



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 20, 2016 – 01:53 AM GMT

PDB ID : 5COD
Title : Bovine heart complex I membrane domain
Authors : Zhu, J.; Hirst, J.; King, M.S.; Yu, M.; Leslie, A.G.W.; Klipcan, L.
Deposited on : 2015-07-20
Resolution : 6.74 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

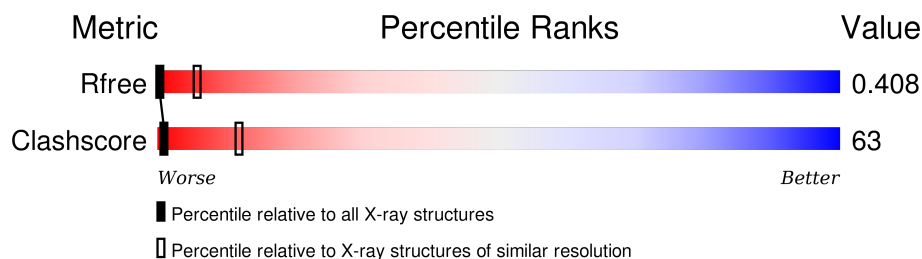
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

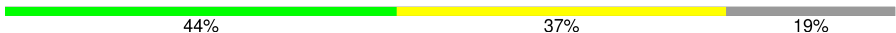
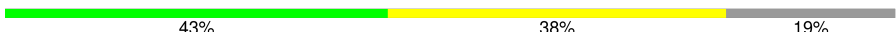

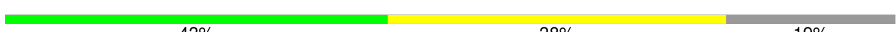
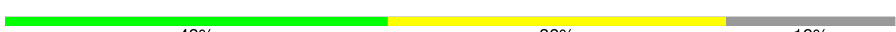
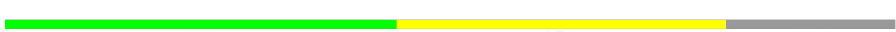



The reported resolution of this entry is 6.74 Å.

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.






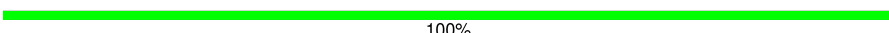
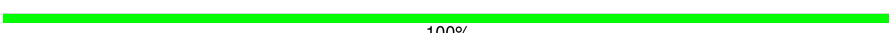
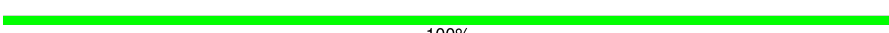









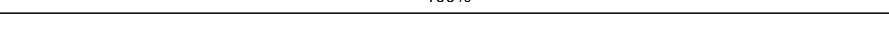
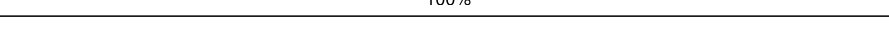
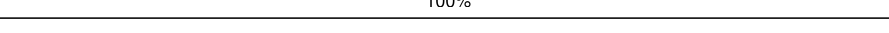
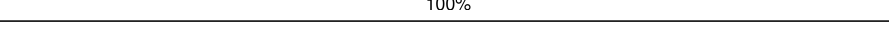
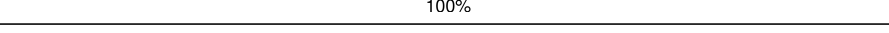
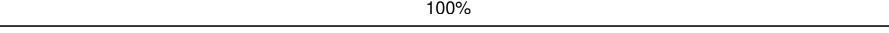
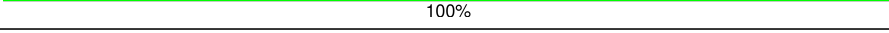
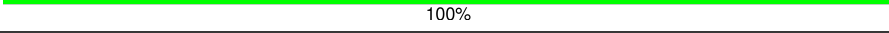
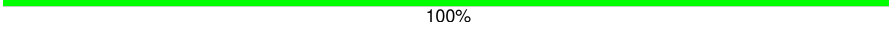
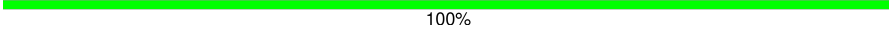
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	91344	1014 (9.50-3.66)
Clashscore	102246	1062 (9.50-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L1	606	
1	L2	606	
1	L3	606	
1	L4	606	
1	L5	606	
1	L6	606	
2	M1	459	
2	M2	459	
2	M3	459	

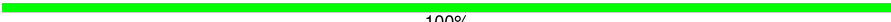
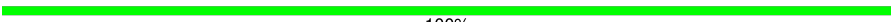













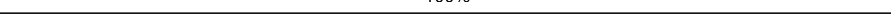
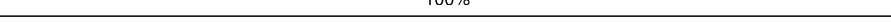
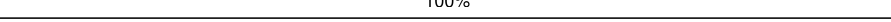
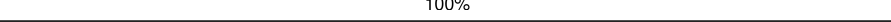
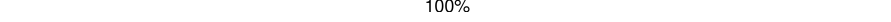
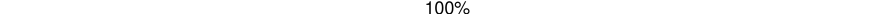
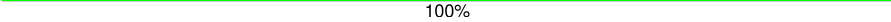
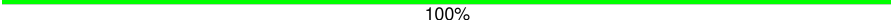

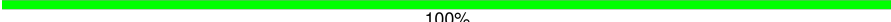
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Mol	Chain	Length	Quality of chain
2	M4	459	 47% 48%
2	M5	459	 48% 47%
2	M6	459	 48% 47%
3	f1	30	 100%
3	f2	30	 100%
3	f3	30	 100%
3	f4	30	 100%
3	f5	30	 100%
3	f6	30	 100%
3	h1	30	 100%
3	h2	30	 100%
3	h3	30	 100%
3	h4	30	 100%
3	h5	30	 100%
3	h6	30	 100%
3	i1	30	 100%
3	i2	30	 100%
3	i3	30	 100%
3	i4	30	 100%
3	i5	30	 100%
3	i6	30	 100%
4	g1	22	 100%
4	g2	22	 100%
4	g3	22	 100%
4	g4	22	 100%

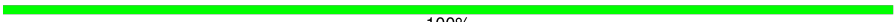













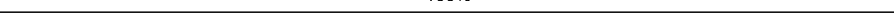
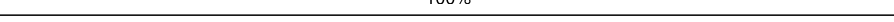
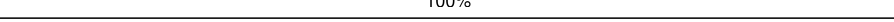
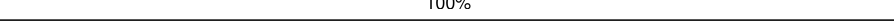
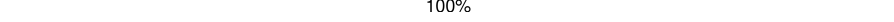
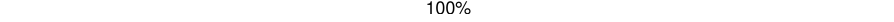
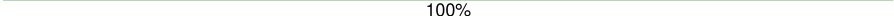




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Mol	Chain	Length	Quality of chain
4	g5	22	 100%
4	g6	22	 100%
5	j1	28	 100%
5	j2	28	 100%
5	j3	28	 100%
5	j4	28	 100%
5	j5	28	 100%
5	j6	28	 100%
5	k1	28	 100%
5	k2	28	 100%
5	k3	28	 100%
5	k4	28	 100%
5	k5	28	 100%
5	k6	28	 100%
5	p1	28	 100%
5	p2	28	 100%
5	p3	28	 100%
5	p4	28	 100%
5	p5	28	 100%
5	p6	28	 100%
5	s1	28	 100%
5	s2	28	 100%
5	s3	28	 100%
5	s4	28	 100%
5	s5	28	 100%

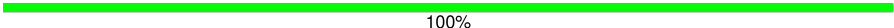
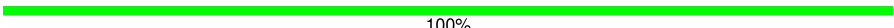
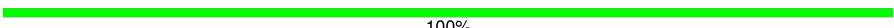
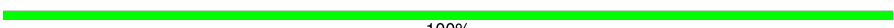









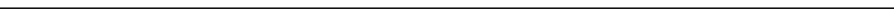

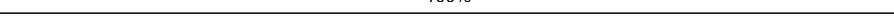
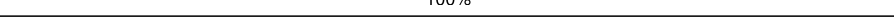
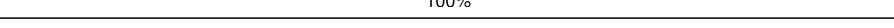
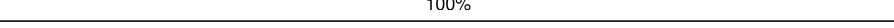
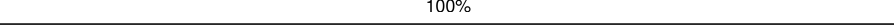
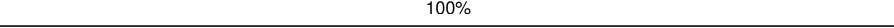
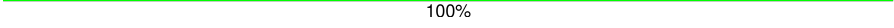
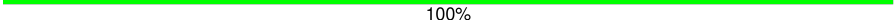
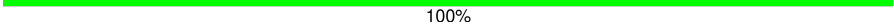
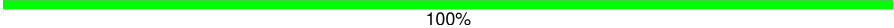
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Mol	Chain	Length	Quality of chain
5	s6	28	 100%
6	l1	13	 100%
6	l2	13	 100%
6	l3	13	 100%
6	l4	13	 100%
6	l5	13	 100%
6	l6	13	 100%
7	U1	88	 55% 31% 15%
7	U2	88	 57% 28% 15%
7	U3	88	 55% 31% 15%
7	U4	88	 57% 28% 15%
7	U5	88	 55% 31% 15%
7	U6	88	 57% 28% 15%
8	n1	59	 100%
8	n2	59	 100%
8	n3	59	 100%
8	n4	59	 100%
8	n5	59	 100%
8	n6	59	 100%
9	o1	21	 100%
9	o2	21	 100%
9	o3	21	 100%
9	o4	21	 100%
9	o5	21	 100%
9	o6	21	 100%


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Mol	Chain	Length	Quality of chain
10	t1	57	 100%
10	t2	57	 100%
10	t3	57	 100%
10	t4	57	 100%
10	t5	57	 100%
10	t6	57	 100%
11	u1	15	 100%
11	u2	15	 100%
11	u3	15	 100%
11	u4	15	 100%
11	u5	15	 100%
11	u6	15	 100%
12	v1	32	 100%
12	v2	32	 100%
12	v3	32	 100%
12	v4	32	 100%
12	v5	32	 100%
12	v6	32	 100%
13	w1	27	 100%
13	w2	27	 100%
13	w3	27	 100%
13	w4	27	 100%
13	w5	27	 100%
13	w6	27	 100%
14	BA	146	 85% 14%

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Mol	Chain	Length	Quality of chain
14	BB	146	 86% 13% •
14	BC	146	 84% 15% •
14	BD	146	 84% 15% •
14	BE	146	 83% 16% •
14	BF	146	 86% 14% •

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 48030 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 NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	L1	493	Total	C	N	O	0	0	0
			2465	1479	493	493			
1	L2	493	Total	C	N	O	0	0	0
			2465	1479	493	493			
1	L3	493	Total	C	N	O	0	0	0
			2465	1479	493	493			
1	L4	493	Total	C	N	O	0	0	0
			2465	1479	493	493			
1	L5	493	Total	C	N	O	0	0	0
			2465	1479	493	493			
1	L6	493	Total	C	N	O	0	0	0
			2465	1479	493	493			

- Molecule 2 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M1	439	Total	C	N	O	0	0	0
			2195	1317	439	439			
2	M2	439	Total	C	N	O	0	0	0
			2195	1317	439	439			
2	M3	439	Total	C	N	O	0	0	0
			2195	1317	439	439			
2	M4	439	Total	C	N	O	0	0	0
			2195	1317	439	439			
2	M5	439	Total	C	N	O	0	0	0
			2195	1317	439	439			
2	M6	439	Total	C	N	O	0	0	0
			2195	1317	439	439			

- Molecule 3 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	f1	30	Total 150	C 90	N 30	O 30	0	0	0
3	h1	30	Total 150	C 90	N 30	O 30	0	0	0
3	i1	30	Total 150	C 90	N 30	O 30	0	0	0
3	f2	30	Total 150	C 90	N 30	O 30	0	0	0
3	h2	30	Total 150	C 90	N 30	O 30	0	0	0
3	i2	30	Total 150	C 90	N 30	O 30	0	0	0
3	f3	30	Total 150	C 90	N 30	O 30	0	0	0
3	h3	30	Total 150	C 90	N 30	O 30	0	0	0
3	i3	30	Total 150	C 90	N 30	O 30	0	0	0
3	f4	30	Total 150	C 90	N 30	O 30	0	0	0
3	h4	30	Total 150	C 90	N 30	O 30	0	0	0
3	i4	30	Total 150	C 90	N 30	O 30	0	0	0
3	f5	30	Total 150	C 90	N 30	O 30	0	0	0
3	h5	30	Total 150	C 90	N 30	O 30	0	0	0
3	i5	30	Total 150	C 90	N 30	O 30	0	0	0
3	f6	30	Total 150	C 90	N 30	O 30	0	0	0
3	h6	30	Total 150	C 90	N 30	O 30	0	0	0
3	i6	30	Total 150	C 90	N 30	O 30	0	0	0

- Molecule 4 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	g1	22	Total 110	C 66	N 22	O 22	0	0	0
4	g2	22	Total 110	C 66	N 22	O 22	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	g3	22	Total 110	C 66	N 22	O 22	0	0	0
4	g4	22	Total 110	C 66	N 22	O 22	0	0	0
4	g5	22	Total 110	C 66	N 22	O 22	0	0	0
4	g6	22	Total 110	C 66	N 22	O 22	0	0	0

- Molecule 5 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	j1	28	Total 140	C 84	N 28	O 28	0	0	0
5	k1	28	Total 140	C 84	N 28	O 28	0	0	0
5	p1	28	Total 140	C 84	N 28	O 28	0	0	0
5	s1	28	Total 140	C 84	N 28	O 28	0	0	0
5	j2	28	Total 140	C 84	N 28	O 28	0	0	0
5	k2	28	Total 140	C 84	N 28	O 28	0	0	0
5	p2	28	Total 140	C 84	N 28	O 28	0	0	0
5	s2	28	Total 140	C 84	N 28	O 28	0	0	0
5	j3	28	Total 140	C 84	N 28	O 28	0	0	0
5	k3	28	Total 140	C 84	N 28	O 28	0	0	0
5	p3	28	Total 140	C 84	N 28	O 28	0	0	0
5	s3	28	Total 140	C 84	N 28	O 28	0	0	0
5	j4	28	Total 140	C 84	N 28	O 28	0	0	0
5	k4	28	Total 140	C 84	N 28	O 28	0	0	0
5	p4	28	Total 140	C 84	N 28	O 28	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	s4	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	j5	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	k5	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	p5	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	s5	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	j6	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	k6	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	p6	28	Total	C	N	O	0	0	0
			140	84	28	28			
5	s6	28	Total	C	N	O	0	0	0
			140	84	28	28			

- Molecule 6 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	l1	13	Total	C	N	O	0	0	0
			65	39	13	13			
6	l2	13	Total	C	N	O	0	0	0
			65	39	13	13			
6	l3	13	Total	C	N	O	0	0	0
			65	39	13	13			
6	l4	13	Total	C	N	O	0	0	0
			65	39	13	13			
6	l5	13	Total	C	N	O	0	0	0
			65	39	13	13			
6	l6	13	Total	C	N	O	0	0	0
			65	39	13	13			

- Molecule 7 is a protein called SDAP.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	U1	75	Total	C	N	O	0	0	0
			375	225	75	75			
7	U2	75	Total	C	N	O	0	0	0
			375	225	75	75			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	U3	75	Total	C	N	O	0	0	0
			375	225	75	75			
7	U4	75	Total	C	N	O	0	0	0
			375	225	75	75			
7	U5	75	Total	C	N	O	0	0	0
			375	225	75	75			
7	U6	75	Total	C	N	O	0	0	0
			375	225	75	75			

- Molecule 8 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	n1	59	Total	C	N	O	0	0	0
			295	177	59	59			
8	n2	59	Total	C	N	O	0	0	0
			295	177	59	59			
8	n3	59	Total	C	N	O	0	0	0
			295	177	59	59			
8	n4	59	Total	C	N	O	0	0	0
			295	177	59	59			
8	n5	59	Total	C	N	O	0	0	0
			295	177	59	59			
8	n6	59	Total	C	N	O	0	0	0
			295	177	59	59			

- Molecule 9 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	o1	21	Total	C	N	O	0	0	0
			105	63	21	21			
9	o2	21	Total	C	N	O	0	0	0
			105	63	21	21			
9	o3	21	Total	C	N	O	0	0	0
			105	63	21	21			
9	o4	21	Total	C	N	O	0	0	0
			105	63	21	21			
9	o5	21	Total	C	N	O	0	0	0
			105	63	21	21			
9	o6	21	Total	C	N	O	0	0	0
			105	63	21	21			

- Molecule 10 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	t1	57	Total	C	N	O	0	0	0
			285	171	57	57			
10	t2	57	Total	C	N	O	0	0	0
			285	171	57	57			
10	t3	57	Total	C	N	O	0	0	0
			285	171	57	57			
10	t4	57	Total	C	N	O	0	0	0
			285	171	57	57			
10	t5	57	Total	C	N	O	0	0	0
			285	171	57	57			
10	t6	57	Total	C	N	O	0	0	0
			285	171	57	57			

- Molecule 11 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	u1	15	Total	C	N	O	0	0	0
			75	45	15	15			
11	u2	15	Total	C	N	O	0	0	0
			75	45	15	15			
11	u3	15	Total	C	N	O	0	0	0
			75	45	15	15			
11	u4	15	Total	C	N	O	0	0	0
			75	45	15	15			
11	u5	15	Total	C	N	O	0	0	0
			75	45	15	15			
11	u6	15	Total	C	N	O	0	0	0
			75	45	15	15			

- Molecule 12 is a protein called Unknown structure.

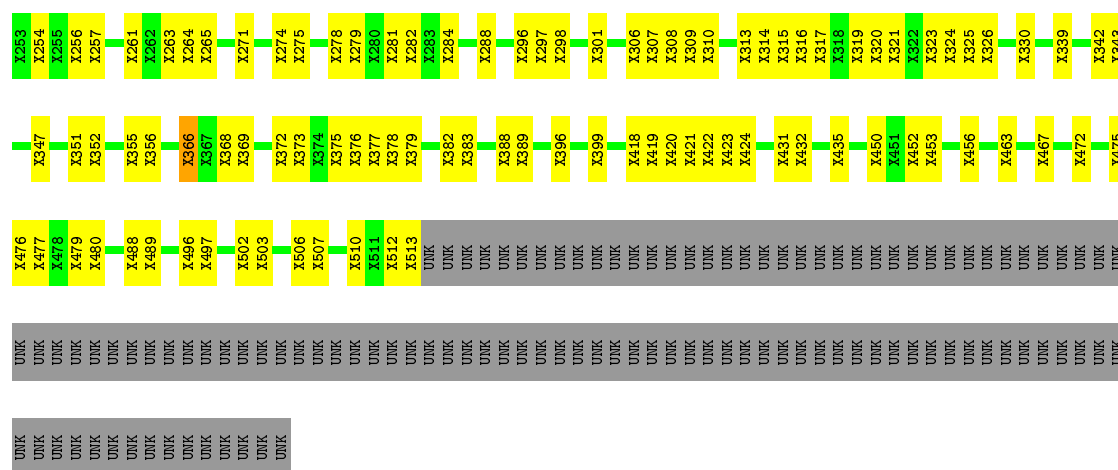
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	v1	32	Total	C	N	O	0	0	0
			160	96	32	32			
12	v2	32	Total	C	N	O	0	0	0
			160	96	32	32			
12	v3	32	Total	C	N	O	0	0	0
			160	96	32	32			
12	v4	32	Total	C	N	O	0	0	0
			160	96	32	32			
12	v5	32	Total	C	N	O	0	0	0
			160	96	32	32			
12	v6	32	Total	C	N	O	0	0	0
			160	96	32	32			

- Molecule 13 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	w1	27	Total	C	N	O	0	0	0
			135	81	27	27			
13	w2	27	Total	C	N	O	0	0	0
			135	81	27	27			
13	w3	27	Total	C	N	O	0	0	0
			135	81	27	27			
13	w4	27	Total	C	N	O	0	0	0
			135	81	27	27			
13	w5	27	Total	C	N	O	0	0	0
			135	81	27	27			
13	w6	27	Total	C	N	O	0	0	0
			135	81	27	27			

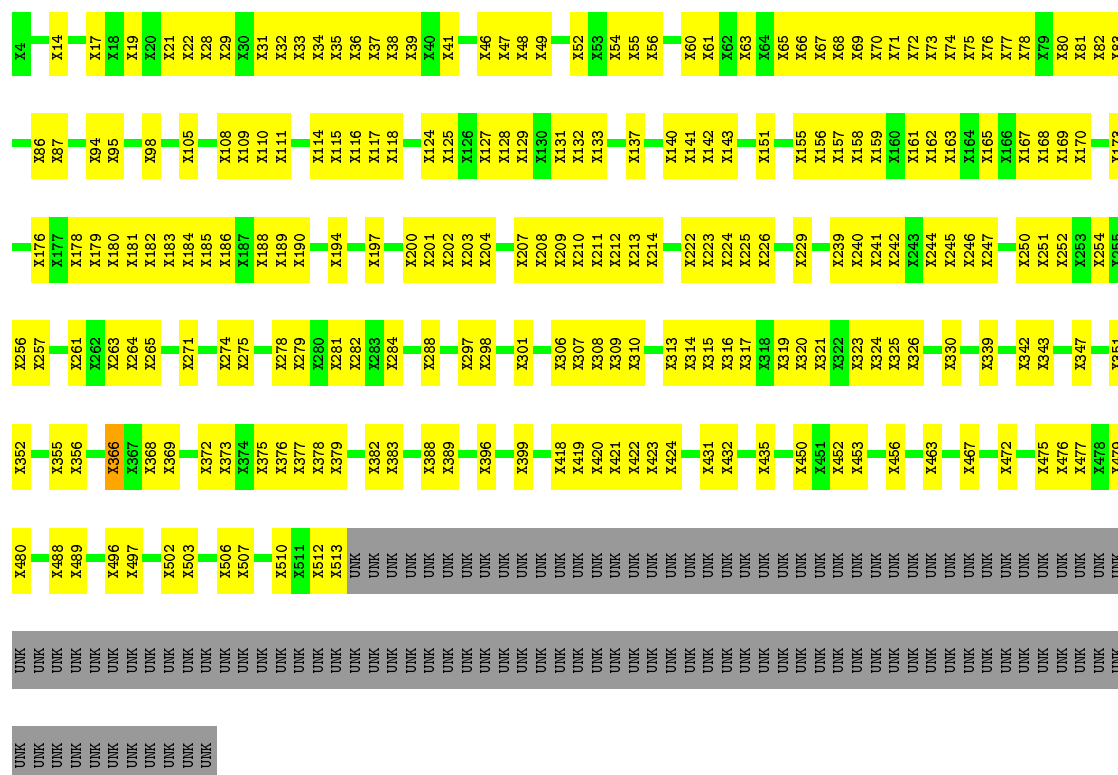
- Molecule 14 is a protein called Unknown structure.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	BA	146	Total	C	N	O	0	0	0
			730	438	146	146			
14	BB	146	Total	C	N	O	0	0	0
			730	438	146	146			
14	BC	146	Total	C	N	O	0	0	0
			730	438	146	146			
14	BD	146	Total	C	N	O	0	0	0
			730	438	146	146			
14	BE	146	Total	C	N	O	0	0	0
			730	438	146	146			
14	BF	146	Total	C	N	O	0	0	0
			730	438	146	146			



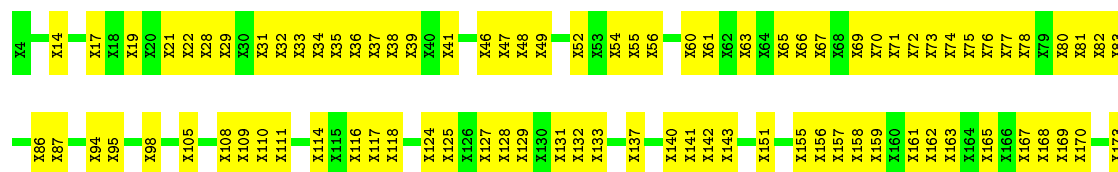
• Molecule 1: NADH-ubiquinone oxidoreductase chain 5

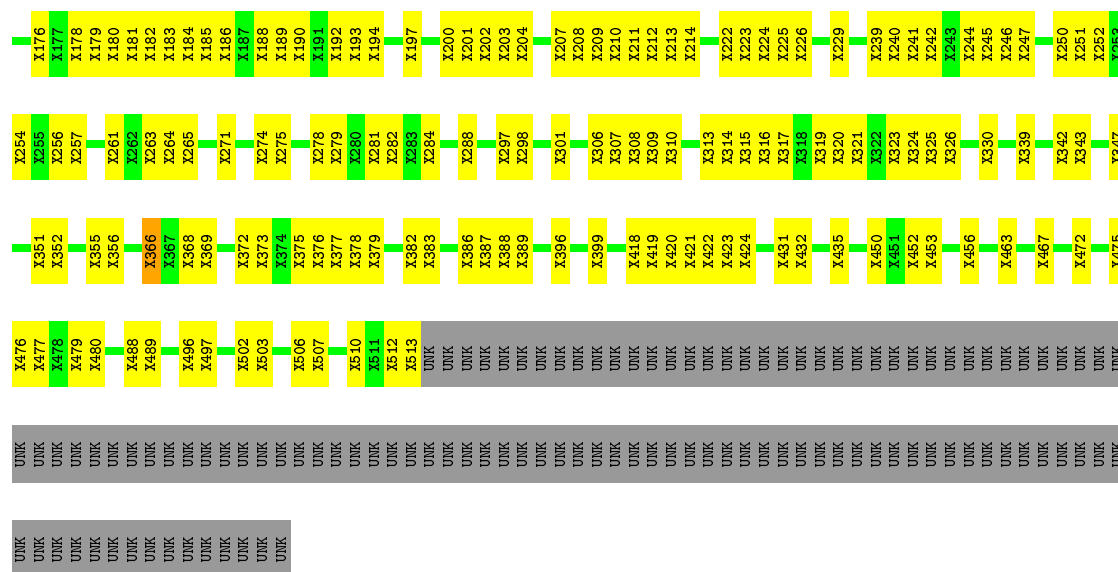
Chain L3: 44% 37% 19%



• Molecule 1: NADH-ubiquinone oxidoreductase chain 5

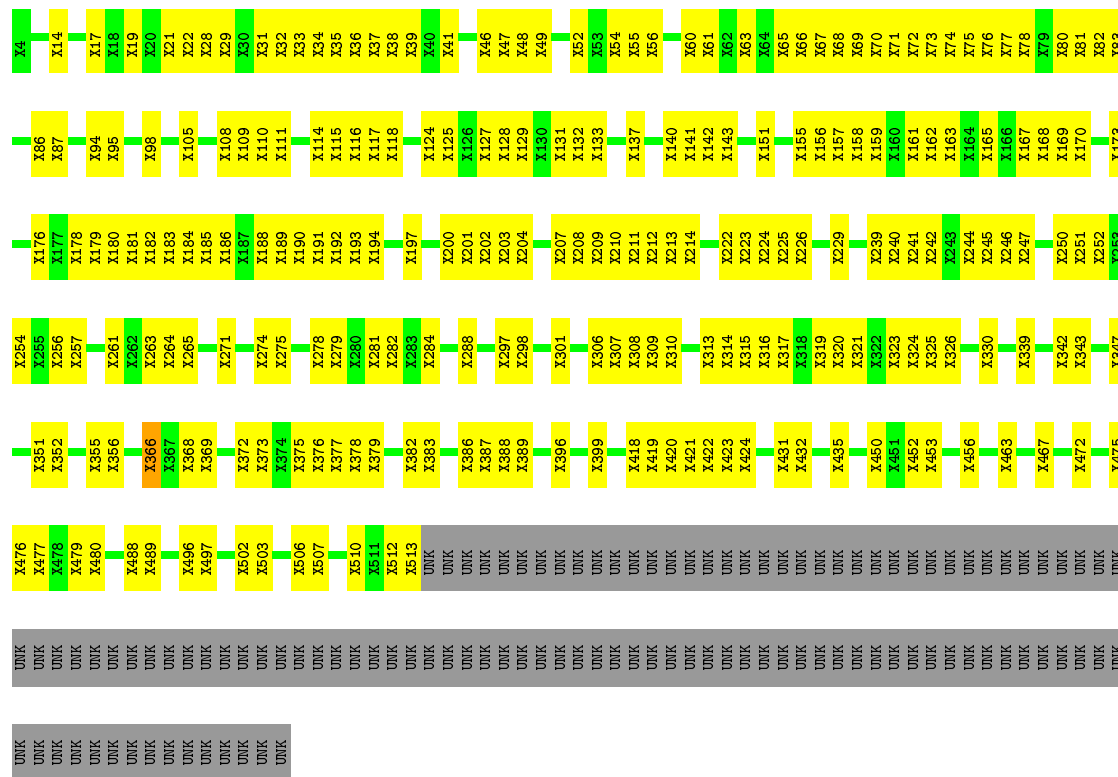
Chain L4: 43% 38% 19%





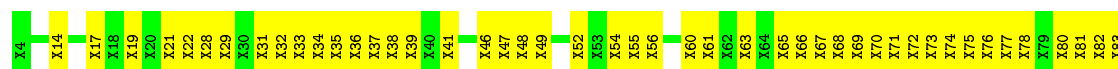
• Molecule 1: NADH-ubiquinone oxidoreductase chain 5

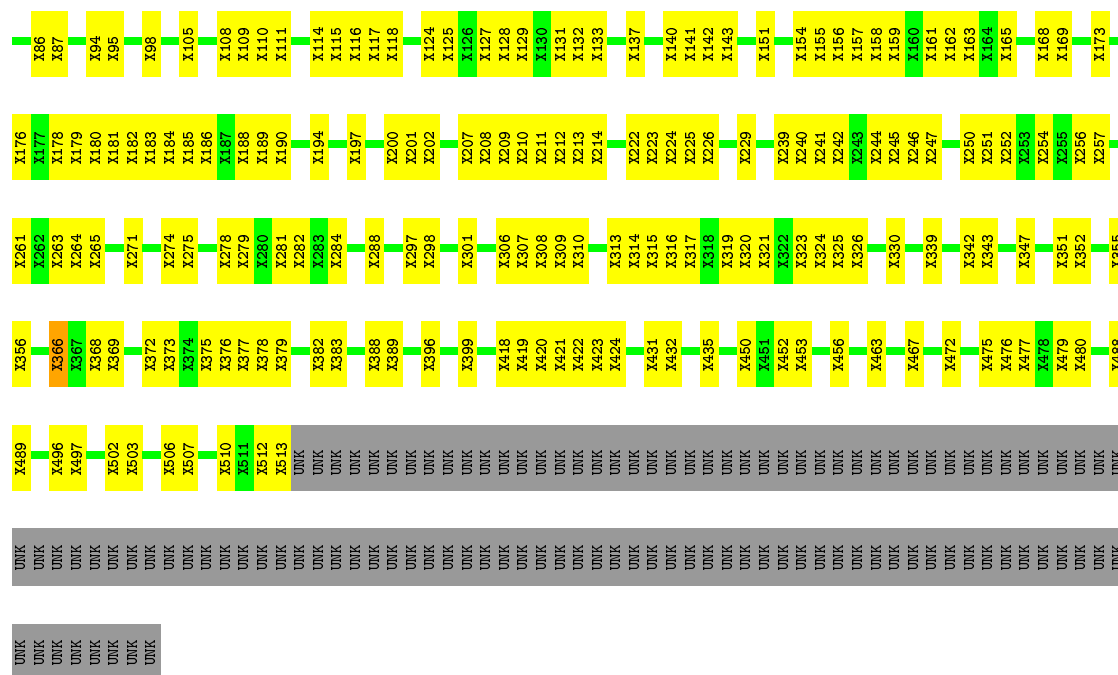
Chain L5:



• Molecule 1: NADH-ubiquinone oxidoreductase chain 5

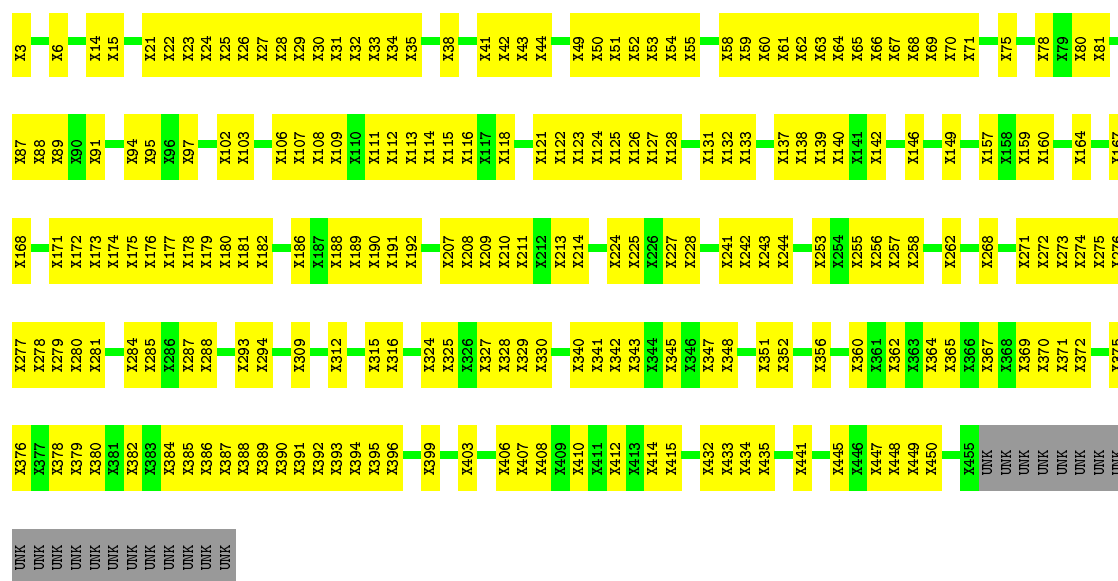
Chain L6:





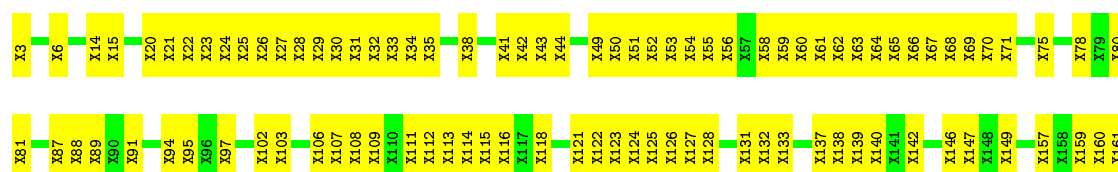
• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

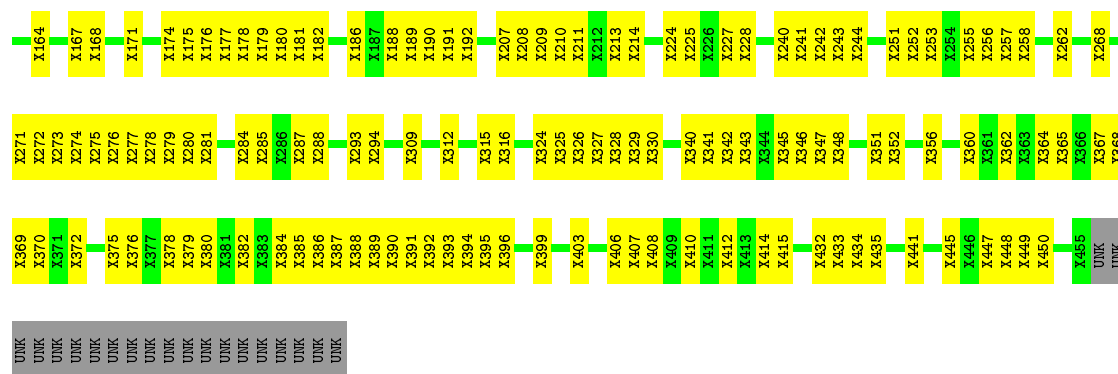
Chain M1: 48% 47%



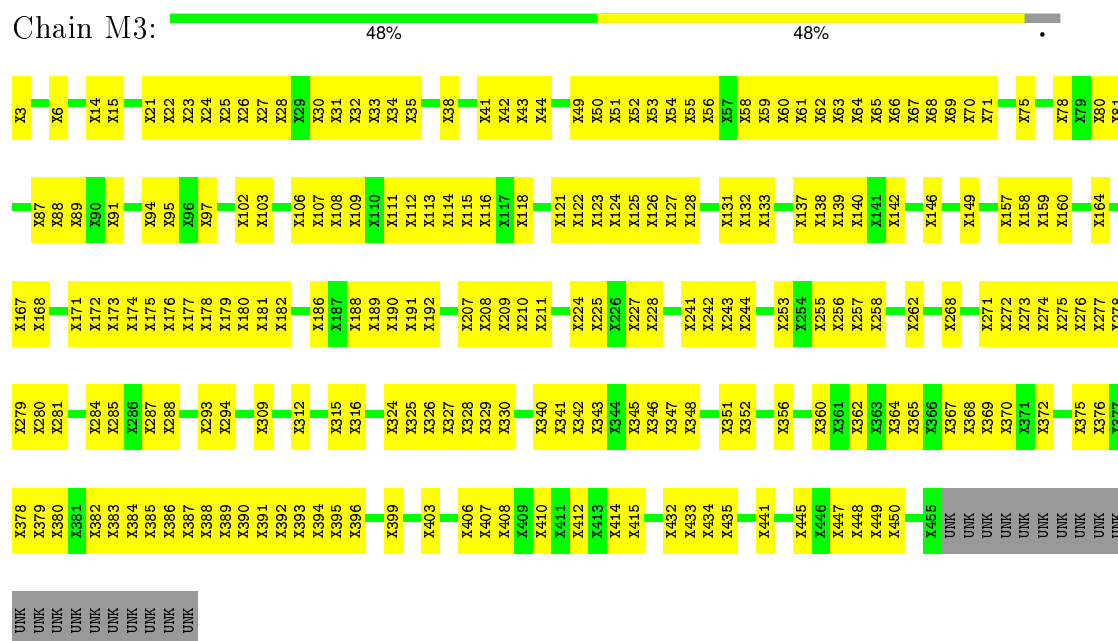
• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

Chain M2: 47% 49%

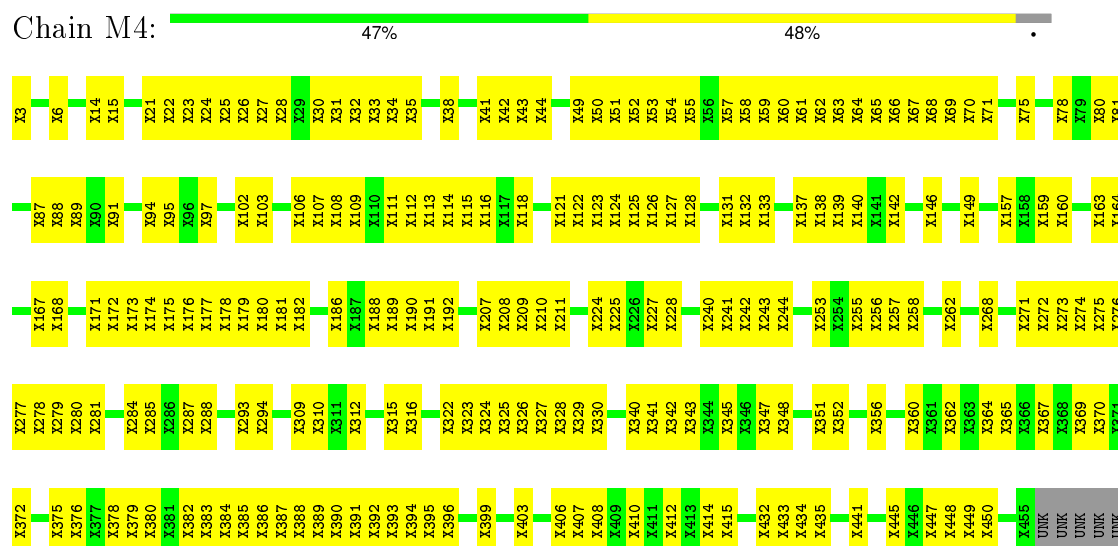




- Molecule 2: NADH-ubiquinone oxidoreductase chain 4



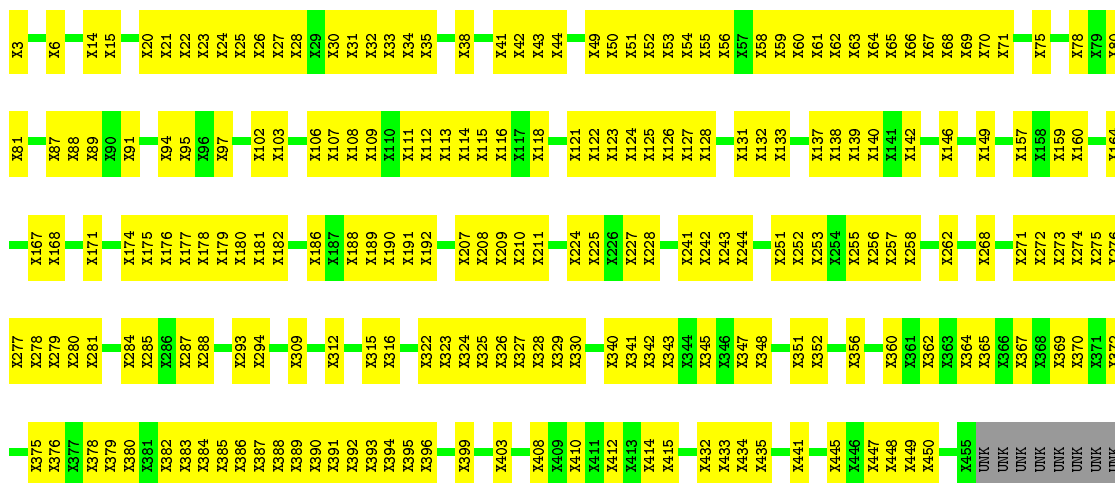
- Molecule 2: NADH-ubiquinone oxidoreductase chain 4



UNK
UNK
UNK
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UNK
UNK

• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

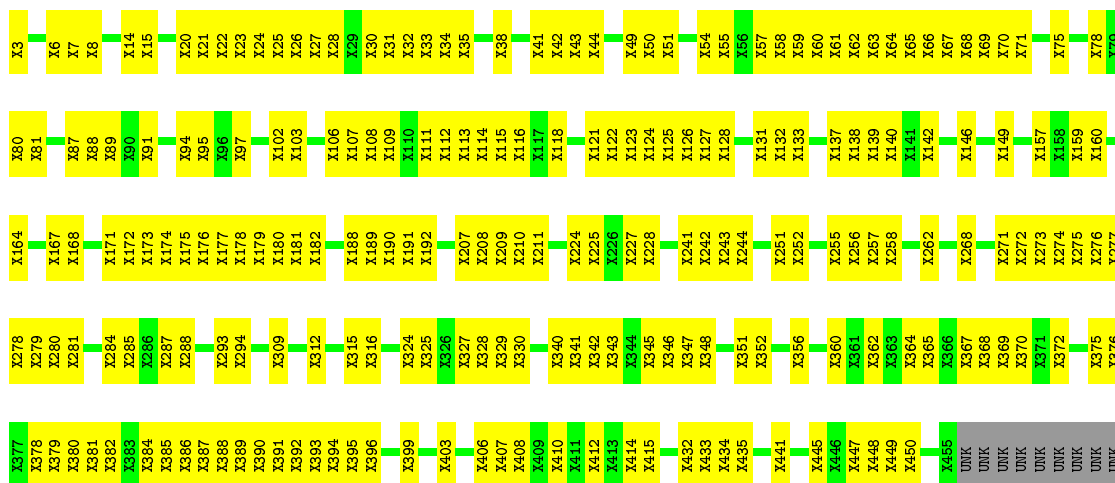
Chain M5:  48% 47%



UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK

• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

Chain M6:  48% 47%



UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK

• Molecule 3: Unknown structure

Chain f1:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain h1:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain i1:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain f2:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain h2:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain i2:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain f3:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain h3:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain i3:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain f4:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain h4:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain i4:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain f5:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain h5:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain i5:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain f6:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain h6:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Unknown structure

Chain i6:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Unknown structure

Chain g1:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Unknown structure

Chain g2:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Unknown structure

Chain g3:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Unknown structure

Chain g4:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Unknown structure

Chain g5:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Unknown structure

Chain g6:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain j1:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain k1:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain p1:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain s1:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain j2:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain k2:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain p2:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain s2:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain j3:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain k3:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain p3:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain s3:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain j4:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain k4:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain p4:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain s4:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain j5:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain k5:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain p5:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain s5:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain j6:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain k6:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain p6:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Unknown structure

Chain s6:  100%

- Molecule 6: Unknown structure

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown structure

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown structure

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown structure

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown structure

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown structure

There are no outlier residues recorded for this chain.

- Molecule 7: SDAP

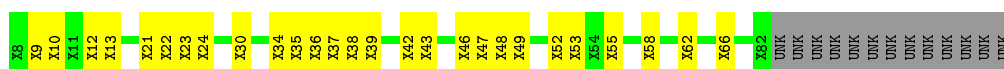
[illegible]

- Molecule 7: SDAP

X8	X9	X10	X11	X12	X13		X21	X22	X23	X24		X30	X34	X35	X36	X37	X38	X39	X42	X43	X44	X46	X47	X48	X49		X53	X54	X55		X58	X62	X66	X67	X68	X69	X70	X71	X72	X73	X74	X75	X76	X77	X78	X79	X80	X81	X82	X83	X84	X85	X86	X87	X88	X89	X90	X91	X92	X93	X94	X95	X96	X97	X98	X99	X100	X101	X102	X103	X104	X105	X106	X107	X108	X109	X110	X111	X112	X113	X114	X115	X116	X117	X118	X119	X120	X121	X122	X123	X124	X125	X126	X127	X128	X129	X130	X131	X132	X133	X134	X135	X136	X137	X138	X139	X140	X141	X142	X143	X144	X145	X146	X147	X148	X149	X150	X151	X152	X153	X154	X155	X156	X157	X158	X159	X160	X161	X162	X163	X164	X165	X166	X167	X168	X169	X170	X171	X172	X173	X174	X175	X176	X177	X178	X179	X180	X181	X182	X183	X184	X185	X186	X187	X188	X189	X190	X191	X192	X193	X194	X195	X196	X197	X198	X199	X200	X201	X202	X203	X204	X205	X206	X207	X208	X209	X210	X211	X212	X213	X214	X215	X216	X217	X218	X219	X220	X221	X222	X223	X224	X225	X226	X227	X228	X229	X230	X231	X232	X233	X234	X235	X236	X237	X238	X239	X240	X241	X242	X243	X244	X245	X246	X247	X248	X249	X250	X251	X252	X253	X254	X255	X256	X257	X258	X259	X260	X261	X262	X263	X264	X265	X266	X267	X268	X269	X270	X271	X272	X273	X274	X275	X276	X277	X278	X279	X280	X281	X282	X283	X284	X285	X286	X287	X288	X289	X290	X291	X292	X293	X294	X295	X296	X297	X298	X299	X300	X301	X302	X303	X304	X305	X306	X307	X308	X309	X310	X311	X312	X313	X314	X315	X316	X317	X318	X319	X320	X321	X322	X323	X324	X325	X326	X327	X328	X329	X330	X331	X332	X333	X334	X335	X336	X337	X338	X339	X340	X341	X342	X343	X344	X345	X346	X347	X348	X349	X350	X351	X352	X353	X354	X355	X356	X357	X358	X359	X360	X361	X362	X363	X364	X365	X366	X367	X368	X369	X370	X371	X372	X373	X374	X375	X376	X377	X378	X379	X380	X381	X382	X383	X384	X385	X386	X387	X388	X389	X390	X391	X392	X393	X394	X395	X396	X397	X398	X399	X400	X401	X402	X403	X404	X405	X406	X407	X408	X409	X410	X411	X412	X413	X414	X415	X416	X417	X418	X419	X420	X421	X422	X423	X424	X425	X426	X427	X428	X429	X430	X431	X432	X433	X434	X435	X436	X437	X438	X439	X440	X441	X442	X443	X444	X445	X446	X447	X448	X449	X450	X451	X452	X453	X454	X455	X456	X457	X458	X459	X460	X461	X462	X463	X464	X465	X466	X467	X468	X469	X470	X471	X472	X473	X474	X475	X476	X477	X478	X479	X480	X481	X482	X483	X484	X485	X486	X487	X488	X489	X490	X491	X492	X493	X494	X495	X496	X497	X498	X499	X500	X501	X502	X503	X504	X505	X506	X507	X508	X509	X510	X511	X512	X513	X514	X515	X516	X517	X518	X519	X520	X521	X522	X523	X524	X525	X526	X527	X528	X529	X530	X531	X532	X533	X534	X535	X536	X537	X538	X539	X540	X541	X542	X543	X544	X545	X546	X547	X548	X549	X550	X551	X552	X553
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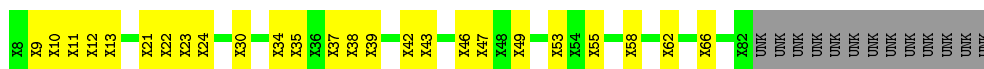
- Molecule 7: SDAP





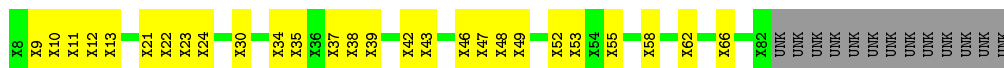
- Molecule 7: SDAP

Chain U4: 57% 28% 15%



- Molecule 7: SDAP

Chain U5: 55% 31% 15%



- Molecule 7: SDAP

Chain U6: 57% 28% 15%



- Molecule 8: Unknown structure

Chain n1: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Unknown structure

Chain n2: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Unknown structure

Chain n3: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Unknown structure

Chain n4: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Unknown structure

Chain n5: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Unknown structure

Chain n6:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure

Chain o1:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure

Chain o2:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure

Chain o3:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure

Chain o4:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure

Chain o5:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure

Chain o6:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown structure

Chain t1:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown structure

Chain t2:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown structure

Chain t3:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown structure

Chain t4:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown structure

Chain t5:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown structure

Chain t6:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Unknown structure

Chain u1:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Unknown structure

Chain u2:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Unknown structure

Chain u3:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Unknown structure

Chain u4:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Unknown structure

Chain u5:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: Unknown structure

Chain u6:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Unknown structure

Chain v1:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Unknown structure

Chain v2:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Unknown structure

Chain v3:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Unknown structure

Chain v4:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Unknown structure

Chain v5:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: Unknown structure

Chain v6:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: Unknown structure

Chain w1:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: Unknown structure

Chain w2:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: Unknown structure

Chain w3:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: Unknown structure

Chain w4:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: Unknown structure

Chain w5:  100%


There are no outlier residues recorded for this chain.

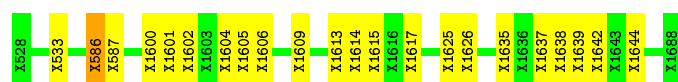
- Molecule 13: Unknown structure

Chain w6:  100%


There are no outlier residues recorded for this chain.

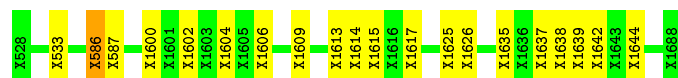
- Molecule 14: Unknown structure

Chain BA:  85% 14%




- Molecule 14: Unknown structure

Chain BB:  86% 13%




- Molecule 14: Unknown structure

Chain BC:  84% 15%




- Molecule 14: Unknown structure

Chain BD:  84% 15%

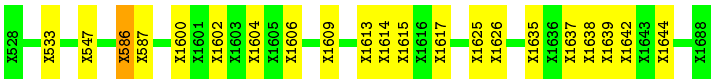
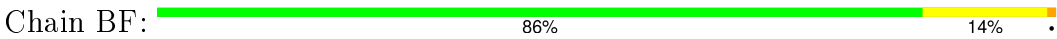


- Molecule 14: Unknown structure

Chain BE:  83% 16%



- Molecule 14: Unknown structure



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	244.83Å 251.41Å 412.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.69 – 6.74 49.44 – 6.74	Depositor EDS
% Data completeness (in resolution range)	97.2 (41.69-6.74) 90.7 (49.44-6.74)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 6.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.425 , 0.435 0.401 , 0.408	Depositor DCC
R_{free} test set	2227 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	495.7	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 102.6	EDS
Estimated twinning fraction	0.037 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	1 of 44280 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.42	EDS
Total number of atoms	48030	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	L1	0	2
1	L2	0	2
1	L3	0	2
1	L4	0	2
1	L5	0	2
1	L6	0	2
14	BA	0	3
14	BB	0	3
14	BC	0	3
14	BD	0	3
14	BE	0	3
14	BF	0	3
All	All	0	30

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	BA	533	UNK	Mainchain,Peptide
14	BA	586	UNK	Mainchain
1	L1	133	UNK	Peptide
1	L1	366	UNK	Peptide
1	L2	133	UNK	Peptide

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	L1	2465	0	517	226	0
1	L2	2465	0	517	228	0
1	L3	2465	0	517	227	0
1	L4	2465	0	517	227	0
1	L5	2465	0	517	227	0
1	L6	2465	0	517	221	0
2	M1	2195	0	455	202	0
2	M2	2195	0	455	209	0
2	M3	2195	0	455	206	0
2	M4	2195	0	455	205	0
2	M5	2195	0	455	201	0
2	M6	2195	0	455	206	0
3	f1	150	0	33	0	0
3	f2	150	0	33	0	0
3	f3	150	0	33	0	0
3	f4	150	0	33	0	0
3	f5	150	0	33	0	0
3	f6	150	0	33	0	0
3	h1	150	0	32	0	0
3	h2	150	0	32	0	0
3	h3	150	0	32	0	0
3	h4	150	0	32	0	0
3	h5	150	0	32	0	0
3	h6	150	0	32	0	0
3	i1	150	0	33	0	0
3	i2	150	0	33	0	0
3	i3	150	0	33	0	0
3	i4	150	0	33	0	0
3	i5	150	0	33	0	0
3	i6	150	0	33	0	0
4	g1	110	0	24	0	0
4	g2	110	0	24	0	0
4	g3	110	0	24	0	0
4	g4	110	0	24	0	0
4	g5	110	0	24	0	0
4	g6	110	0	24	0	0
5	j1	140	0	33	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	j2	140	0	33	0	0
5	j3	140	0	33	0	0
5	j4	140	0	33	0	0
5	j5	140	0	33	0	0
5	j6	140	0	33	0	0
5	k1	140	0	30	0	0
5	k2	140	0	30	0	0
5	k3	140	0	30	0	0
5	k4	140	0	30	0	0
5	k5	140	0	30	0	0
5	k6	140	0	30	0	0
5	p1	140	0	30	0	0
5	p2	140	0	30	0	0
5	p3	140	0	30	0	0
5	p4	140	0	30	0	0
5	p5	140	0	30	0	0
5	p6	140	0	30	0	0
5	s1	140	0	31	0	0
5	s2	140	0	31	0	0
5	s3	140	0	31	0	0
5	s4	140	0	31	0	0
5	s5	140	0	31	0	0
5	s6	140	0	31	0	0
6	l1	65	0	15	0	0
6	l2	65	0	15	0	0
6	l3	65	0	15	0	0
6	l4	65	0	15	0	0
6	l5	65	0	15	0	0
6	l6	65	0	15	0	0
7	U1	375	0	80	22	0
7	U2	375	0	80	21	0
7	U3	375	0	80	22	0
7	U4	375	0	80	21	0
7	U5	375	0	80	22	0
7	U6	375	0	80	21	0
8	n1	295	0	61	0	0
8	n2	295	0	61	0	0
8	n3	295	0	61	0	0
8	n4	295	0	61	0	0
8	n5	295	0	61	0	0
8	n6	295	0	61	0	0
9	o1	105	0	23	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	o2	105	0	23	0	0
9	o3	105	0	23	0	0
9	o4	105	0	23	0	0
9	o5	105	0	23	0	0
9	o6	105	0	23	0	0
10	t1	285	0	61	0	0
10	t2	285	0	61	0	0
10	t3	285	0	61	0	0
10	t4	285	0	61	0	0
10	t5	285	0	61	0	0
10	t6	285	0	61	0	0
11	u1	75	0	17	0	0
11	u2	75	0	17	0	0
11	u3	75	0	17	0	0
11	u4	75	0	17	0	0
11	u5	75	0	17	0	0
11	u6	75	0	17	0	0
12	v1	160	0	34	0	0
12	v2	160	0	34	0	0
12	v3	160	0	34	0	0
12	v4	160	0	34	0	0
12	v5	160	0	34	0	0
12	v6	160	0	34	0	0
13	w1	135	0	30	0	0
13	w2	135	0	29	0	0
13	w3	135	0	29	0	0
13	w4	135	0	29	0	0
13	w5	135	0	29	0	0
13	w6	135	0	29	0	0
14	BA	730	0	164	30	0
14	BB	730	0	164	29	0
14	BC	730	0	164	38	0
14	BD	730	0	164	39	0
14	BE	730	0	164	40	0
14	BF	730	0	164	39	0
All	All	48030	0	10213	2873	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 63.

The worst 5 of 2873 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:321:UNK:CB	1:L5:324:UNK:CB	1.91	1.48
14:BA:1609:UNK:CB	14:BA:1642:UNK:CB	1.92	1.47
1:L1:321:UNK:CB	1:L1:324:UNK:CB	1.91	1.47
1:L4:321:UNK:CB	1:L4:324:UNK:CB	1.91	1.47
14:BB:1609:UNK:CB	14:BB:1642:UNK:CB	1.92	1.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
14	BB	9
14	BA	9
14	BF	9
14	BE	9
14	BD	9
14	BC	9
1	L2	4
1	L3	4
1	L1	4
1	L6	4
1	L4	4
1	L5	4
2	M4	1
2	M5	1
2	M2	1
2	M3	1
2	M1	1
2	M6	1

The worst 5 of 84 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	563:UNK	C	571:UNK	N	83.40
1	BB	563:UNK	C	571:UNK	N	83.40
1	BC	563:UNK	C	571:UNK	N	83.40
1	BD	563:UNK	C	571:UNK	N	83.40
1	BE	563:UNK	C	571:UNK	N	83.40

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	L1	0/606	-	-	-	-
1	L2	0/606	-	-	-	-
1	L3	0/606	-	-	-	-
1	L4	0/606	-	-	-	-
1	L5	0/606	-	-	-	-
1	L6	0/606	-	-	-	-
2	M1	0/459	-	-	-	-
2	M2	0/459	-	-	-	-
2	M3	0/459	-	-	-	-
2	M4	0/459	-	-	-	-
2	M5	0/459	-	-	-	-
2	M6	0/459	-	-	-	-
3	f1	0/30	-	-	-	-
3	f2	0/30	-	-	-	-
3	f3	0/30	-	-	-	-
3	f4	0/30	-	-	-	-
3	f5	0/30	-	-	-	-
3	f6	0/30	-	-	-	-
3	h1	0/30	-	-	-	-
3	h2	0/30	-	-	-	-
3	h3	0/30	-	-	-	-
3	h4	0/30	-	-	-	-
3	h5	0/30	-	-	-	-
3	h6	0/30	-	-	-	-
3	i1	0/30	-	-	-	-
3	i2	0/30	-	-	-	-
3	i3	0/30	-	-	-	-
3	i4	0/30	-	-	-	-
3	i5	0/30	-	-	-	-
3	i6	0/30	-	-	-	-
4	g1	0/22	-	-	-	-
4	g2	0/22	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
4	g3	0/22	-	-	-	-
4	g4	0/22	-	-	-	-
4	g5	0/22	-	-	-	-
4	g6	0/22	-	-	-	-
5	j1	0/28	-	-	-	-
5	j2	0/28	-	-	-	-
5	j3	0/28	-	-	-	-
5	j4	0/28	-	-	-	-
5	j5	0/28	-	-	-	-
5	j6	0/28	-	-	-	-
5	k1	0/28	-	-	-	-
5	k2	0/28	-	-	-	-
5	k3	0/28	-	-	-	-
5	k4	0/28	-	-	-	-
5	k5	0/28	-	-	-	-
5	k6	0/28	-	-	-	-
5	p1	0/28	-	-	-	-
5	p2	0/28	-	-	-	-
5	p3	0/28	-	-	-	-
5	p4	0/28	-	-	-	-
5	p5	0/28	-	-	-	-
5	p6	0/28	-	-	-	-
5	s1	0/28	-	-	-	-
5	s2	0/28	-	-	-	-
5	s3	0/28	-	-	-	-
5	s4	0/28	-	-	-	-
5	s5	0/28	-	-	-	-
5	s6	0/28	-	-	-	-
6	l1	0/13	-	-	-	-
6	l2	0/13	-	-	-	-
6	l3	0/13	-	-	-	-
6	l4	0/13	-	-	-	-
6	l5	0/13	-	-	-	-
6	l6	0/13	-	-	-	-
7	U1	0/88	-	-	-	-
7	U2	0/88	-	-	-	-
7	U3	0/88	-	-	-	-
7	U4	0/88	-	-	-	-
7	U5	0/88	-	-	-	-
7	U6	0/88	-	-	-	-
8	n1	0/59	-	-	-	-
8	n2	0/59	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
8	n3	0/59	-	-	-	-
8	n4	0/59	-	-	-	-
8	n5	0/59	-	-	-	-
8	n6	0/59	-	-	-	-
9	o1	0/21	-	-	-	-
9	o2	0/21	-	-	-	-
9	o3	0/21	-	-	-	-
9	o4	0/21	-	-	-	-
9	o5	0/21	-	-	-	-
9	o6	0/21	-	-	-	-
10	t1	0/57	-	-	-	-
10	t2	0/57	-	-	-	-
10	t3	0/57	-	-	-	-
10	t4	0/57	-	-	-	-
10	t5	0/57	-	-	-	-
10	t6	0/57	-	-	-	-
11	u1	0/15	-	-	-	-
11	u2	0/15	-	-	-	-
11	u3	0/15	-	-	-	-
11	u4	0/15	-	-	-	-
11	u5	0/15	-	-	-	-
11	u6	0/15	-	-	-	-
12	v1	0/32	-	-	-	-
12	v2	0/32	-	-	-	-
12	v3	0/32	-	-	-	-
12	v4	0/32	-	-	-	-
12	v5	0/32	-	-	-	-
12	v6	0/32	-	-	-	-
13	w1	0/27	-	-	-	-
13	w2	0/27	-	-	-	-
13	w3	0/27	-	-	-	-
13	w4	0/27	-	-	-	-
13	w5	0/27	-	-	-	-
13	w6	0/27	-	-	-	-
14	BA	0/146	-	-	-	-
14	BB	0/146	-	-	-	-
14	BC	0/146	-	-	-	-
14	BD	0/146	-	-	-	-
14	BE	0/146	-	-	-	-
14	BF	0/146	-	-	-	-
All	All	0/10482	-	-	-	-

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.