



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 07:05 PM UTC

PDB ID : 1PBQ / pdb_00001pbq
Title : CRYSTAL STRUCTURE OF THE NR1 LIGAND BINDING CORE IN COM-
PLEX WITH 5,7-DICHLOROKYNURENIC ACID (DCKA) AT 1.90
ANGSTROMS RESOLUTION
Authors : Furukawa, H.; Gouaux, E.
Deposited on : 2003-05-14
Resolution : 1.90 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)
Xtrriage (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

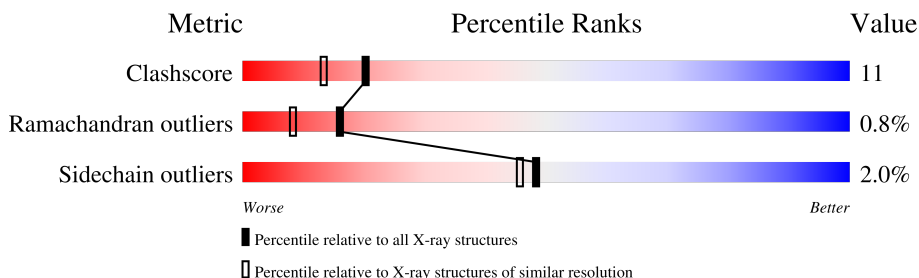
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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	292	 76% 16% • 6%
1	B	292	 71% 18% • 9%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4613 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.

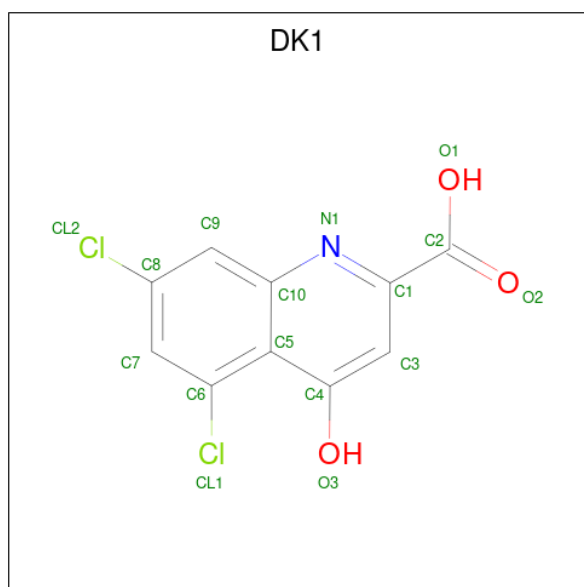
- Molecule 1 is a protein called N-methyl-D-aspartate Receptor Subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2065	1320	347	382	16			
1	B	266	Total	C	N	O	S	0	0	0
			2005	1281	339	369	16			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	GLN	cloning artifact	UNP P35439
A	153	GLY	-	SEE REMARK 999	UNP P35439
A	154	THR	-	SEE REMARK 999	UNP P35439

- Molecule 2 is 5,7-DICHLORO-4-HYDROXYQUINOLINE-2-CARBOXYLIC ACID (CCD ID: DK1) (formula: C₁₀H₅Cl₂NO₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 16	C 10	Cl 2	N 1	O 3	0	0
2	B	1	Total 16	C 10	Cl 2	N 1	O 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	254	Total 254	O 254	0	0
3	B	257	Total 257	O 257	0	0

Note EDS was not executed.

- Chain B:
-
- 71% 18% 9%
- GLY MET SER THR R5 E31 F32 T33 D37 K41 T45 GLY PRO ASN ASP THR SER PRO GLY SER PRO ARG HIS THR VAL P60 K73 L74 A75 R76 T77 K78 R79 F80 H85 L86 V87 A88 E96 ARG VAL ASN ASN SER ASN LYS K104 M109 E112 L122 A123 P124 N128 I129 M130 R131 K139 F140 F141 Q144 I159 L164 Y173 A174 T175 Y184 Q188 V189 E190 M194 H197 N202 V213 R214 L218 F230 Q234 K235 C236 D237 L238 V239 T240 S248 S258 P259 W260 V264 S271 N274 C275 F276 M277 D281 W284 V285 R286 Y287 Q288 D291 SER

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	85.70Å 65.30Å 124.30Å 90.00° 98.10° 90.00°	Depositor
Resolution (Å)	9.99 – 1.90	Depositor
% Data completeness (in resolution range)	87.4 (9.99-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.231 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4613	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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: DK1

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	0.38	0/2111	0.90	5/2867 (0.2%)
1	B	0.37	0/2048	0.87	6/2779 (0.2%)
All	All	0.38	0/4159	0.89	11/5646 (0.2%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	166	ASN	CA-C-N	9.32	129.38	119.78
1	A	166	ASN	C-N-CA	9.32	129.38	119.78
1	B	285	VAL	N-CA-C	8.08	118.18	110.42
1	B	139	LYS	N-CA-C	-6.15	101.60	110.08
1	B	284	TRP	N-CA-C	5.78	120.99	113.88

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	2065	0	1914	42	0
1	B	2005	0	1871	47	0
2	A	16	0	3	0	0
2	B	16	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	254	0	0	3	0
3	B	257	0	0	2	0
All	All	4613	0	3791	89	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 11.

The worst 5 of 89 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:128:ASN:C	1:A:128:ASN:HD22	1.89	0.80
1:B:128:ASN:C	1:B:128:ASN:HD22	1.89	0.79
1:A:94:THR:H	1:A:107:ASN:ND2	1.84	0.75
1:B:173:TYR:H	1:B:197:HIS:HE1	1.33	0.74
1:B:128:ASN:ND2	1:B:131:ARG:H	1.86	0.74

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	270/292 (92%)	258 (96%)	9 (3%)	3 (1%)	11	4
1	B	260/292 (89%)	251 (96%)	8 (3%)	1 (0%)	30	22
All	All	530/584 (91%)	509 (96%)	17 (3%)	4 (1%)	16	8

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	288	GLN
1	A	288	GLN

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Mol	Chain	Res	Type
1	A	248	SER
1	A	261	LYS

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	207/260 (80%)	202 (98%)	5 (2%)	43	38
1	B	202/260 (78%)	199 (98%)	3 (2%)	57	56
All	All	409/520 (79%)	401 (98%)	8 (2%)	48	46

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	274	ASN
1	B	144	GLN
1	A	274	ASN
1	A	247	ARG
1	B	128	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	274	ASN
1	B	128	ASN
1	B	274	ASN
1	B	85	HIS
1	B	129	ASN

5.3.3 RNA ⓘ

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](#)

2 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	DK1	B	1002	-	17,17,17	2.33	8 (47%)	24,25,25	1.80	7 (29%)
2	DK1	A	1001	-	17,17,17	2.18	5 (29%)	24,25,25	1.82	8 (33%)

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	DK1	B	1002	-	-	0/4/4/4	0/2/2/2
2	DK1	A	1001	-	-	0/4/4/4	0/2/2/2

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1002	DK1	O3-C4	-4.12	1.24	1.36
2	B	1002	DK1	C4-C5	4.08	1.50	1.43
2	B	1002	DK1	C3-C4	3.91	1.47	1.37
2	A	1001	DK1	O3-C4	-3.86	1.25	1.36
2	A	1001	DK1	C4-C5	3.84	1.49	1.43

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	DK1	C3-C4-C5	-3.97	116.24	120.55
2	A	1001	DK1	O2-C2-C1	-3.88	113.50	121.30
2	B	1002	DK1	C1-N1-C10	3.75	123.23	117.56
2	B	1002	DK1	C3-C4-C5	-3.63	116.62	120.55
2	B	1002	DK1	O2-C2-C1	-3.44	114.37	121.30

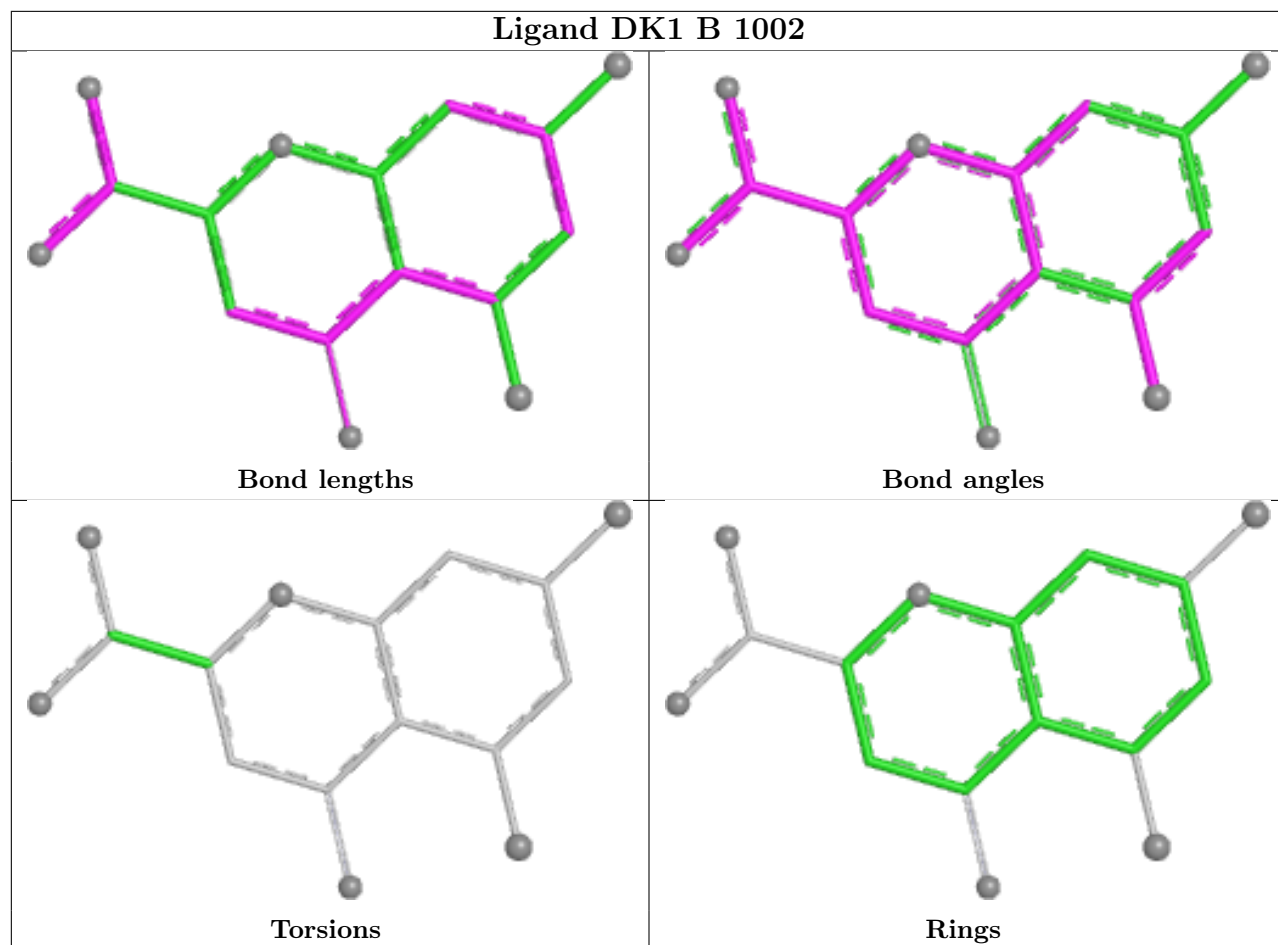
There are no chirality outliers.

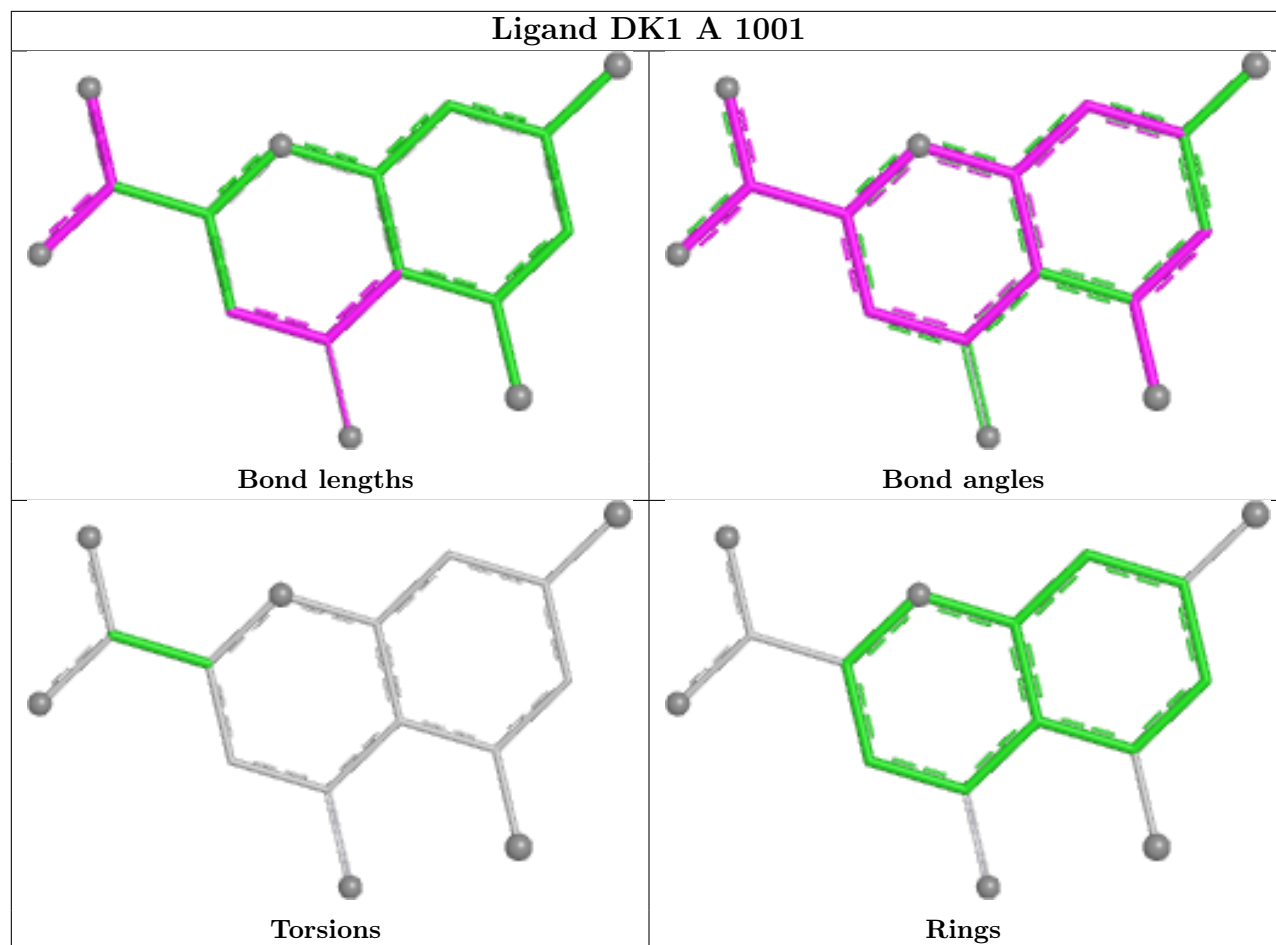
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.