



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 10:22 PM EDT

PDB ID : 1OCO / pdb_00001oco
Title : BOVINE HEART CYTOCHROME C OXIDASE IN CARBON MONOXIDE-
BOUND STATE
Authors : Tsukihara, T.; Yao, M.
Deposited on : 1998-07-09
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)	:	2.50

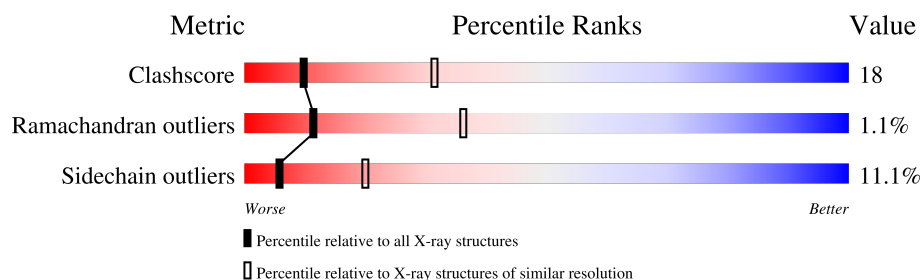
1 Overall quality at a glance

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)

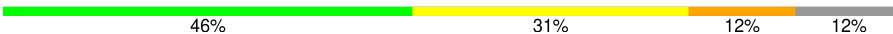
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	514	
1	N	514	
2	B	227	
2	O	227	
3	C	261	
3	P	261	
4	D	147	
4	Q	147	

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Mol	Chain	Length	Quality of chain
5	E	109	
5	R	109	
6	F	98	
6	S	98	
7	G	84	
7	T	84	
8	H	85	
8	U	85	
9	I	73	
9	V	73	
10	J	59	
10	W	59	
11	K	56	
11	X	56	
12	L	47	
12	Y	47	
13	M	46	
13	Z	46	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 28810 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 CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	0	0
			4025	2690	623	677	35			
1	N	514	Total	C	N	O	S	0	0	0
			4025	2690	623	677	35			

- Molecule 2 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	227	Total	C	N	O	S	0	5	0
			1863	1207	288	350	18			
2	O	227	Total	C	N	O	S	0	5	0
			1863	1207	288	350	18			

- Molecule 3 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	261	Total	C	N	O	S	0	0	0
			2124	1420	338	353	13			
3	P	261	Total	C	N	O	S	0	0	0
			2124	1420	338	353	13			

- Molecule 4 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			
4	Q	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			

- Molecule 5 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	109	Total	C	N	O	S	0	0	0
			878	558	150	168	2			
5	R	109	Total	C	N	O	S	0	0	0
			878	558	150	168	2			

- Molecule 6 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			
6	S	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			

- Molecule 7 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	84	Total	C	N	O	S	0	0	0
			672	431	129	111	1			
7	T	84	Total	C	N	O	S	0	0	0
			672	431	129	111	1			

- Molecule 8 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	75	Total	C	N	O	S	0	0	0
			628	395	114	114	5			
8	U	75	Total	C	N	O	S	0	0	0
			628	395	114	114	5			

- Molecule 9 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	73	Total	C	N	O	S	0	0	0
			598	388	107	99	4			
9	V	73	Total	C	N	O	S	0	0	0
			598	388	107	99	4			

- Molecule 10 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	56	Total	C	N	O	S	0	0	0
			441	285	73	80	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	56	Total	C	N	O	S	0	0	0
			441	285	73	80	3			

- Molecule 11 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	49	Total	C	N	O	S	0	0	0
			384	250	65	67	2			
11	X	49	Total	C	N	O	S	0	0	0
			384	250	65	67	2			

- Molecule 12 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	47	Total	C	N	O	S	0	0	0
			386	257	65	62	2			
12	Y	47	Total	C	N	O	S	0	0	0
			386	257	65	62	2			

- Molecule 13 is a protein called CYTOCHROME C OXIDASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	43	Total	C	N	O	0	0	0
			335	223	53	59			
13	Z	43	Total	C	N	O	0	0	0
			335	223	53	59			

- Molecule 14 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	1	Total	Cu	0	0
			1	1		
14	B	2	Total	Cu	0	0
			2	2		
14	N	1	Total	Cu	0	0
			1	1		
14	O	2	Total	Cu	0	0
			2	2		

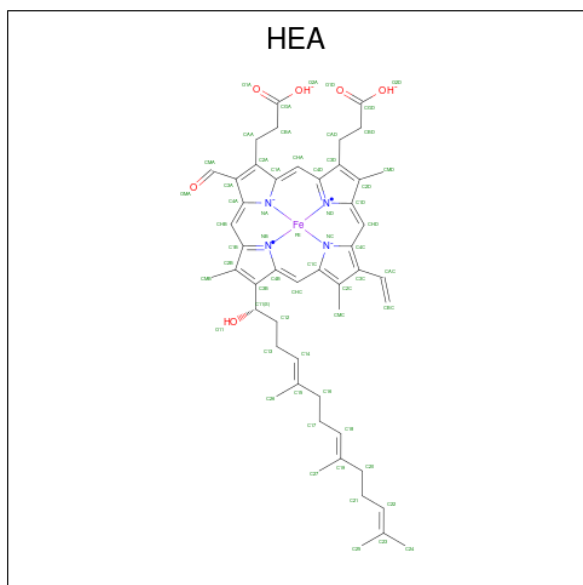
- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	A	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0

- Molecule 16 is SODIUM ION (CCD ID: NA) (formula: Na).

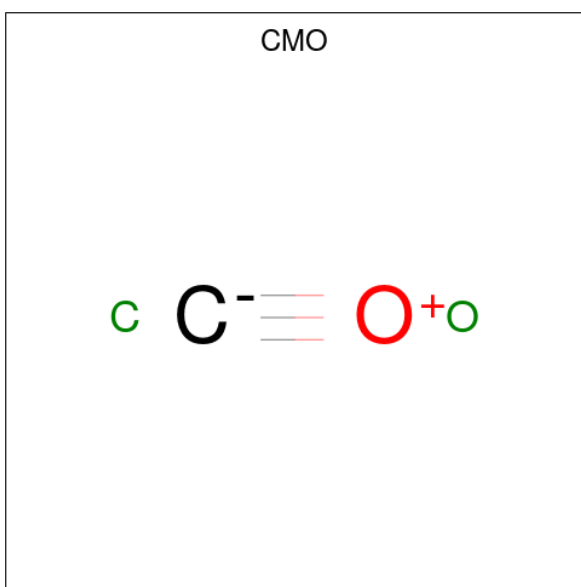
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	A	1	Total Na 1 1	0	0
16	N	1	Total Na 1 1	0	0

- Molecule 17 is HEME-A (CCD ID: HEA) (formula: C₄₉H₅₆FeN₄O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	1	Total C Fe N O 60 49 1 4 6	0	0
17	A	1	Total C Fe N O 60 49 1 4 6	0	0
17	N	1	Total C Fe N O 60 49 1 4 6	0	0
17	N	1	Total C Fe N O 60 49 1 4 6	0	0

- Molecule 18 is CARBON MONOXIDE (CCD ID: CMO) (formula: CO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	A	1	Total	C	O	0	0
			2	1	1		
18	N	1	Total	C	O	0	0
			2	1	1		

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

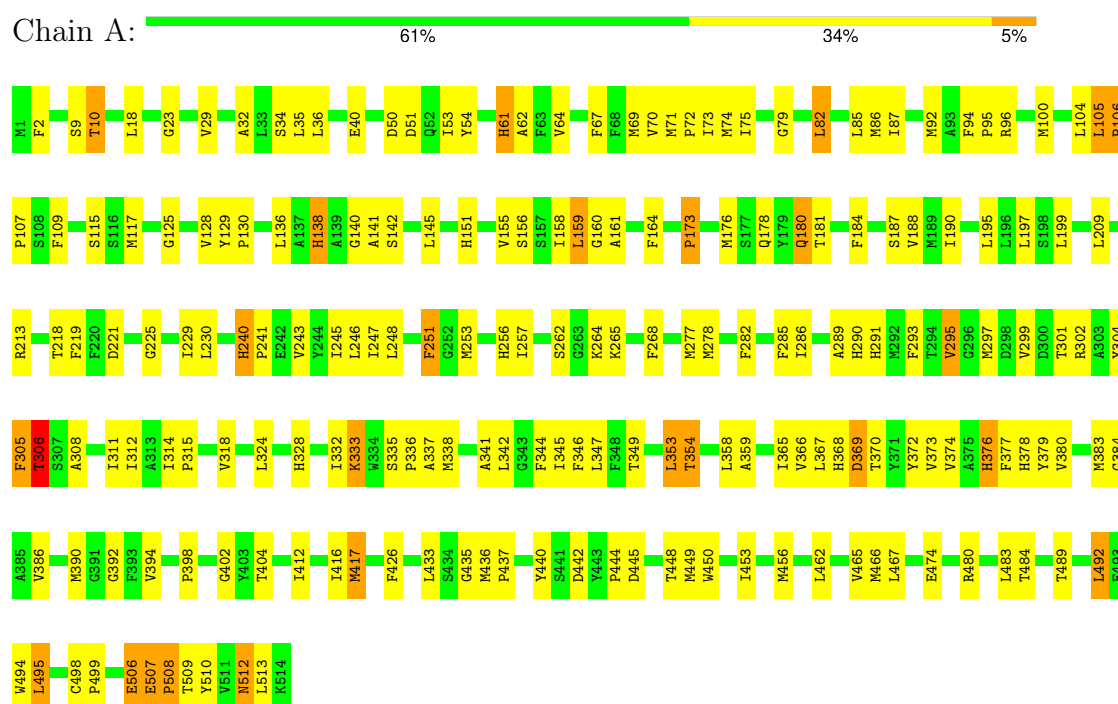
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	F	1	Total	Zn	0	0
			1	1		
19	S	1	Total	Zn	0	0
			1	1		

3 Residue-property plots

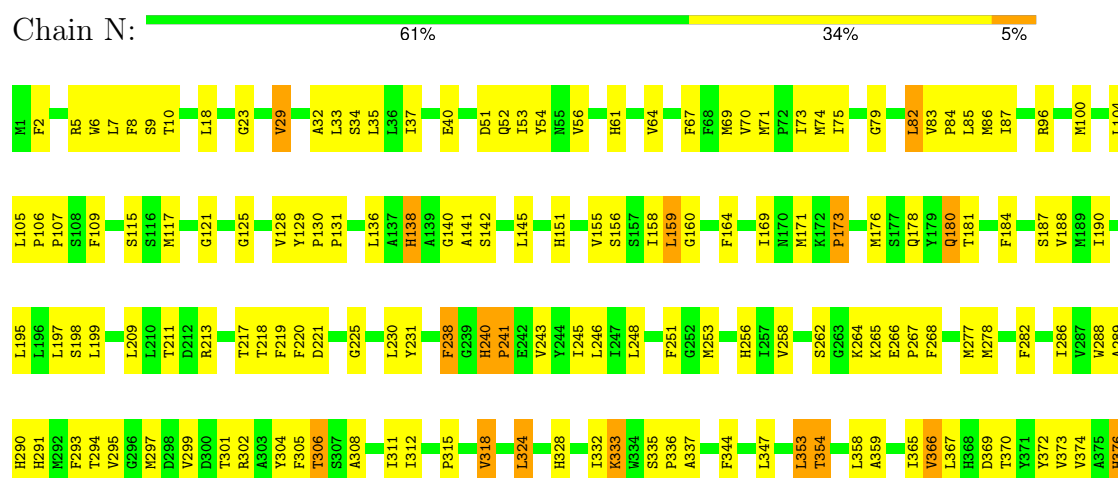
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

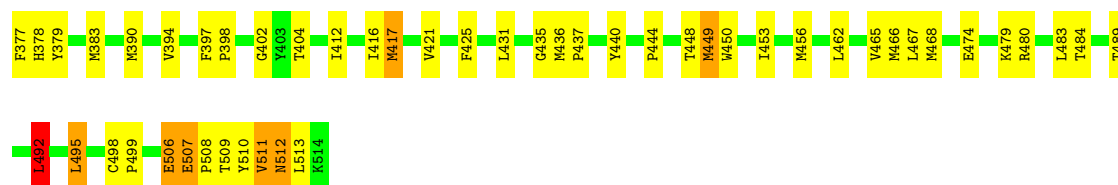
Note EDS was not executed.

• Molecule 1: CYTOCHROME C OXIDASE

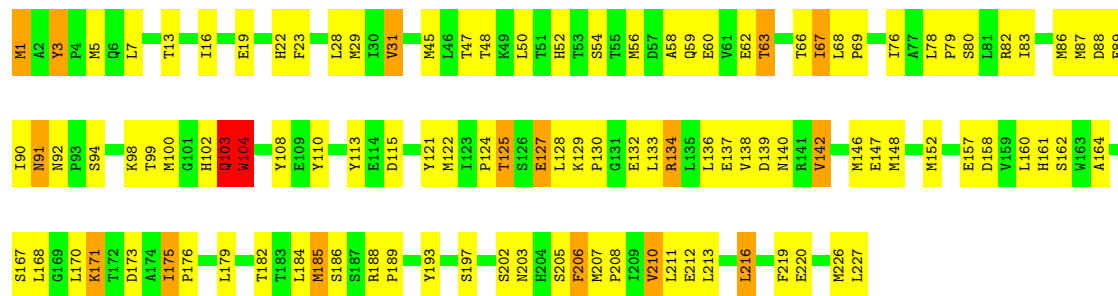


• Molecule 1: CYTOCHROME C OXIDASE

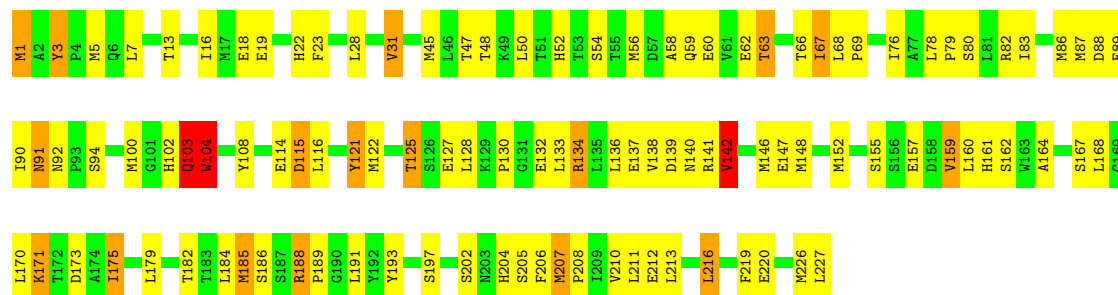




• Molecule 2: CYTOCHROME C OXIDASE



• Molecule 2: CYTOCHROME C OXIDASE

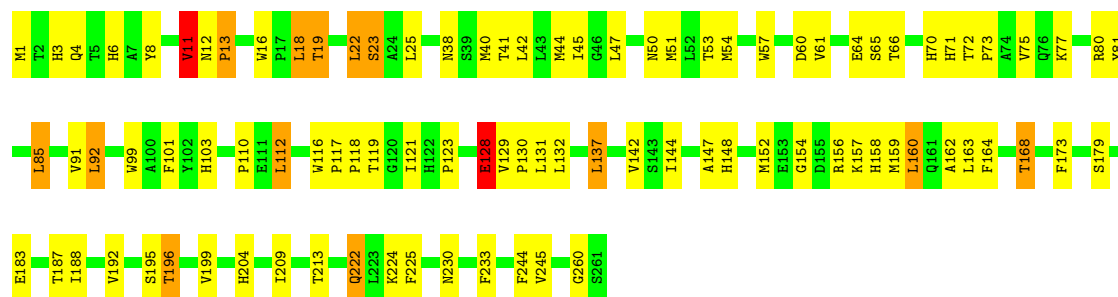


• Molecule 3: CYTOCHROME C OXIDASE



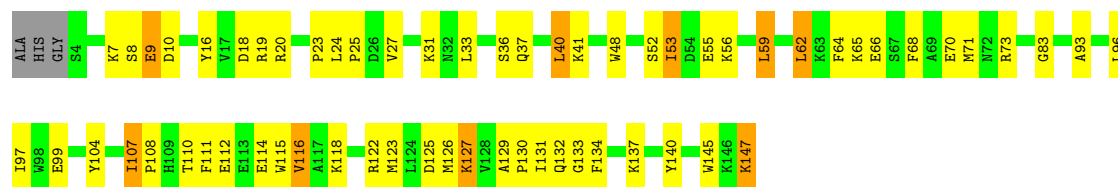
• Molecule 3: CYTOCHROME C OXIDASE





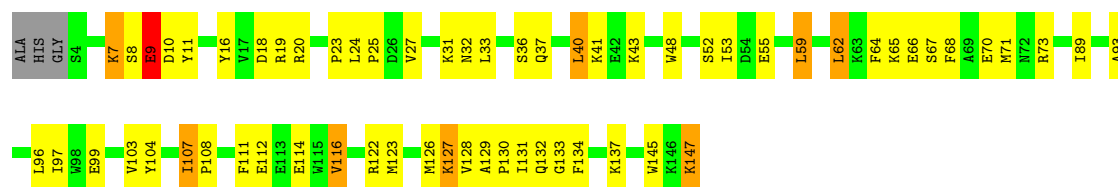
• Molecule 4: CYTOCHROME C OXIDASE

Chain D: 56% 36% 6%



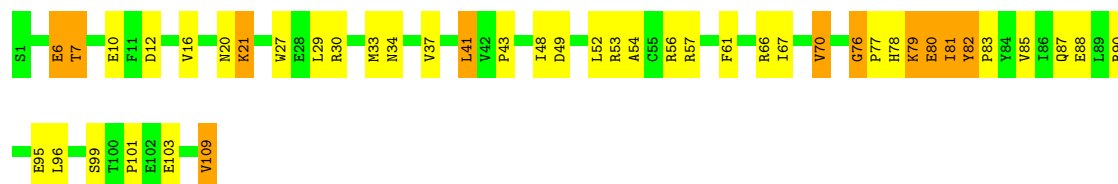
• Molecule 4: CYTOCHROME C OXIDASE

Chain Q: 56% 36% 5%



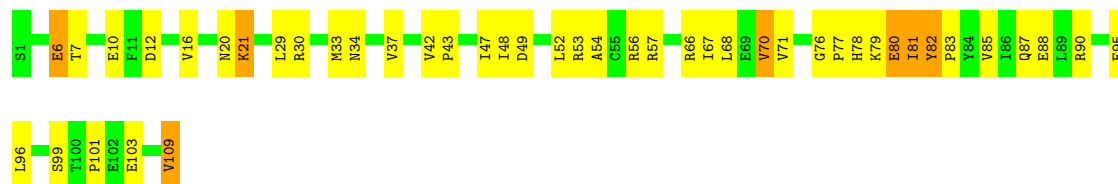
• Molecule 5: CYTOCHROME C OXIDASE

Chain E: 60% 30% 10%

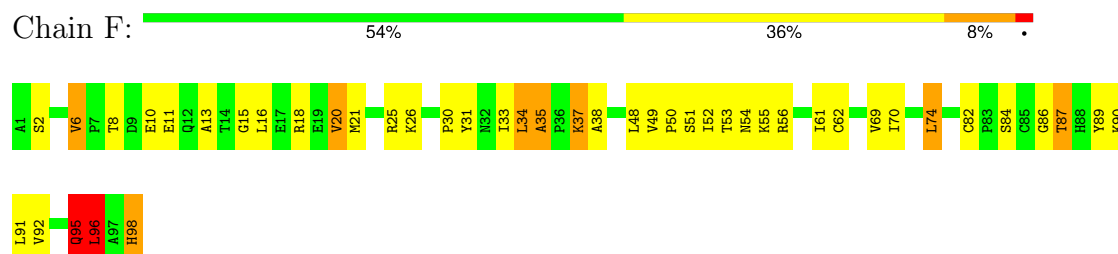


• Molecule 5: CYTOCHROME C OXIDASE

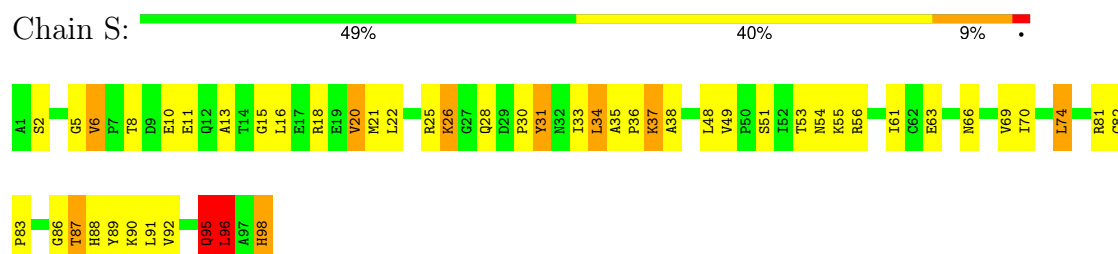
Chain R: 59% 35% 6%



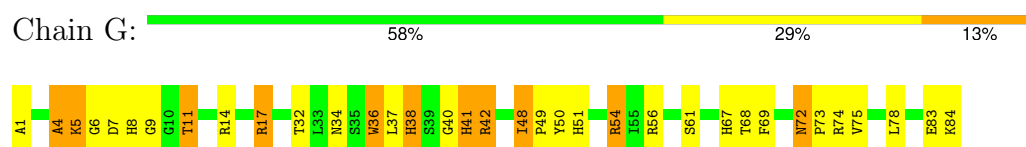
- Molecule 6: CYTOCHROME C OXIDASE



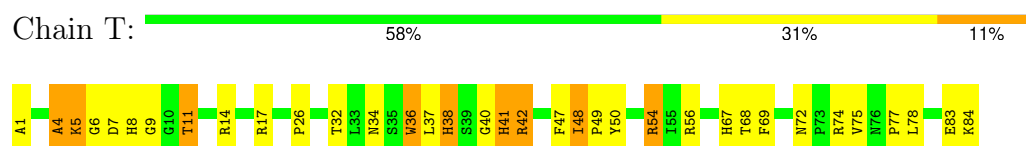
- Molecule 6: CYTOCHROME C OXIDASE



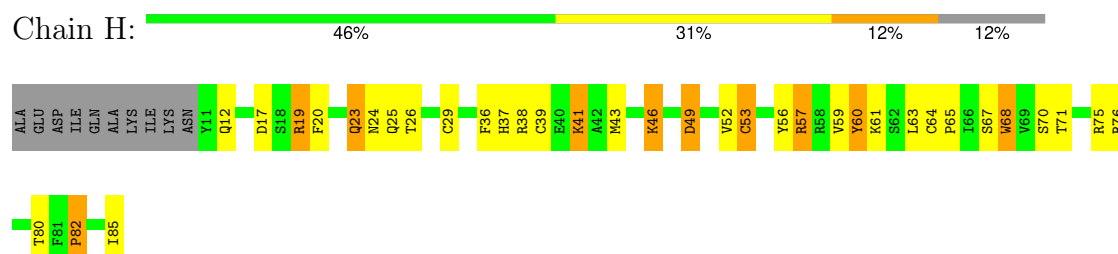
- Molecule 7: CYTOCHROME C OXIDASE



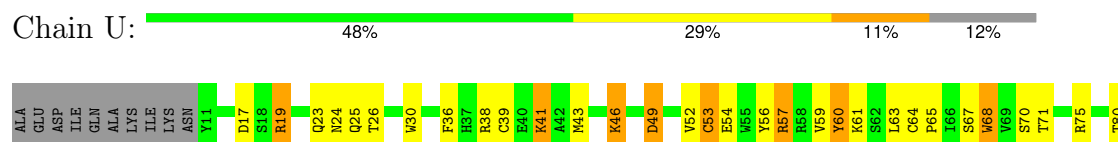
- Molecule 7: CYTOCHROME C OXIDASE



- Molecule 8: CYTOCHROME C OXIDASE



- Molecule 8: CYTOCHROME C OXIDASE





• Molecule 9: CYTOCHROME C OXIDASE

Chain I: 58% 37% 5%



• Molecule 9: CYTOCHROME C OXIDASE

Chain V: 51% 42% 7%



• Molecule 10: CYTOCHROME C OXIDASE

Chain J: 58% 27% 10% 5%



• Molecule 10: CYTOCHROME C OXIDASE

Chain W: 63% 22% 7% 5%



• Molecule 11: CYTOCHROME C OXIDASE

Chain K: 61% 23% 12%



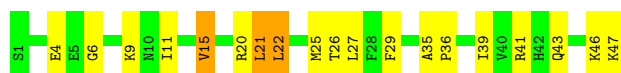
• Molecule 11: CYTOCHROME C OXIDASE

Chain X: 55% 27% 5% 12%

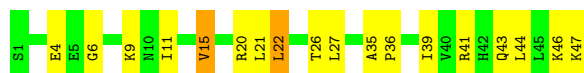


• Molecule 12: CYTOCHROME C OXIDASE

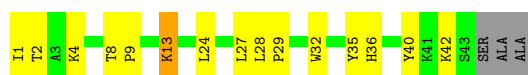
Chain L: 60% 34% 6%



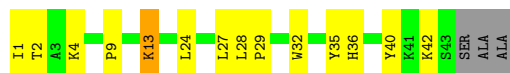
• Molecule 12: CYTOCHROME C OXIDASE



• Molecule 13: CYTOCHROME C OXIDASE



• Molecule 13: CYTOCHROME C OXIDASE



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	189.10Å 210.50Å 178.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.80	Depositor
% Data completeness (in resolution range)	97.3 (7.00-2.80)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.84	Depositor
R, R_{free}	0.213 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	28810	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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: HEA, CMO, MG, CU, ZN, NA

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	1.02	5/4164 (0.1%)	1.28	44/5688 (0.8%)
1	N	0.90	5/4164 (0.1%)	1.25	41/5688 (0.7%)
2	B	0.92	2/1909 (0.1%)	1.21	8/2601 (0.3%)
2	O	0.82	2/1909 (0.1%)	1.19	11/2601 (0.4%)
3	C	0.85	0/2211	1.12	11/3023 (0.4%)
3	P	0.80	0/2211	1.10	8/3023 (0.3%)
4	D	0.79	0/1229	1.07	5/1658 (0.3%)
4	Q	0.66	0/1229	1.06	9/1658 (0.5%)
5	E	0.75	0/898	1.09	9/1218 (0.7%)
5	R	0.68	0/898	1.07	6/1218 (0.5%)
6	F	0.91	0/765	1.16	4/1038 (0.4%)
6	S	0.84	0/765	1.20	4/1038 (0.4%)
7	G	0.82	0/699	1.22	6/950 (0.6%)
7	T	0.76	0/699	1.23	5/950 (0.5%)
8	H	0.80	0/648	1.20	9/877 (1.0%)
8	U	0.71	0/648	1.20	10/877 (1.1%)
9	I	0.80	0/611	1.07	4/810 (0.5%)
9	V	0.76	0/611	1.04	4/810 (0.5%)
10	J	0.80	0/451	1.06	2/610 (0.3%)
10	W	0.72	1/451 (0.2%)	1.04	1/610 (0.2%)
11	K	0.83	0/398	1.02	2/546 (0.4%)
11	X	0.71	0/398	1.04	2/546 (0.4%)
12	L	0.89	0/399	1.01	3/534 (0.6%)
12	Y	0.73	0/399	1.00	2/534 (0.4%)
13	M	0.89	0/345	1.15	1/470 (0.2%)
13	Z	0.69	0/345	1.06	1/470 (0.2%)
All	All	0.85	15/29454 (0.1%)	1.17	212/40046 (0.5%)

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	2
1	N	0	2
2	B	0	2
2	O	0	1
3	C	0	1
3	P	0	1
5	E	0	1
5	R	0	1
All	All	0	11

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	378	HIS	ND1-CE1	8.78	1.41	1.32
1	N	61	HIS	CG-CD2	8.62	1.45	1.35
1	N	378	HIS	CG-CD2	8.30	1.45	1.35
1	A	61	HIS	CG-CD2	7.92	1.44	1.35
1	A	378	HIS	ND1-CE1	6.72	1.39	1.32

The worst 5 of 212 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	61	HIS	ND1-CE1-NE2	10.92	119.32	108.40
1	A	378	HIS	ND1-CE1-NE2	10.08	118.48	108.40
1	A	61	HIS	ND1-CE1-NE2	9.81	118.21	108.40
1	N	332	ILE	N-CA-C	9.46	121.70	108.93
13	Z	27	LEU	N-CA-C	9.41	121.62	111.36

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	HIS	Sidechain
1	A	304	TYR	Sidechain
2	B	110	TYR	Sidechain
2	B	121	TYR	Sidechain
3	C	8	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	4025	0	4002	142	0
1	N	4025	0	4002	145	0
2	B	1863	0	1867	92	0
2	O	1863	0	1867	91	0
3	C	2124	0	2044	69	0
3	P	2124	0	2044	75	0
4	D	1195	0	1183	48	0
4	Q	1195	0	1183	49	0
5	E	878	0	868	36	0
5	R	878	0	868	33	0
6	F	748	0	728	40	0
6	S	748	0	728	47	0
7	G	672	0	645	37	0
7	T	672	0	645	35	0
8	H	628	0	582	53	0
8	U	628	0	582	52	0
9	I	598	0	612	28	0
9	V	598	0	612	30	0
10	J	441	0	439	13	0
10	W	441	0	439	11	0
11	K	384	0	366	11	0
11	X	384	0	366	15	0
12	L	386	0	388	15	0
12	Y	386	0	388	14	0
13	M	335	0	352	16	0
13	Z	335	0	352	15	0
14	A	1	0	0	0	0
14	B	2	0	0	0	0
14	N	1	0	0	0	0
14	O	2	0	0	0	0
15	A	1	0	0	0	0
15	N	1	0	0	0	0
16	A	1	0	0	0	0
16	N	1	0	0	0	0
17	A	120	0	107	13	0
17	N	120	0	107	10	0
18	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	N	2	0	0	0	0
19	F	1	0	0	0	0
19	S	1	0	0	0	0
All	All	28810	0	28366	1002	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 18.

The worst 5 of 1002 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)
8:H:57:ARG:HH11	8:H:57:ARG:HB3	1.23	1.03
8:U:57:ARG:HH11	8:U:57:ARG:HB3	1.20	1.01
1:N:187:SER:HB2	1:N:277:MET:HE1	1.45	0.97
2:B:86:MET:O	2:B:89[B]:GLU:HG2	1.65	0.96
1:A:35:LEU:HD11	1:A:462:LEU:HD13	1.53	0.90

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	512/514 (100%)	477 (93%)	33 (6%)	2 (0%)	30	60
1	N	512/514 (100%)	476 (93%)	36 (7%)	0	100	100
2	B	230/227 (101%)	202 (88%)	24 (10%)	4 (2%)	7	25
2	O	230/227 (101%)	202 (88%)	23 (10%)	5 (2%)	5	19
3	C	259/261 (99%)	249 (96%)	8 (3%)	2 (1%)	16	44
3	P	259/261 (99%)	250 (96%)	8 (3%)	1 (0%)	30	60
4	D	142/147 (97%)	134 (94%)	7 (5%)	1 (1%)	18	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Q	142/147 (97%)	133 (94%)	8 (6%)	1 (1%)	18	47
5	E	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
5	R	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
6	F	96/98 (98%)	85 (88%)	6 (6%)	5 (5%)	1	5
6	S	96/98 (98%)	86 (90%)	5 (5%)	5 (5%)	1	5
7	G	82/84 (98%)	65 (79%)	14 (17%)	3 (4%)	2	9
7	T	82/84 (98%)	64 (78%)	16 (20%)	2 (2%)	4	17
8	H	73/85 (86%)	64 (88%)	8 (11%)	1 (1%)	9	30
8	U	73/85 (86%)	62 (85%)	10 (14%)	1 (1%)	9	30
9	I	71/73 (97%)	66 (93%)	5 (7%)	0	100	100
9	V	71/73 (97%)	66 (93%)	5 (7%)	0	100	100
10	J	54/59 (92%)	49 (91%)	2 (4%)	3 (6%)	1	4
10	W	54/59 (92%)	50 (93%)	1 (2%)	3 (6%)	1	4
11	K	47/56 (84%)	40 (85%)	7 (15%)	0	100	100
11	X	47/56 (84%)	41 (87%)	6 (13%)	0	100	100
12	L	45/47 (96%)	41 (91%)	4 (9%)	0	100	100
12	Y	45/47 (96%)	42 (93%)	3 (7%)	0	100	100
13	M	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
13	Z	41/46 (89%)	40 (98%)	0	1 (2%)	4	17
All	All	3518/3612 (97%)	3230 (92%)	248 (7%)	40 (1%)	11	36

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	91[A]	ASN
2	B	91[B]	ASN
4	D	20	ARG
6	F	87	THR
6	F	96	LEU

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	427/427 (100%)	393 (92%)	34 (8%)	11	34
1	N	427/427 (100%)	390 (91%)	37 (9%)	9	30
2	B	216/211 (102%)	189 (88%)	27 (12%)	4	15
2	O	216/211 (102%)	189 (88%)	27 (12%)	4	15
3	C	226/226 (100%)	199 (88%)	27 (12%)	5	17
3	P	226/226 (100%)	200 (88%)	26 (12%)	5	18
4	D	128/129 (99%)	114 (89%)	14 (11%)	6	21
4	Q	128/129 (99%)	114 (89%)	14 (11%)	6	21
5	E	95/95 (100%)	85 (90%)	10 (10%)	6	22
5	R	95/95 (100%)	86 (90%)	9 (10%)	8	26
6	F	81/81 (100%)	72 (89%)	9 (11%)	6	20
6	S	81/81 (100%)	73 (90%)	8 (10%)	7	24
7	G	68/68 (100%)	55 (81%)	13 (19%)	1	5
7	T	68/68 (100%)	54 (79%)	14 (21%)	1	4
8	H	67/75 (89%)	56 (84%)	11 (16%)	2	8
8	U	67/75 (89%)	57 (85%)	10 (15%)	3	10
9	I	58/58 (100%)	52 (90%)	6 (10%)	7	23
9	V	58/58 (100%)	52 (90%)	6 (10%)	7	23
10	J	47/50 (94%)	39 (83%)	8 (17%)	2	7
10	W	47/50 (94%)	38 (81%)	9 (19%)	1	5
11	K	39/46 (85%)	37 (95%)	2 (5%)	21	54
11	X	39/46 (85%)	37 (95%)	2 (5%)	21	54
12	L	40/40 (100%)	34 (85%)	6 (15%)	3	10
12	Y	40/40 (100%)	33 (82%)	7 (18%)	2	7
13	M	37/38 (97%)	34 (92%)	3 (8%)	11	33
13	Z	37/38 (97%)	34 (92%)	3 (8%)	11	33
All	All	3058/3088 (99%)	2716 (89%)	342 (11%)	6	19

5 of 342 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	205	SER
6	S	37	LYS
3	P	22	LEU
4	Q	9	GLU
7	T	41	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	43	GLN
3	P	204	HIS
11	X	10	HIS
1	N	256	HIS
2	O	203	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 for Mogul analysis.

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
17	HEA	N	516	1	67,67,67	1.47	13 (19%)	81,103,103	1.88	27 (33%)
17	HEA	N	515	1	67,67,67	1.19	7 (10%)	81,103,103	1.96	20 (24%)
18	CMO	N	520	14	0,1,1	-	-	-	-	-
17	HEA	A	516	1	67,67,67	1.54	12 (17%)	81,103,103	2.00	32 (39%)
18	CMO	A	520	14	0,1,1	-	-	-	-	-
17	HEA	A	515	1	67,67,67	1.28	7 (10%)	81,103,103	1.99	18 (22%)

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
17	HEA	N	515	1	-	11/36/76/76	-
17	HEA	A	516	1	-	9/36/76/76	-
17	HEA	N	516	1	-	10/36/76/76	-
17	HEA	A	515	1	-	12/36/76/76	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	A	516	HEA	FE-ND	-3.77	1.83	1.94
17	N	516	HEA	C3C-C2C	-3.49	1.29	1.41
17	A	515	HEA	CMA-C3A	-3.39	1.37	1.45
17	N	516	HEA	FE-NB	-3.29	1.84	1.94
17	A	516	HEA	CMA-C3A	-3.26	1.38	1.45

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	515	HEA	C12-C11-C3B	7.35	123.61	112.12
17	A	515	HEA	C12-C11-C3B	6.49	122.26	112.12
17	A	516	HEA	CMB-C2B-C3B	-5.68	119.30	130.28
17	N	515	HEA	C13-C14-C15	-5.38	115.31	127.62
17	A	515	HEA	C13-C14-C15	-5.16	115.81	127.62

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

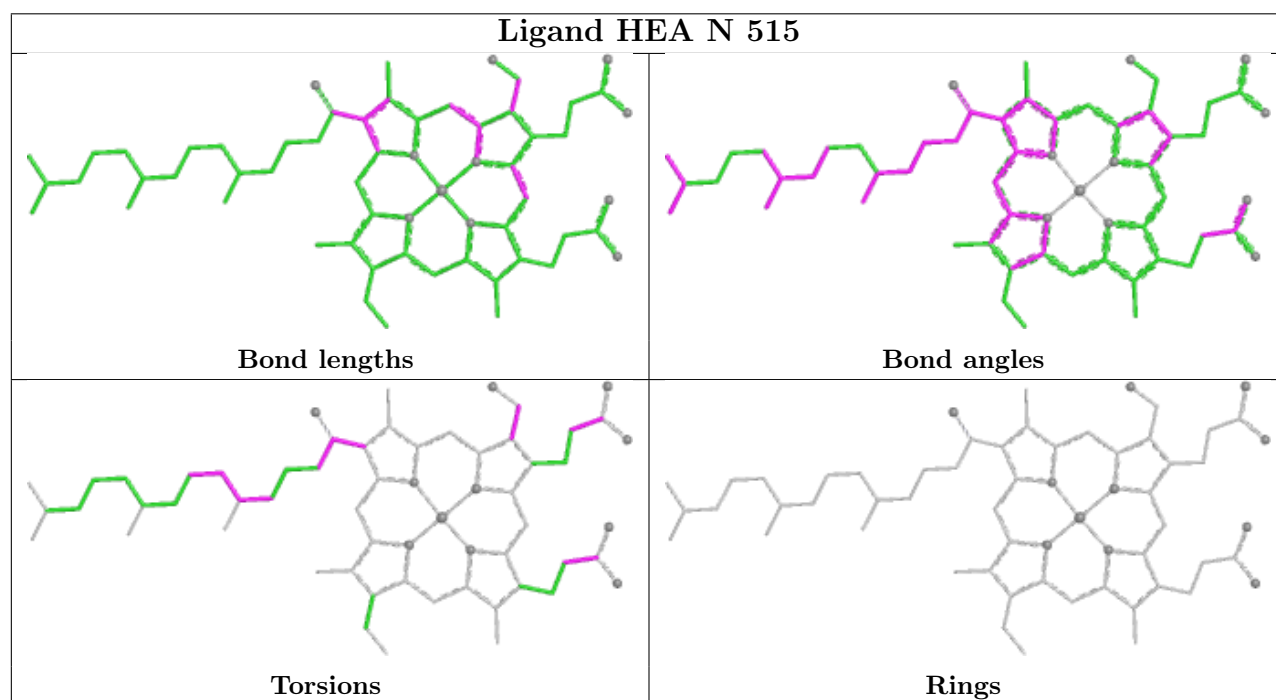
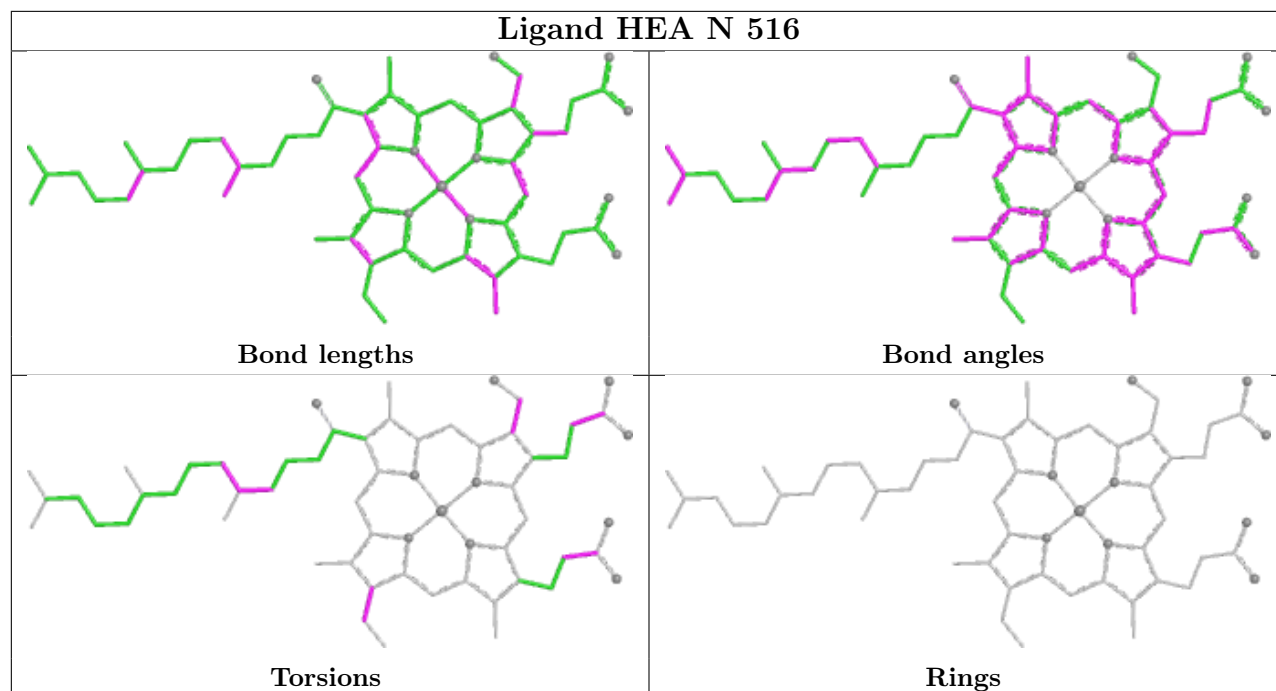
Mol	Chain	Res	Type	Atoms
17	A	515	HEA	C2A-C3A-CMA-OMA
17	A	515	HEA	C4A-C3A-CMA-OMA
17	A	515	HEA	C12-C11-C3B-C2B
17	N	515	HEA	C2A-C3A-CMA-OMA
17	N	515	HEA	C4A-C3A-CMA-OMA

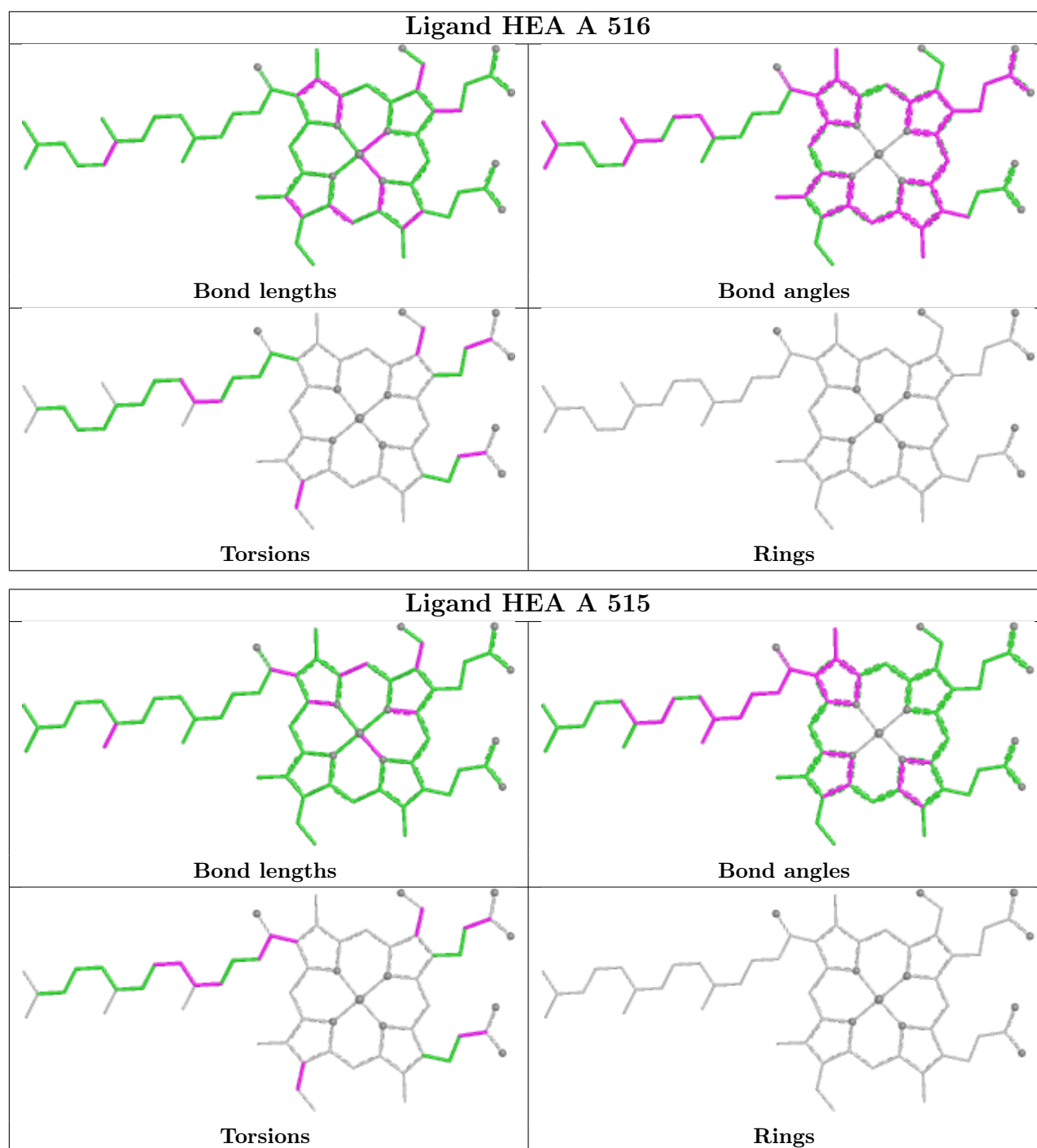
There are no ring outliers.

4 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	N	516	HEA	1	0
17	N	515	HEA	9	0
17	A	516	HEA	3	0
17	A	515	HEA	10	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.