



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:00 AM UTC

PDB ID : 12AS / pdb_000012as
Title : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED
WITH L-ASPARAGINE AND AMP
Authors : Nakatsu, T.; Kato, H.; Oda, J.
Deposited on : 1997-12-02
Resolution : 2.20 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

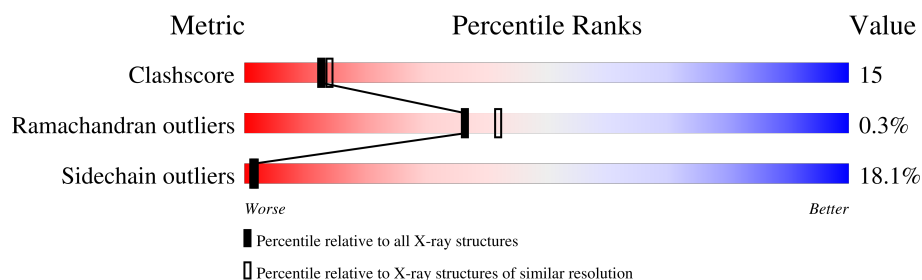
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	330	 60% 28% 11% ..
1	B	330	 59% 28% 11% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5385 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.

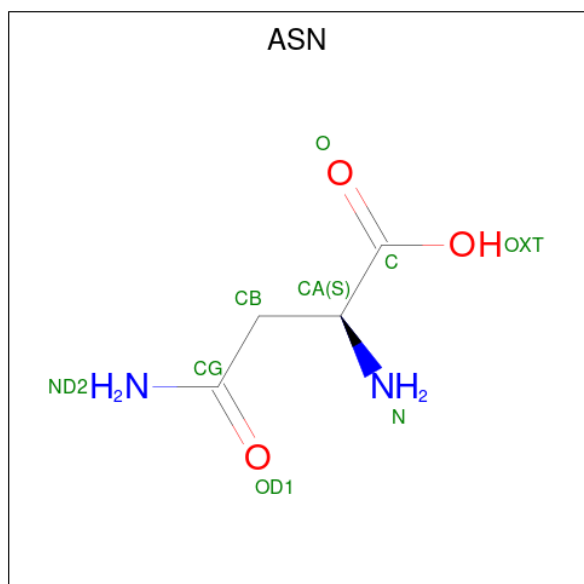
- Molecule 1 is a protein called ASPARAGINE SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2559	1616	455	483	5			
1	B	327	Total	C	N	O	S	0	0	0
			2559	1616	455	483	5			

There are 4 discrepancies between the modelled and reference sequences:

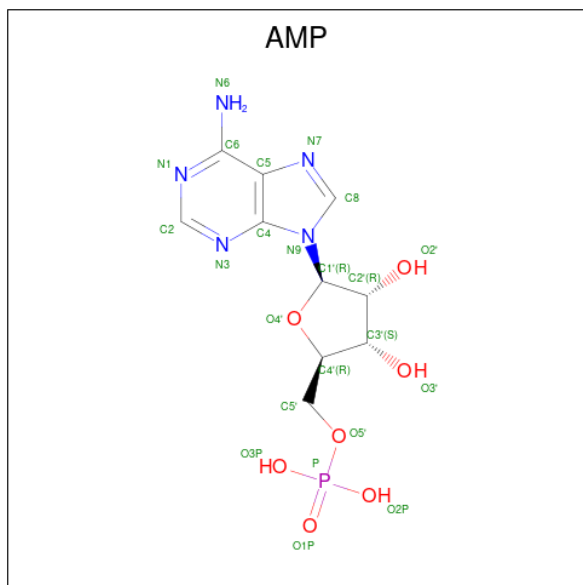
Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ALA	CYS	engineered mutation	UNP P00963
A	315	ALA	CYS	engineered mutation	UNP P00963
B	51	ALA	CYS	engineered mutation	UNP P00963
B	315	ALA	CYS	engineered mutation	UNP P00963

- Molecule 2 is ASPARAGINE (CCD ID: ASN) (formula: $C_4H_8N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	4	2	3		
2	B	1	Total	C	N	O	0	0
			9	4	2	3		

- Molecule 3 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
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	102	Total	O	0	0
			102	102		
4	B	101	Total	O	0	0
			101	101		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.00Å 126.13Å 52.86Å 90.00° 105.59° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	71.1 (10.00-2.20)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.164 , 0.287	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5385	wwPDB-VP
Average B, all atoms (Å ²)	12.0	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: 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	0.53	0/2616	0.90	2/3545 (0.1%)
1	B	0.56	0/2616	0.90	4/3545 (0.1%)
All	All	0.55	0/5232	0.90	6/7090 (0.1%)

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	A	0	19
1	B	0	19
All	All	0	38

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	62	LEU	CA-C-N	5.65	125.27	119.56
1	A	62	LEU	C-N-CA	5.65	125.27	119.56
1	B	217	ASP	N-CA-C	5.55	119.92	113.20
1	B	277	GLU	N-CA-C	5.29	117.13	111.36
1	B	6	ILE	CB-CA-C	-5.14	105.30	111.88
1	B	48	LEU	CB-CA-C	-5.06	110.35	117.23

There are no chirality outliers.

All (38) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	10	ARG	Sidechain
1	A	100	ARG	Sidechain
1	A	105	ARG	Sidechain
1	A	121	ARG	Sidechain
1	A	128	ARG	Sidechain
1	A	176	ARG	Sidechain
1	A	185	ARG	Sidechain
1	A	187	ARG	Sidechain
1	A	21	ARG	Sidechain
1	A	210	ARG	Sidechain
1	A	214	ARG	Sidechain
1	A	255	ARG	Sidechain
1	A	26	ARG	Sidechain
1	A	273	ARG	Sidechain
1	A	284	ARG	Sidechain
1	A	299	ARG	Sidechain
1	A	323	ARG	Sidechain
1	A	39	ARG	Sidechain
1	A	78	ARG	Sidechain
1	B	10	ARG	Sidechain
1	B	100	ARG	Sidechain
1	B	105	ARG	Sidechain
1	B	121	ARG	Sidechain
1	B	128	ARG	Sidechain
1	B	176	ARG	Sidechain
1	B	185	ARG	Sidechain
1	B	187	ARG	Sidechain
1	B	21	ARG	Sidechain
1	B	210	ARG	Sidechain
1	B	214	ARG	Sidechain
1	B	255	ARG	Sidechain
1	B	26	ARG	Sidechain
1	B	273	ARG	Sidechain
1	B	284	ARG	Sidechain
1	B	299	ARG	Sidechain
1	B	323	ARG	Sidechain
1	B	39	ARG	Sidechain
1	B	78	ARG	Sidechain

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	2559	0	2518	80	0
1	B	2559	0	2518	85	0
2	A	9	0	5	2	0
2	B	9	0	5	0	0
3	A	23	0	12	0	0
3	B	23	0	12	0	0
4	A	102	0	0	4	0
4	B	101	0	0	3	0
All	All	5385	0	5070	156	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 (156) 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:100:ARG:HD2	1:B:114:VAL:HG21	1.47	0.95
1:B:210:ARG:HE	1:B:210:ARG:H	0.94	0.94
1:A:189:ILE:HG13	1:A:196:VAL:HG11	1.49	0.92
1:A:216:PRO:HB2	1:A:265:LEU:HD12	1.56	0.87
1:B:210:ARG:H	1:B:210:ARG:NE	1.77	0.82
1:A:173:LEU:HD21	1:A:189:ILE:HB	1.67	0.77
1:B:183:LYS:HD2	1:B:187:ARG:NH1	2.00	0.76
1:A:204:LYS:HE3	1:A:210:ARG:HE	1.52	0.74
1:B:45:GLN:HE22	1:B:71:HIS:H	1.34	0.73
1:B:153:GLU:HG2	4:B:433:HOH:O	1.89	0.72
1:B:204:LYS:H	1:B:204:LYS:HD2	1.55	0.71
1:A:329:LEU:O	1:A:330:LEU:HB2	1.93	0.68
1:B:40:VAL:HG21	1:B:66:GLN:HE21	1.59	0.68
1:B:201:ILE:H	1:B:233:ASN:HD21	1.40	0.68
1:B:11:GLN:O	1:B:15:VAL:HG23	1.94	0.67
1:A:26:ARG:HG2	1:A:26:ARG:HH11	1.59	0.67
1:A:43:GLY:HA2	1:A:276:LEU:HD23	1.76	0.67
1:B:318:TRP:H	1:B:323:ARG:HH21	1.42	0.66
1:B:117:TRP:CZ3	1:B:297:GLN:HA	2.33	0.63
1:B:16:LYS:HZ2	1:B:297:GLN:HB3	1.64	0.62
1:A:60:LYS:HZ1	1:B:104:ASP:HA	1.64	0.62
1:B:69:VAL:HG11	1:B:99:LEU:HB2	1.81	0.62
1:B:210:ARG:HD3	4:B:376:HOH:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:ASP:HB3	1:B:273:ARG:HD3	1.80	0.62
1:A:100:ARG:HE	1:A:114:VAL:HG21	1.65	0.62
1:B:81:LEU:HD21	1:B:91:GLY:HA2	1.82	0.61
1:B:255:ARG:HB2	1:B:290:THR:O	2.01	0.61
1:A:219:ASP:HB2	4:A:411:HOH:O	2.00	0.60
1:A:9:GLN:HG3	1:B:32:VAL:HG22	1.84	0.59
1:B:31:GLU:HG2	1:B:32:VAL:H	1.68	0.59
1:B:169:HIS:CD2	1:B:229:HIS:HB2	2.39	0.58
1:B:196:VAL:HG23	1:B:237:LEU:HB2	1.86	0.58
1:A:32:VAL:O	1:A:94:THR:HG22	2.04	0.58
1:B:100:ARG:HD2	1:B:114:VAL:CG2	2.28	0.57
1:A:117:TRP:CZ3	1:A:300:LEU:HD23	2.40	0.57
1:B:34:ALA:HB1	1:B:73:LEU:HD11	1.87	0.57
1:B:174:LEU:HD13	1:B:185:ARG:CZ	2.36	0.56
1:A:36:ILE:O	1:A:70:VAL:HG23	2.04	0.56
1:B:116:GLN:HA	1:B:295:ILE:O	2.06	0.56
1:A:261:LEU:HD22	1:A:265:LEU:HD13	1.87	0.56
1:A:75:LYS:HE2	1:A:217:ASP:CG	2.31	0.56
1:B:6:ILE:O	1:B:10:ARG:HG2	2.06	0.55
1:B:22:GLN:HE21	1:B:26:ARG:HE	1.53	0.55
1:B:238:VAL:HG23	1:B:247:PHE:HB3	1.87	0.55
1:A:60:LYS:NZ	1:B:104:ASP:HA	2.21	0.55
1:A:265:LEU:HD23	1:A:274:LEU:HD22	1.89	0.54
1:B:78:ARG:HD2	1:B:290:THR:OG1	2.07	0.54
1:A:30:ILE:HD13	1:B:6:ILE:HG23	1.88	0.54
1:A:81:LEU:HD11	1:A:120:GLU:HB3	1.89	0.54
1:A:107:SER:HB2	1:A:108:PRO:HD2	1.90	0.54
1:A:255:ARG:HH22	2:A:331:ASN:N	2.06	0.53
1:B:270:ASP:HB3	1:B:273:ARG:CD	2.38	0.53
1:A:187:ARG:NH1	1:A:191:LYS:HZ1	2.06	0.53
1:A:201:ILE:H	1:A:233:ASN:HD21	1.57	0.53
1:A:78:ARG:HD2	1:A:290:THR:OG1	2.09	0.53
1:B:24:GLU:HB2	1:B:29:LEU:O	2.09	0.53
1:A:256:VAL:HG22	1:A:260:THR:HB	1.91	0.53
1:A:96:MET:SD	1:A:98:ALA:HB2	2.49	0.53
1:A:67:PHE:CE1	1:B:317:VAL:HG11	2.43	0.53
1:A:6:ILE:HG23	1:B:30:ILE:HD13	1.91	0.52
1:A:10:ARG:NH1	1:B:30:ILE:HG22	2.24	0.52
1:A:8:LYS:HE3	1:A:312:GLN:O	2.10	0.52
1:A:17:SER:O	1:A:20:SER:HB2	2.10	0.52
1:B:216:PRO:HG3	1:B:268:THR:OG1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:LYS:O	1:A:138:GLU:HG3	2.11	0.51
1:B:22:GLN:NE2	1:B:26:ARG:HE	2.09	0.51
1:A:280:GLN:HB3	1:A:284:ARG:NH2	2.26	0.51
1:B:265:LEU:HG	1:B:270:ASP:O	2.11	0.50
1:A:171:GLN:HE22	1:A:206:SER:HB3	1.76	0.50
1:A:191:LYS:HB2	1:A:191:LYS:NZ	2.27	0.50
1:B:262:LYS:HE2	4:B:369:HOH:O	2.11	0.50
1:A:172:GLU:HB2	4:A:368:HOH:O	2.11	0.50
1:A:120:GLU:OE2	1:A:255:ARG:HD3	2.11	0.49
1:A:172:GLU:O	1:A:176:ARG:HG3	2.12	0.49
1:B:271:GLU:O	1:B:274:LEU:HB2	2.12	0.49
1:A:320:ALA:HA	1:A:323:ARG:HD2	1.93	0.49
1:B:5:TYR:O	1:B:9:GLN:HG2	2.12	0.49
1:A:317:VAL:HG21	1:B:59:VAL:HG21	1.95	0.49
1:B:186:GLU:O	1:B:189:ILE:HG22	2.12	0.49
1:B:177:TYR:HB2	1:B:185:ARG:HG2	1.94	0.49
2:A:331:ASN:HB2	4:A:371:HOH:O	2.13	0.49
1:B:45:GLN:NE2	1:B:71:HIS:H	2.07	0.49
1:B:96:MET:HE3	1:B:116:GLN:HB2	1.94	0.49
1:B:189:ILE:HG23	1:B:196:VAL:HG21	1.94	0.48
1:B:275:GLU:C	1:B:280:GLN:HE22	2.21	0.48
1:B:310:ILE:O	1:B:313:VAL:HG22	2.13	0.48
1:A:171:GLN:NE2	1:A:206:SER:HB3	2.29	0.48
1:A:265:LEU:HG	1:A:270:ASP:O	2.13	0.48
1:A:193:LEU:HD23	1:A:196:VAL:HG12	1.95	0.48
1:A:73:LEU:O	1:A:77:LYS:HG3	2.14	0.48
1:B:261:LEU:HG	1:B:282:LEU:HD23	1.95	0.48
1:B:204:LYS:HD2	1:B:204:LYS:N	2.24	0.47
1:B:256:VAL:HG13	1:B:257:ASP:O	2.14	0.47
1:B:16:LYS:NZ	1:B:297:GLN:HB3	2.30	0.47
1:A:92:LEU:O	1:A:92:LEU:HD23	2.15	0.46
1:A:223:THR:HB	1:A:232:LEU:HD22	1.97	0.46
1:A:58:LYS:O	1:B:101:PRO:HB2	2.16	0.46
1:A:238:VAL:HG13	1:A:249:LEU:HD23	1.98	0.46
1:B:18:HIS:CD2	1:B:147:THR:HA	2.51	0.46
1:B:240:ASN:HD22	1:B:241:PRO:HD2	1.81	0.45
1:A:13:SER:O	1:A:17:SER:HB2	2.16	0.45
1:A:330:LEU:HD12	4:A:344:HOH:O	2.15	0.45
1:A:204:LYS:CE	1:A:210:ARG:HE	2.23	0.45
1:A:187:ARG:HD2	1:A:245:ASP:OD1	2.17	0.45
1:A:75:LYS:HB3	1:A:278:TRP:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:PRO:HA	1:B:230:ALA:HA	2.00	0.44
1:A:71:HIS:O	1:A:72:SER:HB3	2.16	0.44
1:B:107:SER:OG	1:B:109:LEU:HB2	2.17	0.44
1:A:117:TRP:HZ3	1:A:300:LEU:HD23	1.81	0.44
1:B:233:ASN:ND2	1:B:233:ASN:C	2.75	0.44
1:B:45:GLN:HE22	1:B:71:HIS:N	2.11	0.43
1:A:6:ILE:O	1:A:10:ARG:HG2	2.18	0.43
1:A:191:LYS:HB2	1:A:191:LYS:HZ3	1.82	0.43
1:A:210:ARG:NE	1:A:210:ARG:H	2.16	0.43
1:A:307:LEU:HA	1:A:308:PRO:HD3	1.73	0.43
1:A:169:HIS:O	1:A:172:GLU:HG2	2.18	0.43
1:A:243:LEU:HD13	1:A:243:LEU:HA	1.90	0.43
1:B:107:SER:C	1:B:109:LEU:H	2.27	0.43
1:B:233:ASN:C	1:B:233:ASN:HD22	2.26	0.43
1:A:92:LEU:HD23	1:A:92:LEU:C	2.44	0.43
1:B:187:ARG:HA	1:B:246:ALA:HB2	2.01	0.43
1:A:160:PHE:N	1:A:160:PHE:CD1	2.87	0.43
1:B:174:LEU:HD22	1:B:205:LEU:HD23	2.01	0.43
1:B:193:LEU:HD23	1:B:196:VAL:CG1	2.48	0.42
1:B:13:SER:O	1:B:17:SER:HB2	2.19	0.42
1:A:70:VAL:HG12	1:A:72:SER:H	1.85	0.42
1:A:19:PHE:CE2	1:A:144:ILE:HG13	2.54	0.42
1:B:16:LYS:HA	1:B:117:TRP:HZ2	1.84	0.42
1:B:227:LEU:HD22	1:B:227:LEU:HA	1.80	0.42
1:B:203:GLY:O	1:B:210:ARG:HA	2.20	0.42
1:A:106:LEU:HB3	1:A:318:TRP:CZ3	2.54	0.42
1:A:152:SER:HA	1:A:157:LEU:O	2.20	0.41
1:A:201:ILE:H	1:A:233:ASN:ND2	2.19	0.41
1:B:31:GLU:HG2	1:B:32:VAL:N	2.32	0.41
1:B:223:THR:HA	1:B:224:PRO:HD3	1.83	0.41
1:A:240:ASN:HD22	1:A:241:PRO:HD2	1.86	0.41
1:B:173:LEU:HD13	1:B:185:ARG:HB3	2.03	0.41
1:A:96:MET:HB2	1:A:118:ASP:HB2	2.02	0.41
1:A:225:SER:OG	1:A:227:LEU:HB2	2.20	0.41
1:B:188:ALA:O	1:B:192:ASP:HB2	2.21	0.41
1:A:12:ILE:HG23	1:A:301:THR:HG21	2.01	0.41
1:B:172:GLU:OE1	1:B:176:ARG:NH2	2.54	0.41
1:A:107:SER:HB2	1:A:108:PRO:CD	2.50	0.41
1:A:112:VAL:HG11	1:A:317:VAL:HG22	2.02	0.41
1:A:113:TYR:O	1:A:314:GLN:NE2	2.53	0.41
1:A:327:PRO:O	1:A:328:SER:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:ARG:HD2	1:B:286:GLU:OE2	2.21	0.41
1:B:265:LEU:CD2	1:B:274:LEU:HD23	2.51	0.41
1:A:263:HIS:O	1:A:267:LEU:HG	2.21	0.40
1:A:319:PRO:HD3	1:B:62:LEU:HD21	2.02	0.40
1:B:172:GLU:O	1:B:176:ARG:HD2	2.21	0.40
1:B:81:LEU:CD2	1:B:91:GLY:HA2	2.49	0.40
1:B:107:SER:HB2	1:B:108:PRO:HD2	2.02	0.40
1:B:158:ALA:HA	1:B:159:PRO:HD3	1.88	0.40
1:A:58:LYS:HZ2	1:A:59:VAL:N	2.19	0.40
1:B:240:ASN:HA	1:B:241:PRO:HD2	1.97	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	325/330 (98%)	308 (95%)	16 (5%)	1 (0%)	36	42
1	B	325/330 (98%)	310 (95%)	14 (4%)	1 (0%)	36	42
All	All	650/660 (98%)	618 (95%)	30 (5%)	2 (0%)	36	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	207	ASP
1	B	207	ASP

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	269/272 (99%)	222 (82%)	47 (18%)	2	1
1	B	269/272 (99%)	218 (81%)	51 (19%)	1	1
All	All	538/544 (99%)	440 (82%)	98 (18%)	2	1

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	SER
1	A	21	ARG
1	A	23	LEU
1	A	29	LEU
1	A	32	VAL
1	A	39	ARG
1	A	45	GLN
1	A	48	LEU
1	A	53	LYS
1	A	57	VAL
1	A	58	LYS
1	A	60	LYS
1	A	70	VAL
1	A	75	LYS
1	A	92	LEU
1	A	100	ARG
1	A	112	VAL
1	A	121	ARG
1	A	125	ASP
1	A	128	ARG
1	A	144	ILE
1	A	145	LYS
1	A	168	VAL
1	A	173	LEU
1	A	181	ASP
1	A	191	LYS
1	A	193	LEU
1	A	205	LEU
1	A	206	SER
1	A	210	ARG
1	A	227	LEU
1	A	232	LEU
1	A	233	ASN

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Mol	Chain	Res	Type
1	A	237	LEU
1	A	243	LEU
1	A	249	LEU
1	A	255	ARG
1	A	256	VAL
1	A	260	THR
1	A	261	LEU
1	A	265	LEU
1	A	274	LEU
1	A	277	GLU
1	A	283	LEU
1	A	303	LEU
1	A	322	VAL
1	A	330	LEU
1	B	6	ILE
1	B	17	SER
1	B	23	LEU
1	B	25	GLU
1	B	29	LEU
1	B	32	VAL
1	B	36	ILE
1	B	45	GLN
1	B	48	LEU
1	B	57	VAL
1	B	60	LYS
1	B	64	ASP
1	B	66	GLN
1	B	70	VAL
1	B	92	LEU
1	B	105	ARG
1	B	109	LEU
1	B	123	MET
1	B	128	ARG
1	B	173	LEU
1	B	174	LEU
1	B	179	ASP
1	B	191	LYS
1	B	192	ASP
1	B	193	LEU
1	B	196	VAL
1	B	205	LEU
1	B	210	ARG

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Mol	Chain	Res	Type
1	B	217	ASP
1	B	226	GLU
1	B	227	LEU
1	B	232	LEU
1	B	233	ASN
1	B	237	LEU
1	B	249	LEU
1	B	255	ARG
1	B	256	VAL
1	B	260	THR
1	B	261	LEU
1	B	262	LYS
1	B	265	LEU
1	B	271	GLU
1	B	273	ARG
1	B	274	LEU
1	B	276	LEU
1	B	280	GLN
1	B	283	LEU
1	B	286	GLU
1	B	306	GLN
1	B	322	VAL
1	B	328	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	45	GLN
1	A	83	GLN
1	A	95	HIS
1	A	110	HIS
1	A	116	GLN
1	A	164	GLN
1	A	209	HIS
1	A	211	HIS
1	A	229	HIS
1	A	233	ASN
1	A	240	ASN
1	A	280	GLN
1	A	297	GLN
1	A	312	GLN

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Mol	Chain	Res	Type
1	B	18	HIS
1	B	22	GLN
1	B	45	GLN
1	B	56	GLN
1	B	66	GLN
1	B	84	HIS
1	B	110	HIS
1	B	116	GLN
1	B	171	GLN
1	B	211	HIS
1	B	229	HIS
1	B	233	ASN
1	B	240	ASN
1	B	263	HIS
1	B	280	GLN
1	B	289	GLN
1	B	306	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](#)

4 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
3	AMP	B	332	-	25,25,25	0.97	1 (4%)	37,38,38	1.03	1 (2%)
3	AMP	A	332	-	25,25,25	1.20	2 (8%)	37,38,38	1.15	4 (10%)
2	ASN	B	331	-	7,8,8	0.81	0	6,10,10	0.30	0
2	ASN	A	331	-	7,8,8	0.87	0	6,10,10	0.24	0

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
3	AMP	B	332	-	-	0/10/26/26	0/3/3/3
3	AMP	A	332	-	-	0/10/26/26	0/3/3/3
2	ASN	B	331	-	-	4/8/8/8	-
2	ASN	A	331	-	-	5/8/8/8	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	332	AMP	C8-N7	3.30	1.38	1.31
3	A	332	AMP	C8-N7	2.65	1.36	1.31
3	A	332	AMP	C4-N3	2.14	1.38	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	332	AMP	O4'-C1'-N9	2.67	113.21	108.09
3	A	332	AMP	C2'-C1'-N9	-2.61	106.81	113.30
3	B	332	AMP	C5'-C4'-C3'	-2.31	106.90	115.21
3	A	332	AMP	C5'-C4'-C3'	-2.05	107.81	115.21
3	A	332	AMP	C4-C5-N7	2.00	112.87	110.58

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	331	ASN	OXT-C-CA-N
2	B	331	ASN	CA-CB-CG-ND2
2	A	331	ASN	C-CA-CB-CG
2	B	331	ASN	C-CA-CB-CG

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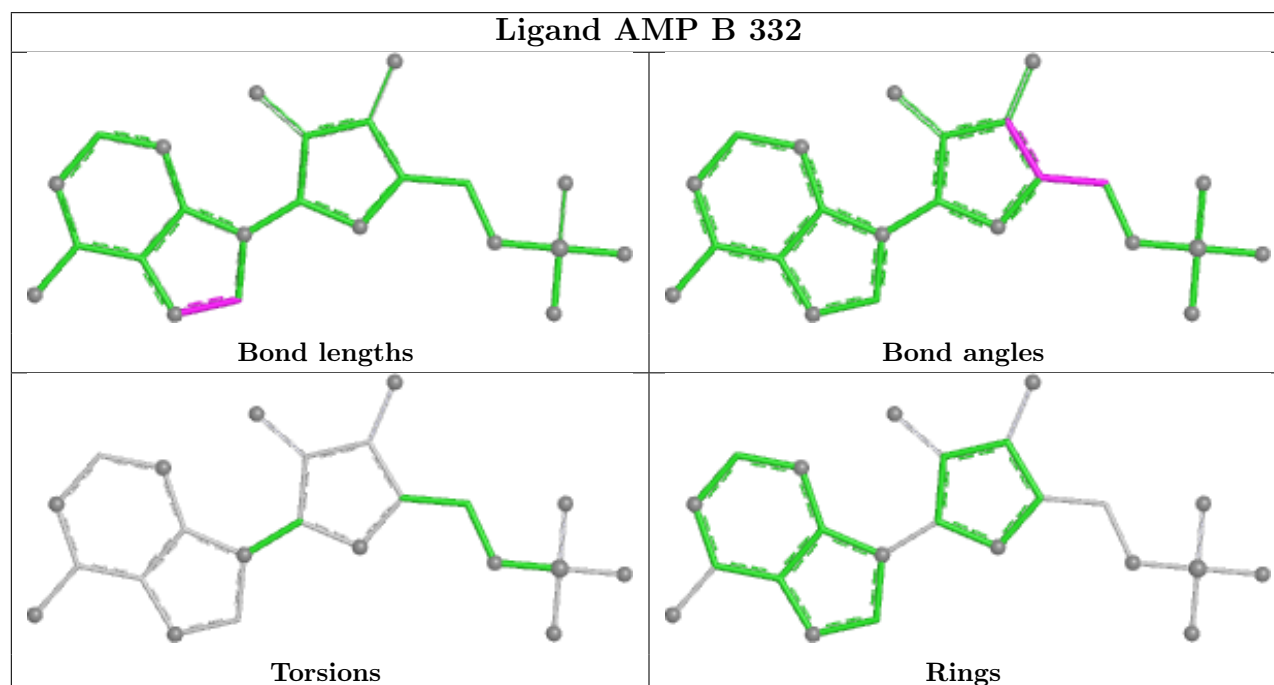
Mol	Chain	Res	Type	Atoms
2	B	331	ASN	CA-CB-CG-OD1
2	A	331	ASN	OXT-C-CA-CB
2	B	331	ASN	O-C-CA-N
2	A	331	ASN	O-C-CA-CB
2	A	331	ASN	O-C-CA-N

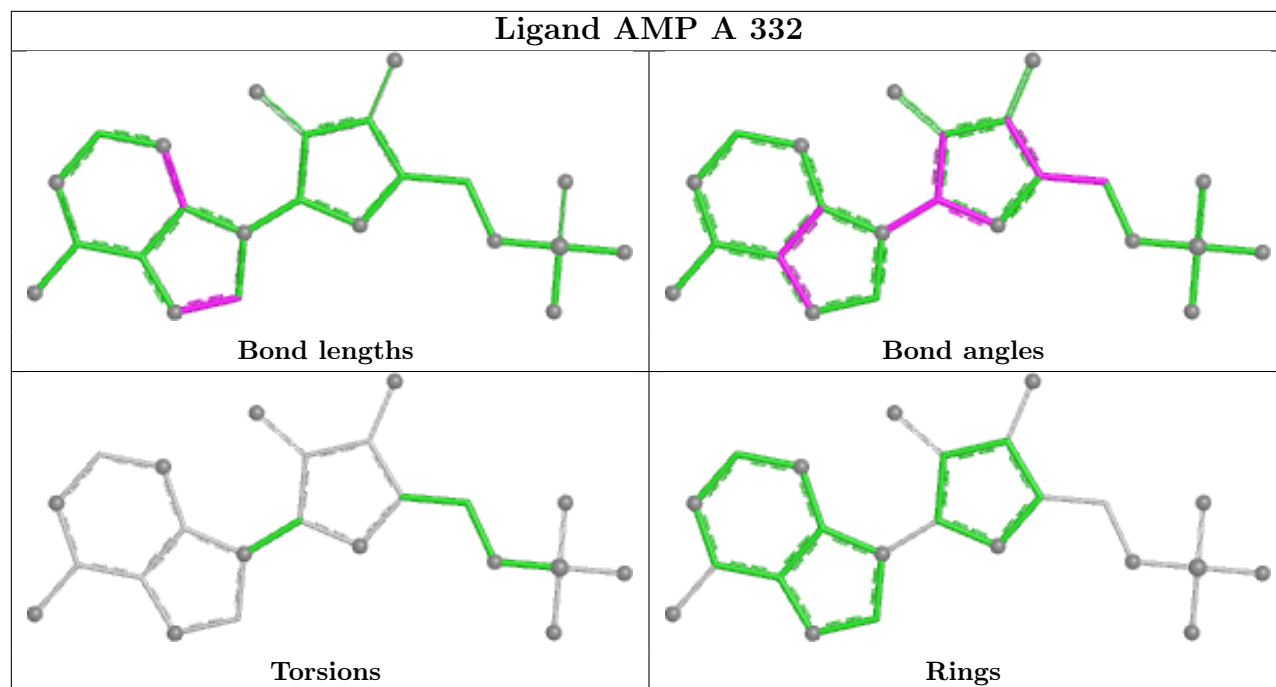
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	331	ASN	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.