



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 4, 2020 – 11:45 pm BST

PDB ID : 1DMA
Title : DOMAIN III OF PSEUDOMONAS AERUGINOSA EXOTOXIN COM-
PLEXED WITH NICOTINAMIDE AND AMP
Authors : Li, M.; Dyda, F.; Benhar, I.; Pastan, I.; Davies, D.
Deposited on : 1995-04-28
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

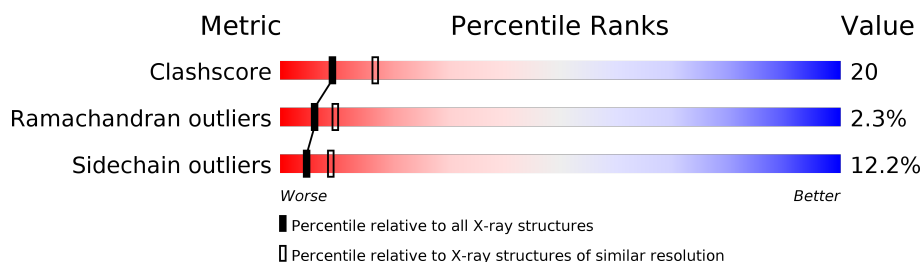
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	214	
1	B	214	

2 Entry composition [i](#)

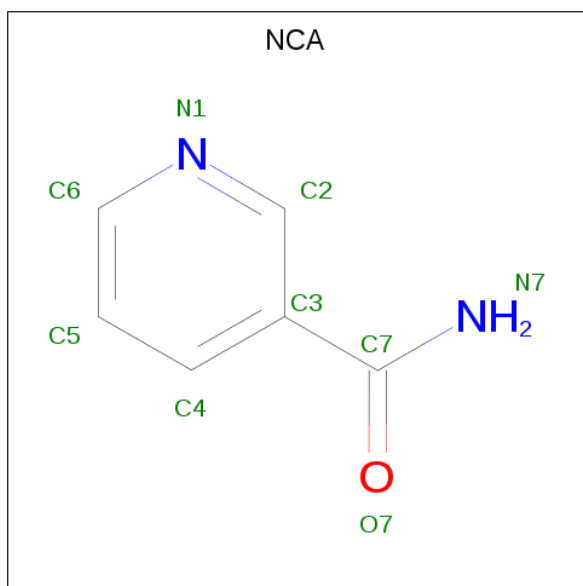
There are 4 unique types of molecules in this entry. The entry contains 3073 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 EXOTOXIN A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	204	Total	C	N	O	5	0	0
			1562	990	280	292			
1	B	189	Total	C	N	O	27	0	0
			1437	914	254	269			

- Molecule 2 is NICOTINAMIDE (three-letter code: NCA) (formula: C₆H₆N₂O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	6	2	1		
2	B	1	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 4 is water.

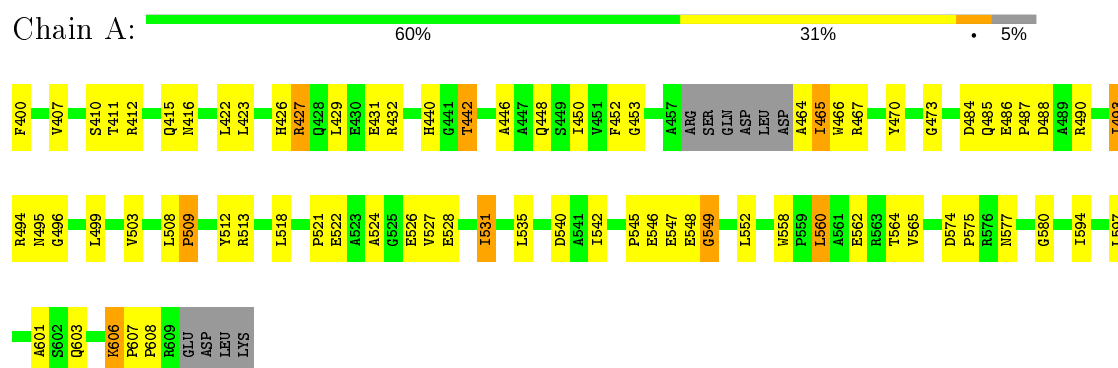
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	18	Total	O	0	0
			18	18		
4	B	15	Total	O	0	0
			15	15		

3 Residue-property plots [i](#)

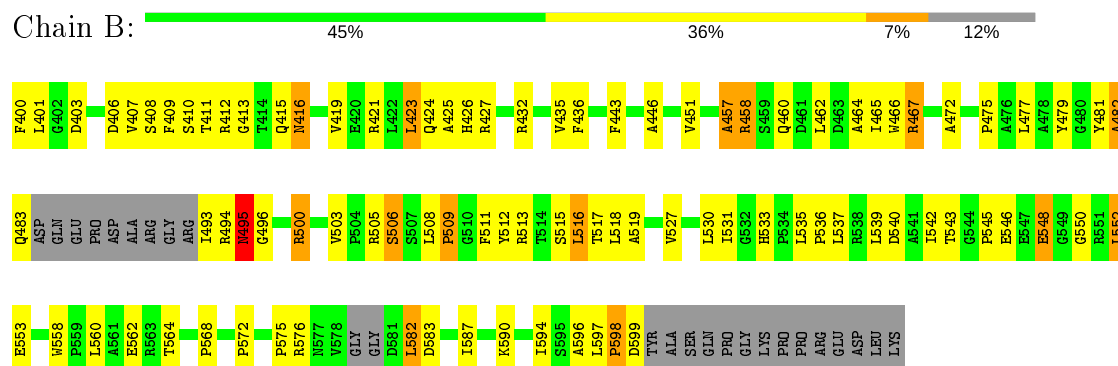
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

Note EDS was not executed.

• Molecule 1: EXOTOXIN A



• Molecule 1: EXOTOXIN A



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	87.51Å 87.51Å 134.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50	Depositor
% Data completeness (in resolution range)	88.9 (8.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.195 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3073	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NCA, AMP

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	0.88	0/1602	1.04	2/2183 (0.1%)
1	B	0.89	1/1471 (0.1%)	1.11	7/2003 (0.3%)
All	All	0.89	1/3073 (0.0%)	1.07	9/4186 (0.2%)

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	575	PRO	CA-C	5.05	1.62	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	537	LEU	CA-CB-CG	7.83	133.30	115.30
1	B	516	LEU	CA-CB-CG	7.79	133.22	115.30
1	B	576	ARG	NE-CZ-NH2	7.11	123.86	120.30
1	B	457	ALA	N-CA-C	7.04	130.02	111.00
1	A	606	LYS	CB-CA-C	5.95	122.30	110.40
1	B	494	ARG	N-CA-C	5.59	126.11	111.00
1	B	495	ASN	O-C-N	-5.45	113.93	123.20
1	A	493	ILE	N-CA-C	-5.32	96.63	111.00
1	B	587	ILE	CB-CA-C	-5.04	101.53	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	495	ASN	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	A	1562	0	1527	42	0
1	B	1437	0	1402	77	0
2	A	9	0	6	0	0
2	B	9	0	6	2	0
3	B	23	0	12	1	0
4	A	18	0	0	0	0
4	B	15	0	0	0	0
All	All	3073	0	2953	117	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 20.

All (117) 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:457:ALA:O	1:B:458:ARG:HB2	1.71	0.89
1:A:400:PHE:HE1	1:B:539:LEU:HD11	1.42	0.82
1:B:482:ALA:HB1	1:B:496:GLY:N	1.93	0.82
1:A:503:VAL:HG12	1:A:564:THR:HG22	1.64	0.79
1:B:598:PRO:HG2	1:B:599:ASP:H	1.47	0.78
1:A:524:ALA:O	1:A:528:GLU:HG3	1.84	0.77
1:B:482:ALA:HB1	1:B:496:GLY:H	1.49	0.76
1:A:429:LEU:HD21	1:A:565:VAL:HG11	1.69	0.73
1:B:558:TRP:O	1:B:562:GLU:HG3	1.89	0.72
1:B:424:GLN:HG3	1:B:427:ARG:HH21	1.53	0.71
1:B:419:VAL:O	1:B:423:LEU:HD22	1.90	0.71
1:A:464:ALA:O	1:A:467:ARG:HG2	1.91	0.69
1:B:436:PHE:HE1	1:B:597:LEU:HD21	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:PHE:HE1	1:B:539:LEU:CD1	2.06	0.68
1:B:426:HIS:CE1	1:B:594:ILE:HG23	2.28	0.68
1:A:465:ILE:HG23	1:A:535:LEU:HD13	1.78	0.65
1:B:512:TYR:HB2	1:B:542:ILE:HD12	1.80	0.64
1:B:582:LEU:HD22	1:B:583:ASP:N	2.12	0.64
1:B:423:LEU:O	1:B:427:ARG:HG3	1.99	0.63
1:B:512:TYR:O	1:B:543:THR:HG22	1.99	0.62
1:B:435:VAL:HG11	1:B:505:ARG:HE	1.65	0.61
1:B:548:GLU:C	1:B:550:GLY:H	2.02	0.61
1:B:596:ALA:O	1:B:597:LEU:HD23	2.00	0.61
1:A:400:PHE:CE1	1:B:539:LEU:HD11	2.32	0.60
1:B:466:TRP:CD1	1:B:519:ALA:HA	2.36	0.60
1:A:407:VAL:HA	1:A:415:GLN:O	2.03	0.59
1:A:440:HIS:HD2	1:A:470:TYR:O	1.86	0.59
1:B:516:LEU:O	1:B:545:PRO:HD2	2.03	0.58
1:B:466:TRP:HH2	1:B:527:VAL:HG21	1.68	0.58
1:B:503:VAL:HG12	1:B:564:THR:HG22	1.84	0.58
1:A:540:ASP:O	1:A:560:LEU:HD12	2.03	0.58
1:B:400:PHE:O	1:B:425:ALA:HB1	2.03	0.58
1:B:560:LEU:O	1:B:564:THR:HG23	2.02	0.58
1:B:407:VAL:HG11	1:B:568:PRO:HG2	1.84	0.57
1:B:472:ALA:HB2	2:B:700:NCA:H5	1.87	0.57
1:B:506:SER:O	1:B:509:PRO:HD2	2.05	0.57
1:A:546:GLU:CD	1:A:549:GLY:HA3	2.26	0.56
1:B:475:PRO:O	1:B:479:TYR:HB2	2.04	0.56
1:B:443:PHE:CZ	1:B:446:ALA:HB2	2.40	0.56
1:A:432:ARG:HH11	1:A:432:ARG:HG2	1.72	0.55
1:B:513:ARG:HG3	1:B:543:THR:HG23	1.88	0.55
1:A:521:PRO:HG2	1:A:522:GLU:OE1	2.05	0.55
1:A:577:ASN:OD1	1:A:580:GLY:HA3	2.07	0.54
1:B:423:LEU:HD21	1:B:590:LYS:HD3	1.90	0.54
1:A:527:VAL:O	1:A:531:ILE:HB	2.07	0.54
1:B:517:THR:HG22	1:B:545:PRO:HG2	1.91	0.53
1:B:548:GLU:C	1:B:550:GLY:N	2.62	0.53
1:B:419:VAL:HG11	1:B:590:LYS:HB2	1.91	0.52
1:B:598:PRO:HG2	1:B:599:ASP:N	2.22	0.52
1:A:410:SER:OG	1:A:412:ARG:HG2	2.10	0.51
1:B:457:ALA:O	1:B:458:ARG:CB	2.53	0.51
1:B:465:ILE:HG23	1:B:535:LEU:HD13	1.91	0.51
1:A:465:ILE:HG22	1:A:466:TRP:CD1	2.46	0.51
1:B:408:SER:HB3	1:B:415:GLN:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:482:ALA:HB1	1:B:496:GLY:CA	2.40	0.51
1:A:426:HIS:NE2	1:A:594:ILE:HG13	2.26	0.50
1:B:481:TYR:CD1	1:B:481:TYR:N	2.80	0.50
1:B:464:ALA:O	1:B:467:ARG:HG2	2.12	0.50
1:B:424:GLN:NE2	1:B:427:ARG:HE	2.10	0.50
1:A:486:GLU:O	1:A:487:PRO:C	2.49	0.49
1:B:500:ARG:HH22	1:B:594:ILE:HG22	1.77	0.49
1:B:401:LEU:HD22	1:B:407:VAL:HG21	1.94	0.49
1:A:547:GLU:O	1:A:548:GLU:HB2	2.10	0.49
1:B:416:ASN:N	1:B:416:ASN:HD22	2.11	0.49
1:A:448:GLN:NE2	1:A:452:PHE:CD2	2.80	0.49
1:B:530:LEU:HD12	1:B:542:ILE:HD11	1.93	0.49
1:A:432:ARG:NH1	1:A:432:ARG:HG2	2.26	0.49
1:B:531:ILE:HG23	1:B:533:HIS:CD2	2.46	0.49
1:B:436:PHE:CE1	1:B:597:LEU:HD21	2.45	0.49
1:B:598:PRO:CG	1:B:599:ASP:H	2.13	0.48
1:A:545:PRO:HA	1:A:552:LEU:HD23	1.96	0.48
1:A:488:ASP:OD1	1:A:488:ASP:C	2.51	0.48
1:B:423:LEU:HD12	1:B:594:ILE:HD11	1.96	0.47
1:B:512:TYR:CD1	1:B:531:ILE:HD12	2.49	0.47
1:B:411:THR:HG23	1:B:495:ASN:OD1	2.15	0.47
1:A:473:GLY:HA3	1:A:597:LEU:HD21	1.96	0.47
1:A:448:GLN:NE2	1:A:452:PHE:HD2	2.13	0.47
1:A:427:ARG:NE	1:A:427:ARG:HA	2.28	0.46
1:B:412:ARG:HD2	1:B:415:GLN:NE2	2.30	0.46
1:B:535:LEU:HB3	1:B:536:PRO:HA	1.98	0.45
1:B:599:ASP:O	1:B:599:ASP:OD1	2.34	0.45
1:A:512:TYR:CD2	1:A:531:ILE:HD12	2.52	0.45
1:A:410:SER:OG	1:A:412:ARG:NE	2.50	0.45
1:B:436:PHE:HE1	1:B:597:LEU:CD2	2.28	0.45
1:A:415:GLN:O	1:A:416:ASN:HB2	2.17	0.44
1:A:558:TRP:O	1:A:562:GLU:HG3	2.18	0.44
1:B:413:GLY:O	1:B:415:GLN:NE2	2.50	0.44
1:A:442:THR:O	1:A:496:GLY:HA3	2.17	0.44
1:B:511:PHE:HD2	1:B:599:ASP:O	2.00	0.44
1:B:435:VAL:HG21	1:B:508:LEU:HD11	1.99	0.43
1:B:553:GLU:HB2	2:B:700:NCA:H6	1.99	0.43
1:A:484:ASP:HB2	1:A:493:ILE:HA	2.01	0.43
1:A:465:ILE:HG23	1:A:535:LEU:CD1	2.45	0.43
1:B:427:ARG:HB2	1:B:427:ARG:CZ	2.49	0.42
1:B:409:PHE:HZ	1:B:451:VAL:HG21	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:512:TYR:HA	1:A:601:ALA:O	2.19	0.42
1:A:546:GLU:HG3	1:A:546:GLU:O	2.20	0.42
1:B:545:PRO:HA	1:B:552:LEU:H	1.84	0.42
1:B:598:PRO:CG	1:B:599:ASP:N	2.77	0.42
1:B:443:PHE:HB3	1:B:483:GLN:H	1.85	0.42
1:B:517:THR:HG22	1:B:545:PRO:O	2.20	0.42
1:B:512:TYR:HB3	1:B:530:LEU:HD13	2.02	0.41
1:B:424:GLN:N	1:B:424:GLN:OE1	2.53	0.41
1:A:607:PRO:HA	1:A:608:PRO:HD2	1.70	0.41
3:B:701:AMP:H2'	3:B:701:AMP:N3	2.36	0.41
1:B:465:ILE:HD13	1:B:465:ILE:HA	1.92	0.41
1:B:458:ARG:HH21	1:B:460:GLN:HB3	1.84	0.41
1:B:443:PHE:CE2	1:B:446:ALA:HB2	2.56	0.41
1:B:515:SER:O	1:B:545:PRO:HG3	2.21	0.41
1:B:432:ARG:HA	1:B:432:ARG:HD3	1.75	0.40
1:B:482:ALA:HB1	1:B:496:GLY:HA3	2.03	0.40
1:B:410:SER:HB3	1:B:415:GLN:NE2	2.36	0.40
1:A:508:LEU:N	1:A:509:PRO:CD	2.84	0.40
1:A:526:GLU:HA	1:A:526:GLU:OE1	2.21	0.40
1:A:574:ASP:OD1	1:A:575:PRO:HD2	2.21	0.40
1:B:458:ARG:NH2	1:B:460:GLN:HB3	2.37	0.40
1:A:446:ALA:O	1:A:450:ILE:HG13	2.22	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	200/214 (94%)	183 (92%)	14 (7%)	3 (2%)	10	18
1	B	183/214 (86%)	165 (90%)	12 (7%)	6 (3%)	4	5
All	All	383/428 (90%)	348 (91%)	26 (7%)	9 (2%)	6	10

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	546	GLU
1	B	548	GLU
1	B	598	PRO
1	B	458	ARG
1	B	482	ALA
1	A	453	GLY
1	A	495	ASN
1	B	495	ASN
1	A	549	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	158/169 (94%)	139 (88%)	19 (12%)	5	9
1	B	146/169 (86%)	128 (88%)	18 (12%)	4	9
All	All	304/338 (90%)	267 (88%)	37 (12%)	5	9

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

Mol	Chain	Res	Type
1	A	411	THR
1	A	422	LEU
1	A	423	LEU
1	A	427	ARG
1	A	431	GLU
1	A	442	THR
1	A	465	ILE
1	A	485	GLN
1	A	490	ARG
1	A	494	ARG
1	A	499	LEU
1	A	509	PRO
1	A	513	ARG
1	A	518	LEU

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Mol	Chain	Res	Type
1	A	531	ILE
1	A	542	ILE
1	A	560	LEU
1	A	603	GLN
1	A	606	LYS
1	B	403	ASP
1	B	406	ASP
1	B	416	ASN
1	B	421	ARG
1	B	423	LEU
1	B	462	LEU
1	B	467	ARG
1	B	477	LEU
1	B	493	ILE
1	B	495	ASN
1	B	500	ARG
1	B	506	SER
1	B	509	PRO
1	B	518	LEU
1	B	540	ASP
1	B	552	LEU
1	B	572	PRO
1	B	582	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	428	GLN
1	A	440	HIS
1	B	415	GLN
1	B	416	ASN
1	B	428	GLN
1	B	448	GLN
1	B	577	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 ⓘ

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NCA	A	700	-	9,9,9	2.00	2 (22%)	11,11,11	1.79	3 (27%)
3	AMP	B	701	-	22,25,25	1.32	3 (13%)	25,38,38	2.09	8 (32%)
2	NCA	B	700	-	9,9,9	2.29	3 (33%)	11,11,11	2.69	6 (54%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NCA	A	700	-	-	0/4/4/4	0/1/1/1
3	AMP	B	701	-	-	4/6/26/26	0/3/3/3
2	NCA	B	700	-	-	0/4/4/4	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	700	NCA	C2-N1	5.01	1.45	1.34
2	A	700	NCA	C3-C7	3.81	1.56	1.50
2	A	700	NCA	C2-N1	3.47	1.41	1.34
3	B	701	AMP	C2'-C1'	-3.28	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	701	AMP	P-O3P	2.81	1.65	1.54
2	B	700	NCA	C4-C3	-2.53	1.35	1.39
2	B	700	NCA	C6-N1	2.21	1.40	1.33
3	B	701	AMP	C5-C4	-2.01	1.35	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	700	NCA	C4-C5-C6	5.33	126.80	118.91
3	B	701	AMP	N3-C2-N1	-4.81	121.16	128.68
3	B	701	AMP	O4'-C1'-C2'	-4.19	100.80	106.93
3	B	701	AMP	O3P-P-O5'	-3.90	96.36	106.73
2	B	700	NCA	O7-C7-N7	3.64	127.75	122.58
2	B	700	NCA	C5-C4-C3	-3.32	116.42	120.34
3	B	701	AMP	O2P-P-O5'	3.29	115.49	106.73
3	B	701	AMP	O4'-C4'-C5'	-3.12	99.09	109.37
2	A	700	NCA	C3-C7-N7	3.00	121.35	117.75
2	A	700	NCA	C4-C3-C2	-2.96	114.28	117.63
2	B	700	NCA	C5-C6-N1	-2.67	114.91	122.58
2	B	700	NCA	C4-C3-C2	2.60	120.58	117.63
2	A	700	NCA	C5-C4-C3	2.52	123.33	120.34
2	B	700	NCA	C3-C7-N7	-2.50	114.74	117.75
3	B	701	AMP	O4'-C4'-C3'	-2.48	100.22	105.11
3	B	701	AMP	O3P-P-O2P	2.11	115.70	107.64
3	B	701	AMP	C1'-N9-C4	-2.03	123.08	126.64

There are no chirality outliers.

All (4) torsion outliers are listed below:

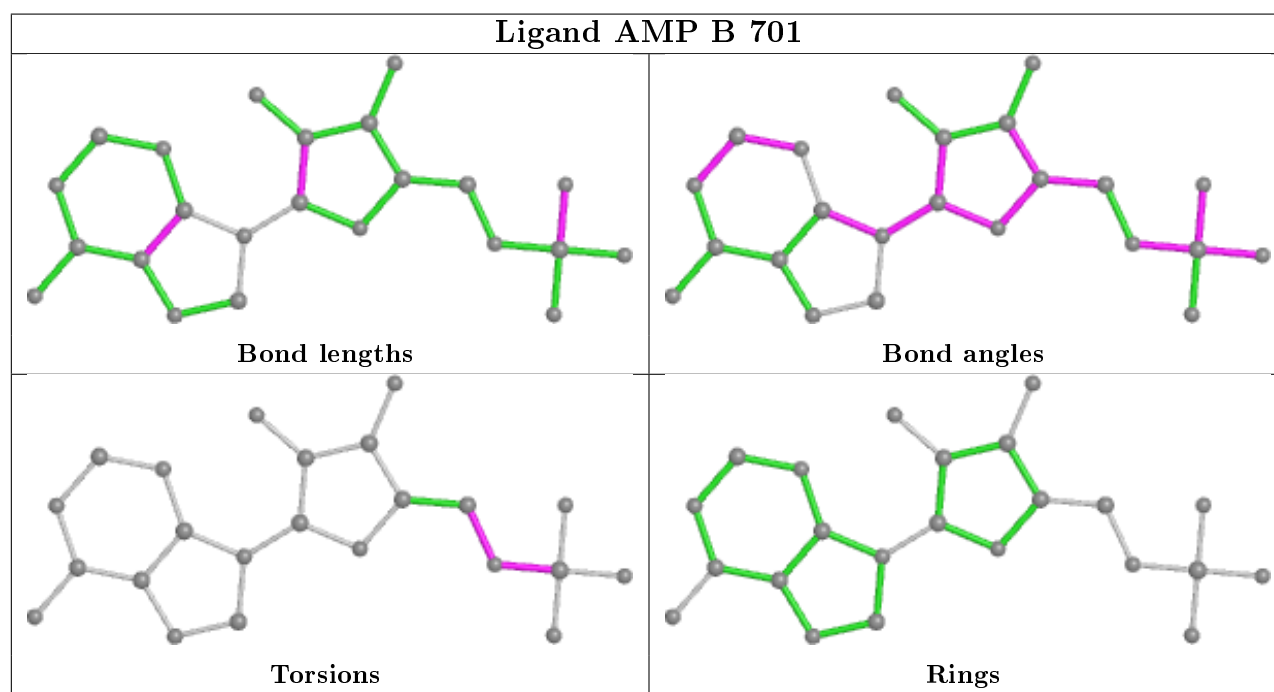
Mol	Chain	Res	Type	Atoms
3	B	701	AMP	C5'-O5'-P-O1P
3	B	701	AMP	C5'-O5'-P-O2P
3	B	701	AMP	C5'-O5'-P-O3P
3	B	701	AMP	C4'-C5'-O5'-P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	701	AMP	1	0
2	B	700	NCA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.