1	A	291	HIS
1	A	314	LEU
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	398	LEU
1	A	406	LEU
1	A	420	ASP
1	A	433	LEU
1	A	437	MET
1	A	445	LEU
1	A	448	LEU
1	A	463	LEU
1	A	472	THR
1	A	481	LEU
1	A	487	ARG
1	A	491	VAL
1	A	516	ARG
1	A	519	LEU
1	A	548	GLN
1	A	549	ASN
1	A	566	GLU
1	A	578	GLU
1	A	589	GLN

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Mol	Chain	Res	Type
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

Sometimes 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	352	GLN
1	A	404	GLN
1	A	429	HIS
1	A	467	GLN
1	A	529	HIS
1	A	548	GLN
1	A	549	ASN
1	A	610	GLN
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 [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	519/519 (100%)	1.64	136 (26%)  	20, 30, 50, 84	0
2	D	2/2 (100%)	6.70	2 (100%)  	39, 39, 39, 79	2 (100%)
All	All	521/521 (100%)	1.66	138 (26%)  	20, 30, 50, 84	2 (0%)

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	1	DC	9.5
1	A	457	THR	7.5
1	A	330	GLU	7.4
1	A	220	ASP	6.6
1	A	331	GLY	6.6
1	A	329	ASN	6.3
1	A	267	GLY	6.2
1	A	460	THR	5.7
1	A	268	GLY	5.6
1	A	589	GLN	5.1
1	A	336	ALA	5.1
1	A	461	GLN	5.0
1	A	269	ALA	4.8
1	A	266	SER	4.6
1	A	455	GLY	4.3
1	A	520	ALA	4.0
1	A	553	ASP	4.0
2	D	2	DA	3.9
1	A	691	LYS	3.9
1	A	328	GLN	3.8
1	A	265	THR	3.8
1	A	692	GLU	3.7
1	A	456	GLY	3.5
1	A	710	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	325	GLU	3.4
1	A	708	TYR	3.3
1	A	332	THR	3.3
1	A	508	GLY	3.3
1	A	548	GLN	3.3
1	A	665	ASN	3.3
1	A	504	ALA	3.3
1	A	557	TYR	3.3
1	A	523	GLY	3.2
1	A	413	GLN	3.2
1	A	237	GLY	3.2
1	A	584	ASP	3.1
1	A	707	TYR	3.1
1	A	459	ASN	3.1
1	A	338	ASN	3.1
1	A	666	GLN	3.1
1	A	334	THR	3.1
1	A	450	ARG	3.0
1	A	524	ILE	3.0
1	A	738	LEU	3.0
1	A	489	GLN	3.0
1	A	273	ASN	2.9
1	A	262	SER	2.9
1	A	713	VAL	2.9
1	A	326	VAL	2.9
1	A	513	LEU	2.9
1	A	706	ASN	2.8
1	A	458	ALA	2.8
1	A	333	LYS	2.8
1	A	436	LEU	2.8
1	A	486	TYR	2.7
1	A	449	SER	2.6
1	A	475	ASN	2.6
1	A	590	ASN	2.6
1	A	705	SER	2.6
1	A	414	PHE	2.6
1	A	725	GLU	2.6
1	A	421	VAL	2.6
1	A	223	GLY	2.6
1	A	678	THR	2.6
1	A	550	ALA	2.6
1	A	221	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	630	ASN	2.5
1	A	588	GLN	2.5
1	A	252	THR	2.5
1	A	737	ASN	2.5
1	A	356	VAL	2.5
1	A	232	ASP	2.5
1	A	720	GLU	2.5
1	A	358	GLY	2.5
1	A	579	TYR	2.5
1	A	465	PHE	2.5
1	A	510	LYS	2.4
1	A	674	THR	2.4
1	A	586	LEU	2.4
1	A	466	SER	2.4
1	A	534	GLU	2.4
1	A	253	TYR	2.4
1	A	372	VAL	2.4
1	A	527	ALA	2.4
1	A	247	THR	2.4
1	A	578	GLU	2.4
1	A	376	PRO	2.4
1	A	500	ASN	2.4
1	A	567	GLU	2.3
1	A	507	ALA	2.3
1	A	222	VAL	2.3
1	A	722	VAL	2.3
1	A	238	ASP	2.3
1	A	501	SER	2.3
1	A	484	PRO	2.3
1	A	696	ARG	2.3
1	A	483	GLY	2.3
1	A	263	ASN	2.3
1	A	339	LEU	2.3
1	A	259	LYS	2.2
1	A	453	THR	2.2
1	A	271	ASN	2.2
1	A	422	PRO	2.2
1	A	497	GLN	2.2
1	A	342	THR	2.2
1	A	424	HIS	2.2
1	A	526	MET	2.2
1	A	446	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	626	HIS	2.2
1	A	644	HIS	2.2
1	A	477	ALA	2.2
1	A	462	THR	2.2
1	A	397	CYS	2.2
1	A	393	SER	2.2
1	A	230	HIS	2.2
1	A	540	ASN	2.1
1	A	659	ASP	2.1
1	A	505	TRP	2.1
1	A	594	GLN	2.1
1	A	552	ARG	2.1
1	A	683	VAL	2.1
1	A	272	ASP	2.1
1	A	532	ASP	2.1
1	A	359	SER	2.1
1	A	638	GLY	2.1
1	A	282	TRP	2.0
1	A	270	THR	2.0
1	A	454	THR	2.0
1	A	593	PRO	2.0
1	A	635	PRO	2.0
1	A	673	ILE	2.0
1	A	560	VAL	2.0
1	A	566	GLU	2.0
1	A	428	ALA	2.0
1	A	658	ALA	2.0
1	A	704	THR	2.0
1	A	384	ASN	2.0
1	A	521	ASN	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

There are no such residues in this entry.