



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 07:40 AM GMT

PDB ID : 1V54  
Title : Bovine heart cytochrome c oxidase at the fully oxidized state  
Authors : Tsukihara, T.; Shimokata, K.; Katayama, Y.; Shimada, H.; Muramoto, K.; Aoyama, H.; Mochizuki, M.; Shinzawa-Itoh, K.; Yamashita, E.; Yao, M.; Ishimura, Y.; Yoshikawa, S.  
Deposited on : 2003-11-21  
Resolution : 1.80 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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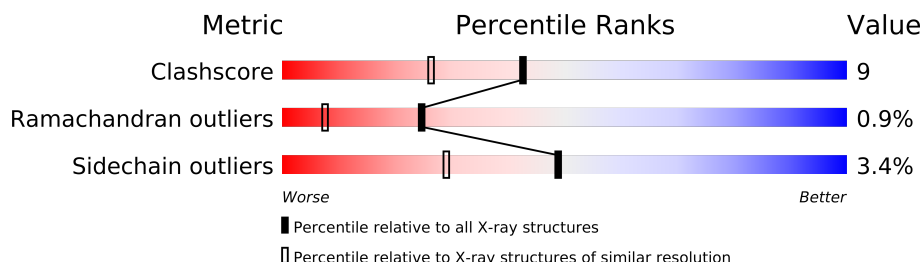
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.80 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	79885	4461 (1.80-1.80)
Ramachandran outliers	78287	4404 (1.80-1.80)
Sidechain outliers	78261	4403 (1.80-1.80)







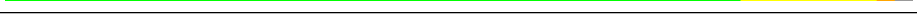

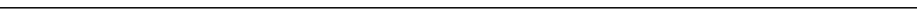
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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	
5	E	109	
5	R	109	
6	F	98	
6	S	98	
7	G	85	
7	T	85	
8	H	85	
8	U	85	
9	I	73	

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Mol	Chain	Length	Quality of chain
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 28 unique types of molecules in this entry. The entry contains 32636 atoms, of which 0 are hydrogen and 0 are deuterium.

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 polypeptide I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			
1	N	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			

- Molecule 2 is a protein called Cytochrome c oxidase polypeptide II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	227	Total	C	N	O	S	0	0	0
			1824	1185	281	340	18			
2	O	227	Total	C	N	O	S	0	0	0
			1824	1185	281	340	18			

- Molecule 3 is a protein called Cytochrome c oxidase polypeptide III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	259	Total	C	N	O	S	0	0	0
			2110	1412	336	350	12			
3	P	259	Total	C	N	O	S	0	0	0
			2110	1412	336	350	12			

- Molecule 4 is a protein called Cytochrome c oxidase subunit IV isoform 1.

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 polypeptide Va.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			
5	R	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			

- Molecule 6 is a protein called Cytochrome c oxidase polypeptide Vb.

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 polypeptide VIa-heart.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
7	G	84	Total 675	C 431	N 129	O 113	P 1	S 1	0	0	0
7	T	84	Total 675	C 431	N 129	O 113	P 1	S 1	0	0	0

- Molecule 8 is a protein called Cytochrome c oxidase polypeptide VIb.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			
8	U	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			

- Molecule 9 is a protein called Cytochrome c oxidase polypeptide VIc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			
9	V	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			

- Molecule 10 is a protein called Cytochrome c oxidase polypeptide VIIa-heart.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

- Molecule 11 is a protein called Cytochrome c oxidase polypeptide VIIb.

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 polypeptide VIIc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	46	Total	C	N	O	S	0	0	0
			380	254	64	60	2			
12	Y	46	Total	C	N	O	S	0	0	0
			380	254	64	60	2			

- Molecule 13 is a protein called Cytochrome c oxidase polypeptide VIII-heart.

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 (three-letter code: CU) (formula: Cu).

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

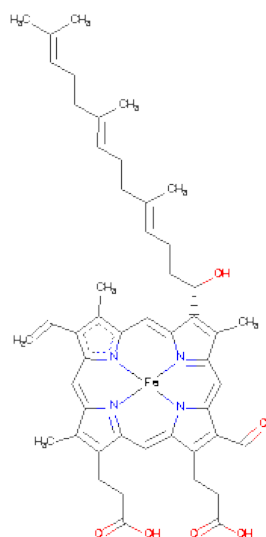
- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 16 is SODIUM ION (three-letter code: NA) (formula: Na).

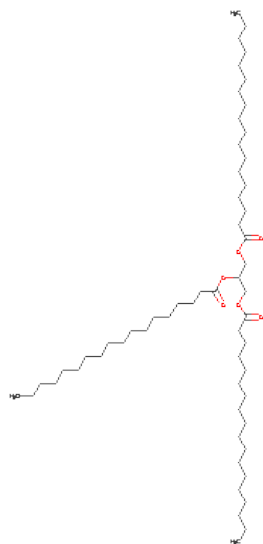
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	1	Total	Na	0	0
			1	1		
16	N	1	Total	Na	0	0
			1	1		

- Molecule 17 is HEME-A (three-letter code: HEA) (formula: C<sub>49</sub>H<sub>56</sub>FeN<sub>4</sub>O<sub>6</sub>).



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

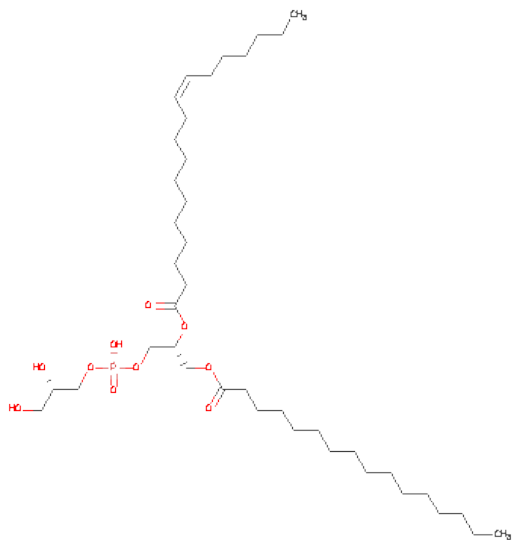
- Molecule 18 is TRISTEAROYLGLYCEROL (three-letter code: TGL) (formula: C<sub>57</sub>H<sub>110</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	A	1	Total	C	O	0	0
			63	57	6		
18	D	1	Total	C	O	0	0
			63	57	6		
18	L	1	Total	C	O	0	0
			63	57	6		
18	N	1	Total	C	O	0	0
			63	57	6		
18	N	1	Total	C	O	0	0
			63	57	6		
18	Q	1	Total	C	O	0	0
			63	57	6		

- Molecule 19 is (1R)-2-{{[[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL(11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: C<sub>40</sub>H<sub>77</sub>O<sub>10</sub>P).





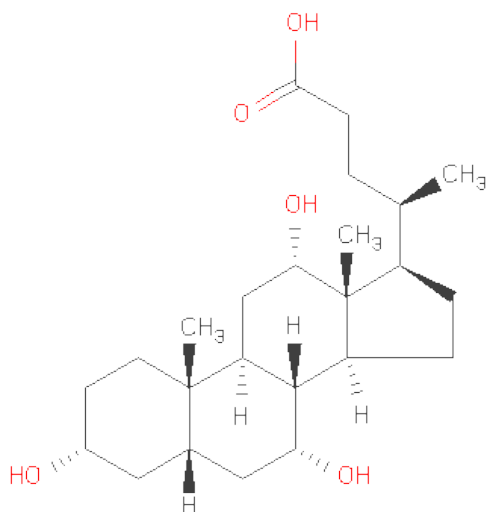
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
19	A	1	Total	C	O	P	0	0
			51	40	10	1		
19	A	1	Total	C	O	P	0	0
			51	40	10	1		
19	C	1	Total	C	O	P	0	0
			51	40	10	1		
19	C	1	Total	C	O	P	0	0
			51	40	10	1		
19	N	1	Total	C	O	P	0	0
			51	40	10	1		
19	N	1	Total	C	O	P	0	0
			51	40	10	1		
19	P	1	Total	C	O	P	0	0
			51	40	10	1		
19	P	1	Total	C	O	P	0	0
			51	40	10	1		

- Molecule 20 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu<sub>2</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	B	1	Total	Cu	0	0
			2	2		
20	O	1	Total	Cu	0	0
			2	2		

- Molecule 21 is CHOLIC ACID (three-letter code: CHD) (formula:  $C_{24}H_{40}O_5$ ).



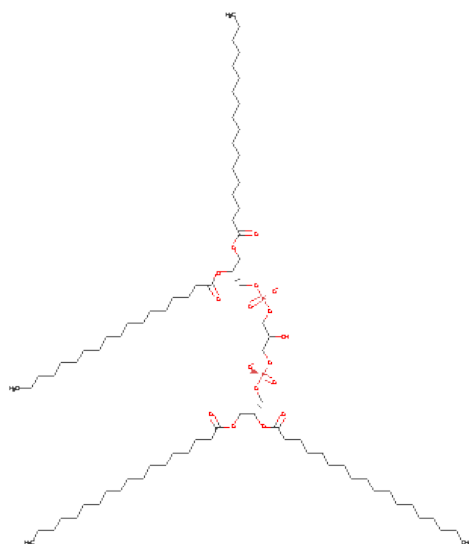
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	B	1	Total	C	O	0	0
			29	24	5		
21	C	1	Total	C	O	0	0
			29	24	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	C	1	Total	C	O	0	0
			29	24	5		
21	J	1	Total	C	O	0	0
			29	24	5		
21	O	1	Total	C	O	0	0
			29	24	5		
21	P	1	Total	C	O	0	0
			29	24	5		
21	P	1	Total	C	O	0	0
			29	24	5		
21	W	1	Total	C	O	0	0
			29	24	5		

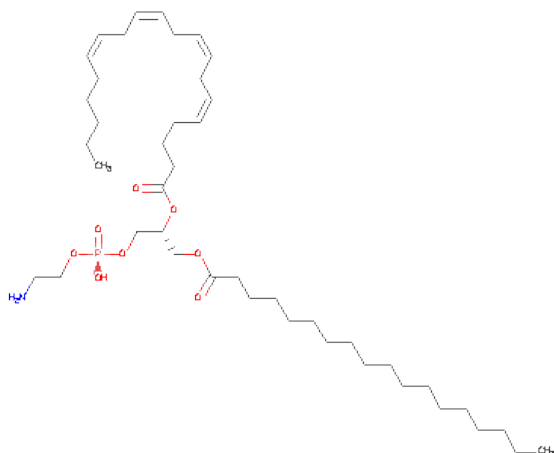
- Molecule 22 is CARDIOLIPIN (three-letter code: CDL) (formula:  $C_{81}H_{156}O_{17}P_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	C	1	Total	C	O	P	0	0
			100	81	17	2		
22	G	1	Total	C	O	P	0	0
			100	81	17	2		
22	P	1	Total	C	O	P	0	0
			100	81	17	2		
22	T	1	Total	C	O	P	0	0
			100	81	17	2		

- Molecule 23 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL(5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE

(three-letter code: PEK) (formula: C<sub>43</sub>H<sub>78</sub>NO<sub>8</sub>P).

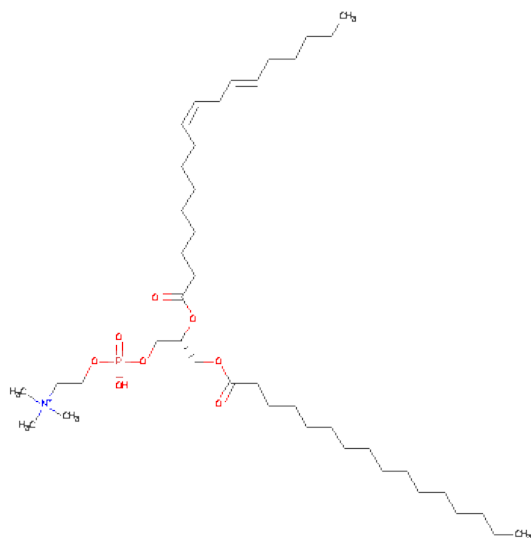


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
23	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
23	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
23	P	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
23	P	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
23	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		

- Molecule 24 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	P	1	Total	X	0	0
			1	1		
24	C	1	Total	X	0	0
			1	1		

- Molecule 25 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (three-letter code: PSC) (formula: C<sub>42</sub>H<sub>81</sub>NO<sub>8</sub>P).

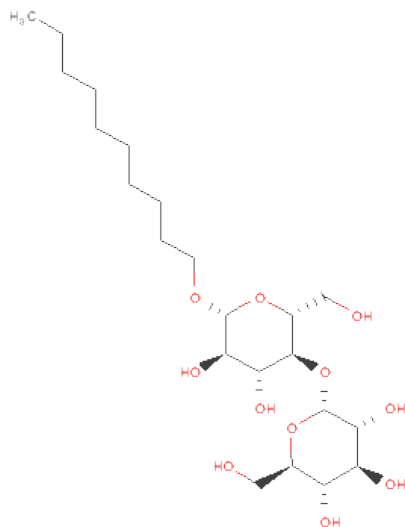


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	E	1	Total	C	N	O	P	0	0
			52	42	1	8	1		
25	O	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 27 is SUGAR (DECYL-BETA-D-MALTOPYRANOSIDE) (three-letter code: DMU) (formula: C<sub>22</sub>H<sub>42</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
27	M	1	Total	C	O	0	0
			33	22	11		
27	Z	1	Total	C	O	0	0
			33	22	11		

- Molecule 28 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	A	227	Total	O	0	0
			227	227		
28	B	180	Total	O	0	0
			180	180		
28	C	116	Total	O	0	0
			116	116		
28	D	109	Total	O	0	0
			109	109		
28	E	68	Total	O	0	0
			68	68		
28	F	80	Total	O	0	0
			80	80		
28	G	59	Total	O	0	0
			59	59		
28	H	71	Total	O	0	0
			71	71		
28	I	61	Total	O	0	0
			61	61		
28	J	21	Total	O	0	0
			21	21		

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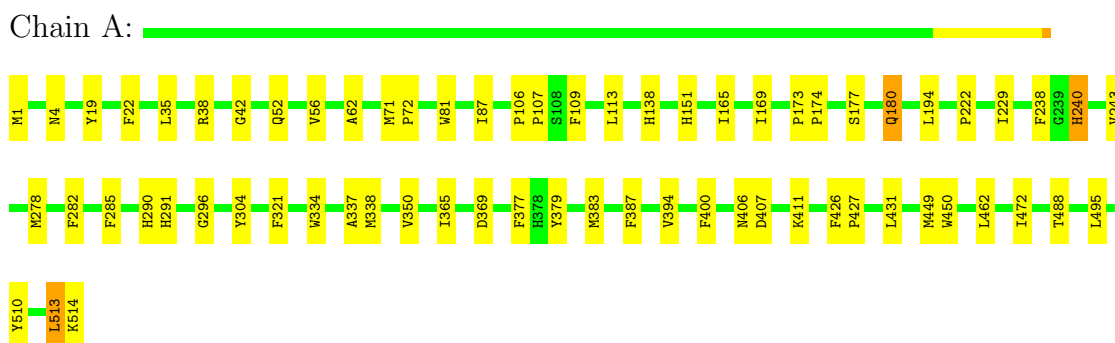
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	K	37	Total 37	O 37	0	0
28	L	23	Total 23	O 23	0	0
28	M	32	Total 32	O 32	0	0
28	N	217	Total 217	O 217	0	0
28	O	146	Total 146	O 146	0	0
28	P	120	Total 120	O 120	0	0
28	Q	73	Total 73	O 73	0	0
28	R	32	Total 32	O 32	0	0
28	S	54	Total 54	O 54	0	0
28	T	58	Total 58	O 58	0	0
28	U	65	Total 65	O 65	0	0
28	V	36	Total 36	O 36	0	0
28	W	13	Total 13	O 13	0	0
28	X	29	Total 29	O 29	0	0
28	Y	25	Total 25	O 25	0	0
28	Z	18	Total 18	O 18	0	0

### 3 Residue-property plots

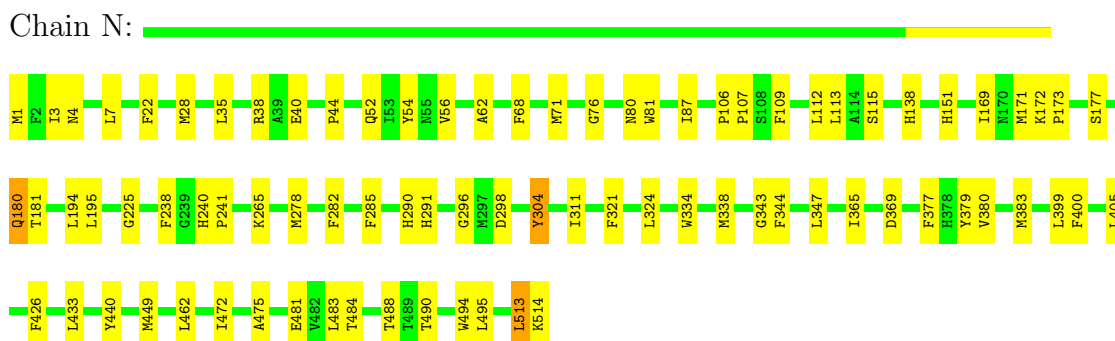
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 was not executed.

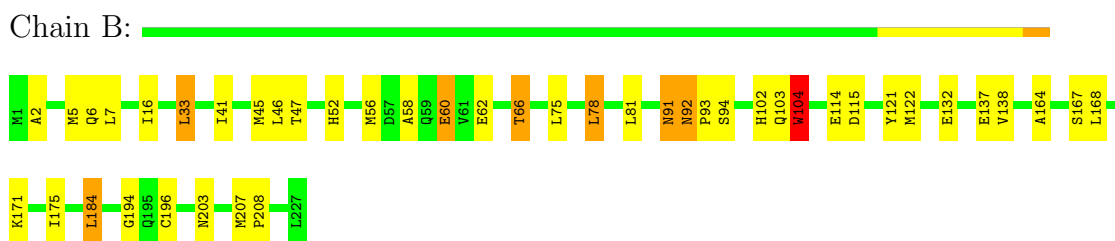
- Molecule 1: Cytochrome c oxidase polypeptide I



- Molecule 1: Cytochrome c oxidase polypeptide I



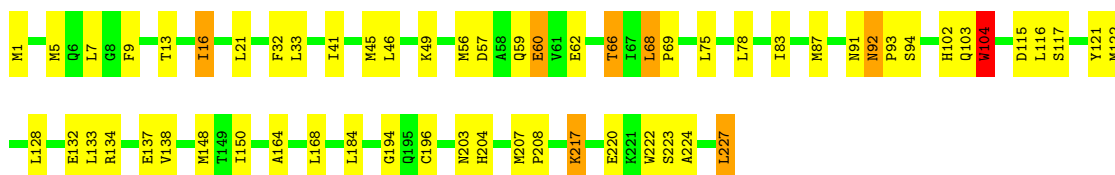
- Molecule 2: Cytochrome c oxidase polypeptide II



- Molecule 2: Cytochrome c oxidase polypeptide II







- Molecule 3: Cytochrome c oxidase polypeptide III

Chain C:



- Molecule 3: Cytochrome c oxidase polypeptide III

Chain P:



- Molecule 4: Cytochrome c oxidase subunit IV isoform 1

Chain D:



- Molecule 4: Cytochrome c oxidase subunit IV isoform 1

Chain Q:



- Molecule 5: Cytochrome c oxidase polypeptide Va

Chain E:



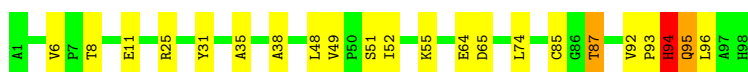
- Molecule 5: Cytochrome c oxidase polypeptide Va

Chain R:



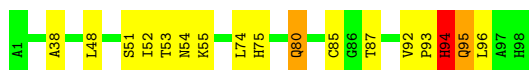
- Molecule 6: Cytochrome c oxidase polypeptide Vb

Chain F:



- Molecule 6: Cytochrome c oxidase polypeptide Vb

Chain S: 



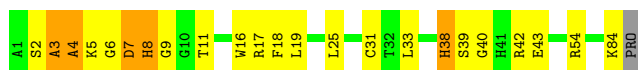
- Molecule 7: Cytochrome c oxidase polypeptide VIa-heart

Chain G: 



- Molecule 7: Cytochrome c oxidase polypeptide VIa-heart

Chain T: 



- Molecule 8: Cytochrome c oxidase polypeptide VIIb

Chain H: 



- Molecule 8: Cytochrome c oxidase polypeptide VIIb

Chain U: 



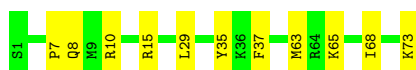
- Molecule 9: Cytochrome c oxidase polypeptide VIc

Chain I: 



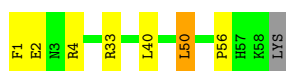
- Molecule 9: Cytochrome c oxidase polypeptide VIc

Chain V: 



- Molecule 10: Cytochrome c oxidase polypeptide VIIa-heart

Chain J: 



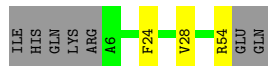
- Molecule 10: Cytochrome c oxidase polypeptide VIIa-heart

Chain W: 



- Molecule 11: Cytochrome c oxidase polypeptide VIIb

Chain K:



- Molecule 11: Cytochrome c oxidase polypeptide VIIb

Chain X:



- Molecule 12: Cytochrome c oxidase polypeptide VIIc

Chain L:



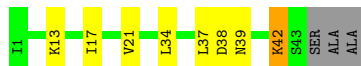
- Molecule 12: Cytochrome c oxidase polypeptide VIIc

Chain Y:



- Molecule 13: Cytochrome c oxidase polypeptide VIII-heart

Chain M:



- Molecule 13: Cytochrome c oxidase polypeptide VIII-heart

Chain Z:



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	182.59Å 205.14Å 178.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.80	Depositor
% Data completeness (in resolution range)	(Not available) (40.00-1.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.202 , 0.227	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	32636	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	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: ZN, CHD, HEA, SAC, CDL, PSC, PEK, MG, TGL, PGV, TPO, UNX, CUA, NA, FME, CU, DMU

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	0.51	0/4156	0.68	0/5678
1	N	0.50	0/4156	0.67	0/5678
2	B	0.48	0/1860	0.79	3/2534 (0.1%)
2	O	0.52	0/1860	0.82	3/2534 (0.1%)
3	C	0.51	0/2197	0.59	0/3005
3	P	0.48	0/2197	0.61	0/3005
4	D	0.48	0/1229	0.66	1/1658 (0.1%)
4	Q	0.51	0/1229	0.66	1/1658 (0.1%)
5	E	0.49	0/871	0.66	0/1182
5	R	0.50	0/871	0.68	0/1182
6	F	0.48	0/765	0.81	2/1038 (0.2%)
6	S	0.51	0/765	0.82	2/1038 (0.2%)
7	G	0.52	0/690	0.69	0/937
7	T	0.55	0/690	0.73	1/937 (0.1%)
8	H	0.47	0/682	0.68	0/921
8	U	0.49	0/682	0.67	0/921
9	I	0.53	0/605	0.60	0/802
9	V	0.53	0/605	0.62	0/802
10	J	0.47	0/471	0.60	0/636
10	W	0.48	0/471	0.64	0/636
11	K	0.50	0/398	0.67	0/546
11	X	0.49	0/398	0.66	0/546
12	L	0.50	0/393	0.56	0/526
12	Y	0.54	0/393	0.58	0/526
13	M	0.47	0/345	0.62	0/470
13	Z	0.43	0/345	0.61	0/470
All	All	0.50	0/29324	0.68	13/39866 (0.0%)

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
8	U	0	1
All	All	0	5

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	S	94	HIS	N-CA-C	6.25	127.89	111.00
2	B	103	GLN	CA-C-N	-6.20	103.55	117.20
6	F	94	HIS	N-CA-C	5.99	127.18	111.00
7	T	33	LEU	CA-CB-CG	5.91	128.88	115.30
2	O	103	GLN	CA-C-N	-5.82	104.40	117.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	19	TYR	Sidechain
1	A	240	HIS	Sidechain
1	N	240	HIS	Sidechain
1	N	304	TYR	Sidechain
8	U	11	TYR	Sidechain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4027	0	4001	62	0
1	N	4027	0	4001	72	0
2	B	1824	0	1833	33	0
2	O	1824	0	1833	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	2110	0	2027	17	0
3	P	2110	0	2027	24	0
4	D	1195	0	1183	15	0
4	Q	1195	0	1183	25	0
5	E	852	0	845	6	0
5	R	852	0	845	11	0
6	F	748	0	728	16	0
6	S	748	0	728	12	0
7	G	675	0	644	25	0
7	T	675	0	644	21	0
8	H	662	0	623	5	0
8	U	662	0	623	8	0
9	I	601	0	613	8	0
9	V	601	0	613	11	0
10	J	460	0	459	6	0
10	W	460	0	459	2	0
11	K	384	0	366	2	0
11	X	384	0	366	8	0
12	L	380	0	380	13	0
12	Y	380	0	380	10	0
13	M	335	0	352	5	0
13	Z	335	0	352	6	0
14	A	1	0	0	0	0
14	N	1	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	108	4	0
17	N	120	0	108	3	0
18	A	63	0	110	11	0
18	D	63	0	110	15	0
18	L	63	0	110	25	0
18	N	126	0	220	38	0
18	Q	63	0	110	15	0
19	A	102	0	152	7	0
19	C	102	0	152	7	0
19	N	102	0	152	5	0
19	P	102	0	152	8	0
20	B	2	0	0	0	0
20	O	2	0	0	0	0
21	B	29	0	39	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	C	58	0	78	3	0
21	J	29	0	39	2	0
21	O	29	0	39	1	0
21	P	58	0	78	2	0
21	W	29	0	39	2	0
22	C	100	0	156	14	0
22	G	100	0	156	14	0
22	P	100	0	156	18	0
22	T	100	0	156	15	0
23	C	106	0	154	7	0
23	G	53	0	77	10	0
23	P	106	0	154	6	0
23	T	53	0	77	9	0
24	C	1	0	0	0	0
24	P	1	0	0	0	0
25	E	52	0	80	13	0
25	O	52	0	80	21	0
26	F	1	0	0	0	0
26	S	1	0	0	0	0
27	M	33	0	36	0	0
27	Z	33	0	36	0	0
28	A	227	0	0	2	0
28	B	180	0	0	8	0
28	C	116	0	0	1	0
28	D	109	0	0	3	0
28	E	68	0	0	2	0
28	F	80	0	0	2	0
28	G	59	0	0	3	0
28	H	71	0	0	1	0
28	I	61	0	0	2	0
28	J	21	0	0	0	0
28	K	37	0	0	0	0
28	L	23	0	0	1	0
28	M	32	0	0	0	0
28	N	217	0	0	5	0
28	O	146	0	0	1	0
28	P	120	0	0	1	0
28	Q	73	0	0	5	0
28	R	32	0	0	0	0
28	S	54	0	0	3	0
28	T	58	0	0	2	0
28	U	65	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	V	36	0	0	2	0
28	W	13	0	0	0	0
28	X	29	0	0	1	0
28	Y	25	0	0	1	0
28	Z	18	0	0	0	0
All	All	32636	0	31222	551	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

The worst 5 of 551 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:84:LYS:HD2	7:G:84:LYS:H	1.14	1.08
3:P:63:ARG:HE	22:P:4270:CDL:HA22	1.24	1.03
22:C:3270:CDL:H662	19:C:3267:PGV:H182	1.41	1.03
7:T:84:LYS:H	7:T:84:LYS:HD2	1.23	1.02
3:C:63:ARG:HE	22:C:3270:CDL:HA22	1.23	1.01

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%)	496 (97%)	16 (3%)	0	100	100
1	N	512/514 (100%)	500 (98%)	12 (2%)	0	100	100
2	B	225/227 (99%)	208 (92%)	14 (6%)	3 (1%)	18	4
2	O	225/227 (99%)	206 (92%)	16 (7%)	3 (1%)	18	4
3	C	257/261 (98%)	252 (98%)	5 (2%)	0	100	100
3	P	257/261 (98%)	252 (98%)	5 (2%)	0	100	100
4	D	142/147 (97%)	138 (97%)	4 (3%)	0	100	100
4	Q	142/147 (97%)	138 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	103/109 (94%)	103 (100%)	0	0	100	100
5	R	103/109 (94%)	102 (99%)	1 (1%)	0	100	100
6	F	96/98 (98%)	89 (93%)	4 (4%)	3 (3%)	7	0
6	S	96/98 (98%)	89 (93%)	4 (4%)	3 (3%)	7	0
7	G	81/85 (95%)	68 (84%)	6 (7%)	7 (9%)	1	0
7	T	81/85 (95%)	65 (80%)	9 (11%)	7 (9%)	1	0
8	H	77/85 (91%)	70 (91%)	5 (6%)	2 (3%)	8	1
8	U	77/85 (91%)	70 (91%)	5 (6%)	2 (3%)	8	1
9	I	71/73 (97%)	67 (94%)	4 (6%)	0	100	100
9	V	71/73 (97%)	67 (94%)	4 (6%)	0	100	100
10	J	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
10	W	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
11	K	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
11	X	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
12	L	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
12	Y	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
13	M	41/46 (89%)	41 (100%)	0	0	100	100
13	Z	41/46 (89%)	41 (100%)	0	0	100	100
All	All	3504/3614 (97%)	3350 (96%)	124 (4%)	30 (1%)	25	7

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	95	GLN
7	G	4	ALA
7	G	7	ASP
7	G	8	HIS
7	G	39	SER

### 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	426/426 (100%)	418 (98%)	8 (2%)	69	56
1	N	426/426 (100%)	415 (97%)	11 (3%)	59	41
2	B	210/210 (100%)	200 (95%)	10 (5%)	35	15
2	O	210/210 (100%)	197 (94%)	13 (6%)	26	9
3	C	224/226 (99%)	220 (98%)	4 (2%)	71	58
3	P	224/226 (99%)	219 (98%)	5 (2%)	64	48
4	D	128/129 (99%)	126 (98%)	2 (2%)	75	63
4	Q	128/129 (99%)	126 (98%)	2 (2%)	75	63
5	E	92/95 (97%)	90 (98%)	2 (2%)	64	48
5	R	92/95 (97%)	88 (96%)	4 (4%)	40	19
6	F	81/81 (100%)	79 (98%)	2 (2%)	60	42
6	S	81/81 (100%)	77 (95%)	4 (5%)	35	15
7	G	67/68 (98%)	61 (91%)	6 (9%)	14	3
7	T	67/68 (98%)	62 (92%)	5 (8%)	19	6
8	H	71/75 (95%)	69 (97%)	2 (3%)	56	38
8	U	71/75 (95%)	67 (94%)	4 (6%)	30	11
9	I	57/57 (100%)	53 (93%)	4 (7%)	21	7
9	V	57/57 (100%)	55 (96%)	2 (4%)	48	28
10	J	49/50 (98%)	48 (98%)	1 (2%)	68	53
10	W	49/50 (98%)	48 (98%)	1 (2%)	68	53
11	K	39/46 (85%)	39 (100%)	0	100	100
11	X	39/46 (85%)	38 (97%)	1 (3%)	59	41
12	L	39/40 (98%)	39 (100%)	0	100	100
12	Y	39/40 (98%)	37 (95%)	2 (5%)	33	14
13	M	37/38 (97%)	32 (86%)	5 (14%)	6	1
13	Z	37/38 (97%)	33 (89%)	4 (11%)	9	2
All	All	3040/3082 (99%)	2936 (97%)	104 (3%)	49	29

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	109	PHE
2	O	33	LEU
10	W	50	LEU

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Mol	Chain	Res	Type
1	N	115	SER
1	N	241	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	8	GLN
1	N	178	GLN
6	S	94	HIS
1	N	80	ASN
1	N	180	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	FME	A	1	1	9,9,10	5.89	2 (22%)	6,9,11	0.95	1 (16%)
2	FME	B	1	2	9,9,10	6.19	2 (22%)	6,9,11	1.96	1 (16%)
7	TPO	G	11	7	10,10,11	6.49	3 (30%)	12,14,16	1.06	1 (8%)
9	SAC	I	1	9	8,8,9	7.14	4 (50%)	6,9,11	4.25	2 (33%)
1	FME	N	1	1	9,9,10	5.41	1 (11%)	6,9,11	1.75	1 (16%)
2	FME	O	1	2	9,9,10	6.10	1 (11%)	6,9,11	1.23	1 (16%)
7	TPO	T	11	7	10,10,11	6.27	3 (30%)	12,14,16	1.08	1 (8%)
9	SAC	V	1	9	8,8,9	7.26	4 (50%)	6,9,11	4.34	4 (66%)

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
1	FME	A	1	1	-	1/7/9/11	0/0/0/0
2	FME	B	1	2	-	1/7/9/11	0/0/0/0
7	TPO	G	11	7	-	0/9/11/13	0/0/0/0
9	SAC	I	1	9	-	0/6/8/10	0/0/0/0
1	FME	N	1	1	-	1/7/9/11	0/0/0/0
2	FME	O	1	2	-	1/7/9/11	0/0/0/0
7	TPO	T	11	7	-	0/9/11/13	0/0/0/0
9	SAC	V	1	9	-	0/6/8/10	0/0/0/0

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	11	TPO	O-C	19.62	1.24	1.11
7	T	11	TPO	O-C	18.87	1.24	1.11
9	V	1	SAC	O-C	18.82	1.24	1.11
9	I	1	SAC	O-C	18.62	1.24	1.11
2	B	1	FME	O-C	18.23	1.24	1.11

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	V	1	SAC	CA-N-C1A	-8.47	110.25	122.01
9	I	1	SAC	CB-CA-N	7.53	118.90	109.48
9	I	1	SAC	CA-N-C1A	-6.76	112.62	122.01
9	V	1	SAC	CB-CA-N	5.49	116.36	109.48
2	B	1	FME	CA-N-CN	-4.54	115.46	122.97

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	O	1	FME	O1-CN-N-CA
2	B	1	FME	O1-CN-N-CA
1	A	1	FME	O1-CN-N-CA
1	N	1	FME	O1-CN-N-CA

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 52 ligands modelled in this entry, 2 are unknown and 8 are monoatomic - leaving 42 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$
19	PGV	A	3266	-	50,50,50	0.92	1 (2%)	56,56,56	0.81	2 (3%)
18	TGL	A	3521	-	62,62,62	0.93	4 (6%)	65,65,65	1.10	6 (9%)
19	PGV	A	3524	-	50,50,50	1.09	4 (8%)	56,56,56	1.18	8 (14%)
17	HEA	A	515	1	67,67,67	1.67	13 (19%)	80,103,103	1.74	22 (27%)
17	HEA	A	516	1	67,67,67	1.84	13 (19%)	80,103,103	1.52	15 (18%)
20	CUA	B	228	2	0,1,1	0.00	-	0,0,0	0.00	-
21	CHD	B	4085	-	32,32,32	0.76	0	51,51,51	1.85	15 (29%)
23	PEK	C	3264	-	52,52,52	1.52	4 (7%)	57,57,57	1.26	7 (12%)
23	PEK	C	3265	-	52,52,52	1.69	10 (19%)	57,57,57	1.08	5 (8%)
19	PGV	C	3267	-	50,50,50	0.81	1 (2%)	56,56,56	0.97	3 (5%)
19	PGV	C	3268	-	50,50,50	1.11	4 (8%)	56,56,56	0.65	0
22	CDL	C	3270	-	99,99,99	0.75	3 (3%)	111,111,111	0.95	7 (6%)
21	CHD	C	3271	-	32,32,32	0.83	1 (3%)	51,51,51	3.68	22 (43%)
21	CHD	C	3525	-	32,32,32	0.83	1 (3%)	51,51,51	1.62	10 (19%)
18	TGL	D	3523	-	62,62,62	1.10	3 (4%)	65,65,65	1.09	7 (10%)
25	PSC	E	3230	-	51,51,51	1.25	4 (7%)	59,59,59	1.10	4 (6%)
22	CDL	G	3269	-	99,99,99	0.95	5 (5%)	111,111,111	0.95	7 (6%)
23	PEK	G	4263	-	52,52,52	1.74	9 (17%)	57,57,57	1.02	3 (5%)
21	CHD	J	3060	-	32,32,32	0.87	1 (3%)	51,51,51	3.27	25 (49%)
18	TGL	L	3522	-	62,62,62	1.32	7 (11%)	65,65,65	1.21	4 (6%)
27	DMU	M	3526	-	34,34,34	3.20	8 (23%)	45,45,45	4.44	20 (44%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
19	PGV	N	4266	-	50,50,50	1.03	3 (6%)	56,56,56	1.07	3 (5%)
18	TGL	N	4521	-	62,62,62	0.95	4 (6%)	65,65,65	1.08	3 (4%)
18	TGL	N	4522	-	62,62,62	1.34	7 (11%)	65,65,65	1.12	5 (7%)
19	PGV	N	4524	-	50,50,50	1.09	4 (8%)	56,56,56	1.13	8 (14%)
17	HEA	N	515	1	67,67,67	1.79	13 (19%)	80,103,103	1.77	24 (30%)
17	HEA	N	516	1	67,67,67	1.87	15 (22%)	80,103,103	1.59	18 (22%)
20	CUA	O	228	2	0,1,1	0.00	-	0,0,0	0.00	-
21	CHD	O	3085	-	32,32,32	0.78	0	51,51,51	1.88	18 (35%)
25	PSC	O	4230	-	51,51,51	1.22	3 (5%)	59,59,59	1.11	4 (6%)
23	PEK	P	4264	-	52,52,52	1.51	5 (9%)	57,57,57	1.37	12 (21%)
23	PEK	P	4265	-	52,52,52	1.72	12 (23%)	57,57,57	1.06	5 (8%)
19	PGV	P	4267	-	50,50,50	0.99	2 (4%)	56,56,56	1.11	5 (8%)
19	PGV	P	4268	-	50,50,50	1.12	4 (8%)	56,56,56	0.67	0
22	CDL	P	4270	-	99,99,99	0.78	3 (3%)	111,111,111	0.93	6 (5%)
21	CHD	P	4271	-	32,32,32	0.79	1 (3%)	51,51,51	3.63	22 (43%)
21	CHD	P	4525	-	32,32,32	0.88	1 (3%)	51,51,51	1.66	9 (17%)
18	TGL	Q	4523	-	62,62,62	1.08	3 (4%)	65,65,65	1.03	3 (4%)
23	PEK	T	3263	-	52,52,52	1.73	10 (19%)	57,57,57	1.00	3 (5%)
22	CDL	T	4269	-	99,99,99	0.92	4 (4%)	111,111,111	0.96	8 (7%)
21	CHD	W	4060	-	32,32,32	0.94	1 (3%)	51,51,51	3.23	25 (49%)
27	DMU	Z	4526	-	34,34,34	3.17	8 (23%)	45,45,45	4.40	20 (44%)

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
19	PGV	A	3266	-	-	0/55/55/55	0/0/0/0
18	TGL	A	3521	-	-	0/65/65/65	0/0/0/0
19	PGV	A	3524	-	-	0/55/55/55	0/0/0/0
17	HEA	A	515	1	-	0/30/76/76	0/0/8/8
17	HEA	A	516	1	-	0/30/76/76	0/0/8/8
20	CUA	B	228	2	-	0/0/0/0	0/0/0/0
21	CHD	B	4085	-	-	0/9/74/74	0/0/4/4
23	PEK	C	3264	-	-	0/56/56/56	0/0/0/0
23	PEK	C	3265	-	-	0/56/56/56	0/0/0/0
19	PGV	C	3267	-	-	0/55/55/55	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	PGV	C	3268	-	-	0/55/55/55	0/0/0/0
22	CDL	C	3270	-	1/1/9/9	0/110/110/110	0/0/0/0
21	CHD	C	3271	-	5/5/12/12	0/9/74/74	0/0/4/4
21	CHD	C	3525	-	-	0/9/74/74	0/0/4/4
18	TGL	D	3523	-	-	2/65/65/65	0/0/0/0
25	PSC	E	3230	-	-	0/55/55/55	0/0/0/0
22	CDL	G	3269	-	1/1/9/9	0/110/110/110	0/0/0/0
23	PEK	G	4263	-	-	0/56/56/56	0/0/0/0
21	CHD	J	3060	-	5/5/12/12	0/9/74/74	0/0/4/4
18	TGL	L	3522	-	-	0/65/65/65	0/0/0/0
27	DMU	M	3526	-	5/5/10/10	0/19/59/59	0/2/2/2
19	PGV	N	4266	-	-	0/55/55/55	0/0/0/0
18	TGL	N	4521	-	-	0/65/65/65	0/0/0/0
18	TGL	N	4522	-	-	0/65/65/65	0/0/0/0
19	PGV	N	4524	-	-	0/55/55/55	0/0/0/0
17	HEA	N	515	1	-	0/30/76/76	0/0/8/8
17	HEA	N	516	1	-	0/30/76/76	0/0/8/8
20	CUA	O	228	2	-	0/0/0/0	0/0/0/0
21	CHD	O	3085	-	-	0/9/74/74	0/0/4/4
25	PSC	O	4230	-	-	0/55/55/55	0/0/0/0
23	PEK	P	4264	-	-	0/56/56/56	0/0/0/0
23	PEK	P	4265	-	-	0/56/56/56	0/0/0/0
19	PGV	P	4267	-	-	0/55/55/55	0/0/0/0
19	PGV	P	4268	-	-	0/55/55/55	0/0/0/0
22	CDL	P	4270	-	1/1/9/9	0/110/110/110	0/0/0/0
21	CHD	P	4271	-	5/5/12/12	0/9/74/74	0/0/4/4
21	CHD	P	4525	-	-	0/9/74/74	0/0/4/4
18	TGL	Q	4523	-	-	1/65/65/65	0/0/0/0
23	PEK	T	3263	-	-	0/56/56/56	0/0/0/0
22	CDL	T	4269	-	1/1/9/9	0/110/110/110	0/0/0/0
21	CHD	W	4060	-	5/5/12/12	0/9/74/74	0/0/4/4
27	DMU	Z	4526	-	5/5/10/10	0/19/59/59	0/2/2/2

The worst 5 of 199 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	M	3526	DMU	O7-C3	-8.70	1.22	1.43
27	Z	4526	DMU	O7-C3	-8.49	1.22	1.43
17	A	516	HEA	C4A-C3A	7.11	1.50	1.41
27	Z	4526	DMU	O16-C6	-6.96	1.27	1.40
27	M	3526	DMU	O1-C9	-6.89	1.27	1.44



The worst 5 of 393 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	M	3526	DMU	C10-C5-C7	11.29	131.95	110.00
27	Z	4526	DMU	C10-C5-C7	11.17	131.73	110.00
27	Z	4526	DMU	C1-C2-C3	10.52	132.50	109.61
27	M	3526	DMU	C1-C2-C3	10.49	132.43	109.61
21	C	3271	CHD	C17-C13-C14	10.35	110.64	100.07

5 of 34 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
22	G	3269	CDL	CA4
27	Z	4526	DMU	C4
27	Z	4526	DMU	C6
27	Z	4526	DMU	C5
27	Z	4526	DMU	C2

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	D	3523	TGL	CG2-OG2-CB1-CB2
18	D	3523	TGL	CG2-OG2-CB1-OB1
18	Q	4523	TGL	CG2-OG2-CB1-CB2

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.