



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:29 AM UTC

PDB ID : 2JID / pdb_00002jid
Title : Human Dipeptidyl peptidase IV in complex with 1-(3,4-Dimethoxy-phenyl) -
3-m-tolyl-piperidine-4-ylamine
Authors : Hennig, M.; Stihle, M.; Luebbbers, T.; Thoma, R.
Deposited on : 2007-02-28
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

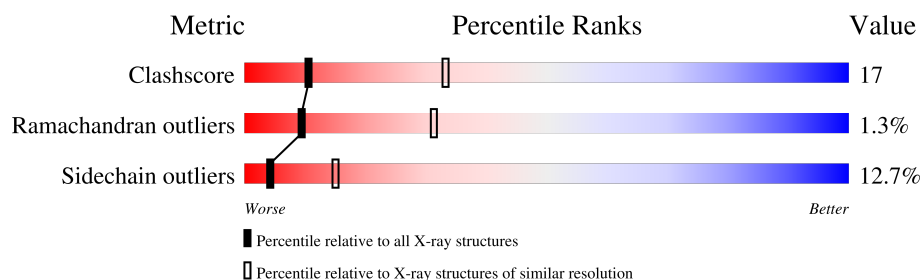
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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	736	
1	B	736	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	1770	X	-	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12214 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 DIPEPTIDYL PEPTIDASE 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			
1	B	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



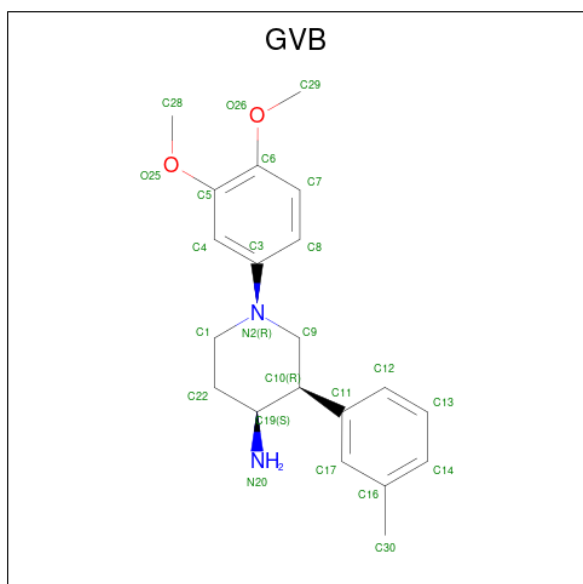
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is (3R,4S)-1-(3,4-DIMETHOXYPHENYL)-3-(3-METHYLPHENYL)PIPERIDI
N-4-AMINE (CCD ID: GVB) (formula: C₂₀H₂₆N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			24	20	2	2		
3	B	1	Total	C	N	O	0	0
			24	20	2	2		

- Molecule 4 is water.

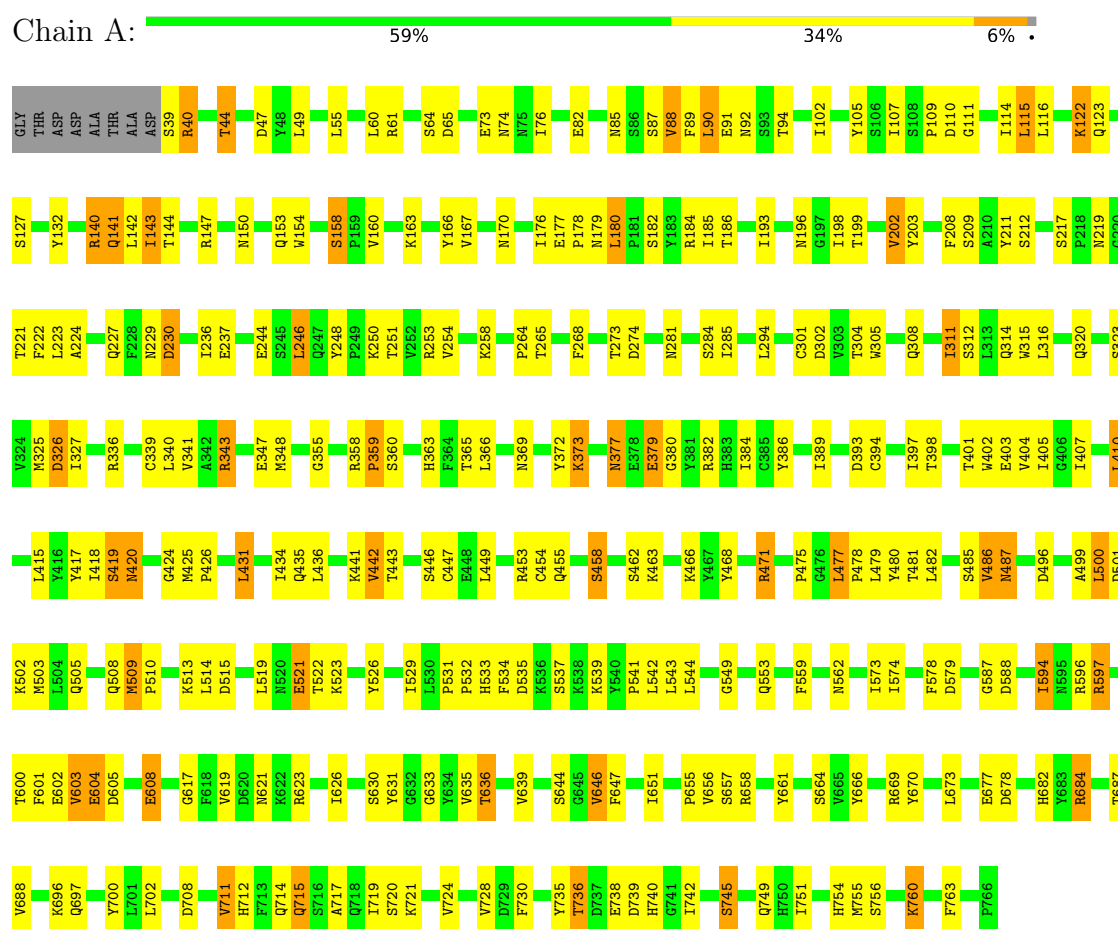
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	55	Total	O	0	0
			55	55		
4	B	73	Total	O	0	0
			73	73		

3 Residue-property plots

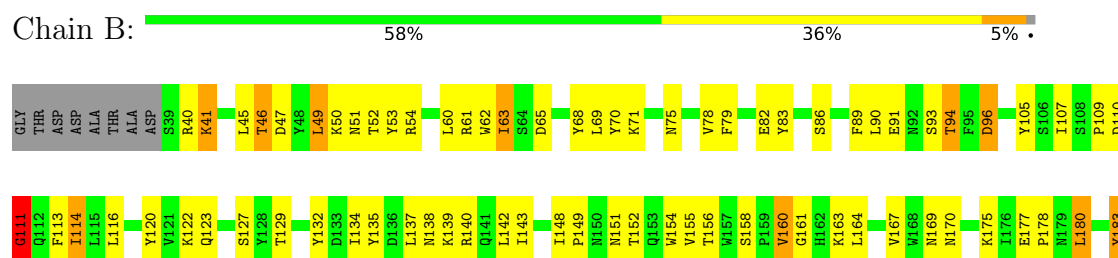
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: DIPEPTIDYL PEPTIDASE 4



• Molecule 1: DIPEPTIDYL PEPTIDASE 4



L765 P766	D678 M679 L680 D681 H682 Y683 R684	T590 N591 H592 A593 T594	R597 L598 G599 T600 F601 E602 V603	T481 L482 H483 V486 R492 L500 M503 N506 M509 P510 K513 L514 D515 F516 I517 I518 L519 N520	Y372 K373 N377 Y381 R382 C385 Y386 F387 Q388 I389 K392 K399 G400 T401 W402 V403 I404 I405 S412 D413 Y414 L415 Y416 Y417 M420 E421 R429 K433 I434 Q435 K441 M450 R453 C454 Y457 S462 K463 E464 L470 R471 C472 P478 L479 Y480	Y279 T280 T283 S284 L285 T288 A289 P290 M293 L294 L295 H298 Y299 L300 C301 D302 W305 A306 R310 I311 S312 L313 Q314 W315 I236 L316 R317 R318 I319 Q320 V324 M325 D326 I327 C328 D329 C339 L340 V341 A342 R343 T350 T351 P359 S360 V270 R361 P362 T365 L366	I193 I194 Y195 I198 W201 V202 F208 S209 L214 N219 G220 T221 P222 L223 A224 Y225 A226 Q227 F228 N229 P234 L235 I236 E237 S242 D243 E244 S245 L246 Q247 Y248 P249 V252 R253 K258 N263 V266 K267 F268 P269 V271 N272 T273 L276 S277 S278
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.25Å 66.82Å 423.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	98.4 (20.00-2.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.223 , 0.303	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12214	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.78	0/6135	1.04	19/8344 (0.2%)
1	B	0.82	2/6135 (0.0%)	1.03	10/8344 (0.1%)
All	All	0.80	2/12270 (0.0%)	1.04	29/16688 (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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	558	VAL	CA-CB	6.13	1.62	1.54
1	B	319	ILE	CA-CB	5.08	1.58	1.53

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	597	ARG	N-CA-C	7.35	119.08	110.41
1	A	454	CYS	N-CA-C	6.84	119.56	108.34
1	B	540	TYR	N-CA-C	6.69	119.14	109.84
1	A	562	ASN	N-CA-C	6.45	116.57	108.45
1	B	96	ASP	N-CA-C	-6.44	105.39	113.18

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	111	GLY	Peptide

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	5963	0	5684	207	0
1	B	5963	0	5681	199	0
2	A	56	0	52	10	0
2	B	56	0	52	3	0
3	A	24	0	26	3	0
3	B	24	0	26	2	0
4	A	55	0	0	5	0
4	B	73	0	0	4	0
All	All	12214	0	11521	396	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 17.

The worst 5 of 396 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:229:ASN:HD21	2:B:1769:NAG:C1	1.47	1.26
1:A:281:ASN:HD21	2:A:1769:NAG:C1	1.51	1.23
1:B:351:THR:HG22	1:B:592:HIS:ND1	1.67	1.09
1:B:193:ILE:HG22	1:B:194:ILE:HG12	1.30	1.07
1:A:608:GLU:HA	1:A:608:GLU:OE1	1.51	1.02

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	726/736 (99%)	639 (88%)	78 (11%)	9 (1%)	10	34
1	B	726/736 (99%)	637 (88%)	79 (11%)	10 (1%)	9	30
All	All	1452/1472 (99%)	1276 (88%)	157 (11%)	19 (1%)	9	31

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	ASP
1	A	486	VAL
1	A	73	GLU
1	A	604	GLU
1	B	94	THR

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	653/658 (99%)	567 (87%)	86 (13%)	4	14
1	B	653/658 (99%)	573 (88%)	80 (12%)	4	16
All	All	1306/1316 (99%)	1140 (87%)	166 (13%)	4	15

5 of 166 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	247	GLN
1	B	472	CYS
1	B	280	THR
1	B	366	LEU
1	B	558	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	298	HIS
1	B	435	GLN
1	B	314	GLN
1	B	383	HIS
1	B	483	HIS

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](#)

10 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	NAG	B	1767	1	14,14,15	0.62	0	17,19,21	1.84	4 (23%)
2	NAG	A	1769	-	14,14,15	0.54	0	17,19,21	0.91	1 (5%)
3	GVB	A	1771	-	26,26,26	0.63	0	33,36,36	1.01	2 (6%)
2	NAG	B	1770	1	14,14,15	0.80	1 (7%)	17,19,21	1.52	3 (17%)
2	NAG	A	1770	1	14,14,15	0.54	0	17,19,21	1.55	2 (11%)
2	NAG	A	1767	-	14,14,15	0.62	0	17,19,21	1.88	6 (35%)
2	NAG	A	1768	-	14,14,15	0.62	0	17,19,21	1.29	2 (11%)
2	NAG	B	1769	-	14,14,15	0.90	0	17,19,21	1.75	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	1768	1	14,14,15	0.61	0	17,19,21	1.40	3 (17%)
3	GVB	B	1771	-	26,26,26	0.60	0	33,36,36	1.09	2 (6%)

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	NAG	B	1767	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1769	-	-	2/6/23/26	0/1/1/1
3	GVB	A	1771	-	-	0/12/25/25	0/3/3/3
2	NAG	B	1770	1	1/1/5/7	4/6/23/26	0/1/1/1
2	NAG	A	1770	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1767	-	-	5/6/23/26	0/1/1/1
2	NAG	A	1768	-	-	2/6/23/26	0/1/1/1
2	NAG	B	1769	-	-	0/6/23/26	0/1/1/1
2	NAG	B	1768	1	-	2/6/23/26	0/1/1/1
3	GVB	B	1771	-	-	0/12/25/25	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1770	NAG	C1-C2	2.58	1.55	1.52

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1770	NAG	C1-O5-C5	4.66	118.44	112.19
2	B	1767	NAG	C1-O5-C5	4.36	118.03	112.19
2	A	1767	NAG	O5-C1-C2	-4.21	104.77	111.29
2	A	1768	NAG	O5-C1-C2	-3.35	106.11	111.29
2	A	1767	NAG	C3-C4-C5	3.35	116.30	110.23

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1770	NAG	C1

5 of 22 torsion outliers are listed below:

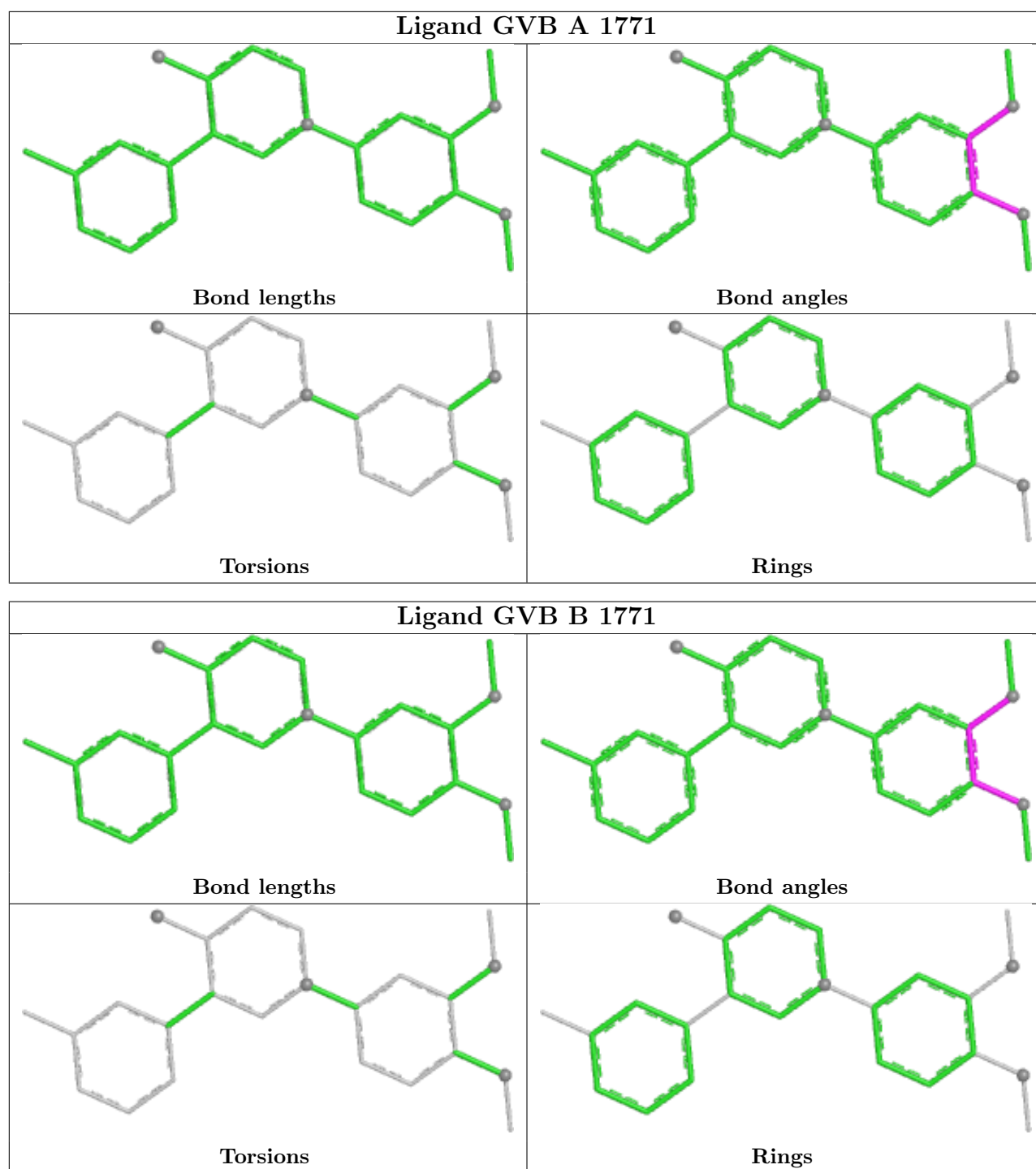
Mol	Chain	Res	Type	Atoms
2	A	1767	NAG	C3-C2-N2-C7
2	A	1767	NAG	C8-C7-N2-C2
2	A	1767	NAG	O7-C7-N2-C2
2	B	1767	NAG	C1-C2-N2-C7
2	B	1767	NAG	C8-C7-N2-C2

There are no ring outliers.

6 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1769	NAG	2	0
3	A	1771	GVB	3	0
2	A	1767	NAG	4	0
2	A	1768	NAG	4	0
2	B	1769	NAG	3	0
3	B	1771	GVB	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.