



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:30 PM UTC

PDB ID : 5COD / pdb_00005cod
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

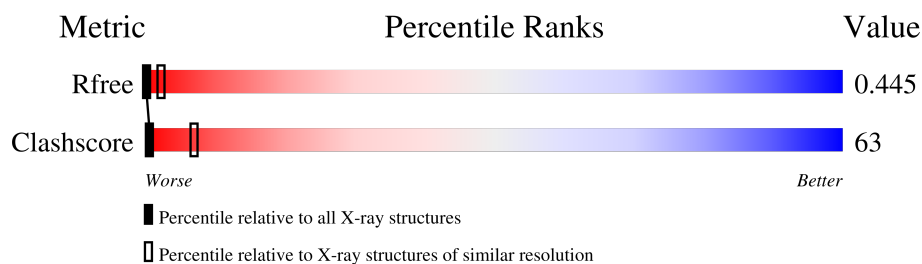
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

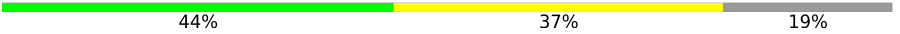
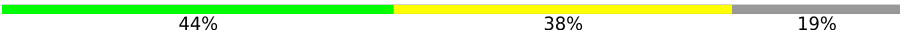
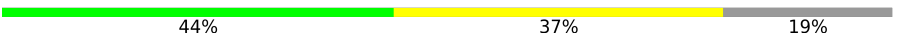


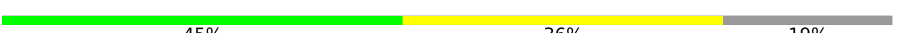
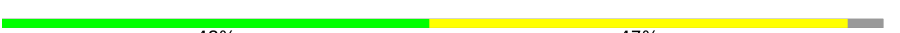


The reported resolution of this entry is 6.74 Å.

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.



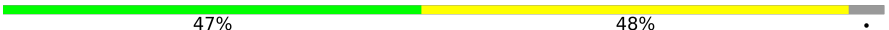









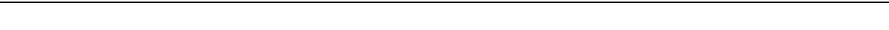

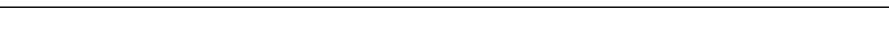
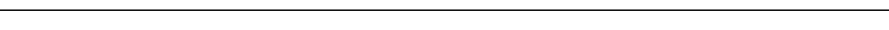











Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1163 (9.44-4.00)
Clashscore	190562	1003 (9.44-4.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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		44%	37%
1	L2	606		44%	38%
1	L3	606		44%	37%
1	L4	606		44%	37%
1	L5	606		43%	38%
1	L6	606		45%	36%
2	M1	459		48%	47%
2	M2	459		47%	49%
2	M3	459		48%	48%


























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












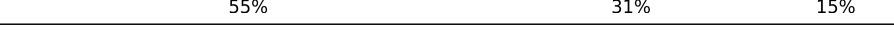







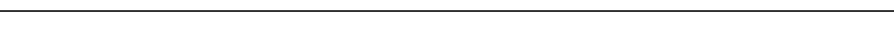

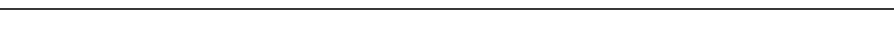
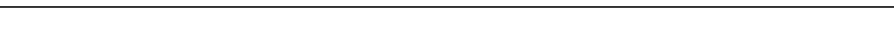


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Mol	Chain	Length	Quality of chain
4	g5	22	 45%55%
4	g6	22	 55%45%
5	j1	28	 68%32%
5	j2	28	 68%32%
5	j3	28	 68%32%
5	j4	28	 68%32%
5	j5	28	 68%32%
5	j6	28	 68%32%
5	k1	28	 82%18%
5	k2	28	 82%18%
5	k3	28	 82%18%
5	k4	28	 82%18%
5	k5	28	 82%18%
5	k6	28	 82%18%
5	p1	28	 79%21%
5	p2	28	 79%21%
5	p3	28	 79%21%
5	p4	28	 79%21%
5	p5	28	 79%21%
5	p6	28	 79%21%
5	s1	28	 61%39%
5	s2	28	 61%39%
5	s3	28	 57%43%
5	s4	28	 57%43%
5	s5	28	 57%43%












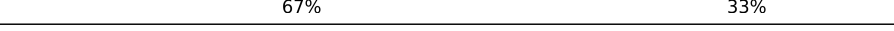







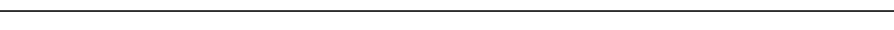

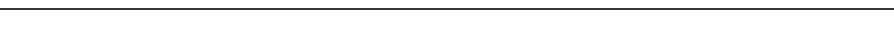
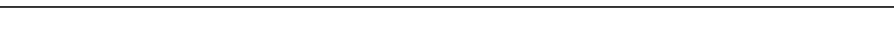


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Mol	Chain	Length	Quality of chain
5	s6	28	 61% 39%
6	l1	13	 54% 46%
6	l2	13	 54% 46%
6	l3	13	 54% 46%
6	l4	13	 54% 46%
6	l5	13	 54% 46%
6	l6	13	 69% 31%
7	U1	88	 55% 31% 15%
7	U2	88	 57% 28% 15%
7	U3	88	 55% 31% 15%
7	U4	88	 57% 28% 15%
7	U5	88	 55% 31% 15%
7	U6	88	 57% 28% 15%
8	n1	59	 56% 44%
8	n2	59	 56% 44%
8	n3	59	 56% 44%
8	n4	59	 53% 47%
8	n5	59	 53% 47%
8	n6	59	 58% 42%
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	 54% 46%
10	t2	57	 56% 44%
10	t3	57	 53% 47%
10	t4	57	 54% 46%
10	t5	57	 56% 44%
10	t6	57	 56% 44%
11	u1	15	 67% 33%
11	u2	15	 80% 20%
11	u3	15	 67% 33%
11	u4	15	 67% 33%
11	u5	15	 67% 33%
11	u6	15	 67% 33%
12	v1	32	 53% 47%
12	v2	32	 53% 47%
12	v3	32	 53% 47%
12	v4	32	 53% 47%
12	v5	32	 53% 47%
12	v6	32	 53% 47%
13	w1	27	 74% 26%
13	w2	27	 74% 26%
13	w3	27	 74% 26%
13	w4	27	 74% 26%
13	w5	27	 74% 26%
13	w6	27	 74% 26%
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	C	N	O	0	0	0
			110	66	22	22			
4	g4	22	Total	C	N	O	0	0	0
			110	66	22	22			
4	g5	22	Total	C	N	O	0	0	0
			110	66	22	22			
4	g6	22	Total	C	N	O	0	0	0
			110	66	22	22			

- Molecule 5 is a protein called Unknown structure.

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

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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			

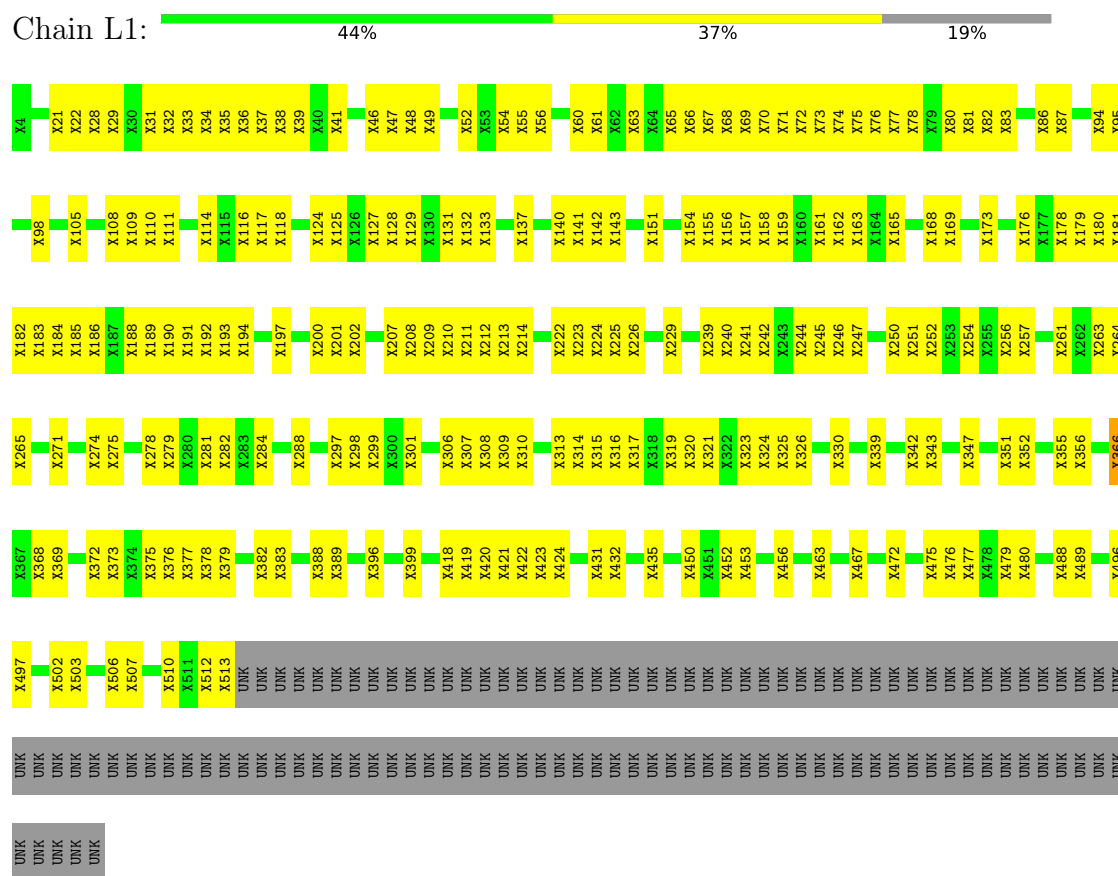
- Molecule 14 is a protein called Unknown structure.

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			

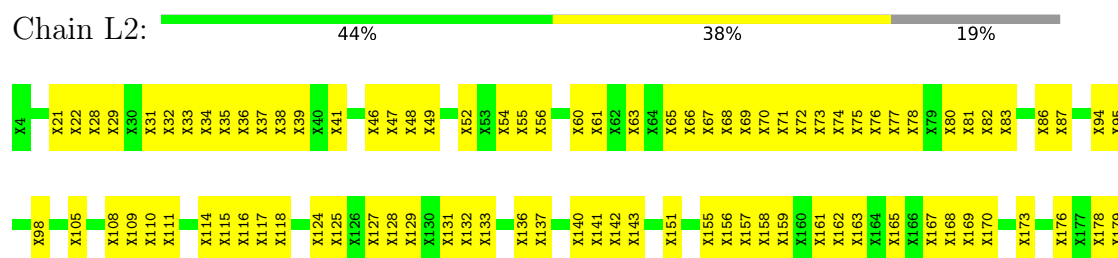
3 Residue-property plots

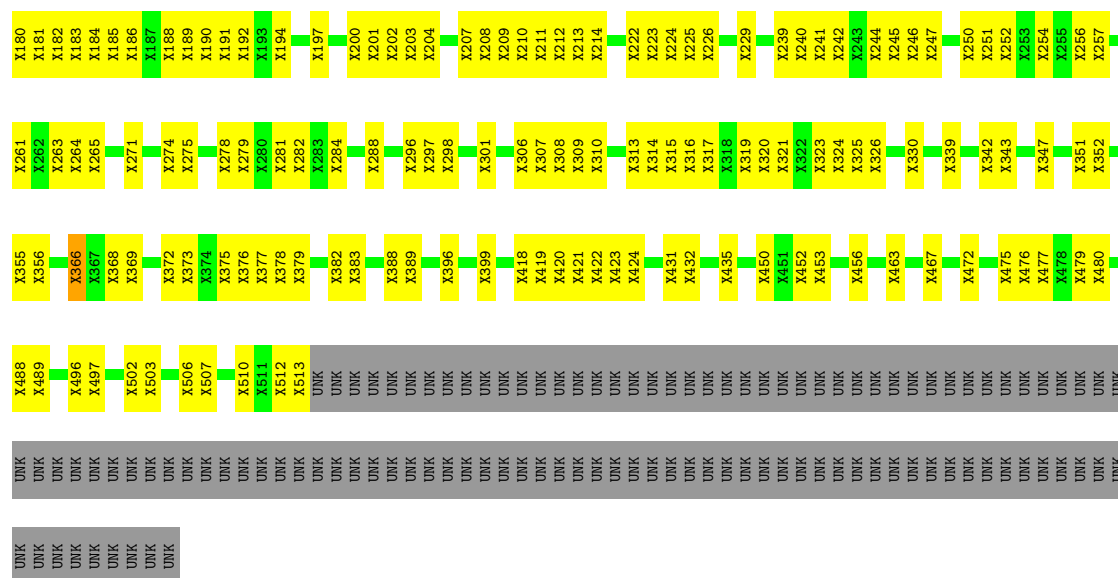
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: NADH-ubiquinone oxidoreductase chain 5



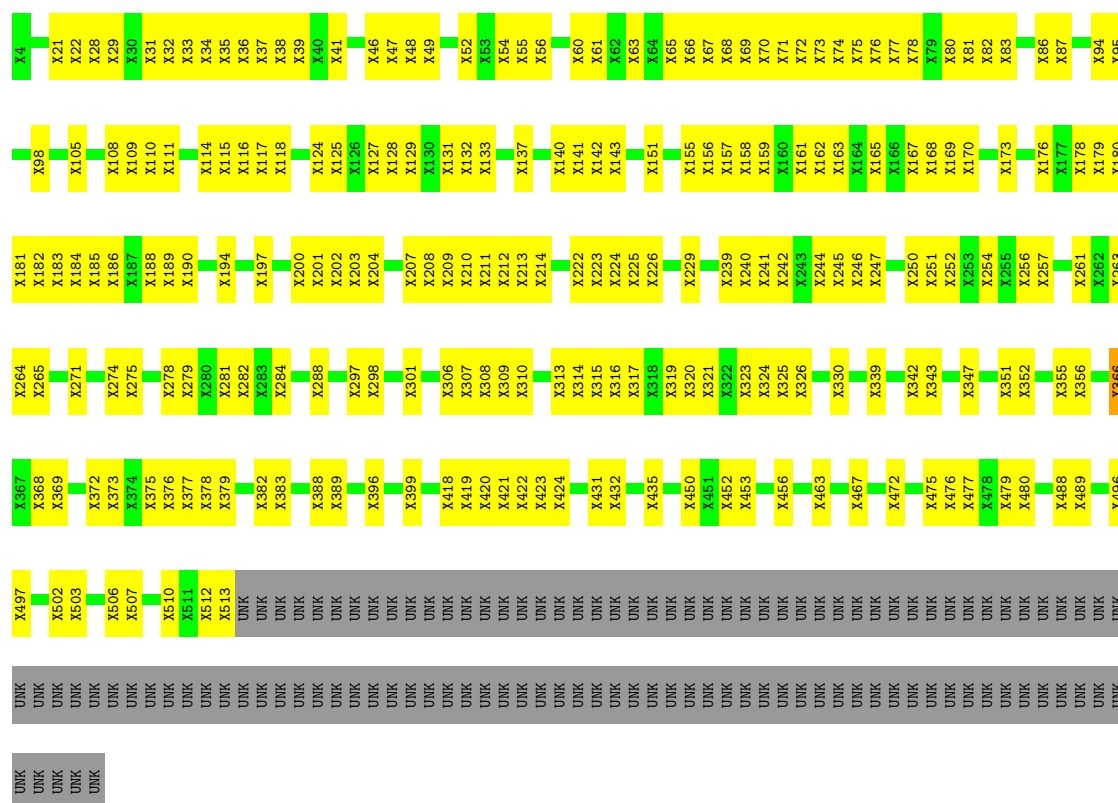
- Molecule 1: NADH-ubiquinone oxidoreductase chain 5





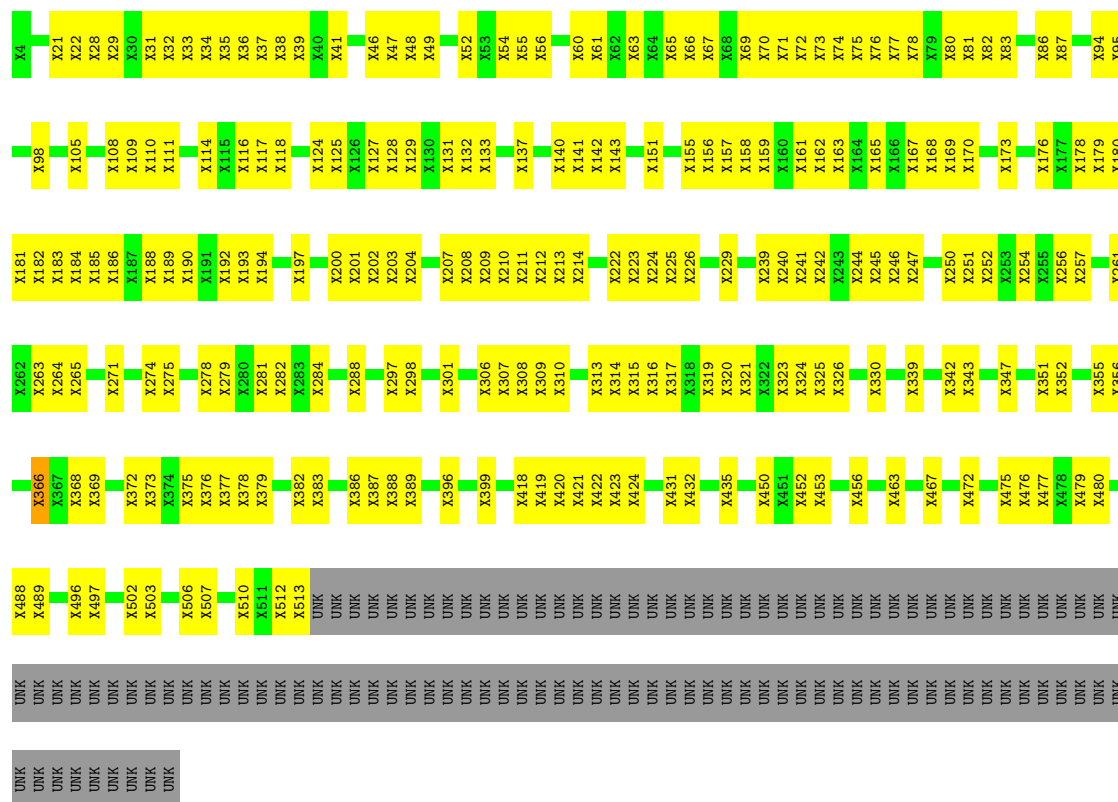
• Molecule 1: NADH-ubiquinone oxidoreductase chain 5

Chain L3: 44% 37% 19%

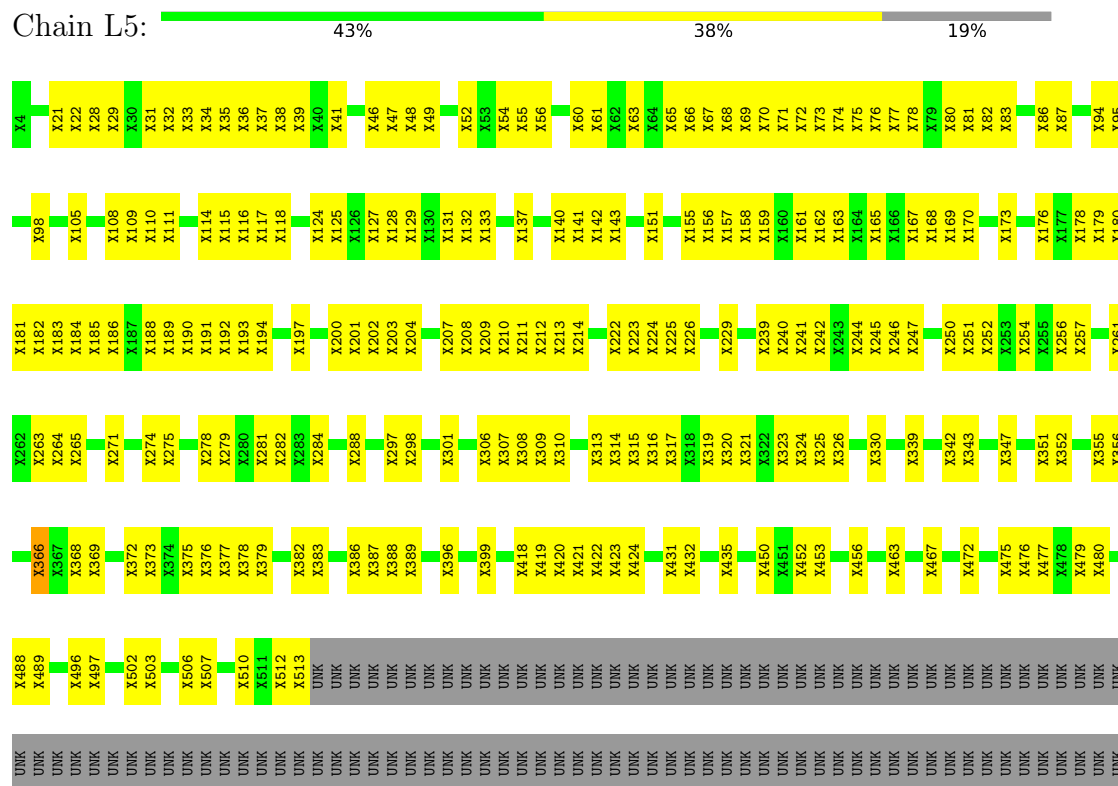


• Molecule 1: NADH-ubiquinone oxidoreductase chain 5

Chain L4: 44% 37% 19%



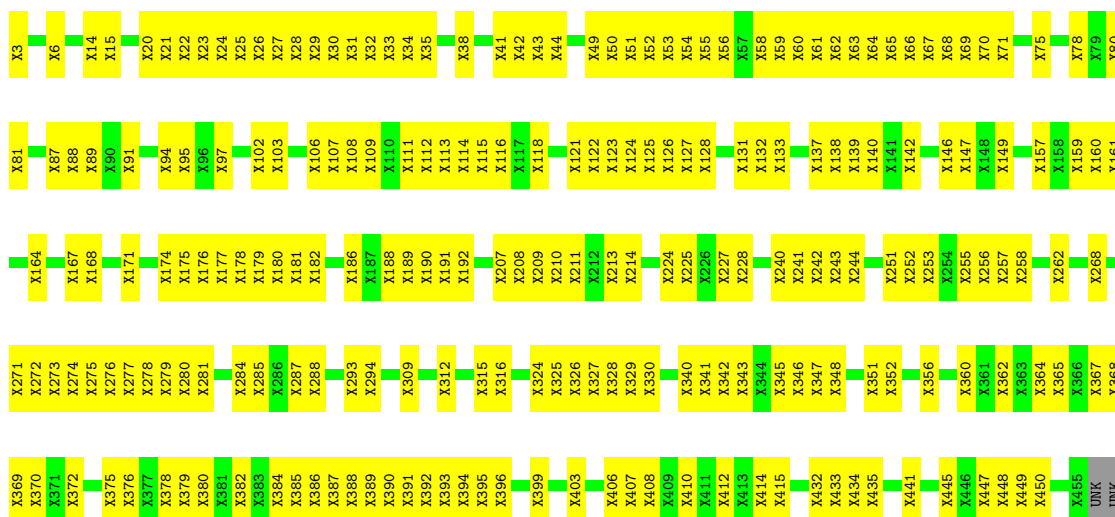
• Molecule 1: NADH-ubiquinone oxidoreductase chain 5



UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK

• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

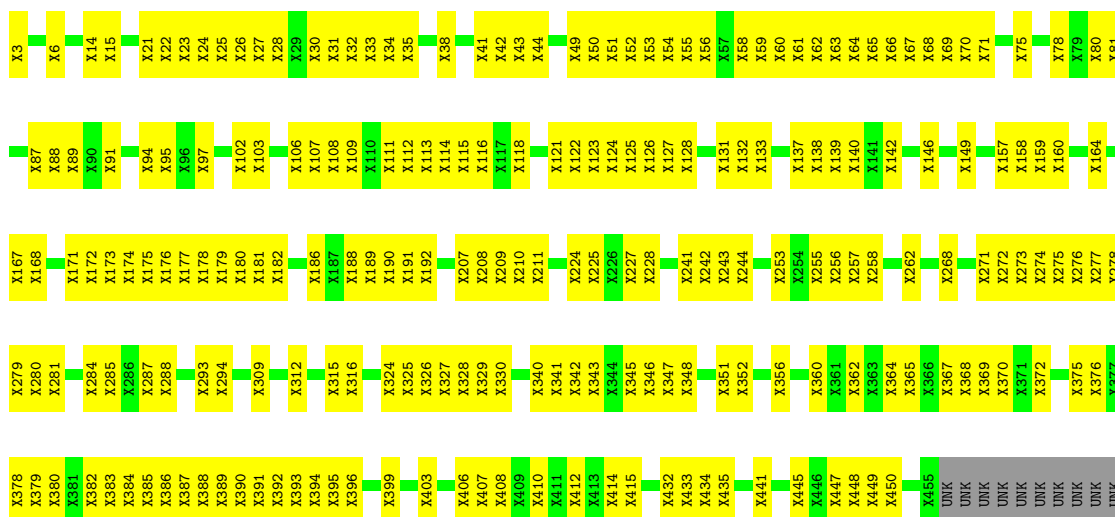
Chain M2:  47% 49% .



UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK

• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

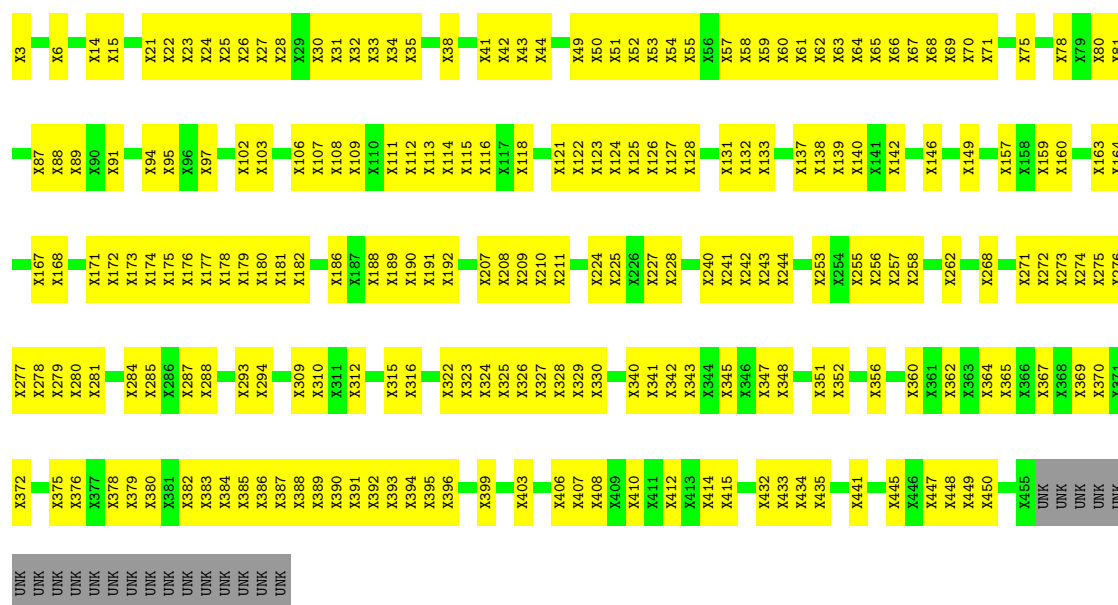
Chain M3:  48% 48% .



UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK
UNK

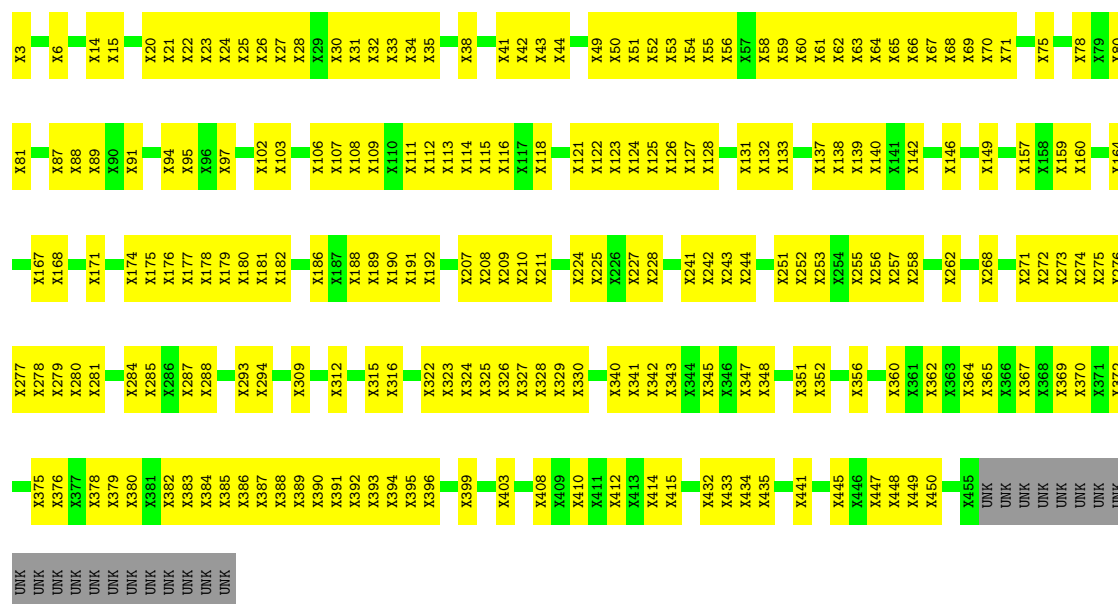
• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

Chain M4:  47% 48% .



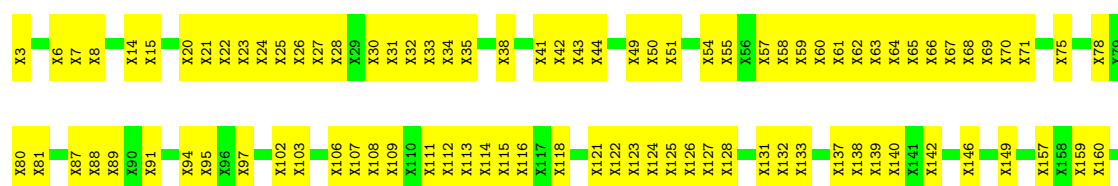
• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

Chain M5:

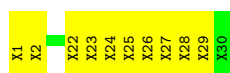


• Molecule 2: NADH-ubiquinone oxidoreductase chain 4

Chain M6:



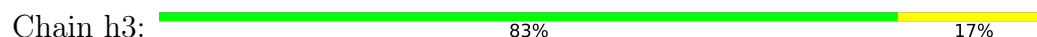




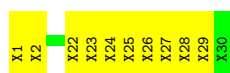
- Molecule 3: Unknown structure



- Molecule 3: Unknown structure



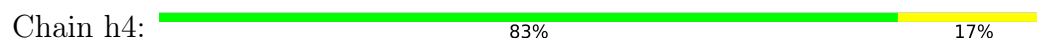
- Molecule 3: Unknown structure



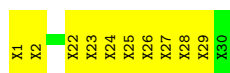
- Molecule 3: Unknown structure



- Molecule 3: Unknown structure



- Molecule 3: Unknown structure

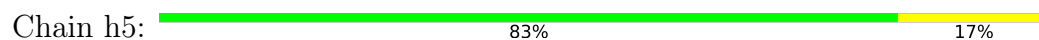


- Molecule 3: Unknown structure

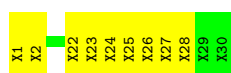




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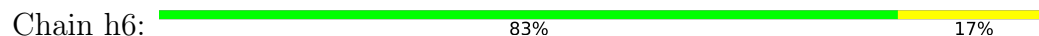
- Molecule 3: Unknown structure



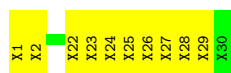
- Molecule 3: Unknown structure



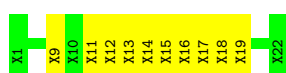
- Molecule 3: Unknown structure



- Molecule 3: Unknown structure

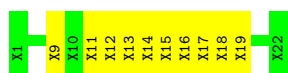


- Molecule 4: Unknown structure

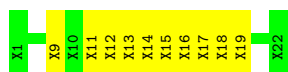


- Molecule 4: Unknown structure

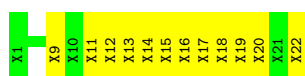




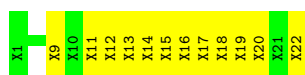
- Molecule 4: Unknown structure



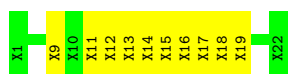
- Molecule 4: Unknown structure



- Molecule 4: Unknown structure



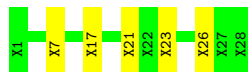
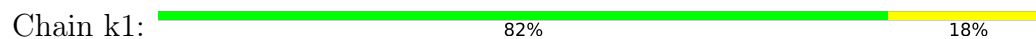
- Molecule 4: Unknown structure



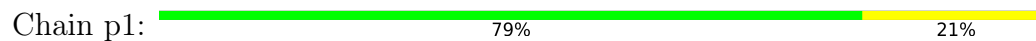
- Molecule 5: Unknown structure

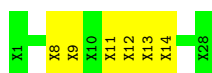


- Molecule 5: Unknown structure



- Molecule 5: Unknown structure





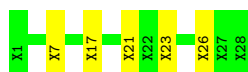
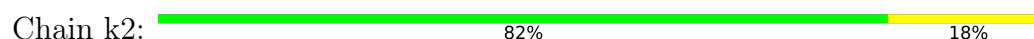
- Molecule 5: Unknown structure



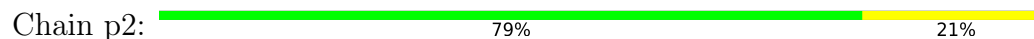
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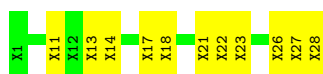
- Molecule 5: Unknown structure



- Molecule 5: Unknown structure



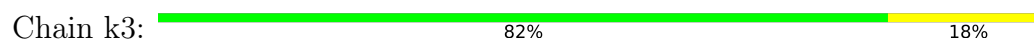
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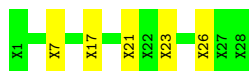


- Molecule 5: Unknown structure

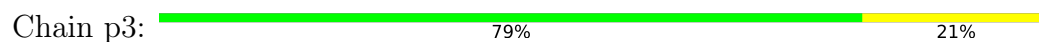


- Molecule 5: Unknown structure





- Molecule 5: Unknown structure



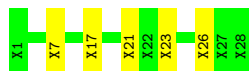
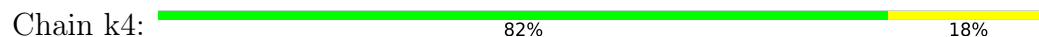
- Molecule 5: Unknown structure



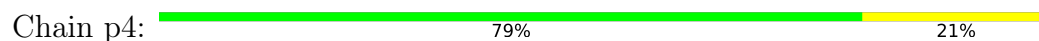
- Molecule 5: Unknown structure



- Molecule 5: Unknown structure



- Molecule 5: Unknown structure



- Molecule 5: Unknown structure

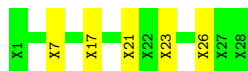
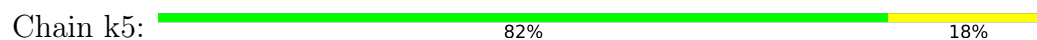


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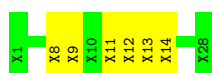
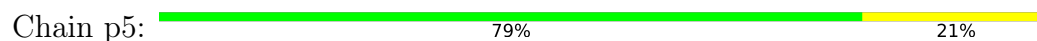




- Molecule 5: Unknown structure



- Molecule 5: Unknown structure



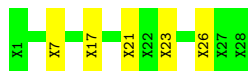
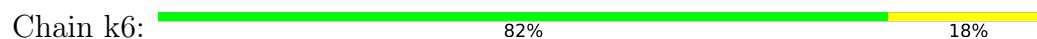
- Molecule 5: Unknown structure



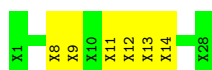
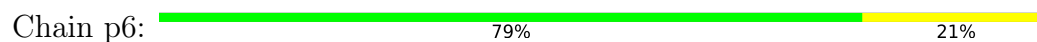
- Molecule 5: Unknown structure



- Molecule 5: Unknown structure



- Molecule 5: Unknown structure

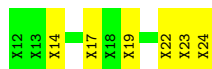


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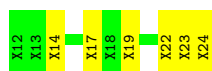




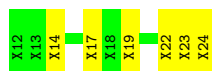
- Molecule 6: Unknown structure



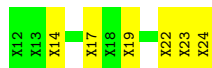
- Molecule 6: Unknown structure



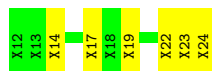
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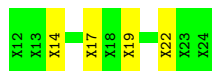
- Molecule 6: Unknown structure



- Molecule 6: Unknown structure

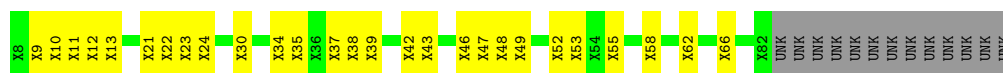


- Molecule 6: Unknown structure

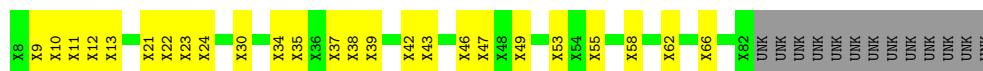


- Molecule 7: SDAP

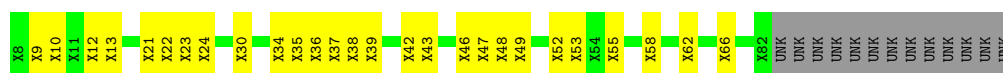




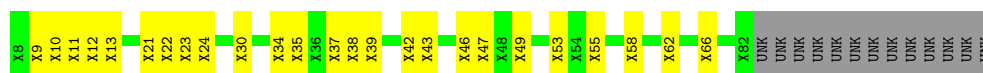
- Molecule 7: SDAP



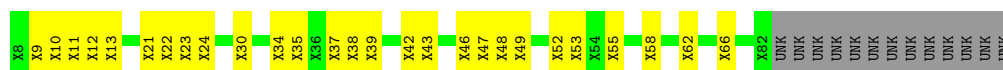
- Molecule 7: SDAP



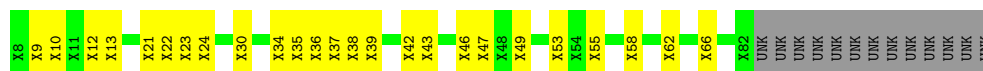
- Molecule 7: SDAP



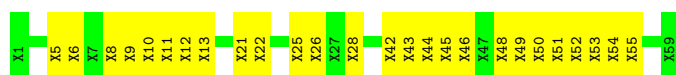
- Molecule 7: SDAP



- Molecule 7: SDAP

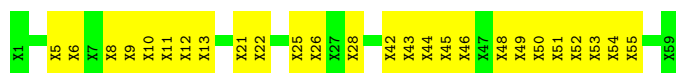


- Molecule 8: Unknown structure

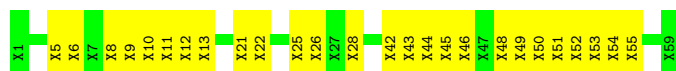


- Molecule 8: Unknown structure





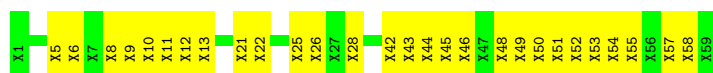
- Molecule 8: Unknown structure



- Molecule 8: Unknown structure



- Molecule 8: Unknown structure



- Molecule 8: Unknown structure



- Molecule 9: Unknown structure



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure



There are no outlier residues recorded for this chain.

- Molecule 9: Unknown structure



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:  54% 46%



- Molecule 10: Unknown structure

Chain t2:  56% 44%



- Molecule 10: Unknown structure

Chain t3:  53% 47%




- Molecule 10: Unknown structure

Chain t4:  54% 46%




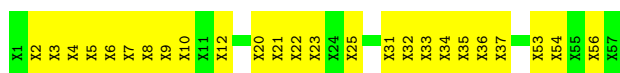
- Molecule 10: Unknown structure

Chain t5:  56% 44%



- Molecule 10: Unknown structure

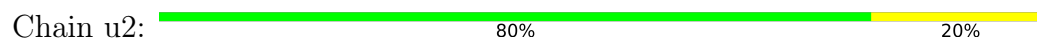
Chain t6:  56% 44%



- Molecule 11: Unknown structure



- Molecule 11: Unknown structure



- Molecule 11: Unknown structure



- Molecule 11: Unknown structure



- Molecule 11: Unknown structure



- Molecule 11: Unknown structure



- Molecule 12: Unknown structure





- Molecule 12: Unknown structure



- Molecule 12: Unknown structure



- Molecule 12: Unknown structure



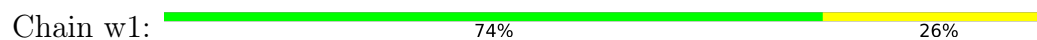
- Molecule 12: Unknown structure



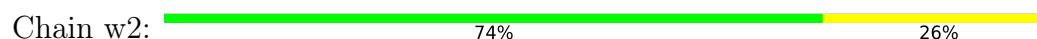
- Molecule 12: Unknown structure

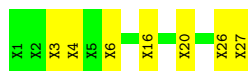


- Molecule 13: Unknown structure

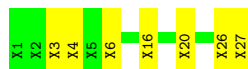
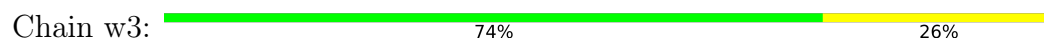


- Molecule 13: Unknown structure

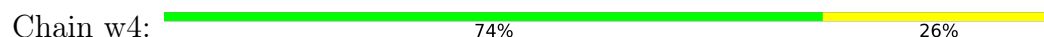




- Molecule 13: Unknown structure



- Molecule 13: Unknown structure



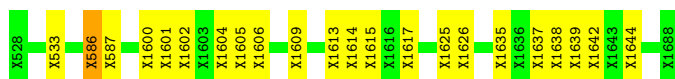
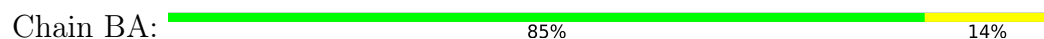
- Molecule 13: Unknown structure



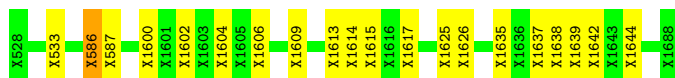
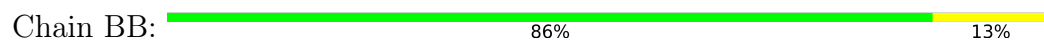
- Molecule 13: Unknown structure



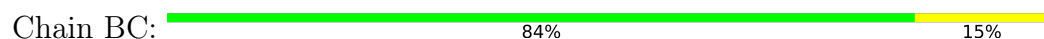
- Molecule 14: Unknown structure



- Molecule 14: Unknown structure

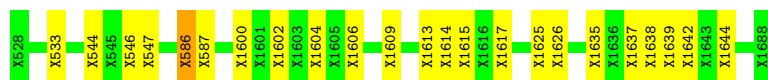
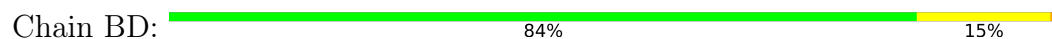


- Molecule 14: Unknown structure

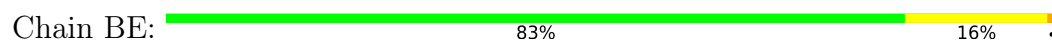




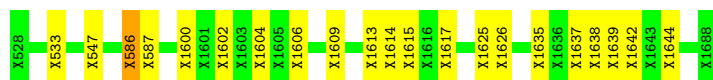
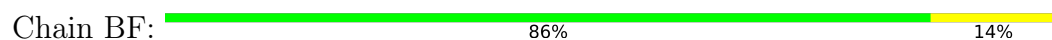
- Molecule 14: Unknown structure



- Molecule 14: Unknown structure



- 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 41.69 – 6.74	Depositor EDS
% Data completeness (in resolution range)	97.2 (41.69-6.74) 90.7 (41.69-6.74)	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 1.9_1692	Depositor
R, R_{free}	0.425 , 0.435 0.425 , 0.445	Depositor DCC
R_{free} test set	2228 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	495.7	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.15 , 731.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.037 for k,h,-l	Xtriage
F_o, F_c correlation	0.78	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	224	0
1	L2	2465	0	517	226	0
1	L3	2465	0	517	225	0
1	L4	2465	0	517	225	0
1	L5	2465	0	517	225	0
1	L6	2465	0	517	219	0
2	M1	2195	0	455	203	0
2	M2	2195	0	455	210	0
2	M3	2195	0	455	207	0
2	M4	2195	0	455	206	0
2	M5	2195	0	455	202	0
2	M6	2195	0	455	207	0
3	f1	150	0	33	7	0
3	f2	150	0	33	7	0
3	f3	150	0	33	7	0
3	f4	150	0	33	7	0
3	f5	150	0	33	7	0
3	f6	150	0	33	7	0
3	h1	150	0	32	8	0
3	h2	150	0	32	8	0
3	h3	150	0	32	8	0
3	h4	150	0	32	7	0
3	h5	150	0	32	8	0
3	h6	150	0	32	8	0
3	i1	150	0	33	14	0
3	i2	150	0	33	14	0
3	i3	150	0	33	13	0
3	i4	150	0	33	14	0
3	i5	150	0	33	13	0
3	i6	150	0	33	14	0
4	g1	110	0	24	9	0
4	g2	110	0	24	9	0
4	g3	110	0	24	9	0
4	g4	110	0	24	10	0
4	g5	110	0	24	10	0
4	g6	110	0	24	9	0
5	j1	140	0	33	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	j2	140	0	33	9	0
5	j3	140	0	33	9	0
5	j4	140	0	33	9	0
5	j5	140	0	33	9	0
5	j6	140	0	33	9	0
5	k1	140	0	30	3	0
5	k2	140	0	30	3	0
5	k3	140	0	30	3	0
5	k4	140	0	30	3	0
5	k5	140	0	30	3	0
5	k6	140	0	30	3	0
5	p1	140	0	30	4	0
5	p2	140	0	30	4	0
5	p3	140	0	30	4	0
5	p4	140	0	30	4	0
5	p5	140	0	30	4	0
5	p6	140	0	30	4	0
5	s1	140	0	31	10	0
5	s2	140	0	31	10	0
5	s3	140	0	31	11	0
5	s4	140	0	31	11	0
5	s5	140	0	31	11	0
5	s6	140	0	31	10	0
6	l1	65	0	15	3	0
6	l2	65	0	15	3	0
6	l3	65	0	15	3	0
6	l4	65	0	15	3	0
6	l5	65	0	15	3	0
6	l6	65	0	15	2	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	26	0
8	n2	295	0	61	26	0
8	n3	295	0	61	25	0
8	n4	295	0	61	27	0
8	n5	295	0	61	27	0
8	n6	295	0	61	24	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	23	0
10	t2	285	0	61	22	0
10	t3	285	0	61	23	0
10	t4	285	0	61	24	0
10	t5	285	0	61	22	0
10	t6	285	0	61	22	0
11	u1	75	0	17	4	0
11	u2	75	0	17	3	0
11	u3	75	0	17	4	0
11	u4	75	0	17	4	0
11	u5	75	0	17	4	0
11	u6	75	0	17	4	0
12	v1	160	0	34	11	0
12	v2	160	0	34	11	0
12	v3	160	0	34	11	0
12	v4	160	0	34	11	0
12	v5	160	0	34	11	0
12	v6	160	0	34	11	0
13	w1	135	0	30	5	0
13	w2	135	0	29	5	0
13	w3	135	0	29	5	0
13	w4	135	0	29	5	0
13	w5	135	0	29	5	0
13	w6	135	0	29	5	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	3668	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 3668 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 oligosaccharides 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	BA	9
14	BB	9
14	BC	9
14	BD	9
14	BE	9
14	BF	9
1	L4	4
1	L1	4
1	L2	4
1	L3	4
1	L5	4
1	L6	4
2	M1	1
2	M2	1
2	M3	1
2	M4	1
2	M5	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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 oligosaccharides 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.