



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:44 PM GMT

PDB ID : 1GZX
Title : OXY T STATE HAEMOGLOBIN: OXYGEN BOUND AT ALL FOUR HAEMS
Authors : Paoli, M.; Liddington, R.; Tame, J.; Wilkinson, A.; Dodson, G.
Deposited on : 2002-06-07
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : **FAILED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

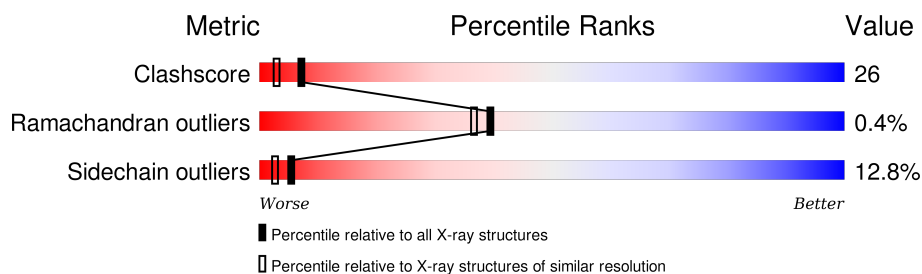
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

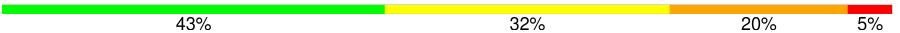
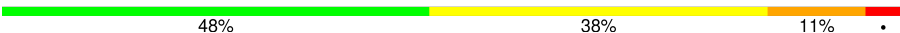


Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)

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. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	141	 43% 32% 20% 5%
1	C	141	 48% 38% 11% •
2	B	146	 49% 38% 11% •
2	D	146	 44% 36% 18% •

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
4	OXY	B	1291	-	-	X	-
4	OXY	D	1691	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4769 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 HEMOGLOBIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			
1	C	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			

- Molecule 2 is a protein called HEMOGLOBIN BETA CHAIN.

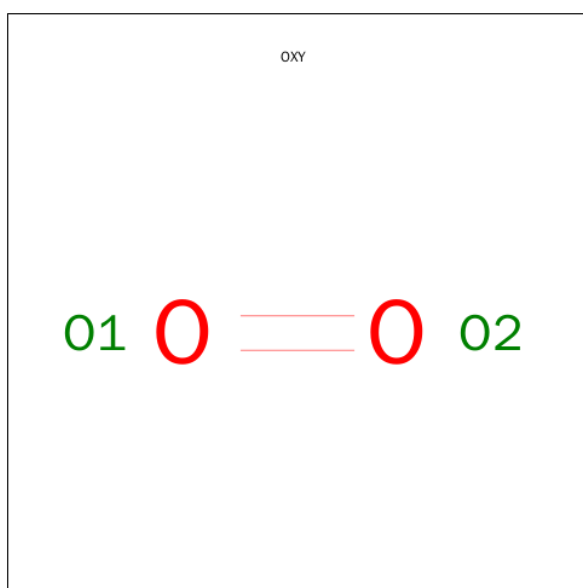
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1123	724	195	201	3			
2	D	146	Total	C	N	O	S	0	0	0
			1123	724	195	201	3			

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 4 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			2	2		
4	B	1	Total	O	0	0
			2	2		
4	C	1	Total	O	0	0
			2	2		
4	D	1	Total	O	0	0
			2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	62	Total	O	0	0
			62	62		
5	B	55	Total	O	0	0
			55	55		

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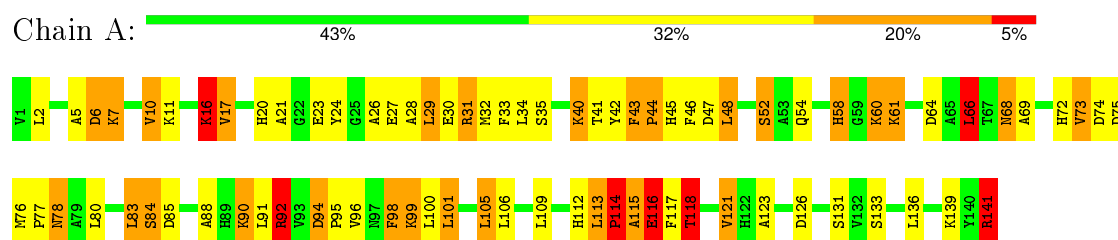
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	45	Total	O	0	0
			45	45		
5	D	43	Total	O	0	0
			43	43		

3 Residue-property plots

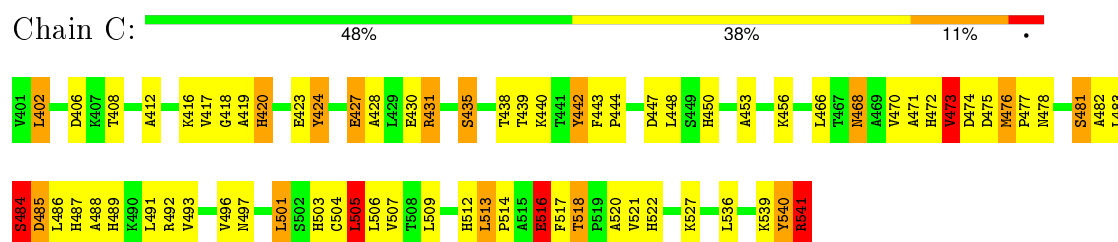
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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 failed to run properly.

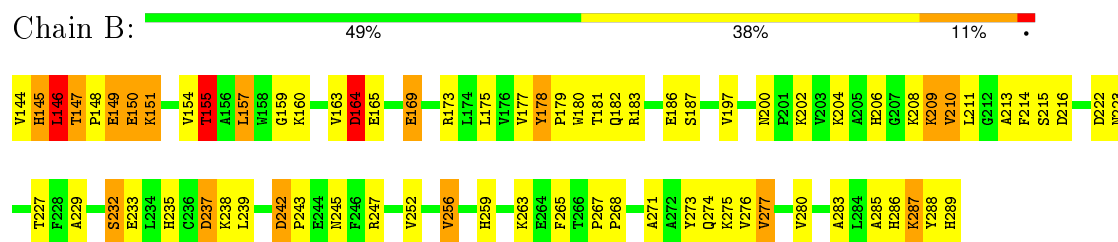
• Molecule 1: HEMOGLOBIN ALPHA CHAIN



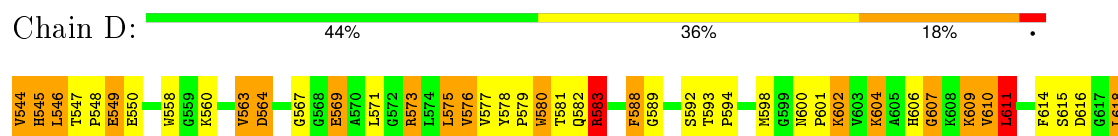
• Molecule 1: HEMOGLOBIN ALPHA CHAIN



• Molecule 2: HEMOGLOBIN BETA CHAIN



• Molecule 2: HEMOGLOBIN BETA CHAIN



L619	L620	L621	L622	L625	L626	L627	L628	L629	L630	L633	L634	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L660	L661	L662	L663	L666	L667	L668	L669	L670	L673	L674	L675	L676	L677	L684	L685	L686	L687	L688	L689
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4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 2 A	Depositor
Cell constants a, b, c, α , β , γ	97.05Å 99.50Å 66.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.10	Depositor
% Data completeness (in resolution range)	95.0 (10.00-2.10)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.199 , 0.221	Depositor
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Outliers	(Not available)	Xtriage
Total number of atoms	4769	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1.13	1/1097 (0.1%)	2.57	80/1491 (5.4%)
1	C	1.11	2/1097 (0.2%)	2.54	68/1491 (4.6%)
2	B	1.13	0/1153	2.76	76/1566 (4.9%)
2	D	1.12	1/1153 (0.1%)	2.44	58/1566 (3.7%)
All	All	1.12	4/4500 (0.1%)	2.58	282/6114 (4.6%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	487	HIS	CA-CB	6.06	1.67	1.53
2	D	549	GLU	CD-OE2	5.73	1.31	1.25
1	C	541	ARG	CD-NE	-5.41	1.37	1.46
1	A	141	ARG	NE-CZ	5.15	1.39	1.33

The worst 5 of 282 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	183	ARG	NE-CZ-NH1	26.47	133.54	120.30
2	B	247	ARG	NE-CZ-NH1	-23.71	108.44	120.30
2	B	247	ARG	CD-NE-CZ	22.18	154.66	123.60
1	A	92	ARG	CD-NE-CZ	20.71	152.59	123.60
1	C	431	ARG	NE-CZ-NH2	-17.30	111.65	120.30

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	1069	0	1073	46	0
1	C	1069	0	1070	50	0
2	B	1123	0	1115	53	0
2	D	1123	0	1112	105	0
3	A	43	0	30	3	0
3	B	43	0	30	1	0
3	C	43	0	30	0	0
3	D	43	0	30	9	0
4	A	2	0	0	0	0
4	B	2	0	0	2	0
4	C	2	0	0	0	0
4	D	2	0	0	2	0
5	A	62	0	0	4	0
5	B	55	0	0	7	0
5	C	45	0	0	2	1
5	D	43	0	0	8	0
All	All	4769	0	4490	237	1

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 26.

The worst 5 of 237 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)
2:D:638:LYS:NZ	2:D:638:LYS:HB2	1.27	1.28
1:C:470:VAL:O	1:C:473:VAL:HG22	1.39	1.18
2:D:547:THR:HG22	2:D:549:GLU:N	1.64	1.13
2:D:649:LEU:HD23	3:D:1690:HEM:HBB2	1.32	1.09
2:D:638:LYS:NZ	2:D:638:LYS:CB	2.17	1.08

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:2027:HOH:O	5:C:2027:HOH:O[2_545]	1.90	0.30

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	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
1	C	139/141 (99%)	128 (92%)	10 (7%)	1 (1%)	26	21
2	B	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
2	D	144/146 (99%)	138 (96%)	5 (4%)	1 (1%)	26	21
All	All	566/574 (99%)	543 (96%)	21 (4%)	2 (0%)	39	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	419	ALA
2	D	663	LYS

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	113/113 (100%)	92 (81%)	21 (19%)	2	1
1	C	113/113 (100%)	101 (89%)	12 (11%)	8	5
2	B	118/118 (100%)	106 (90%)	12 (10%)	9	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	118/118 (100%)	104 (88%)	14 (12%)	6	3
All	All	462/462 (100%)	403 (87%)	59 (13%)	5	3

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	163	VAL
1	C	402	LEU
2	D	618	LEU
2	B	164	ASP
2	B	211	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	472	HIS
2	D	686	HIS
2	D	620	HIS
2	B	245	ASN
1	C	497	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	HEM	A	1142	1,4	30,50,50	2.77	11 (36%)	24,82,82	3.56	16 (66%)
4	OXY	A	1143	3	1,1,1	0.10	0	0,0,0	0.00	-
3	HEM	B	1290	2,4	30,50,50	2.53	8 (26%)	24,82,82	3.65	15 (62%)
4	OXY	B	1291	3	1,1,1	0.40	0	0,0,0	0.00	-
3	HEM	C	1542	1,4	30,50,50	2.69	8 (26%)	24,82,82	2.84	13 (54%)
4	OXY	C	1543	3	1,1,1	0.32	0	0,0,0	0.00	-
3	HEM	D	1690	2,4	30,50,50	2.87	12 (40%)	24,82,82	3.36	12 (50%)
4	OXY	D	1691	3	1,1,1	0.04	0	0,0,0	0.00	-

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	HEM	A	1142	1,4	-	0/10/54/54	0/0/8/8
4	OXY	A	1143	3	-	0/0/0/0	0/0/0/0
3	HEM	B	1290	2,4	-	0/10/54/54	0/0/8/8
4	OXY	B	1291	3	-	0/0/0/0	0/0/0/0
3	HEM	C	1542	1,4	-	0/10/54/54	0/0/8/8
4	OXY	C	1543	3	-	0/0/0/0	0/0/0/0
3	HEM	D	1690	2,4	-	0/10/54/54	0/0/8/8
4	OXY	D	1691	3	-	0/0/0/0	0/0/0/0

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1690	HEM	C3B-C4B	-8.48	1.44	1.51
3	A	1142	HEM	C3B-C4B	-7.97	1.44	1.51
3	C	1542	HEM	C2D-C3D	-7.35	1.32	1.54
3	D	1690	HEM	C2D-C3D	-7.20	1.32	1.54
3	B	1290	HEM	C3B-C4B	-6.82	1.45	1.51

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1142	HEM	CAA-C2A-C1A	-9.10	117.13	127.01
3	B	1290	HEM	CAA-C2A-C1A	-8.51	117.77	127.01
3	D	1690	HEM	CMA-C3A-C4A	-6.00	118.44	128.36
3	B	1290	HEM	CMA-C3A-C4A	-5.76	118.83	128.36
3	D	1690	HEM	CAA-C2A-C1A	-5.59	120.94	127.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1142	HEM	3	0
3	B	1290	HEM	1	0
4	B	1291	OXY	2	0
3	D	1690	HEM	9	0
4	D	1691	OXY	2	0

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 failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.