



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 01:55 am BST

PDB ID : 1ASC
Title : THE STRUCTURAL BASIS FOR THE REDUCED ACTIVITY OF THE
D223A(D222A) ACTIVE SITE MUTANT OF E. COLI ASPARTATE
AMINOTRANSFERASE
Authors : Schumacher, C.; Ringe, D.
Deposited on : 1993-08-27
Resolution : 2.40 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

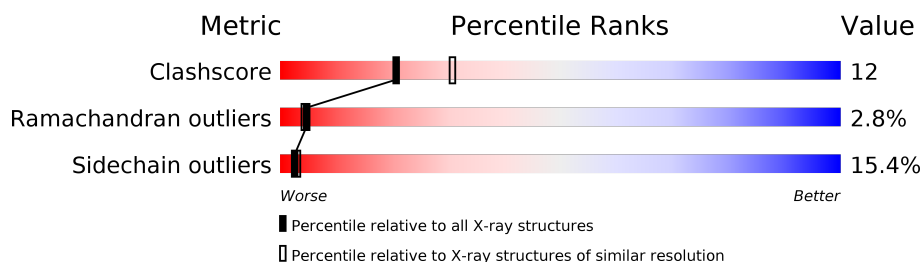
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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	396	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3105 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.

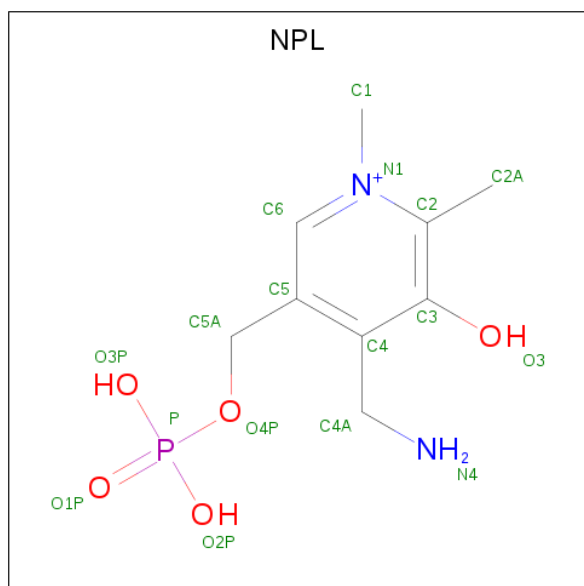
- Molecule 1 is a protein called ASPARTATE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	3066	1935	536	582	13	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	223	ALA	ASP	ENGINEERED MUTATION	UNP P00509

- Molecule 2 is N-METHYL-4-DEOXY-4-AMINO-PYRIDOXAL-5-PHOSPHATE (three-letter code: NPL) (formula: $C_9H_{16}N_2O_5P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	17	9	2	5	1	0	0

- Molecule 3 is water.

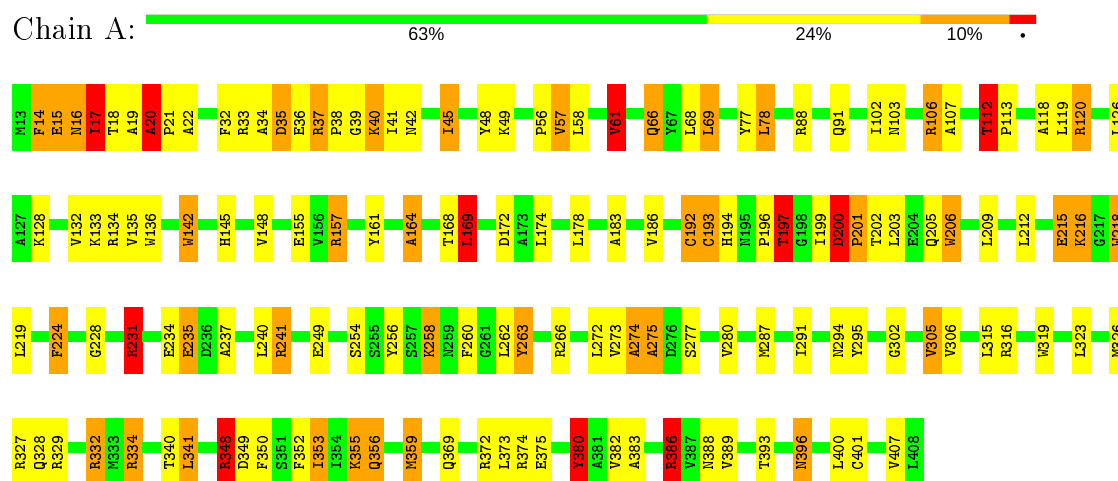
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	22	Total	O	0	0
			22	22		

3 Residue-property plots

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: ASPARTATE AMINOTRANSFERASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	157.50 Å 85.00 Å 78.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.214 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3105	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: NPL

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	0.84	1/3127 (0.0%)	1.71	81/4236 (1.9%)

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	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	61	VAL	CA-CB	5.01	1.65	1.54

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	348	ARG	NE-CZ-NH1	11.38	125.99	120.30
1	A	355	LYS	CA-C-N	-9.67	95.92	117.20
1	A	193	CYS	CA-C-N	-9.56	96.16	117.20
1	A	334	ARG	NE-CZ-NH1	9.53	125.06	120.30
1	A	218	TRP	CD1-CG-CD2	9.44	113.85	106.30
1	A	120	ARG	NE-CZ-NH1	8.28	124.44	120.30
1	A	327	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	A	192	CYS	CA-CB-SG	-8.03	99.54	114.00
1	A	319	TRP	CD1-CG-CD2	7.80	112.54	106.30
1	A	112	THR	N-CA-CB	-7.68	95.71	110.30
1	A	20	ALA	N-CA-C	7.65	131.66	111.00
1	A	372	ARG	NE-CZ-NH2	-7.55	116.53	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	193	CYS	CA-CB-SG	-7.53	100.44	114.00
1	A	218	TRP	CE2-CD2-CG	-7.51	101.29	107.30
1	A	136	TRP	CD1-CG-CD2	7.46	112.27	106.30
1	A	18	THR	N-CA-C	-7.43	90.94	111.00
1	A	142	TRP	CD1-CG-CD2	7.39	112.21	106.30
1	A	33	ARG	CA-C-N	-7.36	101.00	117.20
1	A	37	ARG	NE-CZ-NH2	7.34	123.97	120.30
1	A	200	ASP	N-CA-C	7.19	130.41	111.00
1	A	200	ASP	CA-C-N	7.18	137.21	117.10
1	A	21	PRO	N-CA-C	7.14	130.66	112.10
1	A	33	ARG	CA-CB-CG	7.02	128.84	113.40
1	A	120	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	A	319	TRP	CE2-CD2-CG	-6.90	101.78	107.30
1	A	35	ASP	N-CA-C	6.88	129.57	111.00
1	A	157	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	A	206	TRP	CE2-CD2-CG	-6.79	101.87	107.30
1	A	164	ALA	N-CA-CB	6.76	119.57	110.10
1	A	319	TRP	CG-CD2-CE3	6.66	139.89	133.90
1	A	263	TYR	CB-CG-CD2	-6.55	117.07	121.00
1	A	374	ARG	NE-CZ-NH2	-6.53	117.03	120.30
1	A	136	TRP	CE2-CD2-CG	-6.53	102.08	107.30
1	A	142	TRP	CE2-CD2-CG	-6.53	102.08	107.30
1	A	218	TRP	CG-CD1-NE1	-6.40	103.70	110.10
1	A	206	TRP	CD1-CG-CD2	6.37	111.39	106.30
1	A	356	GLN	N-CA-C	-6.17	94.33	111.00
1	A	215	GLU	CA-CB-CG	6.06	126.74	113.40
1	A	241	ARG	CG-CD-NE	6.02	124.44	111.80
1	A	231	ARG	NE-CZ-NH1	5.99	123.30	120.30
1	A	372	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	A	193	CYS	N-CA-C	5.96	127.09	111.00
1	A	88	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	A	22	ALA	N-CA-C	5.93	127.01	111.00
1	A	329	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	332	ARG	NE-CZ-NH1	5.85	123.23	120.30
1	A	305	VAL	CG1-CB-CG2	-5.84	101.55	110.90
1	A	15	GLU	CA-C-N	-5.78	104.50	117.20
1	A	33	ARG	O-C-N	5.75	131.91	122.70
1	A	77	TYR	CB-CG-CD2	-5.75	117.55	121.00
1	A	17	ILE	CA-C-N	-5.74	104.58	117.20
1	A	274	ALA	N-CA-C	5.71	126.43	111.00
1	A	319	TRP	CG-CD1-NE1	-5.68	104.42	110.10
1	A	329	ARG	NE-CZ-NH1	5.66	123.13	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	353	ILE	CA-CB-CG1	-5.65	100.27	111.00
1	A	241	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	215	GLU	N-CA-CB	-5.54	100.64	110.60
1	A	20	ALA	CA-C-N	5.53	132.60	117.10
1	A	193	CYS	O-C-N	5.52	131.53	122.70
1	A	169	LEU	CA-CB-CG	5.50	127.94	115.30
1	A	275	ALA	N-CA-CB	5.48	117.77	110.10
1	A	316	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	A	35	ASP	CA-C-N	5.36	129.00	117.20
1	A	332	ARG	CA-CB-CG	5.34	125.16	113.40
1	A	200	ASP	N-CA-CB	-5.33	101.00	110.60
1	A	183	ALA	CA-C-N	5.31	126.82	116.20
1	A	16	ASN	CA-C-N	-5.26	105.62	117.20
1	A	57	VAL	CG1-CB-CG2	-5.24	102.51	110.90
1	A	327	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	A	212	LEU	CA-CB-CG	5.21	127.29	115.30
1	A	319	TRP	CB-CG-CD1	-5.17	120.28	127.00
1	A	359	MET	CG-SD-CE	-5.17	91.93	100.20
1	A	69	LEU	CA-CB-CG	5.16	127.17	115.30
1	A	275	ALA	CB-CA-C	-5.15	102.37	110.10
1	A	386	ARG	CB-CG-CD	-5.14	98.23	111.60
1	A	15	GLU	O-C-N	5.09	130.85	122.70
1	A	380	TYR	CB-CG-CD2	-5.08	117.95	121.00
1	A	197	THR	N-CA-C	5.08	124.71	111.00
1	A	197	THR	N-CA-CB	-5.04	100.72	110.30
1	A	48	TYR	CB-CG-CD2	-5.04	117.98	121.00
1	A	256	TYR	CB-CG-CD1	-5.02	117.99	121.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	20	ALA	Peptide
1	A	355	LYS	Mainchain
1	A	380	TYR	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	3066	0	3019	74	0
2	A	17	0	13	4	0
3	A	22	0	0	1	0
All	All	3105	0	3032	75	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 12.

All (75) 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:35:ASP:HB2	1:A:40:LYS:HD2	1.39	1.03
1:A:16:ASN:HB3	1:A:17:ILE:HD12	1.57	0.86
1:A:193:CYS:SG	1:A:200:ASP:HA	2.19	0.83
1:A:112:THR:HG21	1:A:118:ALA:HB2	1.61	0.81
1:A:196:PRO:HB3	1:A:386:ARG:HG3	1.68	0.76
1:A:201:PRO:HB2	1:A:205:GLN:HB2	1.69	0.74
1:A:78:LEU:HB2	3:A:513:HOH:O	1.92	0.69
1:A:197:THR:HG23	1:A:199:ILE:H	1.61	0.66
1:A:39:GLY:O	1:A:41:ILE:HG13	1.97	0.65
1:A:237:ALA:O	1:A:241:ARG:HG3	1.96	0.65
1:A:202:THR:H	1:A:205:GLN:HE21	1.43	0.65
1:A:200:ASP:HB2	1:A:201:PRO:O	1.98	0.64
1:A:192:CYS:HB2	1:A:224:PHE:CE1	2.33	0.64
2:A:409:NPL:HN41	2:A:409:NPL:H52	1.64	0.62
1:A:35:ASP:HB2	1:A:40:LYS:CD	2.22	0.60
1:A:260:PHE:HB3	1:A:262:LEU:HD22	1.83	0.60
1:A:145:HIS:NE2	2:A:409:NPL:H23	2.16	0.60
1:A:45:ILE:HD13	1:A:49:LYS:HE2	1.84	0.60
1:A:168:THR:HG22	1:A:169:LEU:H	1.66	0.59
1:A:169:LEU:HD21	1:A:174:LEU:HD12	1.86	0.58
1:A:334:ARG:HG2	1:A:389:VAL:HG11	1.86	0.58
1:A:145:HIS:CE1	2:A:409:NPL:H23	2.39	0.57
1:A:193:CYS:SG	1:A:200:ASP:CA	2.91	0.57
1:A:91:GLN:HE21	1:A:102:ILE:HG23	1.69	0.57
1:A:258:LYS:HD3	1:A:263:TYR:HE1	1.70	0.57
1:A:340:THR:HB	1:A:401:CYS:SG	2.45	0.57
1:A:106:ARG:HH11	1:A:106:ARG:HB2	1.69	0.56
1:A:61:VAL:HB	1:A:305:VAL:HG11	1.86	0.56
1:A:178:LEU:HB3	1:A:218:TRP:CH2	2.40	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ASP:CB	1:A:40:LYS:HD2	2.26	0.54
1:A:277:SER:O	1:A:280:VAL:HG12	2.10	0.52
1:A:91:GLN:NE2	1:A:102:ILE:HG23	2.24	0.51
1:A:228:GLY:HA3	1:A:323:LEU:HD21	1.92	0.51
1:A:348:ARG:HG3	1:A:348:ARG:HH11	1.75	0.51
1:A:369:GLN:HG2	1:A:407:VAL:HG12	1.94	0.50
1:A:194:HIS:CG	1:A:197:THR:HG22	2.47	0.49
1:A:258:LYS:HD3	1:A:263:TYR:CE1	2.47	0.49
1:A:106:ARG:O	1:A:273:VAL:HA	2.13	0.47
1:A:119:LEU:HD11	2:A:409:NPL:H12	1.96	0.47
1:A:58:LEU:HB2	1:A:61:VAL:HG13	1.94	0.47
1:A:202:THR:H	1:A:205:GLN:NE2	2.12	0.47
1:A:291:ILE:HG23	1:A:295:TYR:CZ	2.51	0.46
1:A:57:VAL:HG12	1:A:61:VAL:HG22	1.98	0.46
1:A:393:THR:H	1:A:396:ASN:HB2	1.80	0.46
1:A:302:GLY:O	1:A:306:VAL:HG23	2.16	0.46
1:A:161:TYR:HE2	1:A:197:THR:HG21	1.79	0.46
1:A:142:TRP:HE3	1:A:145:HIS:CD2	2.34	0.45
1:A:359:MET:HB3	1:A:388:ASN:OD1	2.16	0.45
1:A:194:HIS:HB3	1:A:197:THR:HG22	1.99	0.45
1:A:112:THR:HG21	1:A:118:ALA:CB	2.39	0.44
1:A:249:GLU:HG2	1:A:274:ALA:HA	1.98	0.44
1:A:107:ALA:HA	1:A:272:LEU:O	2.18	0.43
1:A:135:VAL:HA	1:A:186:VAL:O	2.18	0.43
1:A:113:PRO:HD3	1:A:295:TYR:CZ	2.53	0.43
1:A:194:HIS:ND1	1:A:197:THR:HG22	2.34	0.43
1:A:380:TYR:N	1:A:380:TYR:CD1	2.87	0.43
1:A:66:GLN:HA	1:A:66:GLN:HE21	1.84	0.43
1:A:266:ARG:HD2	1:A:266:ARG:HA	1.75	0.42
1:A:14:PHE:O	1:A:16:ASN:N	2.52	0.42
1:A:200:ASP:HB2	1:A:201:PRO:C	2.39	0.42
1:A:216:LYS:HG2	1:A:218:TRP:CZ2	2.55	0.42
1:A:224:PHE:O	1:A:254:SER:HA	2.19	0.42
1:A:42:ASN:OD1	1:A:45:ILE:HG23	2.19	0.42
1:A:323:LEU:HD12	1:A:326:MET:HE3	2.00	0.42
1:A:341:LEU:HA	1:A:341:LEU:HD12	1.93	0.42
1:A:35:ASP:O	1:A:37:ARG:N	2.39	0.41
1:A:119:LEU:HD13	1:A:145:HIS:HD2	1.85	0.41
1:A:132:VAL:HG11	1:A:186:VAL:HG23	2.03	0.41
1:A:32:PHE:CE1	1:A:40:LYS:HG2	2.55	0.41
1:A:201:PRO:HD2	1:A:206:TRP:CZ2	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:PHE:O	1:A:353:ILE:HB	2.21	0.41
1:A:231:ARG:HB2	1:A:235:GLU:HB3	2.03	0.40
1:A:142:TRP:HE3	1:A:145:HIS:NE2	2.19	0.40
1:A:352:PHE:HD1	1:A:356:GLN:HE22	1.70	0.40
1:A:119:LEU:HB3	1:A:148:VAL:HG11	2.03	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	394/396 (100%)	355 (90%)	28 (7%)	11 (3%)	5 4

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	ALA
1	A	34	ALA
1	A	164	ALA
1	A	200	ASP
1	A	19	ALA
1	A	275	ALA
1	A	383	ALA
1	A	15	GLU
1	A	40	LYS
1	A	38	PRO
1	A	17	ILE

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	319/319 (100%)	270 (85%)	49 (15%)	2 3

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	PHE
1	A	36	GLU
1	A	45	ILE
1	A	56	PRO
1	A	61	VAL
1	A	66	GLN
1	A	68	LEU
1	A	69	LEU
1	A	78	LEU
1	A	103	ASN
1	A	106	ARG
1	A	112	THR
1	A	120	ARG
1	A	126	LEU
1	A	128	LYS
1	A	133	LYS
1	A	134	ARG
1	A	155	GLU
1	A	157	ARG
1	A	169	LEU
1	A	172	ASP
1	A	197	THR
1	A	200	ASP
1	A	201	PRO
1	A	203	LEU
1	A	209	LEU
1	A	215	GLU
1	A	216	LYS
1	A	219	LEU
1	A	224	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	231	ARG
1	A	234	GLU
1	A	235	GLU
1	A	240	LEU
1	A	258	LYS
1	A	287	MET
1	A	294	ASN
1	A	315	LEU
1	A	328	GLN
1	A	332	ARG
1	A	341	LEU
1	A	348	ARG
1	A	349	ASP
1	A	373	LEU
1	A	375	GLU
1	A	382	VAL
1	A	386	ARG
1	A	396	ASN
1	A	400	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	66	GLN
1	A	91	GLN
1	A	111	GLN
1	A	150	ASN
1	A	205	GLN
1	A	294	ASN
1	A	297	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

1 ligand is 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	NPL	A	409	-	17,17,17	1.91	6 (35%)	22,25,25	1.62	4 (18%)

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	NPL	A	409	-	-	2/8/8/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	409	NPL	C2A-C2	-3.32	1.43	1.49
2	A	409	NPL	C3-C2	-3.02	1.36	1.39
2	A	409	NPL	C4A-C4	2.96	1.61	1.51
2	A	409	NPL	P-O3P	-2.80	1.44	1.54
2	A	409	NPL	C1-N1	-2.75	1.41	1.47
2	A	409	NPL	P-O2P	-2.58	1.44	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	409	NPL	C2A-C2-C3	-4.08	118.34	121.02
2	A	409	NPL	O4P-P-O1P	-4.02	95.21	106.47
2	A	409	NPL	C2A-C2-N1	2.28	122.31	119.66

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	409	NPL	C4-C4A-N4	2.07	125.80	115.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

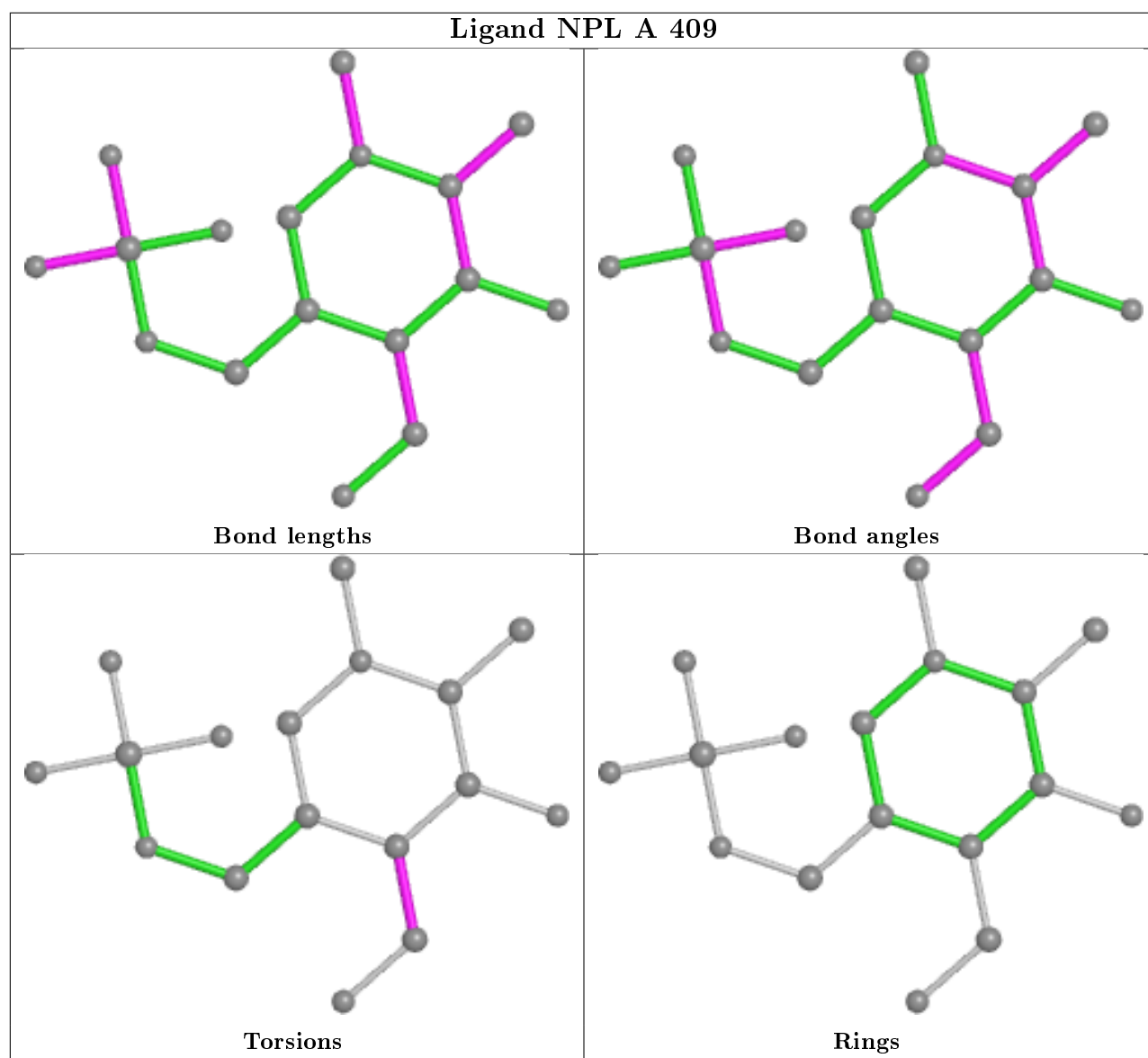
Mol	Chain	Res	Type	Atoms
2	A	409	NPL	C3-C4-C4A-N4
2	A	409	NPL	C5-C4-C4A-N4

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	409	NPL	4	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.