



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 04:48 PM GMT

PDB ID : 3ABK
Title : Bovine heart cytochrome c oxidase at the NO-bound fully reduced state (50K)
Authors : Ohta, K.; Muramoto, K.; Shinzawa-Itoh, K.; Yamashita, E.; Yoshikawa, S.;
Tsukihara, T.
Deposited on : 2009-12-16
Resolution : 2.00 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

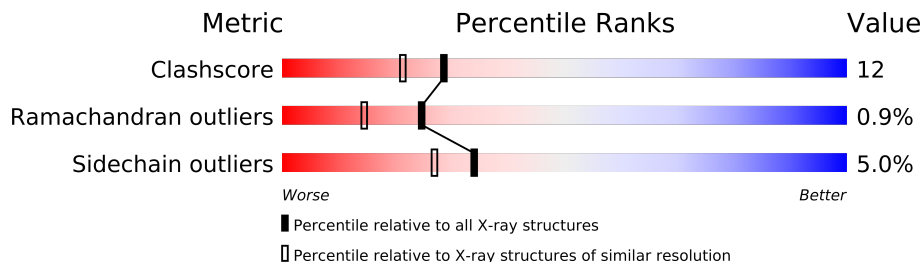
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	FAILED
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 2.00 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	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)







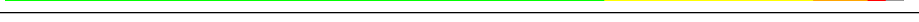

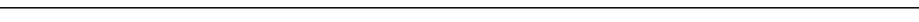
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The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

Note EDS failed to run properly.

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 29 unique types of molecules in this entry. The entry contains 32382 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 subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	5	0
			4060	2712	628	684	36			
1	N	514	Total	C	N	O	S	0	5	0
			4060	2712	628	684	36			

- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

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 subunit 3.

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 4 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 subunit 5A.

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 subunit 5B.

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 subunit 6A2.

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 subunit 6B1.

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 subunit 6C.

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 7A1.

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 subunit 7B.

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			

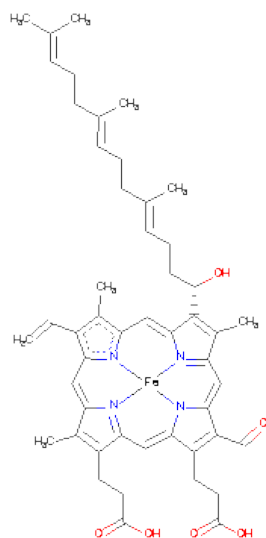
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C.

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 subunit 8B.

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 HEME-A (three-letter code: HEA) (formula: C₄₉H₅₆FeN₄O₆).



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

- Molecule 15 is NITRIC OXIDE (three-letter code: NO) (formula: NO).



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

- Molecule 16 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

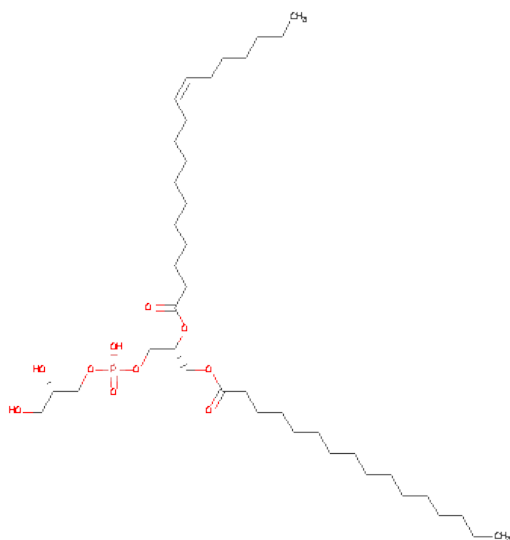
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 18 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- 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: C₄₀H₇₇O₁₀P).



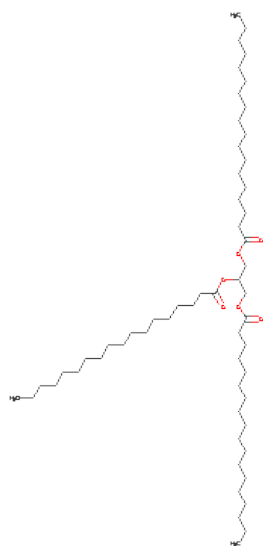
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
19	A	1	Total	C	O	P	0	0
			51	40	10	1		
19	A	1	Total	C	O	P	0	0
			51	40	10	1		
19	C	1	Total	C	O	P	0	0
			51	40	10	1		
19	C	1	Total	C	O	P	0	0
			51	40	10	1		
19	N	1	Total	C	O	P	0	0
			51	40	10	1		
19	N	1	Total	C	O	P	0	0
			51	40	10	1		
19	P	1	Total	C	O	P	0	0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

- Molecule 20 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



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 TRISTEAROYLGLYCEROL (three-letter code: TGL) (formula: $C_{57}H_{110}O_6$).



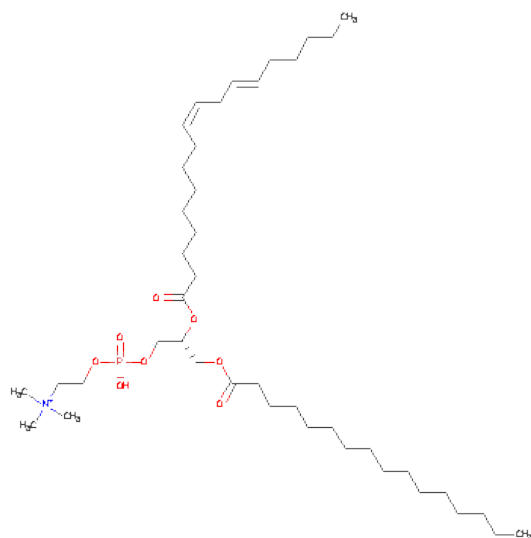
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	B	1	Total	C	O	0	0
			63	57	6		
21	D	1	Total	C	O	0	0
			63	57	6		

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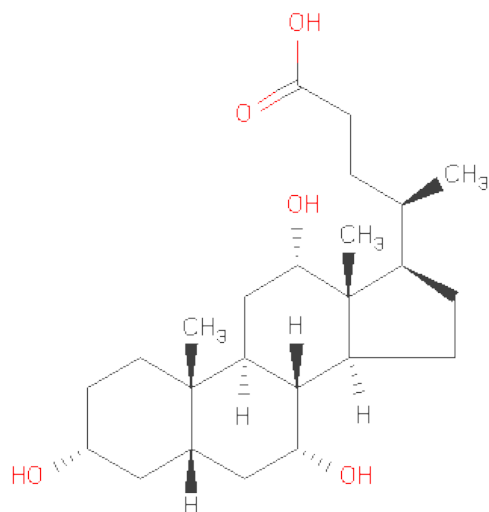
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	L	1	Total	C	O	0	0
			63	57	6		
21	N	1	Total	C	O	0	0
			63	57	6		
21	O	1	Total	C	O	0	0
			63	57	6		
21	Y	1	Total	C	O	0	0
			63	57	6		

- Molecule 22 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 M4-OXIDE (three-letter code: PSC) (formula: $C_{42}H_{81}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
22	B	1	Total	C	N	O	P	0	0
			52	42	1	8	1		
22	R	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

- Molecule 23 is CHOLIC ACID (three-letter code: CHD) (formula: $C_{24}H_{40}O_5$).

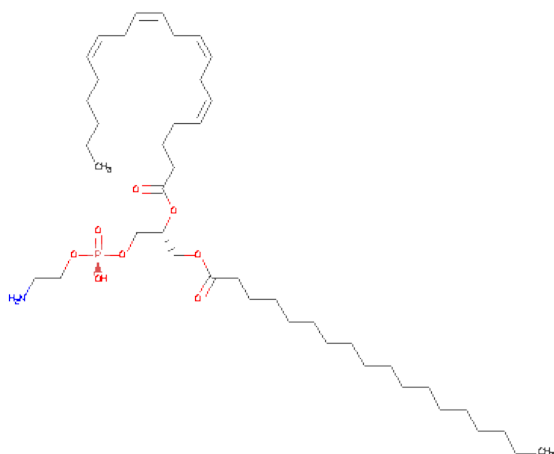


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
23	B	1	Total	C	O	0	0
			29	24	5		
23	C	1	Total	C	O	0	0
			29	24	5		
23	C	1	Total	C	O	0	0
			29	24	5		
23	J	1	Total	C	O	0	0
			29	24	5		
23	O	1	Total	C	O	0	0
			29	24	5		
23	P	1	Total	C	O	0	0
			29	24	5		
23	P	1	Total	C	O	0	0
			29	24	5		
23	W	1	Total	C	O	0	0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

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

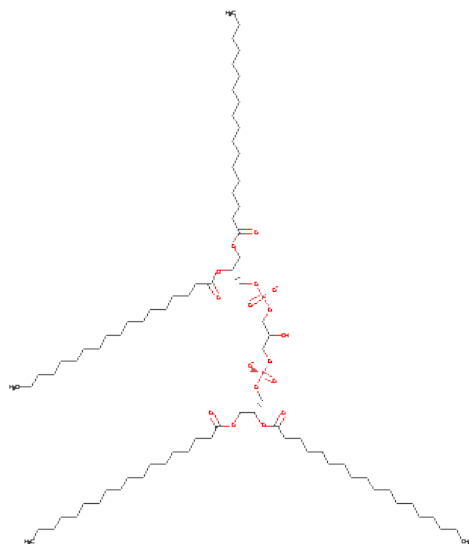
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	P	1	Total	X	0	0
			1	1		
24	C	1	Total	X	0	0
			1	1		

- Molecule 25 is (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: C₄₃H₇₈NO₈P).



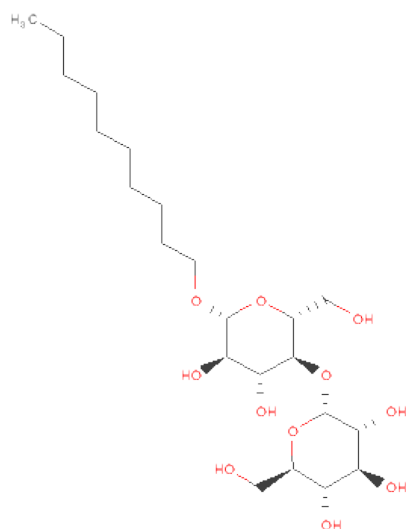
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	P	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		

- Molecule 26 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



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

- Molecule 27 is SUGAR (DECYL-BETA-D-MALTOPYRANOSIDE) (three-letter code: DMU) (formula: $C_{22}H_{42}O_{11}$).



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

- Molecule 28 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 29 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	A	217	Total	O	0	0
			217	217		
29	B	127	Total	O	0	0
			127	127		
29	C	93	Total	O	0	0
			93	93		
29	D	86	Total	O	0	0
			86	86		
29	E	52	Total	O	0	0
			52	52		
29	F	72	Total	O	0	0
			72	72		
29	G	42	Total	O	0	0
			42	42		
29	H	46	Total	O	0	0
			46	46		
29	I	31	Total	O	0	0
			31	31		
29	J	28	Total	O	0	0
			28	28		
29	K	27	Total	O	0	0
			27	27		
29	L	16	Total	O	0	0
			16	16		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	M	20	Total 20	O 20	0	0
29	N	207	Total 207	O 207	0	0
29	O	105	Total 105	O 105	0	0
29	P	96	Total 96	O 96	0	0
29	Q	57	Total 57	O 57	0	0
29	R	35	Total 35	O 35	0	0
29	S	63	Total 63	O 63	0	0
29	T	44	Total 44	O 44	0	0
29	U	43	Total 43	O 43	0	0
29	V	20	Total 20	O 20	0	0
29	W	17	Total 17	O 17	0	0
29	X	13	Total 13	O 13	0	0
29	Y	12	Total 12	O 12	0	0
29	Z	11	Total 11	O 11	0	0

3 Residue-property plots

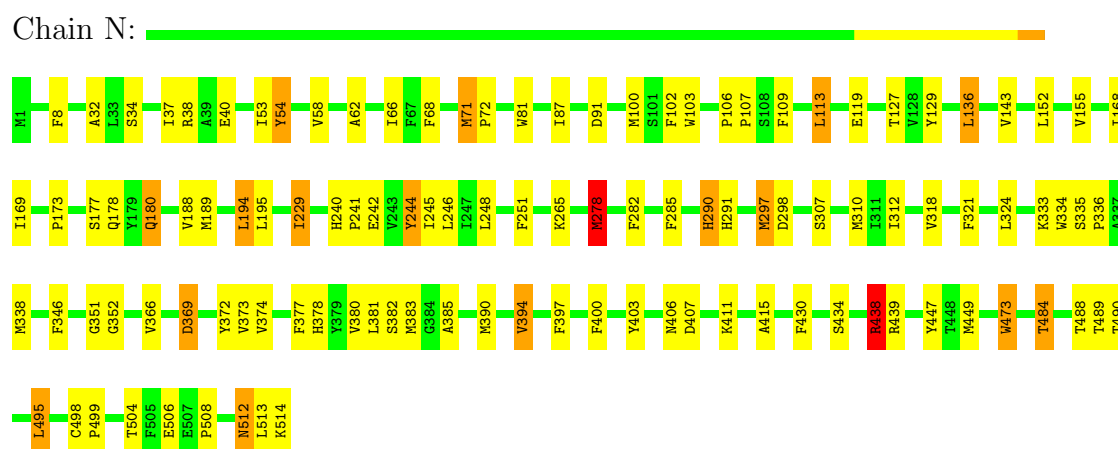
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 failed to run properly.

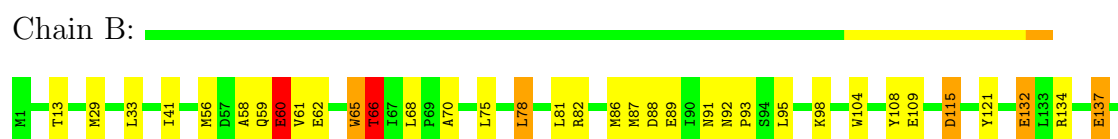
- Molecule 1: Cytochrome c oxidase subunit 1



- Molecule 1: Cytochrome c oxidase subunit 1



- Molecule 2: Cytochrome c oxidase subunit 2





• Molecule 2: Cytochrome c oxidase subunit 2

Chain O:



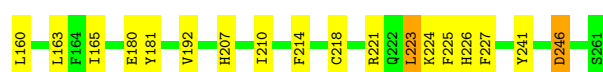
• Molecule 3: Cytochrome c oxidase subunit 3

Chain C:



• Molecule 3: Cytochrome c oxidase subunit 3

Chain P:



• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain D:



• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain Q:



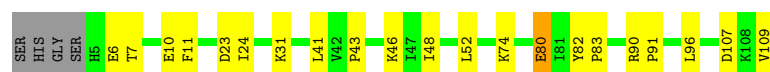
• Molecule 5: Cytochrome c oxidase subunit 5A

Chain E:



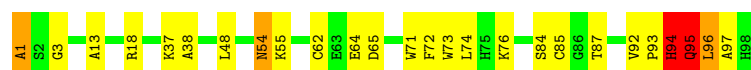
• Molecule 5: Cytochrome c oxidase subunit 5A

Chain R: 



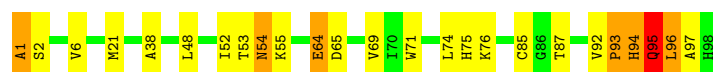
- Molecule 6: Cytochrome c oxidase subunit 5B

Chain F: 



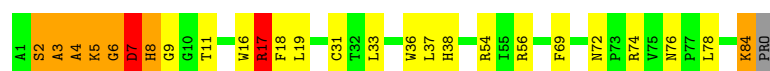
- Molecule 6: Cytochrome c oxidase subunit 5B

Chain S: 



- Molecule 7: Cytochrome c oxidase subunit 6A2

Chain G: 



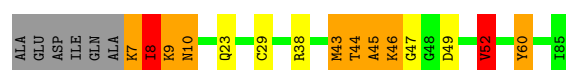
- Molecule 7: Cytochrome c oxidase subunit 6A2

Chain T: 



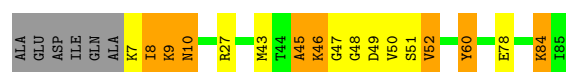
- Molecule 8: Cytochrome c oxidase subunit 6B1

Chain H: 



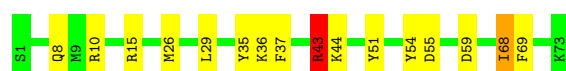
- Molecule 8: Cytochrome c oxidase subunit 6B1

Chain U: 



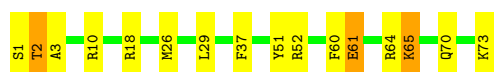
- Molecule 9: Cytochrome c oxidase subunit 6C

Chain I: 



- Molecule 9: Cytochrome c oxidase subunit 6C

Chain V: 



- Molecule 10: Cytochrome c oxidase polypeptide 7A1

Chain J:



- Molecule 10: Cytochrome c oxidase polypeptide 7A1

Chain W:



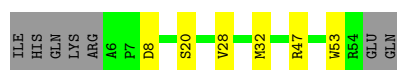
- Molecule 11: Cytochrome c oxidase subunit 7B

Chain K:



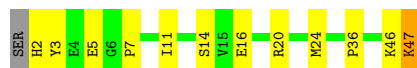
- Molecule 11: Cytochrome c oxidase subunit 7B

Chain X:



- Molecule 12: Cytochrome c oxidase subunit 7C

Chain L:



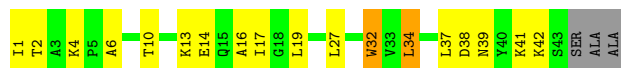
- Molecule 12: Cytochrome c oxidase subunit 7C

Chain Y:



- Molecule 13: Cytochrome c oxidase subunit 8B

Chain M:



- Molecule 13: Cytochrome c oxidase subunit 8B

Chain Z:

I1	T2	T10	K13	E14	G18	L34	D38	N39	Y40	K41	K42	S43	SER	ALA	ALA
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4 Data and refinement statistics i

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	182.25Å 207.94Å 178.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (40.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.3	Depositor
R, R_{free}	0.183 , 0.219	Depositor
Wilson B-factor (Å ²)	33.0	Xtriage
Anisotropy	0.521	Xtriage
Estimated twinning fraction	0.014 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	2 of 444413 reflections (0.000%)	Xtriage
Total number of atoms	32382	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEK, ZN, CHD, HEA, SAC, CDL, PSC, NO, 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	1.64	40/4189 (1.0%)	1.27	19/5722 (0.3%)
1	N	1.46	26/4189 (0.6%)	1.20	22/5722 (0.4%)
2	B	1.54	15/1860 (0.8%)	1.32	11/2534 (0.4%)
2	O	1.32	7/1860 (0.4%)	1.14	9/2534 (0.4%)
3	C	1.43	15/2197 (0.7%)	1.13	10/3005 (0.3%)
3	P	1.36	9/2197 (0.4%)	1.16	11/3005 (0.4%)
4	D	1.33	2/1229 (0.2%)	1.11	5/1658 (0.3%)
4	Q	1.24	5/1229 (0.4%)	1.04	5/1658 (0.3%)
5	E	1.32	4/871 (0.5%)	0.98	0/1182
5	R	1.15	0/871	0.98	1/1182 (0.1%)
6	F	1.44	6/765 (0.8%)	1.23	1/1038 (0.1%)
6	S	1.33	3/765 (0.4%)	1.17	1/1038 (0.1%)
7	G	1.38	3/690 (0.4%)	1.28	7/937 (0.7%)
7	T	1.36	3/690 (0.4%)	1.21	6/937 (0.6%)
8	H	1.34	0/682	1.12	2/921 (0.2%)
8	U	1.16	0/682	0.97	0/921
9	I	1.32	3/605 (0.5%)	1.20	5/802 (0.6%)
9	V	1.22	1/605 (0.2%)	0.97	1/802 (0.1%)
10	J	1.26	2/471 (0.4%)	1.09	2/636 (0.3%)
10	W	1.25	0/471	1.10	2/636 (0.3%)
11	K	1.36	0/398	1.19	4/546 (0.7%)
11	X	1.11	0/398	0.95	1/546 (0.2%)
12	L	1.42	2/393 (0.5%)	1.09	0/526
12	Y	1.35	1/393 (0.3%)	1.00	1/526 (0.2%)
13	M	1.41	1/345 (0.3%)	1.23	2/470 (0.4%)
13	Z	1.17	0/345	0.99	0/470
All	All	1.41	148/29390 (0.5%)	1.16	128/39954 (0.3%)

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
5	E	0	1
6	F	0	1
6	S	0	2
12	Y	0	1
All	All	0	5

The worst 5 of 148 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	36	TRP	CB-CG	10.56	1.69	1.50
7	T	36	TRP	CB-CG	10.45	1.69	1.50
1	A	380[A]	VAL	CB-CG1	-9.14	1.33	1.52
1	A	380[B]	VAL	CB-CG1	-9.14	1.33	1.52
3	P	180	GLU	CD-OE1	8.86	1.35	1.25

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	17	ARG	NE-CZ-NH2	-14.38	113.11	120.30
1	A	71	MET	CG-SD-CE	-14.02	77.77	100.20
7	G	17	ARG	NE-CZ-NH1	12.88	126.74	120.30
3	P	246	ASP	CB-CG-OD1	-12.27	107.26	118.30
1	N	278	MET	CG-SD-CE	-11.92	81.12	100.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	5	HIS	Peptide
6	F	93	PRO	Peptide
6	S	93	PRO	Peptide
6	S	95	GLN	Peptide
12	Y	46	LYS	Peptide

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	4060	0	4037	74	0
1	N	4060	0	4037	86	0
2	B	1824	0	1833	25	0
2	O	1824	0	1833	50	0
3	C	2110	0	2027	24	0
3	P	2110	0	2027	35	0
4	D	1195	0	1183	19	0
4	Q	1195	0	1183	20	0
5	E	852	0	845	10	0
5	R	852	0	845	19	0
6	F	748	0	728	22	0
6	S	748	0	728	40	0
7	G	675	0	643	45	0
7	T	675	0	643	43	0
8	H	662	0	623	19	0
8	U	662	0	623	20	0
9	I	601	0	613	8	0
9	V	601	0	613	9	0
10	J	460	0	459	13	0
10	W	460	0	459	12	0
11	K	384	0	366	2	0
11	X	384	0	366	4	0
12	L	380	0	380	16	0
12	Y	380	0	380	20	0
13	M	335	0	352	13	0
13	Z	335	0	352	6	0
14	A	120	0	108	16	0
14	N	120	0	108	9	0
15	A	2	0	0	0	0
15	N	2	0	0	0	0
16	A	1	0	0	0	0
16	N	1	0	0	0	0
17	A	1	0	0	0	0
17	N	1	0	0	0	0
18	A	1	0	0	0	0
18	N	1	0	0	0	0
19	A	102	0	152	16	0
19	C	102	0	152	10	0
19	N	102	0	152	7	0
19	P	51	0	76	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	U	51	0	76	4	0
20	B	2	0	0	0	0
20	O	2	0	0	0	0
21	B	63	0	110	4	0
21	D	63	0	110	10	0
21	L	63	0	110	15	0
21	N	63	0	110	14	0
21	O	63	0	110	5	0
21	Y	63	0	110	20	0
22	B	52	0	80	20	0
22	R	52	0	80	20	0
23	B	29	0	37	4	0
23	C	58	0	71	4	0
23	J	29	0	36	8	0
23	O	29	0	37	3	0
23	P	58	0	72	5	0
23	W	29	0	35	3	0
24	C	1	0	0	0	0
24	P	1	0	0	0	0
25	C	106	0	154	22	0
25	G	53	0	77	19	0
25	P	53	0	77	6	0
25	T	106	0	154	34	0
26	C	100	0	156	20	0
26	G	100	0	156	33	0
26	P	100	0	156	27	0
26	T	100	0	156	30	0
27	C	33	0	39	4	0
27	M	33	0	39	0	0
27	P	33	0	38	1	0
27	Z	33	0	38	0	0
28	F	1	0	0	0	0
28	S	1	0	0	0	0
29	A	217	0	0	5	0
29	B	127	0	0	3	0
29	C	93	0	0	4	0
29	D	86	0	0	6	0
29	E	52	0	0	0	0
29	F	72	0	0	3	0
29	G	42	0	0	7	0
29	H	46	0	0	1	0
29	I	31	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	J	28	0	0	4	0
29	K	27	0	0	2	0
29	L	16	0	0	1	0
29	M	20	0	0	0	0
29	N	207	0	0	6	0
29	O	105	0	0	2	0
29	P	96	0	0	3	0
29	Q	57	0	0	4	0
29	R	35	0	0	1	0
29	S	63	0	0	5	0
29	T	44	0	0	5	0
29	U	43	0	0	5	0
29	V	20	0	0	0	0
29	W	17	0	0	2	0
29	X	13	0	0	0	0
29	Y	12	0	0	1	0
29	Z	11	0	0	1	0
All	All	32382	0	31350	777	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 12.

The worst 5 of 777 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:T:1265:PEK:H383	26:T:1269:CDL:C27	1.34	1.51
1:N:297:MET:CE	1:N:297:MET:SD	2.10	1.40
25:T:1265:PEK:C38	26:T:1269:CDL:H273	1.51	1.36
10:W:2:GLU:HB2	10:W:4:ARG:NH1	1.50	1.26
25:T:1265:PEK:C38	26:T:1269:CDL:C27	2.12	1.18

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	517/514 (101%)	502 (97%)	15 (3%)	0	100	100
1	N	517/514 (101%)	495 (96%)	22 (4%)	0	100	100
2	B	225/227 (99%)	217 (96%)	7 (3%)	1 (0%)	43	36
2	O	225/227 (99%)	219 (97%)	5 (2%)	1 (0%)	43	36
3	C	257/261 (98%)	251 (98%)	6 (2%)	0	100	100
3	P	257/261 (98%)	250 (97%)	7 (3%)	0	100	100
4	D	142/147 (97%)	138 (97%)	4 (3%)	0	100	100
4	Q	142/147 (97%)	134 (94%)	8 (6%)	0	100	100
5	E	103/109 (94%)	101 (98%)	2 (2%)	0	100	100
5	R	103/109 (94%)	100 (97%)	2 (2%)	1 (1%)	22	12
6	F	96/98 (98%)	90 (94%)	3 (3%)	3 (3%)	7	1
6	S	96/98 (98%)	88 (92%)	5 (5%)	3 (3%)	7	1
7	G	81/85 (95%)	68 (84%)	7 (9%)	6 (7%)	2	0
7	T	81/85 (95%)	67 (83%)	6 (7%)	8 (10%)	1	0
8	H	77/85 (91%)	68 (88%)	3 (4%)	6 (8%)	1	0
8	U	77/85 (91%)	68 (88%)	5 (6%)	4 (5%)	3	0
9	I	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
9	V	71/73 (97%)	67 (94%)	4 (6%)	0	100	100
10	J	56/59 (95%)	56 (100%)	0	0	100	100
10	W	56/59 (95%)	56 (100%)	0	0	100	100
11	K	47/56 (84%)	44 (94%)	3 (6%)	0	100	100
11	X	47/56 (84%)	45 (96%)	2 (4%)	0	100	100
12	L	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
12	Y	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
13	M	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
13	Z	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
All	All	3514/3614 (97%)	3356 (96%)	125 (4%)	33 (1%)	25	14

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	94	HIS
6	F	95	GLN
7	G	4	ALA

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Mol	Chain	Res	Type
7	G	7	ASP
7	G	8	HIS

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	430/426 (101%)	419 (97%)	11 (3%)	59	58
1	N	430/426 (101%)	414 (96%)	16 (4%)	45	40
2	B	210/210 (100%)	200 (95%)	10 (5%)	35	28
2	O	210/210 (100%)	196 (93%)	14 (7%)	23	16
3	C	224/226 (99%)	217 (97%)	7 (3%)	52	49
3	P	224/226 (99%)	219 (98%)	5 (2%)	64	65
4	D	128/129 (99%)	124 (97%)	4 (3%)	52	49
4	Q	128/129 (99%)	121 (94%)	7 (6%)	30	23
5	E	92/95 (97%)	88 (96%)	4 (4%)	40	33
5	R	92/95 (97%)	89 (97%)	3 (3%)	50	46
6	F	81/81 (100%)	76 (94%)	5 (6%)	26	18
6	S	81/81 (100%)	77 (95%)	4 (5%)	35	28
7	G	67/68 (98%)	59 (88%)	8 (12%)	8	4
7	T	67/68 (98%)	58 (87%)	9 (13%)	6	3
8	H	71/75 (95%)	65 (92%)	6 (8%)	15	9
8	U	71/75 (95%)	66 (93%)	5 (7%)	21	14
9	I	57/57 (100%)	50 (88%)	7 (12%)	7	3
9	V	57/57 (100%)	48 (84%)	9 (16%)	4	1
10	J	49/50 (98%)	48 (98%)	1 (2%)	68	69
10	W	49/50 (98%)	48 (98%)	1 (2%)	68	69
11	K	39/46 (85%)	36 (92%)	3 (8%)	18	11
11	X	39/46 (85%)	37 (95%)	2 (5%)	33	26
12	L	39/40 (98%)	38 (97%)	1 (3%)	59	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Y	39/40 (98%)	36 (92%)	3 (8%)	18	11
13	M	37/38 (97%)	33 (89%)	4 (11%)	9	5
13	Z	37/38 (97%)	33 (89%)	4 (11%)	9	5
All	All	3048/3082 (99%)	2895 (95%)	153 (5%)	34	27

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	39	ASN
1	N	508	PRO
9	V	70	GLN
1	N	109	PHE
1	N	290	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	57	HIS
1	N	512	ASN
7	T	8	HIS
1	N	80	ASN
1	N	178	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	5.48	2 (22%)	6,9,11	5.64	3 (50%)
2	FME	B	1	2	9,9,10	7.52	4 (44%)	6,9,11	8.19	3 (50%)
7	TPO	G	11	7	10,10,11	7.53	5 (50%)	12,14,16	1.82	4 (33%)
9	SAC	I	1	9	8,8,9	7.35	4 (50%)	6,9,11	2.98	2 (33%)
1	FME	N	1	1	9,9,10	5.53	1 (11%)	6,9,11	6.10	1 (16%)
2	FME	O	1	2	9,9,10	6.23	2 (22%)	6,9,11	5.24	2 (33%)
7	TPO	T	11	7	10,10,11	7.65	7 (70%)	12,14,16	2.46	5 (41%)
9	SAC	V	1	9	8,8,9	8.05	4 (50%)	6,9,11	3.00	2 (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
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 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	11	TPO	O-C	22.75	1.27	1.11
7	G	11	TPO	O-C	22.75	1.27	1.11
2	B	1	FME	O-C	21.73	1.26	1.11
9	V	1	SAC	O-C	20.35	1.25	1.11
9	I	1	SAC	O-C	19.25	1.24	1.11

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	FME	CA-N-CN	-19.34	90.98	122.97
1	N	1	FME	CA-N-CN	-14.75	98.57	122.97
1	A	1	FME	CA-N-CN	-12.52	102.27	122.97
2	O	1	FME	CA-N-CN	-12.46	102.36	122.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	V	1	SAC	CA-N-C1A	6.27	130.73	122.01

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	N	1	FME	O1-CN-N-CA
1	A	1	FME	O1-CN-N-CA
2	O	1	FME	O1-CN-N-CA
2	B	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 56 ligands modelled in this entry, 2 are unknown and 8 are monoatomic - leaving 46 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	$\# Z > 2$
14	HEA	A	515	1	67,67,67	1.69	16 (23%)	80,103,103	2.11	28 (35%)
14	HEA	A	516	1	67,67,67	1.60	15 (22%)	80,103,103	2.93	35 (43%)
15	NO	A	520	16	0,1,1	0.00	-	0,0,0	0.00	-
19	PGV	A	521	-	50,50,50	1.24	6 (12%)	56,56,56	1.68	13 (23%)
19	PGV	A	524	-	50,50,50	1.28	4 (8%)	56,56,56	1.61	10 (17%)
23	CHD	B	1085	-	32,32,32	1.77	5 (15%)	51,51,51	5.79	34 (66%)
20	CUA	B	228	2	0,1,1	0.00	-	0,0,0	0.00	-
22	PSC	B	229	-	51,51,51	1.17	3 (5%)	59,59,59	1.35	10 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	TGL	B	521	-	62,62,62	1.23	6 (9%)	65,65,65	1.90	12 (18%)
25	PEK	C	264	-	52,52,52	0.92	1 (1%)	57,57,57	1.80	15 (26%)
25	PEK	C	265	-	52,52,52	1.52	6 (11%)	57,57,57	1.57	6 (10%)
19	PGV	C	267	-	50,50,50	0.85	2 (4%)	56,56,56	1.30	6 (10%)
19	PGV	C	268	-	50,50,50	1.34	4 (8%)	56,56,56	1.68	9 (16%)
26	CDL	C	270	-	99,99,99	1.46	17 (17%)	111,111,111	1.45	16 (14%)
23	CHD	C	271	-	32,32,32	0.81	1 (3%)	51,51,51	4.89	32 (62%)
27	DMU	C	272	-	34,34,34	1.45	3 (8%)	45,45,45	3.52	25 (55%)
23	CHD	C	525	-	32,32,32	1.51	6 (18%)	51,51,51	5.56	38 (74%)
21	TGL	D	523	-	62,62,62	1.52	7 (11%)	65,65,65	1.49	15 (23%)
25	PEK	G	1263	-	52,52,52	1.29	3 (5%)	57,57,57	1.43	7 (12%)
26	CDL	G	269	-	99,99,99	1.42	14 (14%)	111,111,111	1.51	19 (17%)
23	CHD	J	60	-	32,32,32	0.96	0	51,51,51	5.26	35 (68%)
21	TGL	L	522	-	62,62,62	1.49	8 (12%)	65,65,65	2.03	16 (24%)
27	DMU	M	526	-	34,34,34	1.09	3 (8%)	45,45,45	3.48	26 (57%)
19	PGV	N	1266	-	50,50,50	0.93	2 (4%)	56,56,56	1.46	9 (16%)
21	TGL	N	1523	-	62,62,62	1.33	7 (11%)	65,65,65	1.39	9 (13%)
19	PGV	N	1524	-	50,50,50	1.05	2 (4%)	56,56,56	1.26	6 (10%)
14	HEA	N	515	1	67,67,67	1.62	11 (16%)	80,103,103	2.07	29 (36%)
14	HEA	N	516	1,15	67,67,67	1.54	16 (23%)	80,103,103	2.89	46 (57%)
15	NO	N	520	14,16	0,1,1	0.00	-	0,0,0	0.00	-
21	TGL	O	1521	-	62,62,62	1.28	6 (9%)	65,65,65	1.58	11 (16%)
20	CUA	O	228	2	0,1,1	0.00	-	0,0,0	0.00	-
23	CHD	O	229	-	32,32,32	1.55	5 (15%)	51,51,51	5.71	32 (62%)
25	PEK	P	1264	-	52,52,52	0.90	2 (3%)	57,57,57	1.74	13 (22%)
19	PGV	P	1267	-	50,50,50	0.90	4 (8%)	56,56,56	1.47	9 (16%)
26	CDL	P	1270	-	99,99,99	1.43	14 (14%)	111,111,111	1.65	19 (17%)
23	CHD	P	1271	-	32,32,32	0.81	1 (3%)	51,51,51	4.99	33 (64%)
23	CHD	P	1525	-	32,32,32	1.59	6 (18%)	51,51,51	5.68	39 (76%)
27	DMU	P	272	-	34,34,34	1.60	5 (14%)	45,45,45	3.44	25 (55%)
22	PSC	R	1229	-	51,51,51	1.30	3 (5%)	59,59,59	1.31	4 (6%)
25	PEK	T	1265	-	52,52,52	1.35	5 (9%)	57,57,57	1.50	7 (12%)
26	CDL	T	1269	-	99,99,99	1.39	15 (15%)	111,111,111	1.55	18 (16%)
25	PEK	T	263	-	52,52,52	1.45	4 (7%)	57,57,57	1.37	7 (12%)
19	PGV	U	1268	-	50,50,50	1.49	2 (4%)	56,56,56	1.97	9 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CHD	W	1059	-	32,32,32	1.19	3 (9%)	51,51,51	5.29	32 (62%)
21	TGL	Y	1522	-	62,62,62	1.61	10 (16%)	65,65,65	2.15	17 (26%)
27	DMU	Z	1526	-	34,34,34	1.08	2 (5%)	45,45,45	3.23	26 (57%)

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
14	HEA	A	515	1	-	0/30/76/76	0/0/8/8
14	HEA	A	516	1	-	0/30/76/76	0/0/8/8
15	NO	A	520	16	-	0/0/0/0	0/0/0/0
19	PGV	A	521	-	-	0/55/55/55	0/0/0/0
19	PGV	A	524	-	-	0/55/55/55	0/0/0/0
23	CHD	B	1085	-	-	0/9/74/74	0/0/4/4
20	CUA	B	228	2	-	0/0/0/0	0/0/0/0
22	PSC	B	229	-	-	0/55/55/55	0/0/0/0
21	TGL	B	521	-	-	0/65/65/65	0/0/0/0
25	PEK	C	264	-	-	0/56/56/56	0/0/0/0
25	PEK	C	265	-	-	0/56/56/56	0/0/0/0
19	PGV	C	267	-	-	0/55/55/55	0/0/0/0
19	PGV	C	268	-	-	0/55/55/55	0/0/0/0
26	CDL	C	270	-	1/1/9/9	0/110/110/110	0/0/0/0
23	CHD	C	271	-	1/1/12/12	0/9/74/74	0/0/4/4
27	DMU	C	272	-	6/6/10/10	0/19/59/59	0/2/2/2
23	CHD	C	525	-	-	0/9/74/74	0/0/4/4
21	TGL	D	523	-	-	0/65/65/65	0/0/0/0
25	PEK	G	1263	-	-	0/56/56/56	0/0/0/0
26	CDL	G	269	-	1/1/9/9	0/110/110/110	0/0/0/0
23	CHD	J	60	-	2/2/12/12	0/9/74/74	0/0/4/4
21	TGL	L	522	-	-	0/65/65/65	0/0/0/0
27	DMU	M	526	-	4/4/10/10	0/19/59/59	0/2/2/2
19	PGV	N	1266	-	-	0/55/55/55	0/0/0/0
21	TGL	N	1523	-	-	0/65/65/65	0/0/0/0
19	PGV	N	1524	-	-	1/55/55/55	0/0/0/0
14	HEA	N	515	1	-	0/30/76/76	0/0/8/8
14	HEA	N	516	1,15	-	0/30/76/76	0/0/8/8
15	NO	N	520	14,16	-	0/0/0/0	0/0/0/0
21	TGL	O	1521	-	-	0/65/65/65	0/0/0/0
20	CUA	O	228	2	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CHD	O	229	-	-	0/9/74/74	0/0/4/4
25	PEK	P	1264	-	-	0/56/56/56	0/0/0/0
19	PGV	P	1267	-	-	0/55/55/55	0/0/0/0
26	CDL	P	1270	-	1/1/9/9	2/110/110/110	0/0/0/0
23	CHD	P	1271	-	1/1/12/12	0/9/74/74	0/0/4/4
23	CHD	P	1525	-	1/1/12/12	0/9/74/74	0/0/4/4
27	DMU	P	272	-	6/6/10/10	0/19/59/59	0/2/2/2
22	PSC	R	1229	-	-	0/55/55/55	0/0/0/0
25	PEK	T	1265	-	-	0/56/56/56	0/0/0/0
26	CDL	T	1269	-	1/1/9/9	3/110/110/110	0/0/0/0
25	PEK	T	263	-	-	0/56/56/56	0/0/0/0
19	PGV	U	1268	-	-	0/55/55/55	0/0/0/0
23	CHD	W	1059	-	1/1/12/12	0/9/74/74	0/0/4/4
21	TGL	Y	1522	-	-	2/65/65/65	0/0/0/0
27	DMU	Z	1526	-	5/5/10/10	0/19/59/59	0/2/2/2

The worst 5 of 255 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Y	1522	TGL	OG2-CB1	7.30	1.56	1.34
19	U	1268	PGV	O01-C1	6.73	1.54	1.34
21	L	522	TGL	OG2-CB1	6.72	1.54	1.34
27	P	272	DMU	O16-C6	6.52	1.52	1.40
19	C	268	PGV	O01-C1	6.09	1.52	1.34

The worst 5 of 807 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	P	1525	CHD	C1-C10-C5	17.37	126.94	107.79
23	B	1085	CHD	C1-C10-C5	16.74	126.24	107.79
23	C	525	CHD	C1-C10-C5	15.96	125.38	107.79
23	O	229	CHD	C1-C10-C5	15.03	124.36	107.79
23	B	1085	CHD	C6-C5-C10	15.02	128.91	112.67

5 of 31 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
27	Z	1526	DMU	C2
27	Z	1526	DMU	C4
27	Z	1526	DMU	C9
27	Z	1526	DMU	C6

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Mol	Chain	Res	Type	Atom
27	Z	1526	DMU	C5

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
26	P	1270	CDL	CA4-OA6-CA5-C11
26	T	1269	CDL	CA4-OA6-CA5-C11
26	P	1270	CDL	CA4-OA6-CA5-OA7
26	T	1269	CDL	CA4-OA6-CA5-OA7
21	Y	1522	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 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.