



Full wwPDB EM Validation Report ⓘ

Jan 7, 2025 – 04:38 PM JST

PDB ID : 8X03
EMDB ID : EMD-37969
Title : Structure of mitochondrial soluble protein
Authors : Zhang, S.S.; Chen, M.F.
Deposited on : 2023-11-03
Resolution : 3.66 Å(reported)

This is a Full wwPDB EM Validation 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

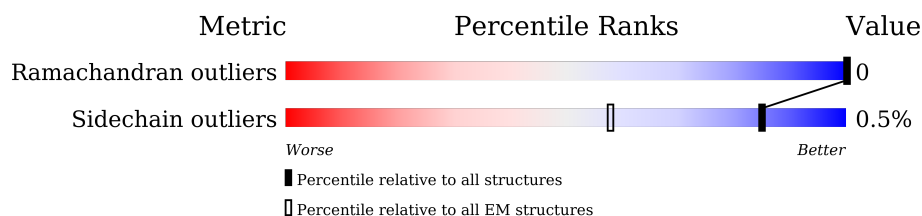
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.66 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)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain	
1	0	647	<div><div></div></div> 35%	65%
1	1	647	<div><div></div></div> 35%	65%
1	2	647	<div><div></div></div> 35%	65%
1	3	647	<div><div></div></div> 35%	65%
1	4	647	<div><div></div></div> 35%	65%
1	5	647	<div><div></div></div> 35%	65%
1	6	647	<div><div></div></div> 35%	65%
1	7	647	<div><div></div></div> 35%	65%
1	A	647	<div><div></div></div> 35%	65%


























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Mol	Chain	Length	Quality of chain	
1	B	647		
1	C	647		
1	D	647		
1	E	647		
1	F	647		
1	G	647		
1	H	647		
1	I	647		
1	J	647		
1	K	647		
1	L	647		
1	M	647		
1	N	647		
1	O	647		
1	P	647		
1	Q	647		
1	R	647		
1	S	647		
1	T	647		
1	U	647		
1	V	647		
1	W	647		
1	X	647		
1	Y	647		
1	Z	647		

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Mol	Chain	Length	Quality of chain	
1	a	647		
1	b	647		
1	c	647		
1	d	647		
1	e	647		
1	f	647		
1	g	647		
1	h	647		
1	i	647		
1	j	647		
1	k	647		
1	l	647		
1	m	647		
1	n	647		
1	o	647		
1	p	647		
1	q	647		
1	r	647		
1	s	647		
1	t	647		
1	u	647		
1	v	647		
1	w	647		
1	x	647		
1	y	647		

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Mol	Chain	Length	Quality of chain
1	z	647	<div><div></div><div>35%</div><div>65%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 105540 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Acetyltransferase component of pyruvate dehydrogenase complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	B	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	C	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	D	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	E	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	F	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	G	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	H	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	I	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	J	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	K	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	L	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	M	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	N	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	O	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	P	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	R	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	S	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	T	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	U	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	V	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	W	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	X	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	Y	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	Z	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	a	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	b	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	c	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	d	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	e	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	f	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	g	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	h	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	i	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	j	229	Total 1759	C 1121	N 304	O 324	S 10	0	0
1	k	229	Total 1759	C 1121	N 304	O 324	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	l	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	m	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	n	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	o	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	p	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	q	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	r	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	s	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	t	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	u	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	v	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	w	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	x	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	y	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	z	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	0	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	1	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	2	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	3	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	4	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	5	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		

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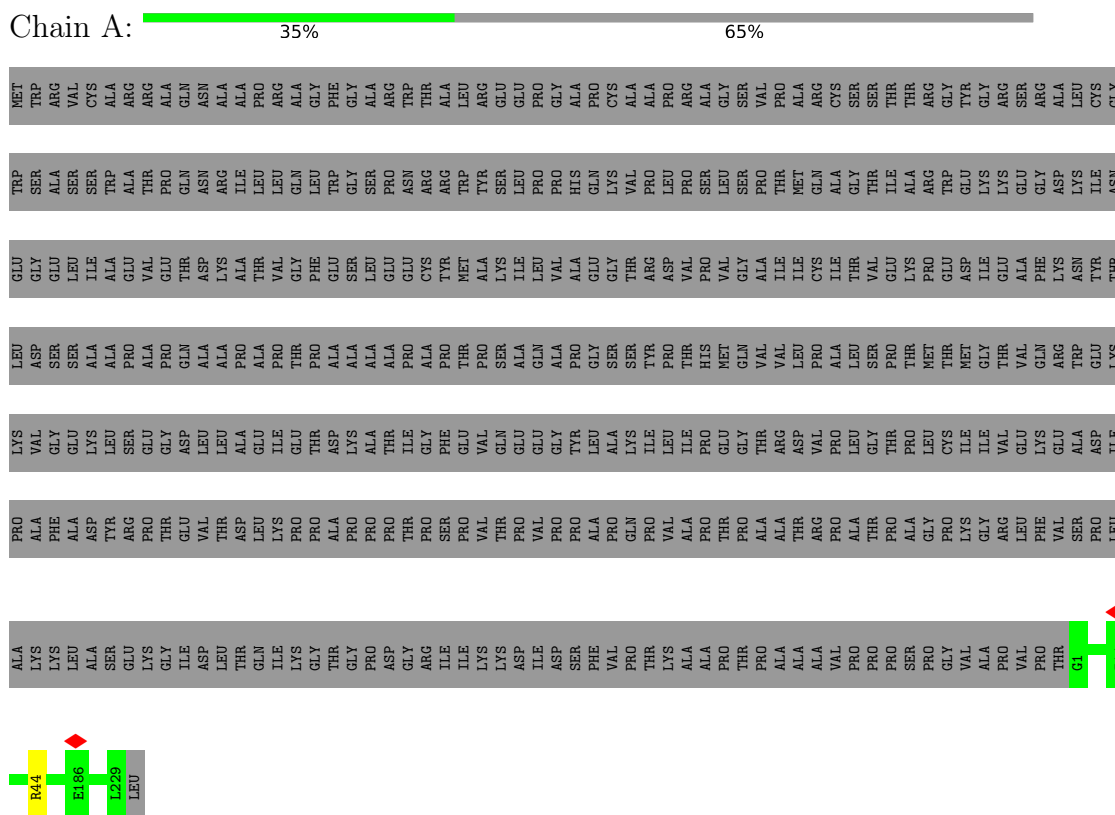
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	6	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		
1	7	229	Total	C	N	O	S	0	0
			1759	1121	304	324	10		

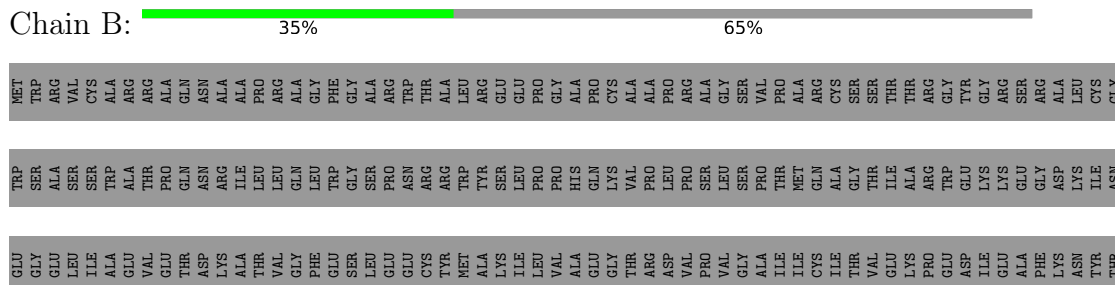
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain C:  35% 65%

[illegible]

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain D: 35% 65%

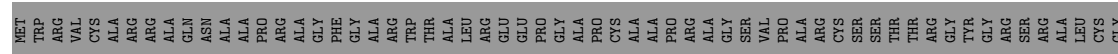
MET	TRP	ALA	ARG	VAL	CYS	ARG	ALA	ARG	ALA	ASN	GLN	ALA	ALA	LEU	GLY	PHI	GLY	ALA	ARG	TRP	THR	ARG	ALA	LEU	GLY	GLU	PRO	PRO	GLY	ALA	ALA	CYS	PRO	VAL	PRO	PRO	ARG	ARG	ALA	ALA	GLY	GLY	SER	SER	VAL	THR	THR	THR	GLY	TYR	ARG	ARG	ALA	CYS	LEU	CYS	GLY		
TRP	SER	ALA	SER	SER	SER	TRP	ALA	TRP	THR	PRO	GLN	ASN	ARG	ILE	LEU	LEU	GLN	TRP	GLY	SER	PRO	ASN	ARG	TRP	THR	SER	LEU	PRO	PRO	HIS	GLN	LYS	VAL	PRO	LEU	PRO	PRO	SER	LEU	GLN	MET	THR	THR	SER	PRO	GLY	ALA	ARG	TRP	GLU	LYS	LYS	GLY	ASP	LYS	ILE	THR	CYS	GLY

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain E: 35% 65%

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

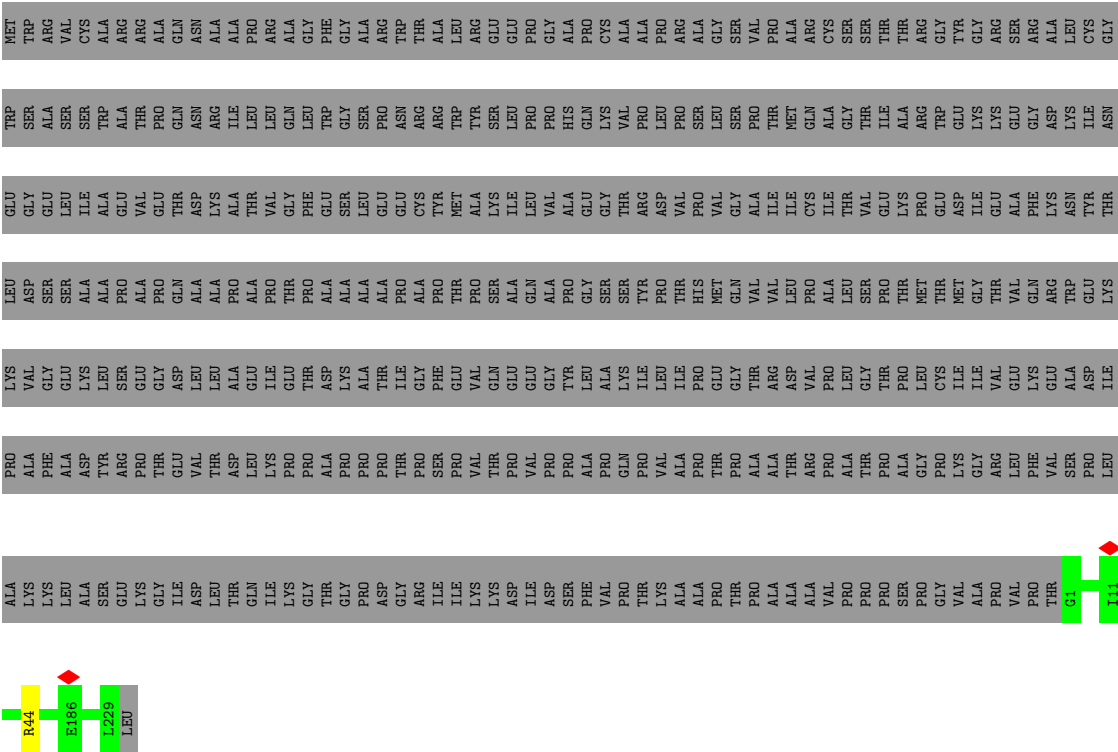
Chain F:  35% 65%



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex





● Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain I: 35% 65%



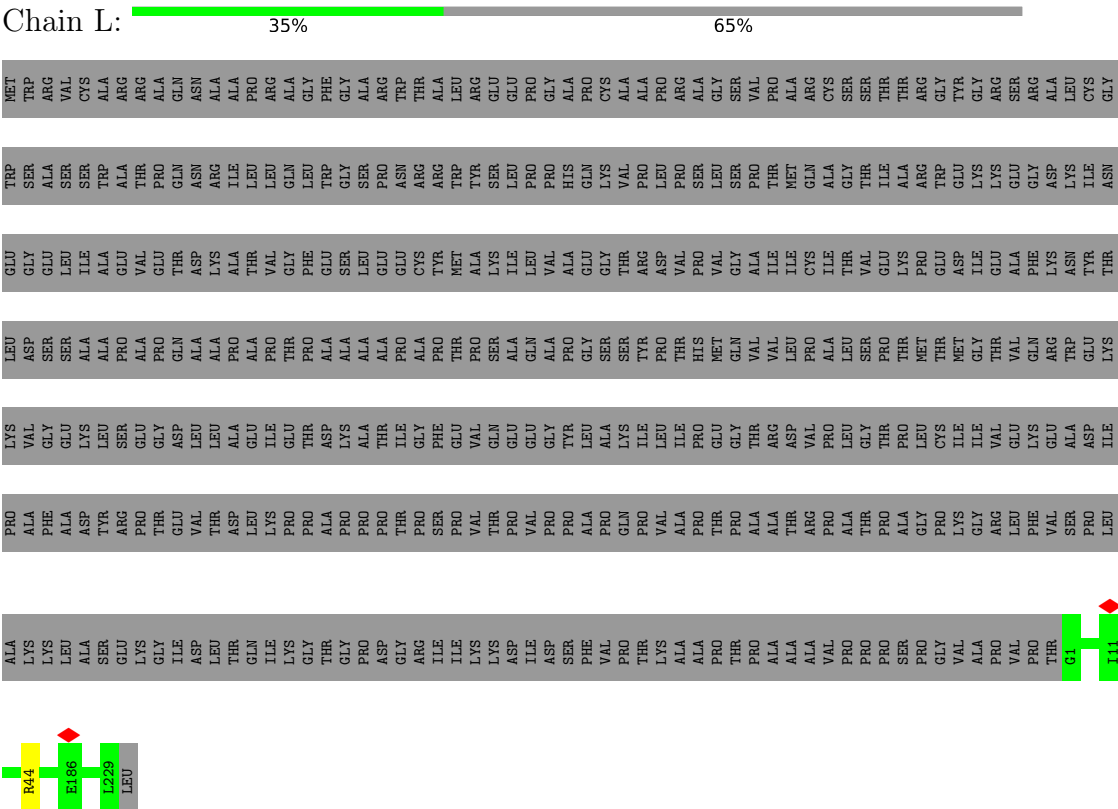
● Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

65%

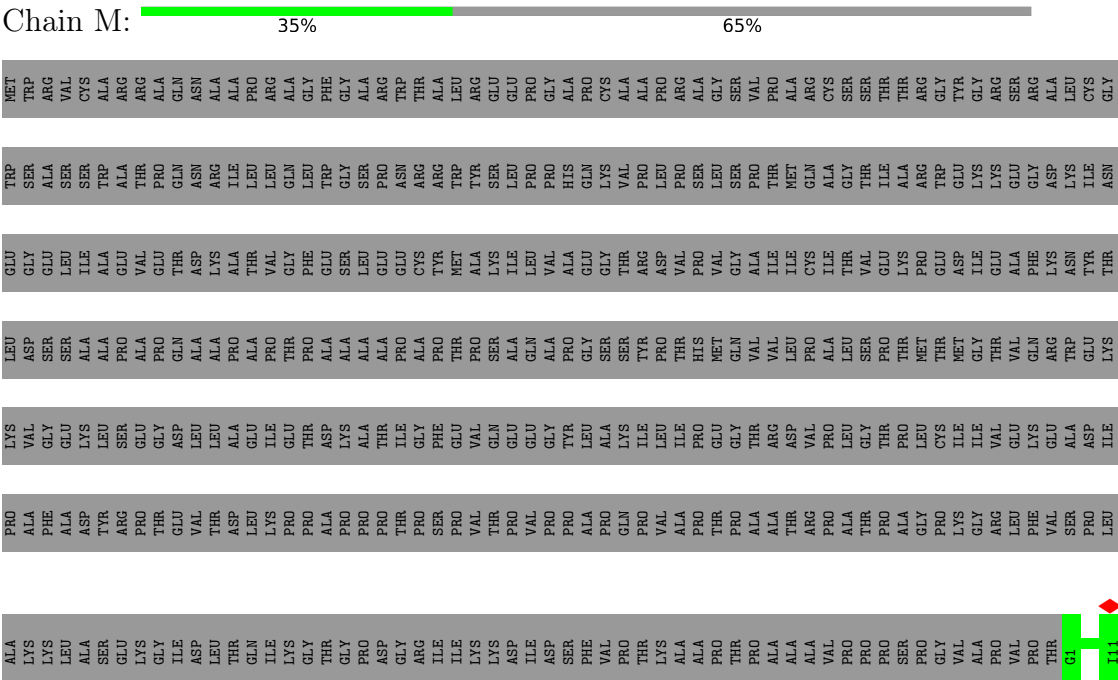
A diagram of a 4-bit register. The bits are labeled R44, E186, L229, and LEU. A red diamond is positioned above the E186 bit.

- 65%

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

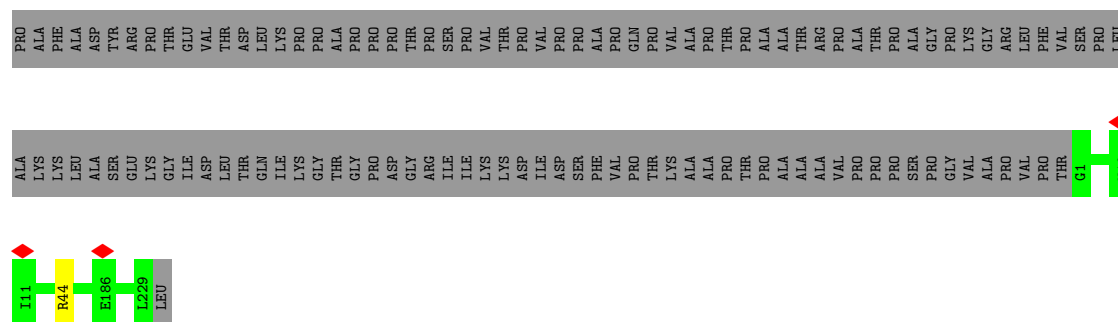
Chain N: 35% 65%

[illegible]

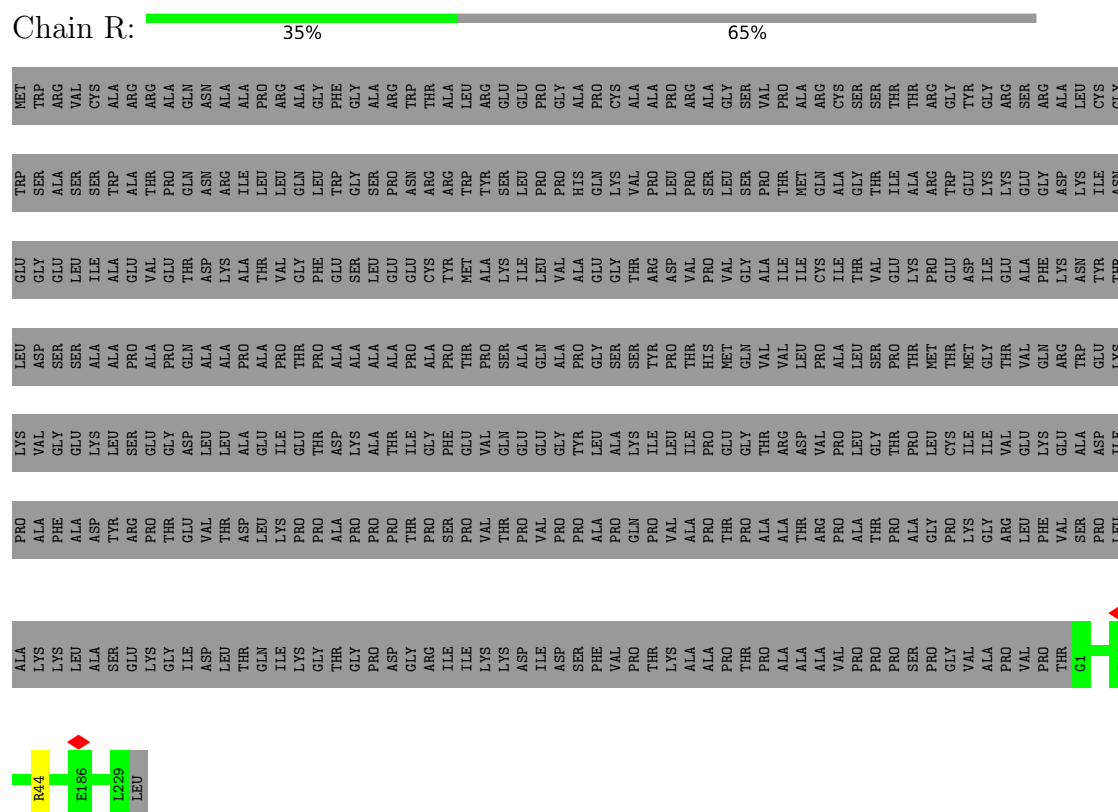
- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain 0:  35% 65%

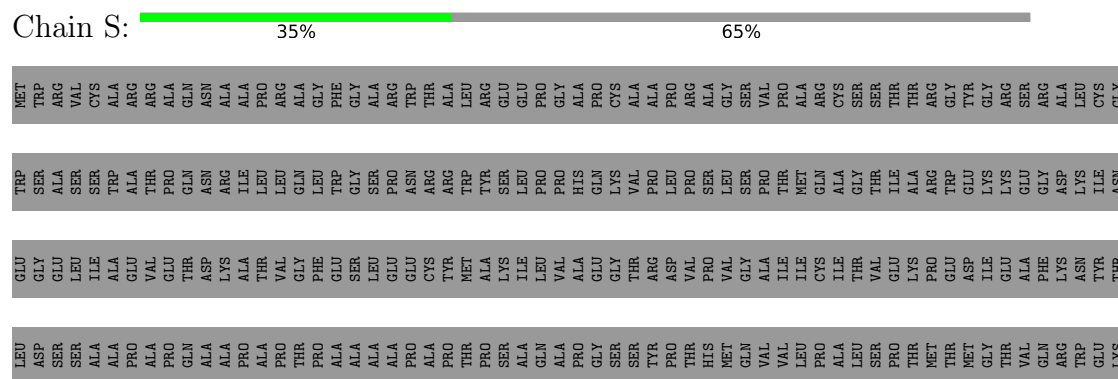
PRO	LYS	LEU	GLU	LEU	ASP	TRP	MET
PHE	GLY	SER	GLY	SER	ASP	SER	ARG
ALA	GLU	SER	LEU	SER	SER	SER	VAL
ASP	LYS	ALA	ILE	ALA	ALA	ILE	CYS
TYR	LEU	ALA	ALA	ALA	PRO	TRP	ALA
ARG	SER	PRO	GLU	VAL	ALA	ALA	ARG
PRO	GLU	PRO	VAL	VAL	GLU	PRO	ALA
THR	GLY	GLN	THR	THR	THR	GLN	ALA
GLU	ASP	ALA	THR	ALA	ASP	ASN	ASN
VAL	LEU	ALA	LYS	LYS	ALA	ARG	ALA
THR	LEU	ALA	ALA	PRO	ALA	ILE	ALA
ASP	ALA	ALA	ALA	ALA	ALA	LEU	PRO
ASP	GLU	ALA	THR	THR	THR	LEU	ARG
LEU	ILE	PRO	VAL	VAL	VAL	GLN	ALA
PRO	LYS	THR	GLY	PRO	THR	GLY	ALA
PRO	THR	PRO	PHE	PRO	THR	LEU	GLY
ALA	GLU	ALA	ASP	ALA	ALA	TRP	PHE
PRO	LYS	ALA	LYS	ALA	ALA	GLY	GLY
PRO	THR	ALA	THR	ALA	ALA	GLY	ALA
ASN	ILE	ALA	GLU	ALA	PRO	ASN	TRP
PRO	GLY	ALA	CYS	ALA	PRO	ARG	THR
SER	PHE	PRO	TTR	THR	THR	ARG	LEU
GLU	GLU	THR	MET	THR	THR	TRP	ALA
PRO	VAL	PRO	ALA	ALA	ALA	ALA	ALA
THR	GLN	SER	LYS	SER	SER	SER	GLY
VAL	GLU	ALA	ILE	ALA	ALA	LEU	PRO
PRO	GLY	ALA	LEU	VAL	ALA	PRO	GLY
PRO	TYR	PRO	ALA	ALA	PRO	HIS	ALA
ALA	LEU	GLY	GLU	GLY	GLY	GLN	PRO
ALA	ALA	SER	GLY	SER	SER	VAL	CYS
GLN	LYS	THR	THR	THR	THR	VAL	ALA
PRO	ILE	TYR	ARG	ARG	PRO	PRO	ALA
VAL	LEU	PRO	ASP	ASP	LEU	LEU	ALA
THR	ILE	THR	VAL	VAL	THR	THR	ARG
ALA	LEU	THR	ILE	ILE	THR	GLY	ALA
ALA	PRO	THR	GLY	SER	GLN	SER	SER
ALA	THR	THR	THR	PRO	VAL	PRO	VAL
THR	PRO	THR	GLU	VAL	VAL	THR	PRO
THR	PRO	THR	LYS	ILE	ILE	ILE	ALA
ALA	PRO	THR	LYS	THR	THR	THR	THR
ALA	GLY	VAL	GLY	THR	GLY	GLY	GLY
ARG	VAL	THR	THR	THR	THR	LYS	ARG
LEU	LYS	VAL	VAL	VAL	GLN	GLY	LEU
PHE	GLY	GLN	PHE	PHE	THR	GLY	ARG
VAL	GLU	ARG	LYS	LYS	ARG	ASP	ALA
SER	ALA	TRP	ASN	ASN	TRP	LYS	LEU
PRO	ASP	GLU	TYR	THR	GLU	ILE	CYS

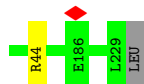


- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

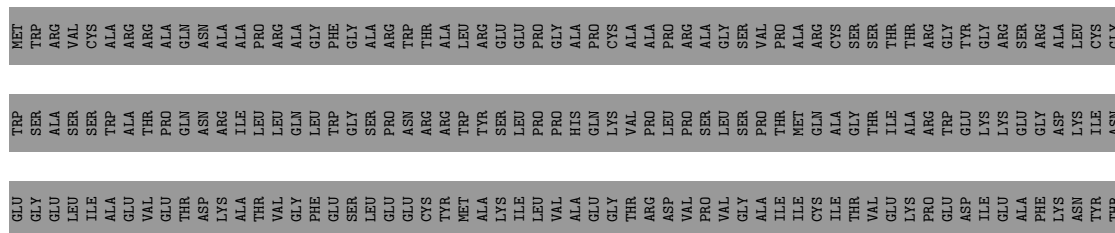




- Chain T:  35% 65%



- Chain U:  35% 65%



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain V: 35% 65%

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain W: 35% 65%

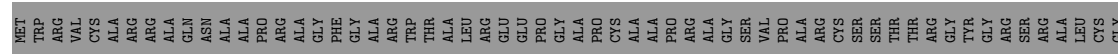
MET	TRP	ALA	ARG	VAL	CYS	ARG	ALA	ARG	ALA	ASN	GLN	ALA	ALA	LEU	GLY	PHI	GLY	ALA	ARG	TRP	THR	ARG	ALA	LEU	GLU	GLY	PRO	GLY	ALA	ALA	VAL	ALA	ALA	PRO	ARG	ARG	ALA	GLY	GLY	SER	SER	VAL	PRO	ARG	ALA	ARG	CYS	SER	SER	THR	THR	GLY	TYR	ARG	ARG	CYS	LEU	CYS	GLY
TRP	SER	ALA	SER	SER	SER	TRP	ALA	TRP	THR	PRO	GLN	ASN	ARG	ILE	LEU	LEU	GLN	TRP	GLY	SER	PRO	ASN	ARG	TRP	THR	SER	PRO	PRO	HIS	GLN	LYS	VAL	PRO	LEU	PRO	SER	PRO	THR	THR	MET	GLN	GLY	ALA	ILE	ARG	TRP	GLU	LYS	LYS	GLY	ASP	LYS	ILE	THR	CYS	GLY			

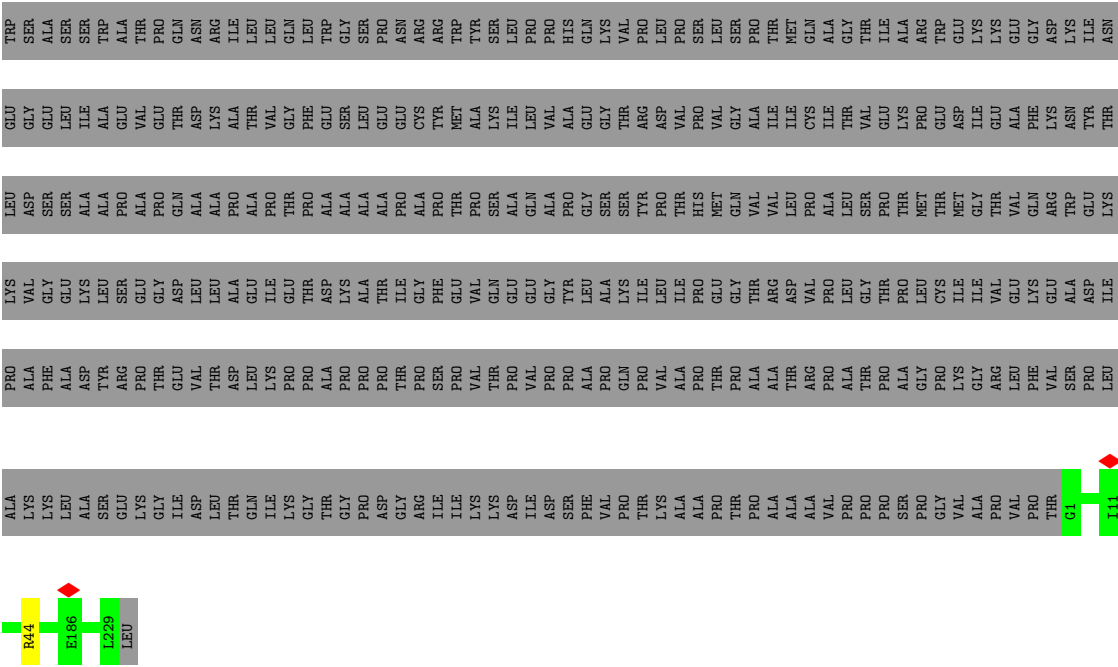
- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain X: 35% 65%

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain Y:  35% 65%



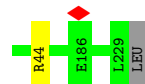


● Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



● Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex





- Chain b: 35% 65%



- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

65%

- 65%

- [illegible]

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

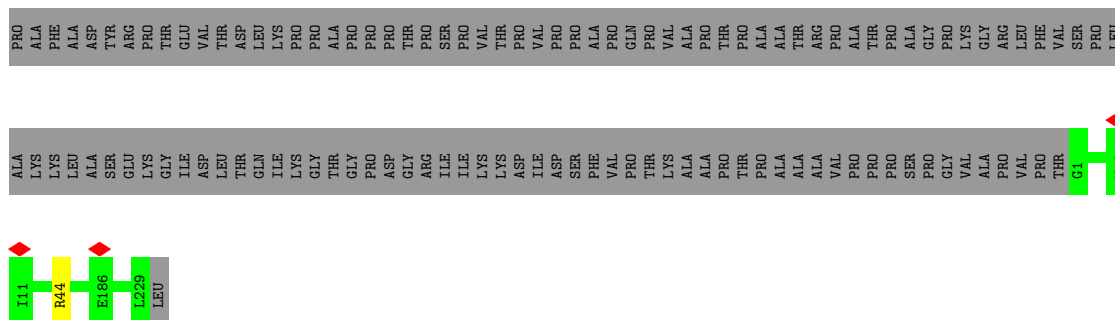
Chain g:  35% 65%

ALA	LYS	ALA	LYS	VAL	PRO	LYS	LEU	ASP	GLY	LEU	ASP	GLY	TRP	MET
LYS	LYS	PHE	ALA	GLY	ASP	VAL	GLY	SER	GLY	SER	GLY	ALA	SER	ARG
LEU	LEU	ALA	ASP	GLY	ALA	LYS	LYS	SER	LEU	SER	ILE	SER	SER	VAL
ALA	SER	THR	THR	LEU	LEU	LEU	LEU	ALA	ALA	ALA	ALA	TRP	TRP	CYS
GLY	GLY	ARG	ARG	SER	PRO	SER	PRO	PRO	GLU	GLU	VAL	ALA	ALA	ARG
LYS	GLY	THR	THR	PRO	THR	GLY	GLY	ALA	VAL	THR	THR	PRO	ALA	ALA
ILE	ILE	GLY	GLY	ASP	VAL	GLY	ASP	GLN	THR	THR	THR	GLN	GLN	ALA
ASP	ASP	VAL	THR	LEU	THR	LEU	LEU	ALA	ALA	ASP	ASP	ASN	ASN	ASN
LEU	LEU	ASP	THR	LEU	THR	LEU	LEU	ALA	LYS	LYS	ASN	ASN	ASN	ALA
THR	THR	ASP	THR	ALA	ASP	ALA	ALA	PRO	ALA	ALA	ILE	ILE	ALA	ALA
ILE	ILE	PRO	PRO	GLY	PRO	LYS	LYS	ALA	ALA	SER	THR	GLY	GLY	ARG
PRO	PRO	PRO	PRO	THR	PRO	THR	THR	ALA	LEU	GLU	VAL	LEU	LEU	ARG
ASP	GLY	THR	THR	THR	THR	ILE	ILE	PRO	GLU	GLU	GLY	GLN	GLN	ALA
ARG	ARG	PRO	THR	THR	THR	GLY	GLY	ALA	ALA	ALA	PHE	THR	THR	THR
ILE	ILE	SER	SER	PHE	SER	PHE	THR	ALA	THR	TYR	ARG	ARG	ARG	ALA
ILE	ILE	PRO	PRO	GLY	PRO	GLY	GLY	THR	THR	TRP	TRP	TRP	TRP	ALA
LYS	LYS	VAL	VAL	GLN	VAL	GLN	GLN	SER	LYS	SER	ALA	TYR	ALA	GLY
LYS	LYS	THR	THR	GLY	PRO	GLY	GLY	ALA	ILE	LEU	ILE	LEU	GLU	GLY
ASP	ILE	VAL	VAL	GLY	VAL	GLY	GLY	GLN	LEU	PRO	VAL	PRO	PRO	PRO
ILE	ILE	VAL	VAL	GLY	VAL	GLY	GLY	ALA	VAL	PRO	ASP	PRO	PRO	GLY
ASP	ASP	PRO	PRO	GLY	PRO	GLY	GLY	ALA	ALA	ALA	THR	THR	THR	THR
SER	PHE	ALA	ALA	LEU	ALA	LEU	LEU	THR	VAL	LEU	THR	THR	THR	THR
VAL	VAL	PRO	PRO	ALA	PRO	ALA	ALA	PRO	VAL	PRO	VAL	GLN	GLN	ARG
PRO	PRO	THR	THR	GLY	THR	THR	THR	HIS	VAL	PRO	VAL	ARG	ARG	ARG
THR	THR	THR	THR	GLY	THR	ILE	GLY	GLN	ARG	PRO	GLY	VAL	VAL	ALA
LYS	LYS	VAL	VAL	ILE	VAL	ILE	LEU	TVR	THR	ASP	THR	THR	THR	ALA
ALA	ALA	PRO	PRO	THR	VAL	THR	THR	PRO	THR	ASP	THR	THR	THR	ALA
ALA	ALA	PRO	PRO	ILE	ALA	ILE	LEU	THR	THR	VAL	VAL	THR	THR	ALA
PRO	PRO	THR	THR	GLY	THR	GLY	GLY	HIS	PRO	PRO	VAL	GLY	GLY	ALA
THR	THR	THR	THR	GLY	THR	THR	THR	MET	VAL	VAL	VAL	LEU	SER	SER
PRO	PRO	ALA	ALA	THR	ALA	THR	THR	GLN	SER	GLY	ALA	PRO	VAL	VAL
ALA	ALA	THR	THR	ARG	ALA	ARG	ILE	VAL	ILE	THR	THR	THR	THR	PRO
ALA	ALA	ARG	ARG	ASP	THR	ASP	ILE	LEU	ILE	ILE	THR	THR	THR	PRO
ALA	ALA	THR	THR	VAL	THR	VAL	VAL	LEU	ILE	ILE	THR	THR	THR	ALA
VAL	VAL	PRO	PRO	VAL	PRO	VAL	CYS	PRO	CYS	GLN	GLN	MET	ALA	ALA
VAL	VAL	PRO	PRO	PRO	PRO	PRO	VAL	PRO	VAL	VAL	VAL	GLY	CYS	ARG
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain h: 35% 65%

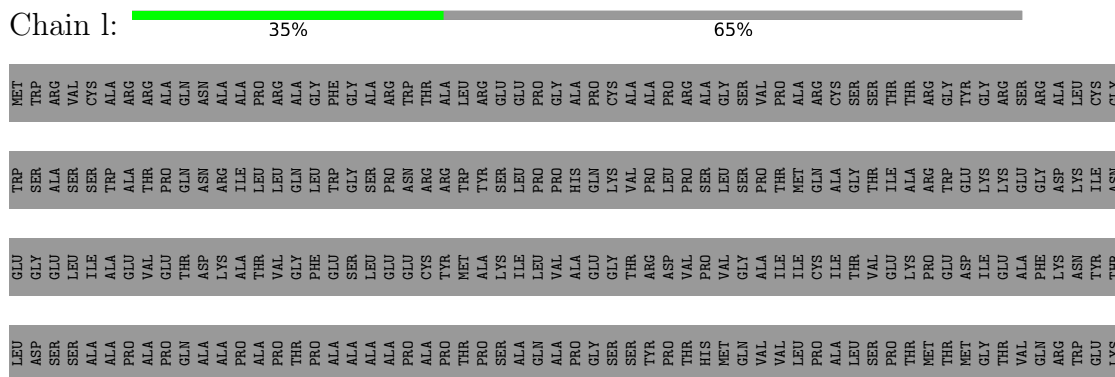
[illegible]

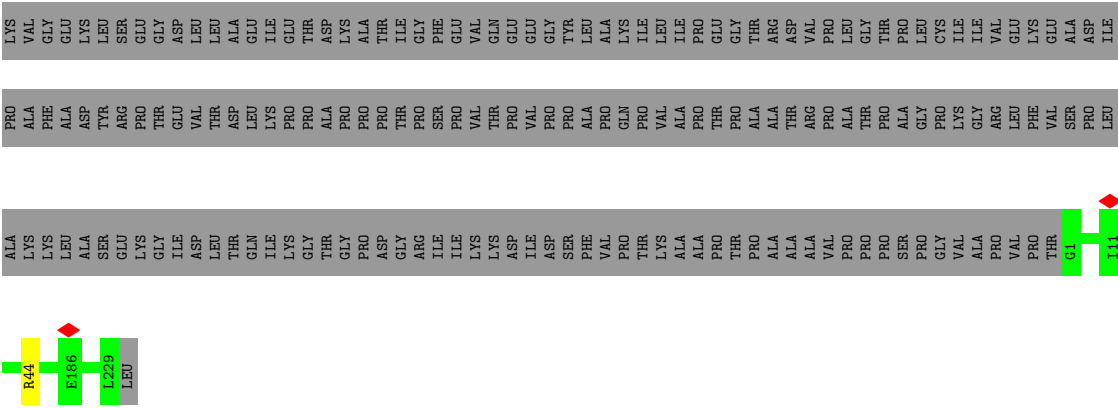


- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



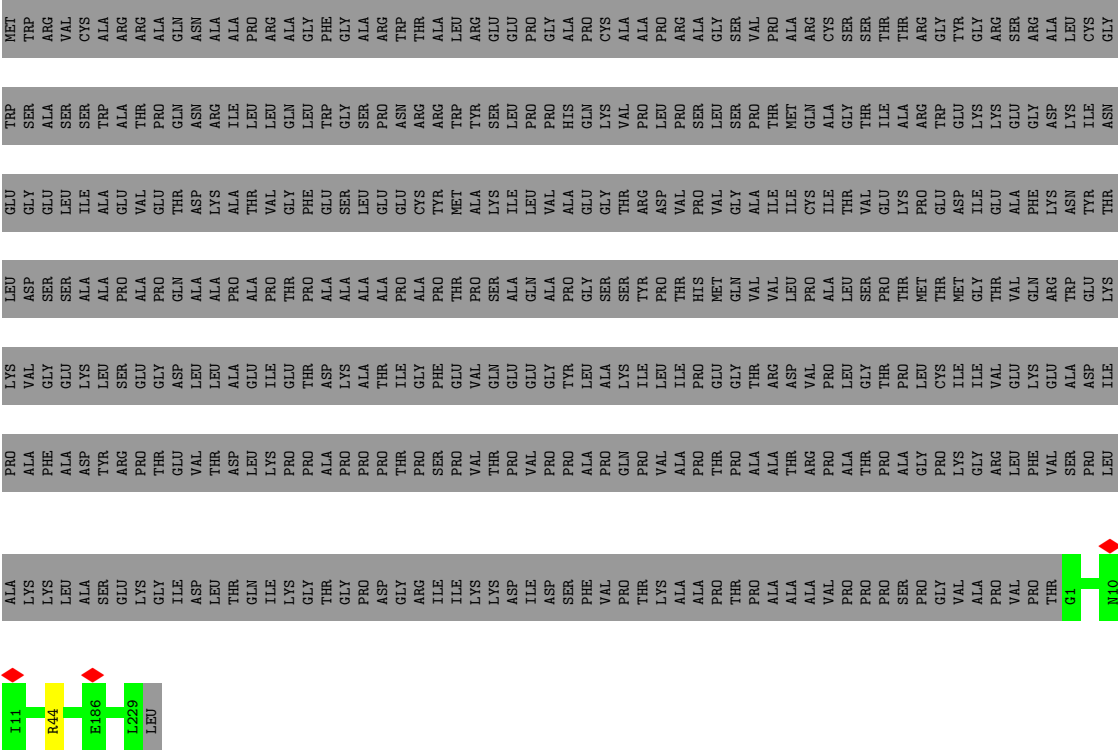
- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex





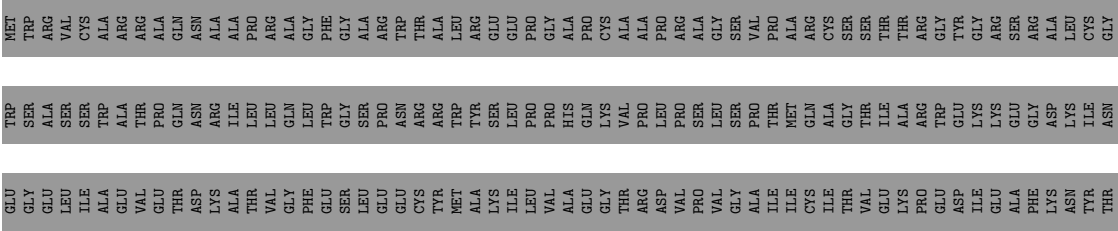
● Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain m: 35% 65%



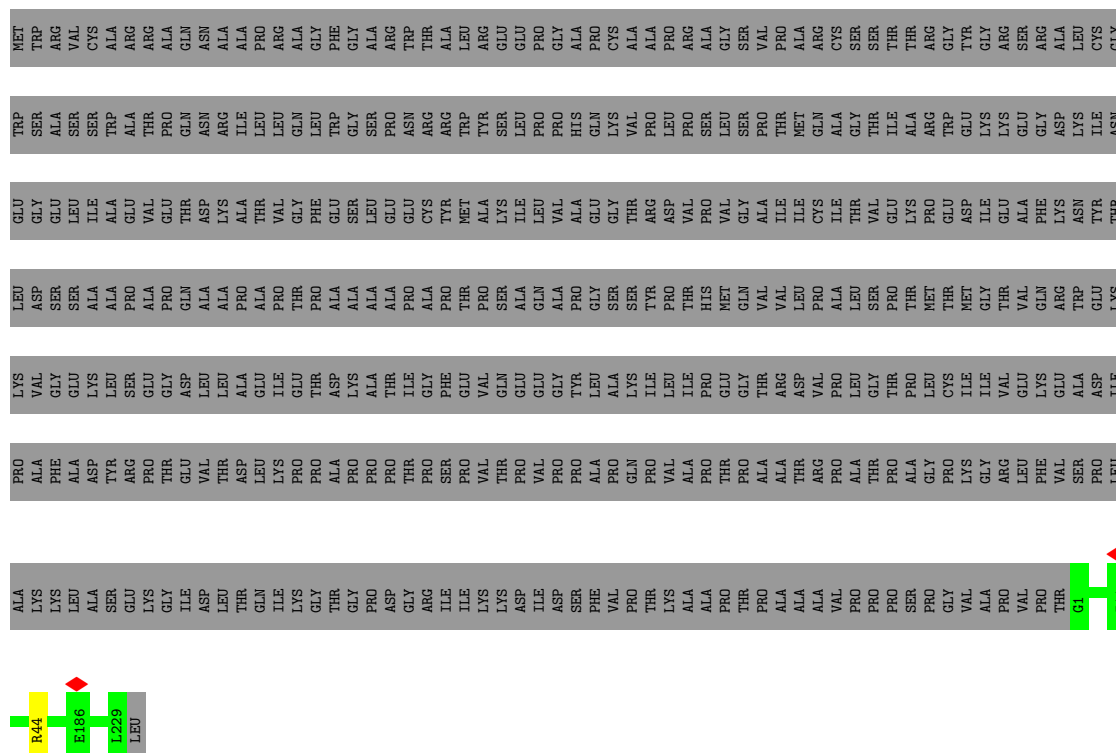
● Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

Chain n: 35% 65%

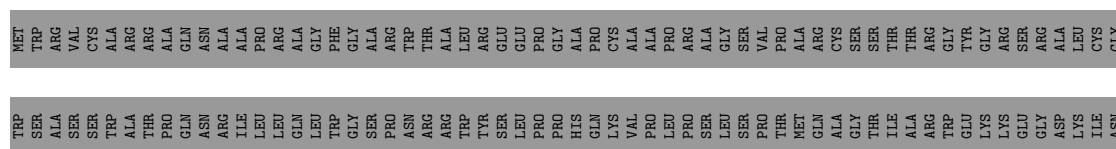


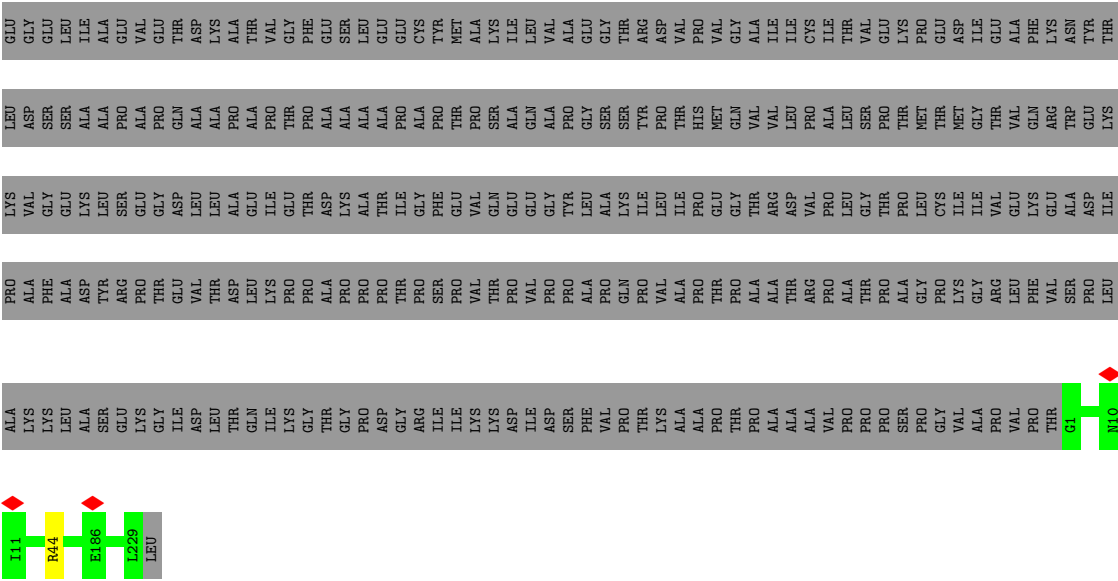


- Chain o:  35% 65%



- Chain p: 35% 65%

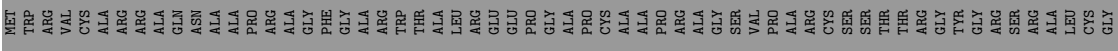




• Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



• Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



A diagram showing a 4x4 grid. The columns are labeled R44, E186, L229, and LEU. A red diamond is placed above the E186 column.

- Chain u:  35% 65%

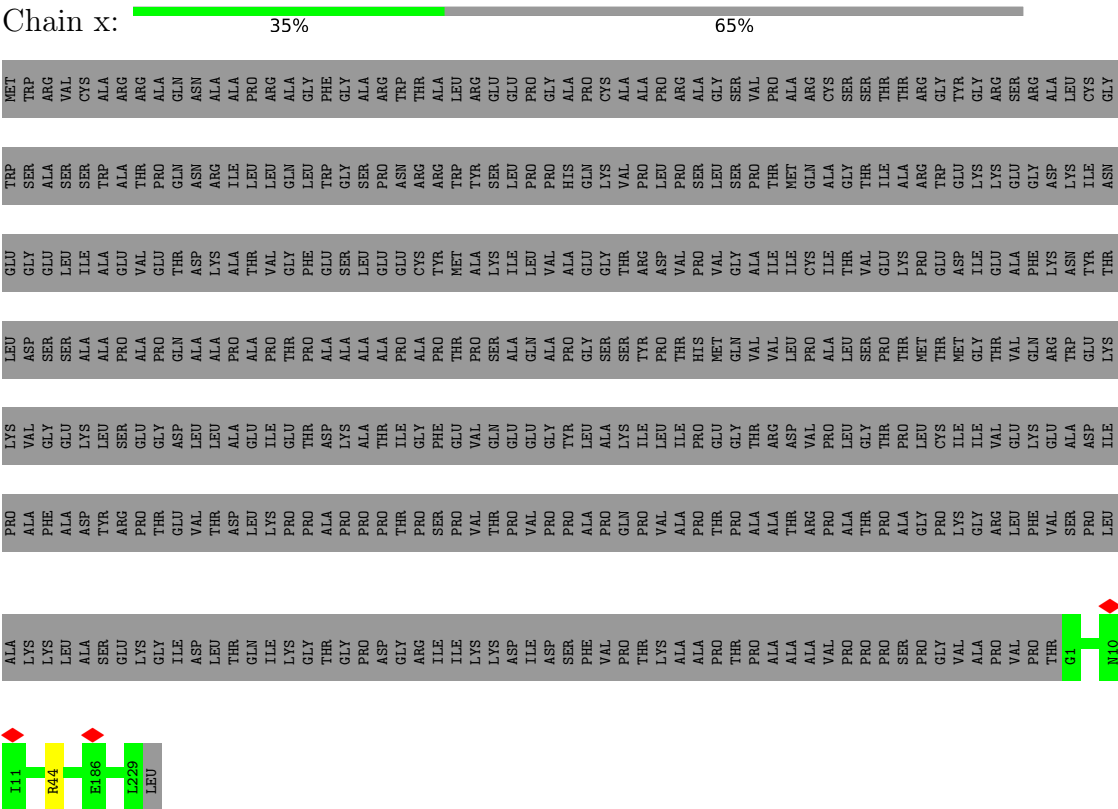
- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

65%

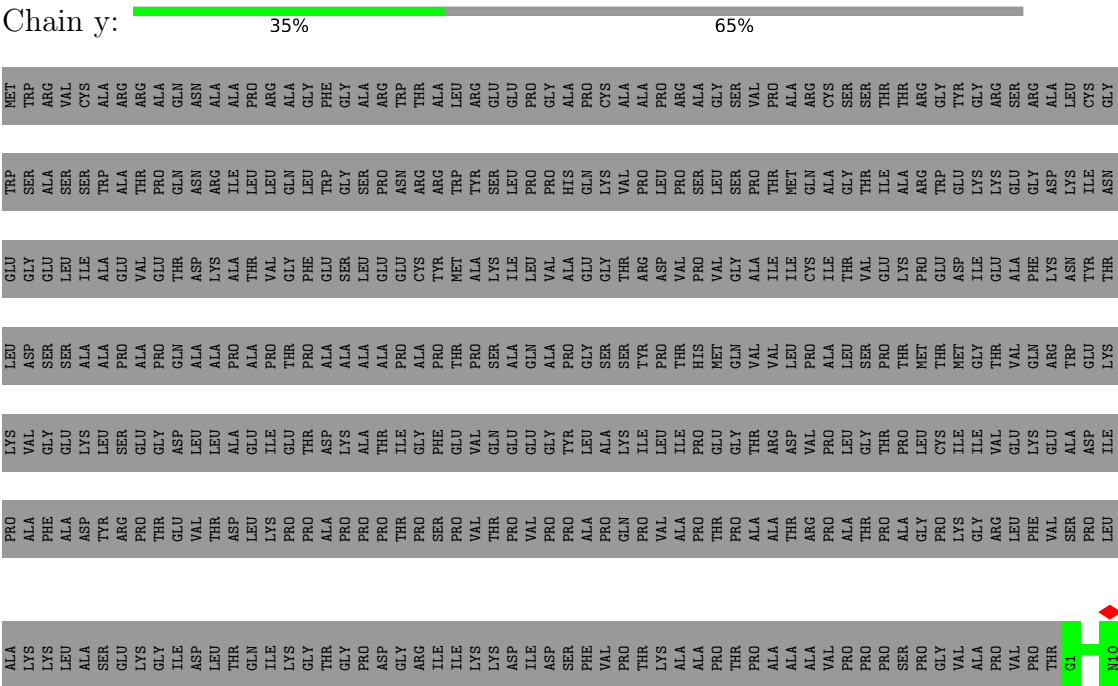
- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

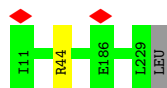
65%

- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex



- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

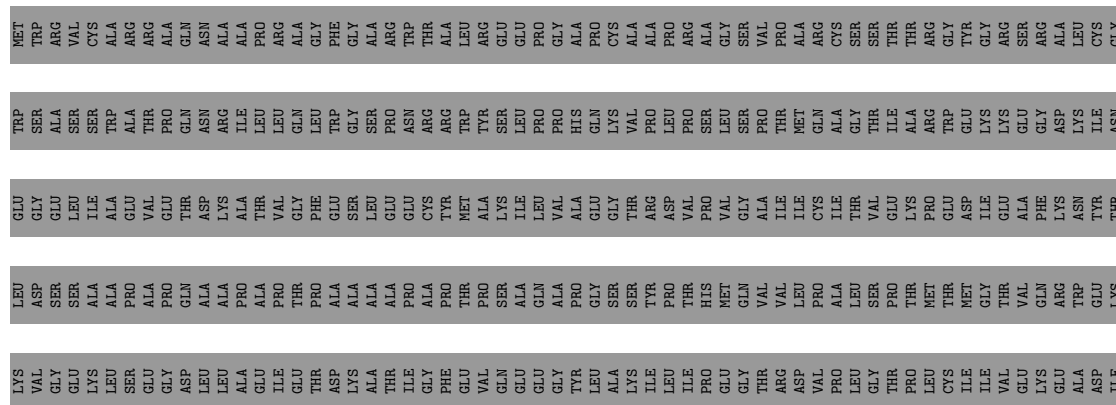


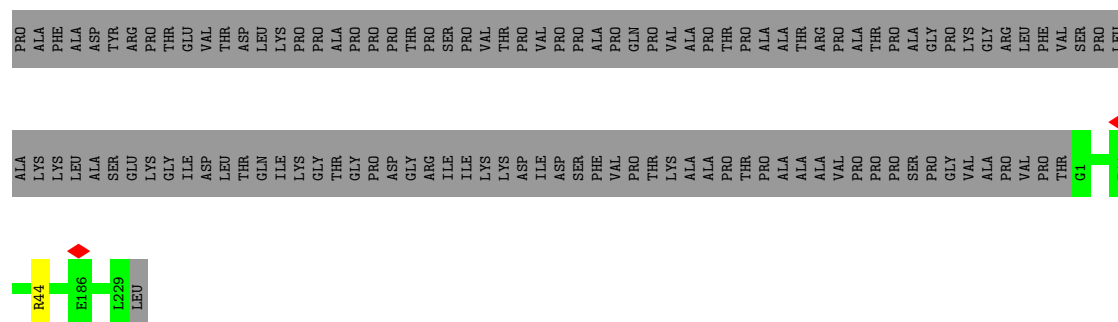


- Chain 1: 

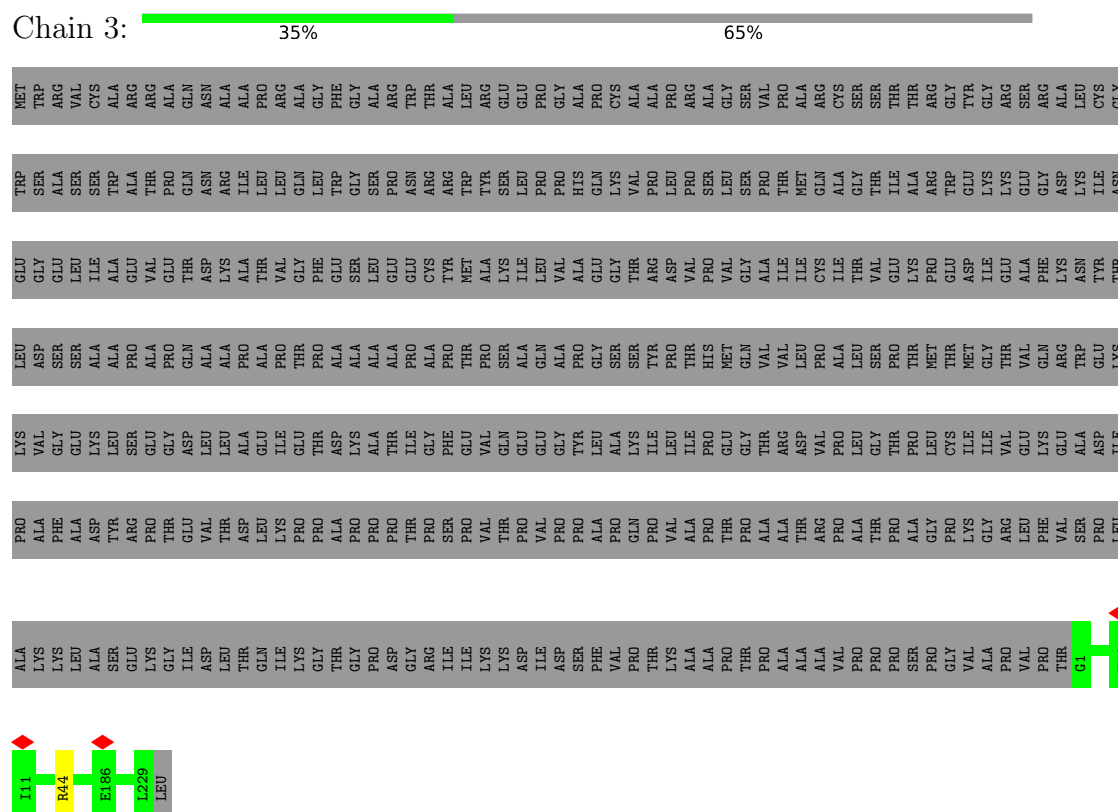


- Chain 2:  35% 65%

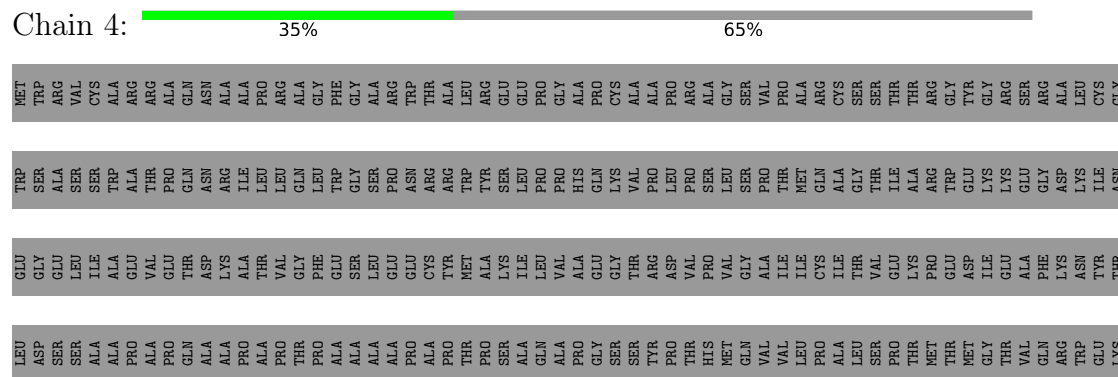


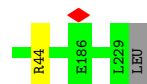


- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

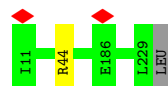


- Molecule 1: Acetyltransferase component of pyruvate dehydrogenase complex

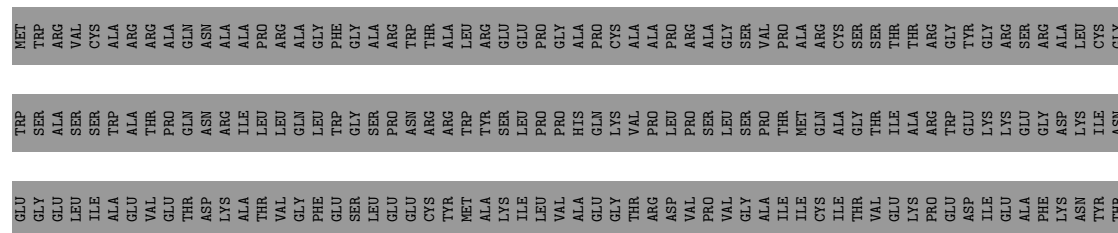




- Chain 5:  35% 65%



- Chain 6:  35% 65%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35220	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.129	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.019	Depositor
Map size (Å)	395.09998, 395.09998, 395.09998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0975, 1.0975, 1.0975	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.30	0/1790	0.52	0/2426
1	1	0.30	0/1790	0.52	0/2426
1	2	0.30	0/1790	0.52	0/2426
1	3	0.30	0/1790	0.52	0/2426
1	4	0.30	0/1790	0.52	0/2426
1	5	0.30	0/1790	0.52	0/2426
1	6	0.30	0/1790	0.52	0/2426
1	7	0.30	0/1790	0.52	0/2426
1	A	0.30	0/1790	0.52	0/2426
1	B	0.30	0/1790	0.52	0/2426
1	C	0.30	0/1790	0.52	0/2426
1	D	0.30	0/1790	0.52	0/2426
1	E	0.30	0/1790	0.52	0/2426
1	F	0.30	0/1790	0.52	0/2426
1	G	0.30	0/1790	0.52	0/2426
1	H	0.30	0/1790	0.52	0/2426
1	I	0.30	0/1790	0.52	0/2426
1	J	0.30	0/1790	0.52	0/2426
1	K	0.30	0/1790	0.52	0/2426
1	L	0.30	0/1790	0.52	0/2426
1	M	0.30	0/1790	0.52	0/2426
1	N	0.30	0/1790	0.52	0/2426
1	O	0.30	0/1790	0.52	0/2426
1	P	0.30	0/1790	0.52	0/2426
1	Q	0.30	0/1790	0.52	0/2426
1	R	0.30	0/1790	0.52	0/2426
1	S	0.30	0/1790	0.52	0/2426
1	T	0.30	0/1790	0.52	0/2426
1	U	0.30	0/1790	0.52	0/2426
1	V	0.30	0/1790	0.52	0/2426
1	W	0.30	0/1790	0.52	0/2426
1	X	0.30	0/1790	0.52	0/2426
1	Y	0.30	0/1790	0.52	0/2426
1	Z	0.30	0/1790	0.52	0/2426

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.30	0/1790	0.52	0/2426
1	b	0.30	0/1790	0.52	0/2426
1	c	0.30	0/1790	0.52	0/2426
1	d	0.30	0/1790	0.52	0/2426
1	e	0.30	0/1790	0.52	0/2426
1	f	0.30	0/1790	0.52	0/2426
1	g	0.30	0/1790	0.52	0/2426
1	h	0.30	0/1790	0.52	0/2426
1	i	0.30	0/1790	0.52	0/2426
1	j	0.30	0/1790	0.52	0/2426
1	k	0.30	0/1790	0.52	0/2426
1	l	0.30	0/1790	0.52	0/2426
1	m	0.30	0/1790	0.52	0/2426
1	n	0.30	0/1790	0.52	0/2426
1	o	0.30	0/1790	0.52	0/2426
1	p	0.30	0/1790	0.52	0/2426
1	q	0.30	0/1790	0.52	0/2426
1	r	0.30	0/1790	0.52	0/2426
1	s	0.30	0/1790	0.52	0/2426
1	t	0.30	0/1790	0.52	0/2426
1	u	0.30	0/1790	0.52	0/2426
1	v	0.30	0/1790	0.52	0/2426
1	w	0.30	0/1790	0.52	0/2426
1	x	0.30	0/1790	0.52	0/2426
1	y	0.30	0/1790	0.52	0/2426
1	z	0.30	0/1790	0.52	0/2426
All	All	0.30	0/107400	0.52	0/145560

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	1	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	2	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	3	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	4	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	5	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	6	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	7	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	A	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	B	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	C	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	D	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	E	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	F	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	G	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	H	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	I	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	J	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	K	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	L	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	M	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	N	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	O	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	P	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	Q	227/647 (35%)	220 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	S	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	T	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	U	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	V	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	W	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	X	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	Y	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	Z	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	a	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	b	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	c	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	d	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	e	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	f	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	g	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	h	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	i	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	j	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	k	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	l	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	m	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	n	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	o	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	p	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	q	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	r	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	s	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	t	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	u	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	v	227/647 (35%)	220 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	x	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	y	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
1	z	227/647 (35%)	220 (97%)	7 (3%)	0	100	100
All	All	13620/38820 (35%)	13200 (97%)	420 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	1	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	2	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	3	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	4	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	5	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	6	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	7	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	A	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	B	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	C	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	D	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	E	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	F	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	G	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	H	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	I	195/526 (37%)	194 (100%)	1 (0%)	86	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	K	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	L	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	M	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	N	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	O	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	P	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	Q	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	R	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	S	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	T	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	U	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	V	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	W	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	X	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	Y	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	Z	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	a	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	b	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	c	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	d	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	e	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	f	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	g	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	h	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	i	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	j	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	k	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	l	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	m	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	n	195/526 (37%)	194 (100%)	1 (0%)	86	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	o	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	p	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	q	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	r	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	s	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	t	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	u	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	v	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	w	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	x	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	y	195/526 (37%)	194 (100%)	1 (0%)	86	92
1	z	195/526 (37%)	194 (100%)	1 (0%)	86	92
All	All	11700/31560 (37%)	11640 (100%)	60 (0%)	85	92

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	B	44	ARG
1	C	44	ARG
1	D	44	ARG
1	E	44	ARG
1	F	44	ARG
1	G	44	ARG
1	H	44	ARG
1	I	44	ARG
1	J	44	ARG
1	K	44	ARG
1	L	44	ARG
1	M	44	ARG
1	N	44	ARG
1	O	44	ARG
1	P	44	ARG
1	Q	44	ARG
1	R	44	ARG
1	S	44	ARG
1	T	44	ARG
1	U	44	ARG

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Mol	Chain	Res	Type
1	V	44	ARG
1	W	44	ARG
1	X	44	ARG
1	Y	44	ARG
1	Z	44	ARG
1	a	44	ARG
1	b	44	ARG
1	c	44	ARG
1	d	44	ARG
1	e	44	ARG
1	f	44	ARG
1	g	44	ARG
1	h	44	ARG
1	i	44	ARG
1	j	44	ARG
1	k	44	ARG
1	l	44	ARG
1	m	44	ARG
1	n	44	ARG
1	o	44	ARG
1	p	44	ARG
1	q	44	ARG
1	r	44	ARG
1	s	44	ARG
1	t	44	ARG
1	u	44	ARG
1	v	44	ARG
1	w	44	ARG
1	x	44	ARG
1	y	44	ARG
1	z	44	ARG
1	0	44	ARG
1	1	44	ARG
1	2	44	ARG
1	3	44	ARG
1	4	44	ARG
1	5	44	ARG
1	6	44	ARG
1	7	44	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (121) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	158	ASN
1	B	17	GLN
1	B	158	ASN
1	C	17	GLN
1	C	158	ASN
1	D	17	GLN
1	D	158	ASN
1	E	17	GLN
1	E	158	ASN
1	F	17	GLN
1	F	158	ASN
1	G	17	GLN
1	G	158	ASN
1	H	17	GLN
1	H	158	ASN
1	I	17	GLN
1	I	158	ASN
1	J	17	GLN
1	J	158	ASN
1	K	17	GLN
1	K	158	ASN
1	L	17	GLN
1	L	158	ASN
1	M	17	GLN
1	M	158	ASN
1	N	17	GLN
1	N	158	ASN
1	O	17	GLN
1	O	158	ASN
1	P	17	GLN
1	P	158	ASN
1	Q	17	GLN
1	Q	158	ASN
1	R	17	GLN
1	R	158	ASN
1	S	17	GLN
1	S	88	GLN
1	S	158	ASN
1	T	17	GLN
1	T	158	ASN
1	U	17	GLN
1	U	158	ASN

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Mol	Chain	Res	Type
1	V	17	GLN
1	V	158	ASN
1	W	17	GLN
1	W	158	ASN
1	X	17	GLN
1	X	158	ASN
1	Y	17	GLN
1	Y	158	ASN
1	Z	17	GLN
1	Z	158	ASN
1	a	17	GLN
1	a	158	ASN
1	b	17	GLN
1	b	158	ASN
1	c	17	GLN
1	c	158	ASN
1	d	17	GLN
1	d	158	ASN
1	e	17	GLN
1	e	158	ASN
1	f	17	GLN
1	f	158	ASN
1	g	17	GLN
1	g	158	ASN
1	h	17	GLN
1	h	158	ASN
1	i	17	GLN
1	i	158	ASN
1	j	17	GLN
1	j	158	ASN
1	k	17	GLN
1	k	158	ASN
1	l	17	GLN
1	l	158	ASN
1	m	17	GLN
1	m	158	ASN
1	n	17	GLN
1	n	158	ASN
1	o	17	GLN
1	o	158	ASN
1	p	17	GLN
1	p	158	ASN

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Mol	Chain	Res	Type
1	q	17	GLN
1	q	158	ASN
1	r	17	GLN
1	r	158	ASN
1	s	17	GLN
1	s	158	ASN
1	t	17	GLN
1	t	158	ASN
1	u	17	GLN
1	u	158	ASN
1	v	17	GLN
1	v	158	ASN
1	w	17	GLN
1	w	158	ASN
1	x	17	GLN
1	x	158	ASN
1	y	17	GLN
1	y	158	ASN
1	z	17	GLN
1	z	158	ASN
1	0	17	GLN
1	0	158	ASN
1	1	17	GLN
1	1	158	ASN
1	2	17	GLN
1	2	158	ASN
1	3	17	GLN
1	3	158	ASN
1	4	17	GLN
1	4	158	ASN
1	5	17	GLN
1	5	158	ASN
1	6	17	GLN
1	6	158	ASN
1	7	17	GLN
1	7	158	ASN

5.3.3 RNA ⓘ

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 [i](#)

There are no chain breaks in this entry.

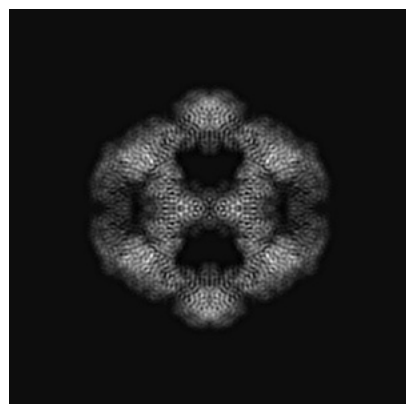
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37969. These allow visual inspection of the internal detail of the map and identification of artifacts.

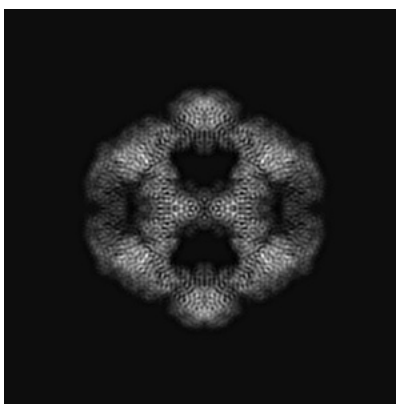
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

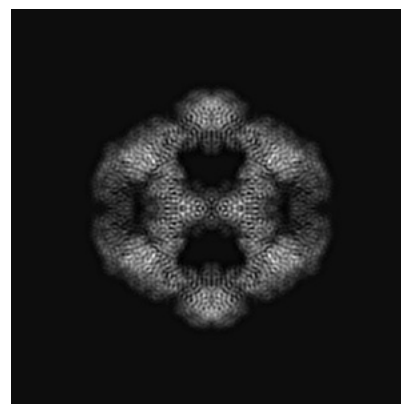
6.1.1 Primary map



X

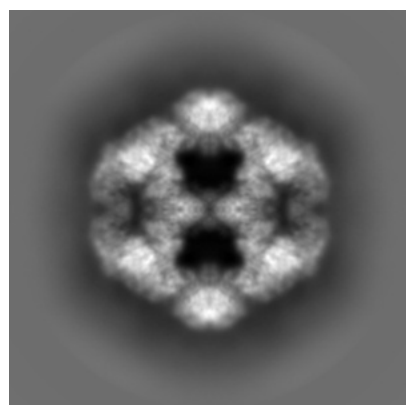


Y

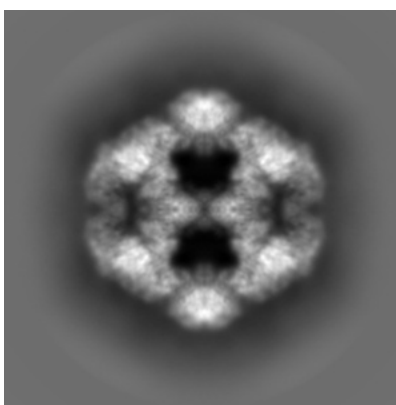


Z

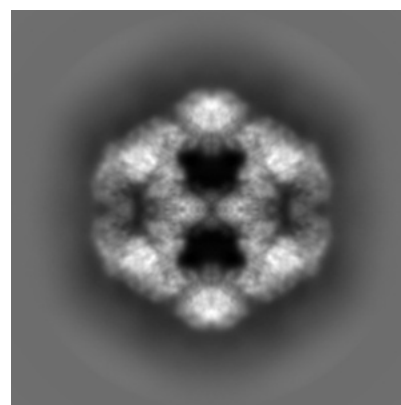
6.1.2 Raw map



X



Y

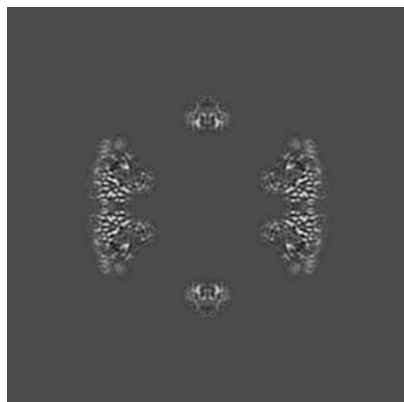


Z

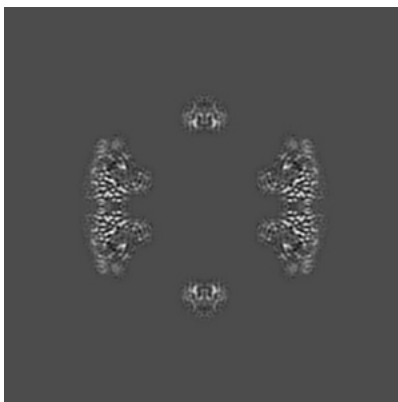
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

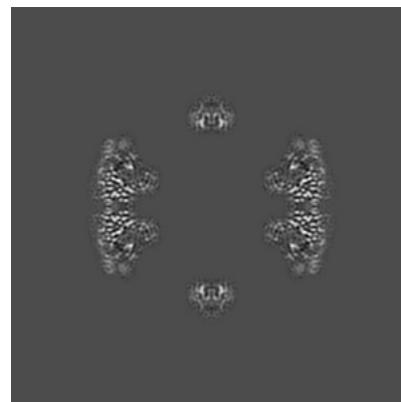
6.2.1 Primary map



X Index: 180

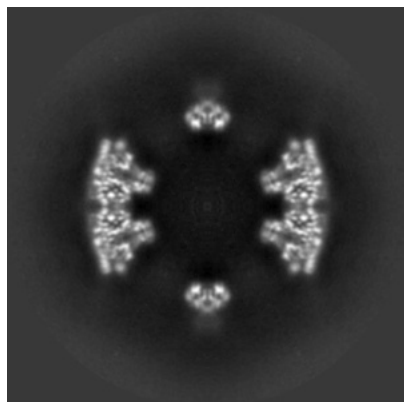


Y Index: 180

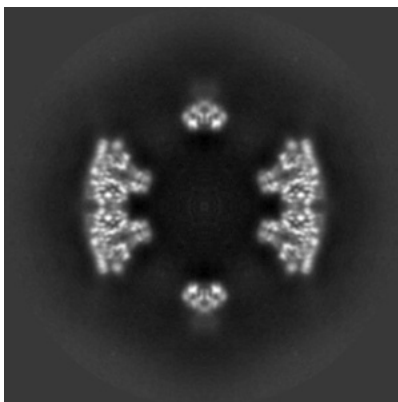


Z Index: 180

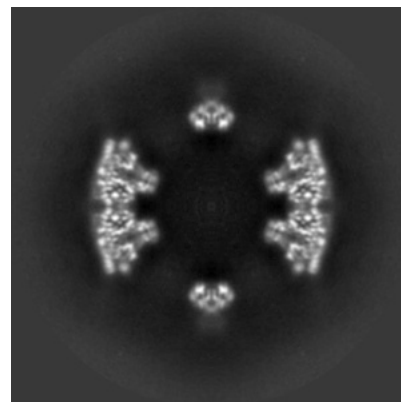
6.2.2 Raw map



X Index: 180



Y Index: 180

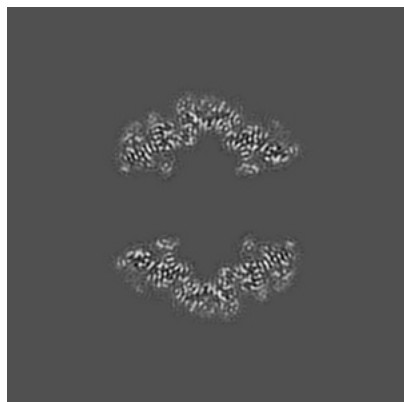


Z Index: 180

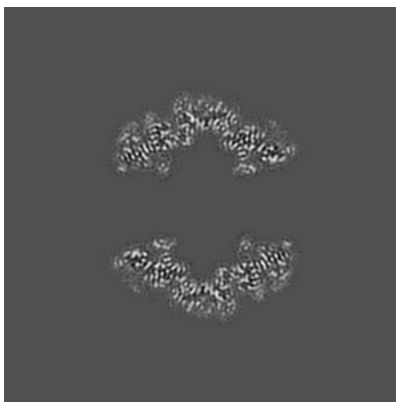
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

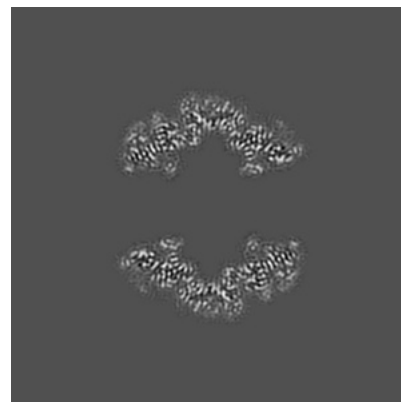
6.3.1 Primary map



X Index: 137

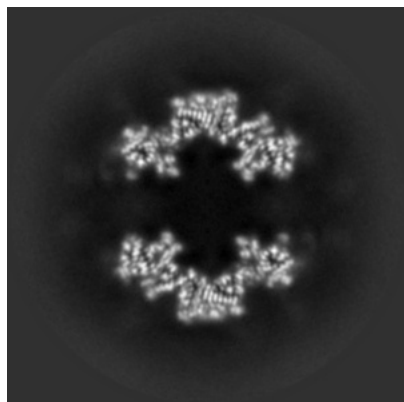


Y Index: 137

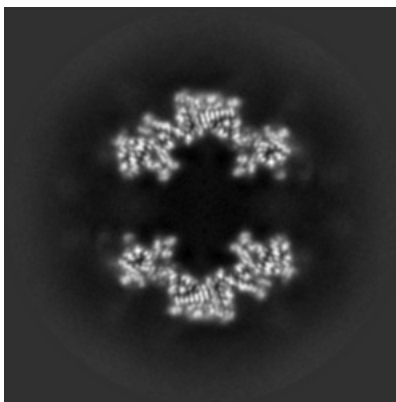


Z Index: 137

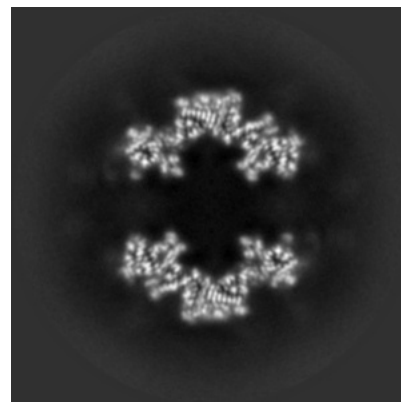
6.3.2 Raw map



X Index: 217



Y Index: 143

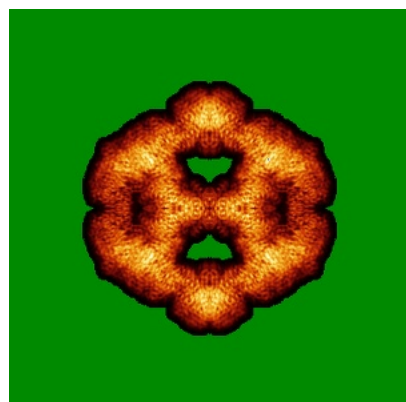


Z Index: 217

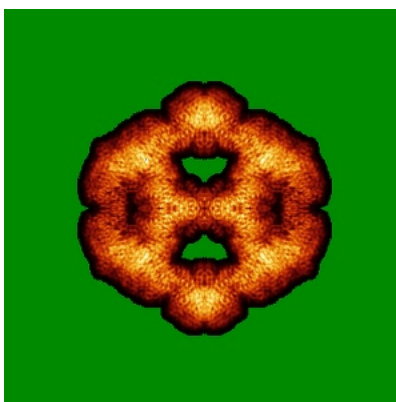
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

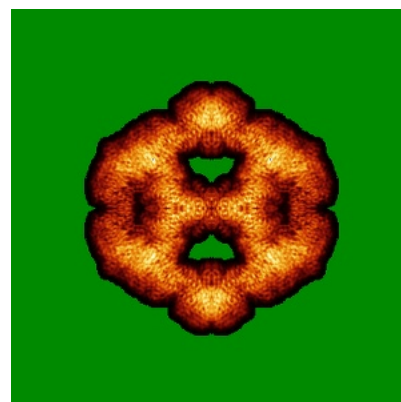
6.4.1 Primary map



X

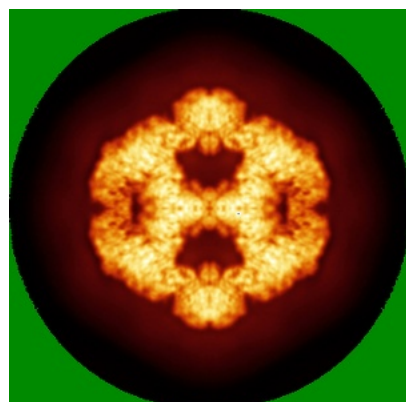


Y

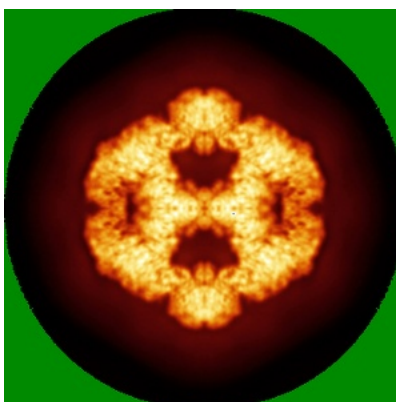


Z

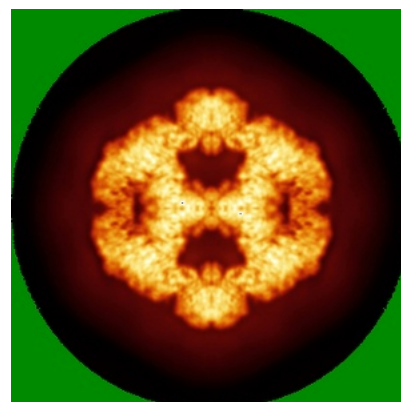
6.4.2 Raw map



X



Y

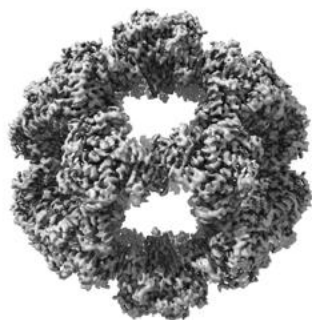


Z

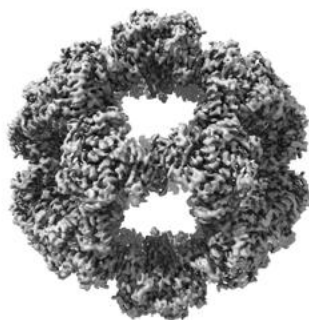
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

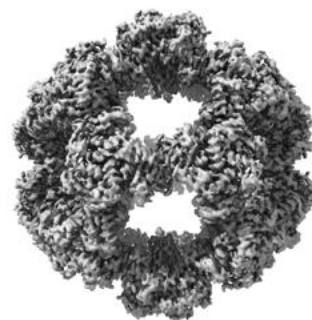
6.5.1 Primary map



X



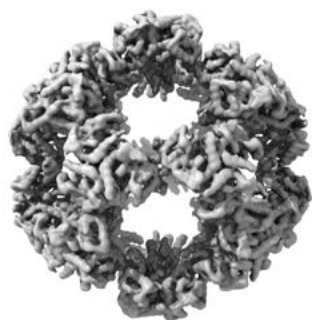
Y



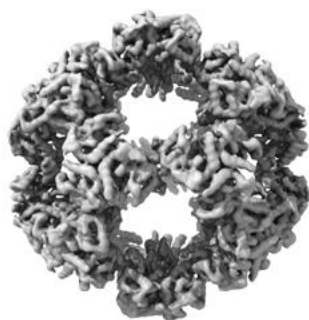
Z

The images above show the 3D surface view of the map at the recommended contour level 0.019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

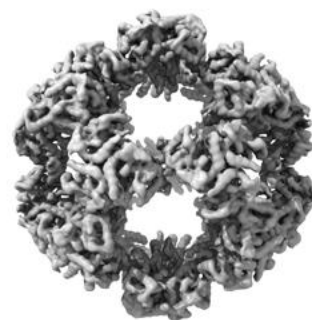
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

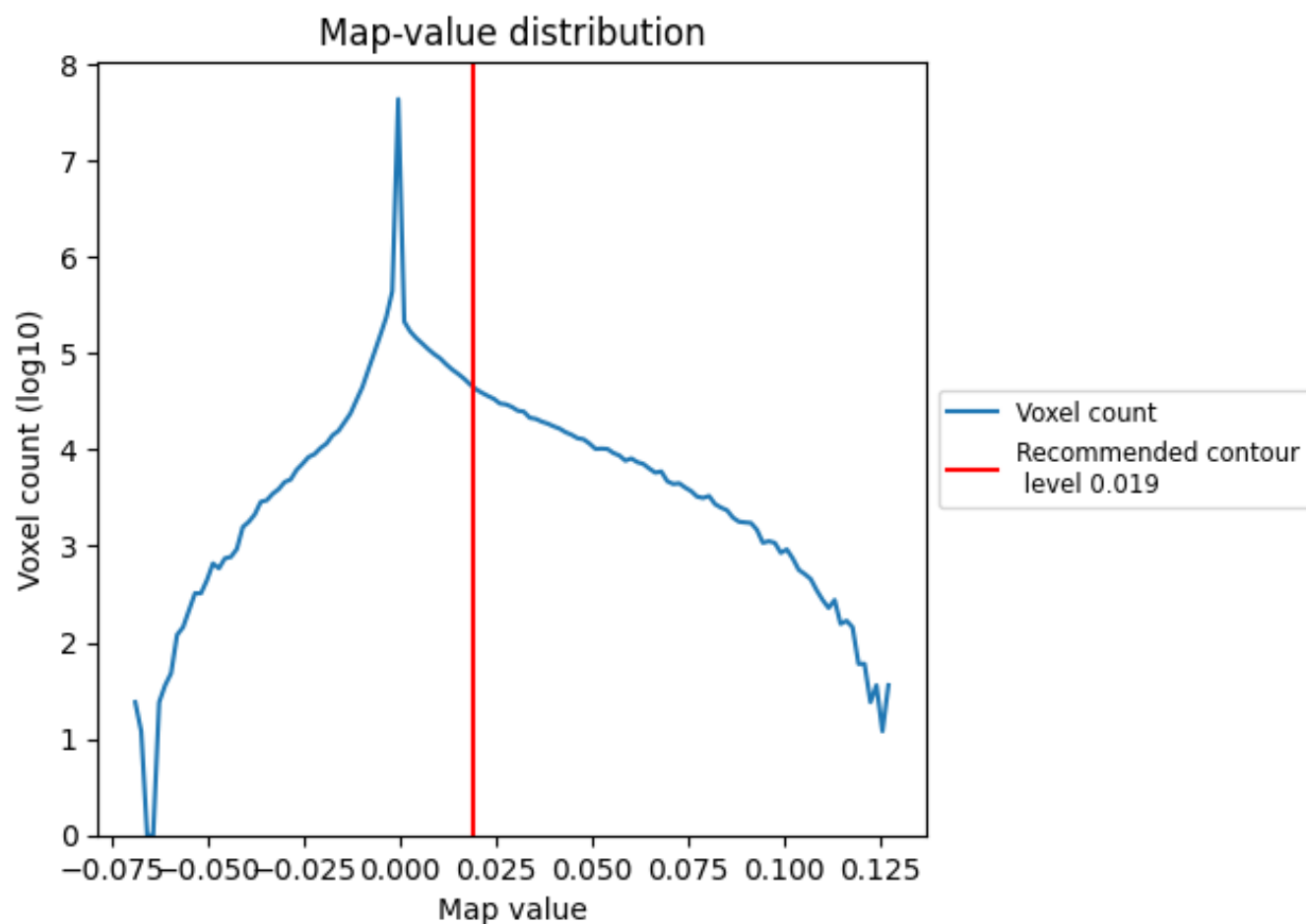
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

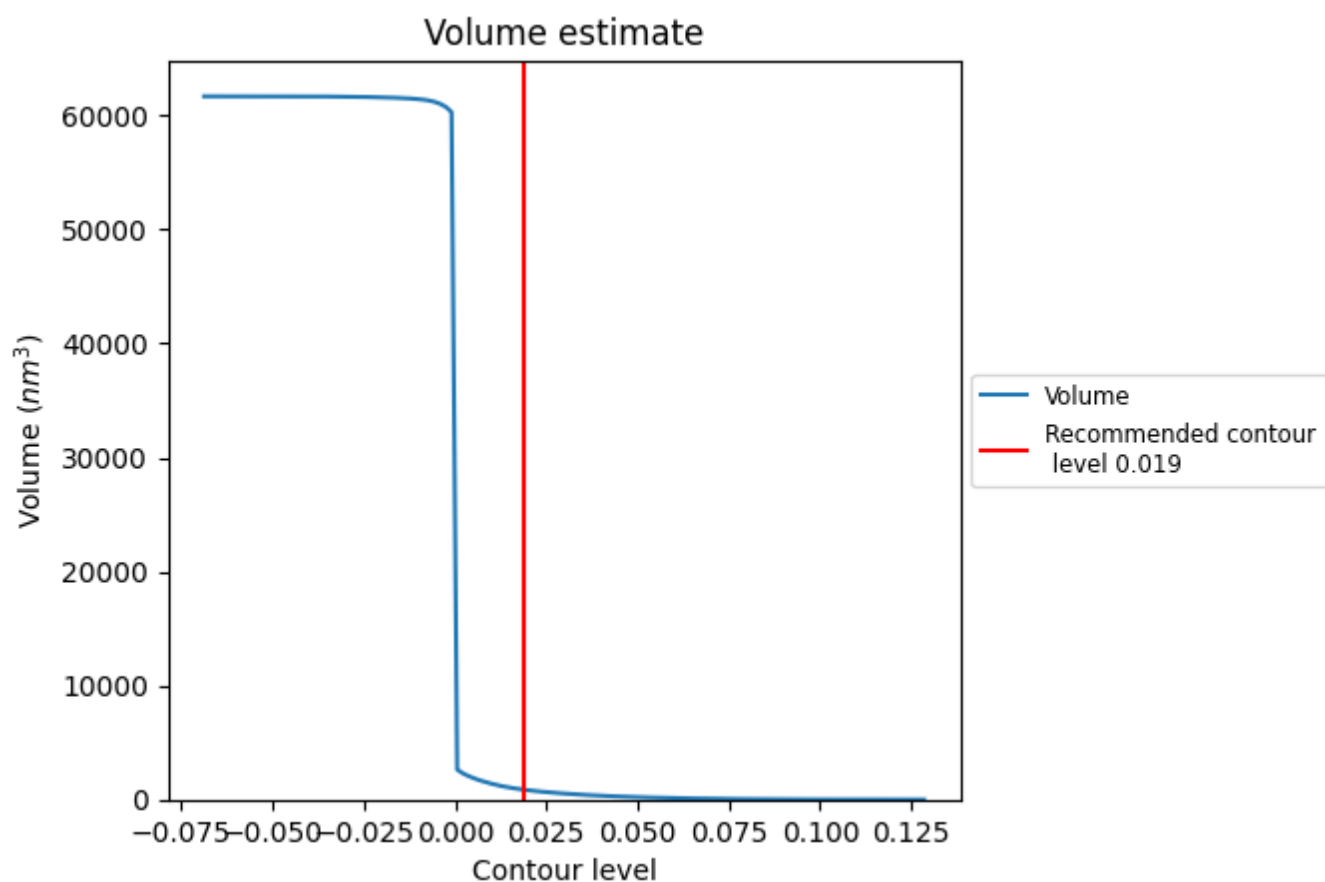
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

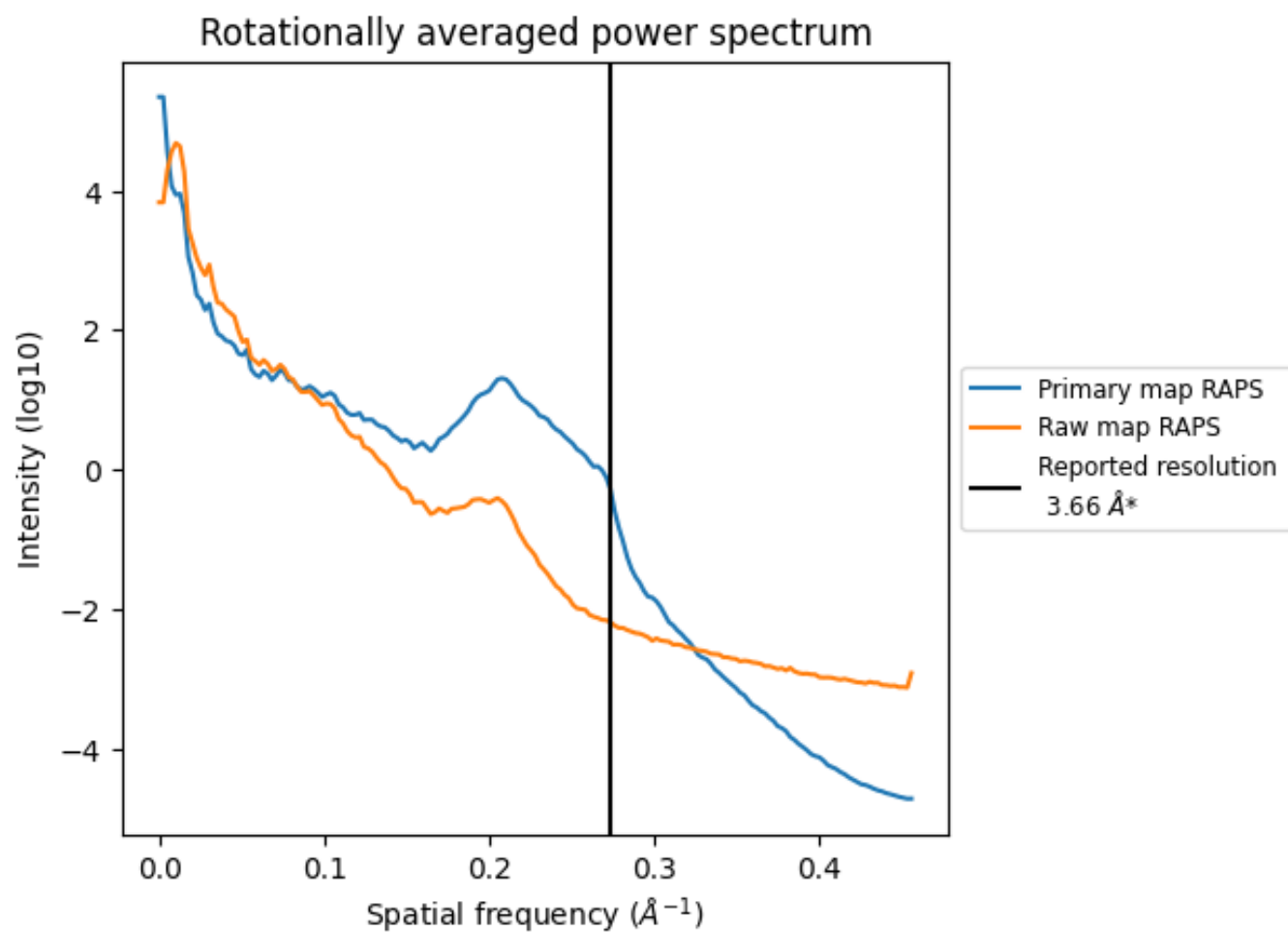
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 855 nm³; this corresponds to an approximate mass of 772 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

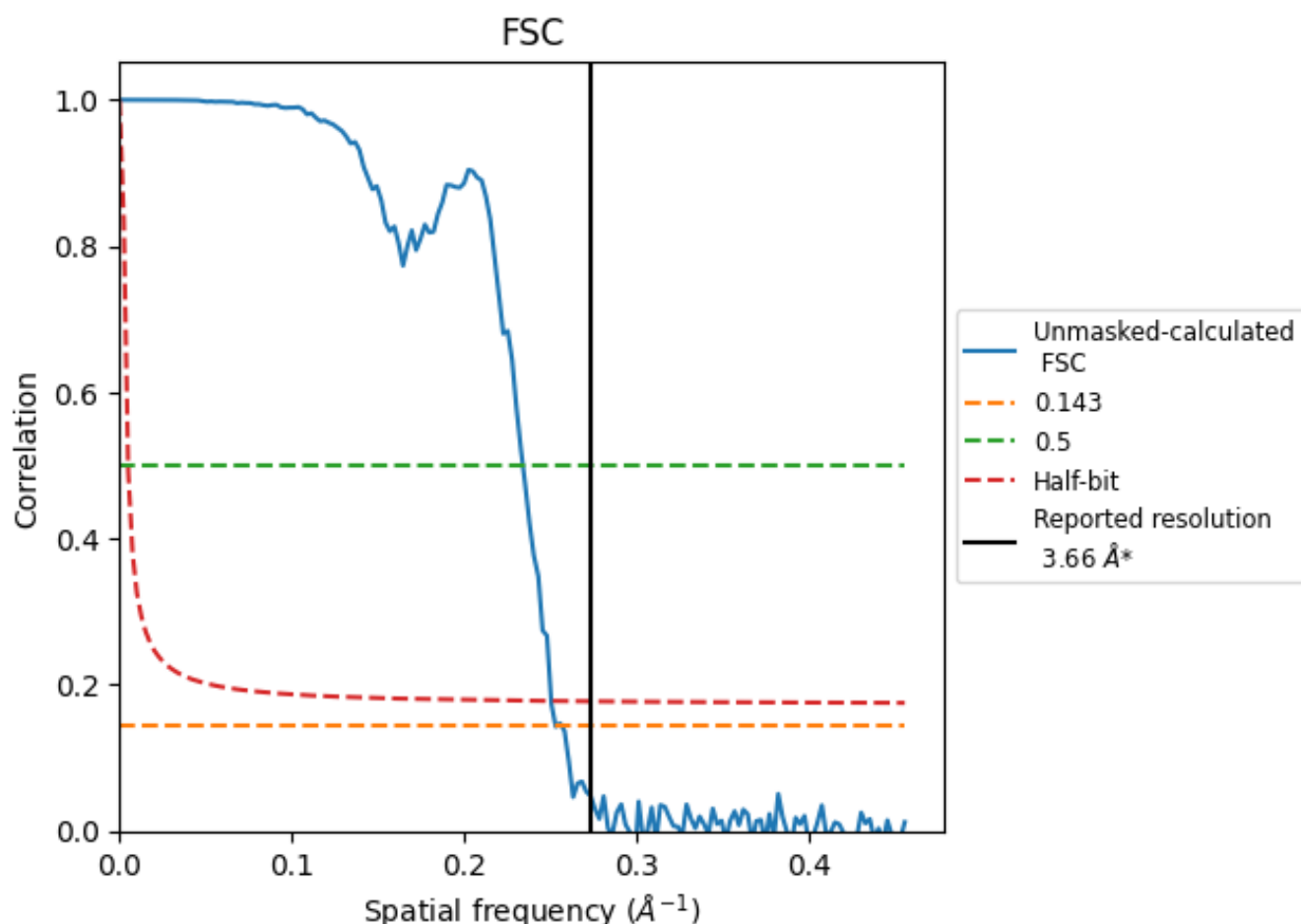


*Reported resolution corresponds to spatial frequency of 0.273 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.273 \AA^{-1}

8.2 Resolution estimates [i](#)

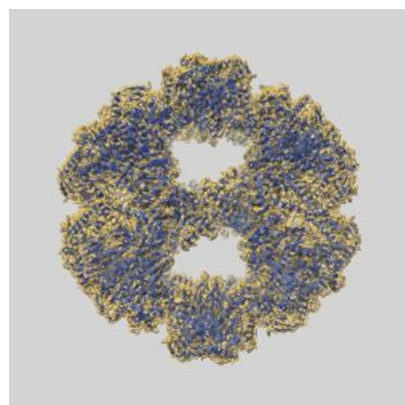
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.66	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.95	4.27	3.99

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

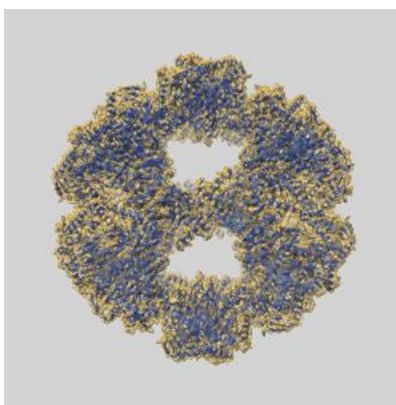
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37969 and PDB model 8X03. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

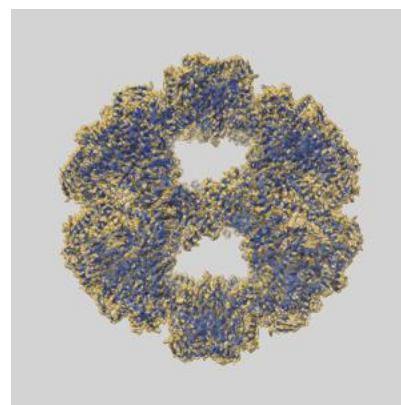
9.1 Map-model overlay [i](#)



X



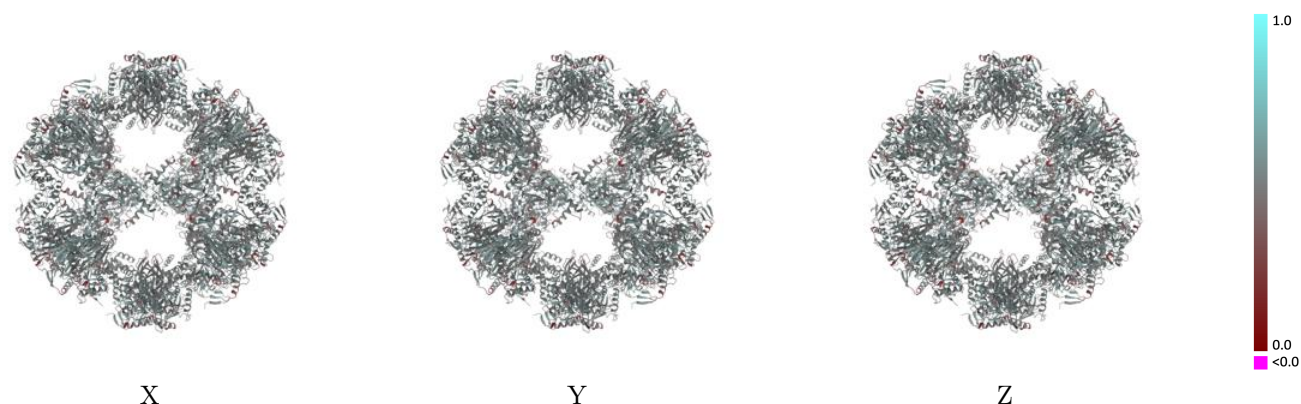
Y



Z

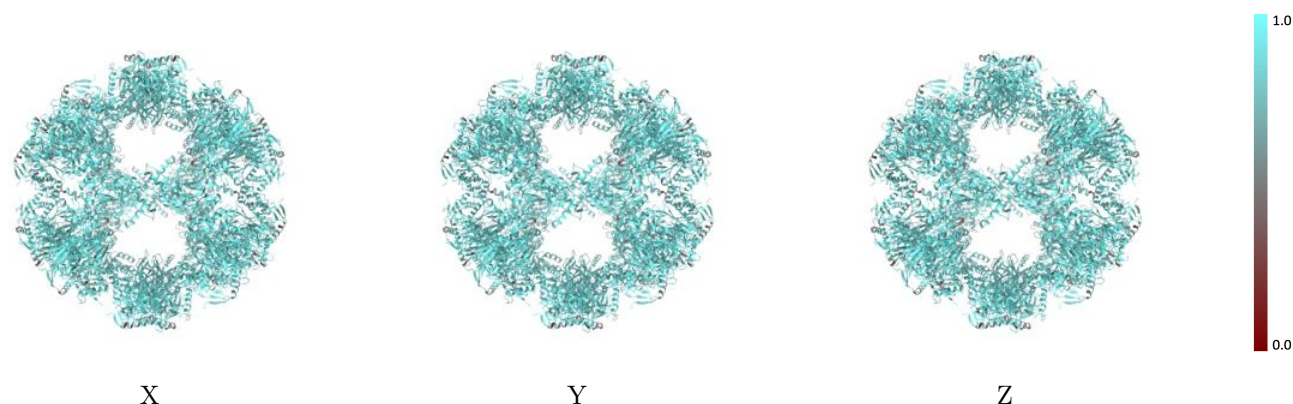
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



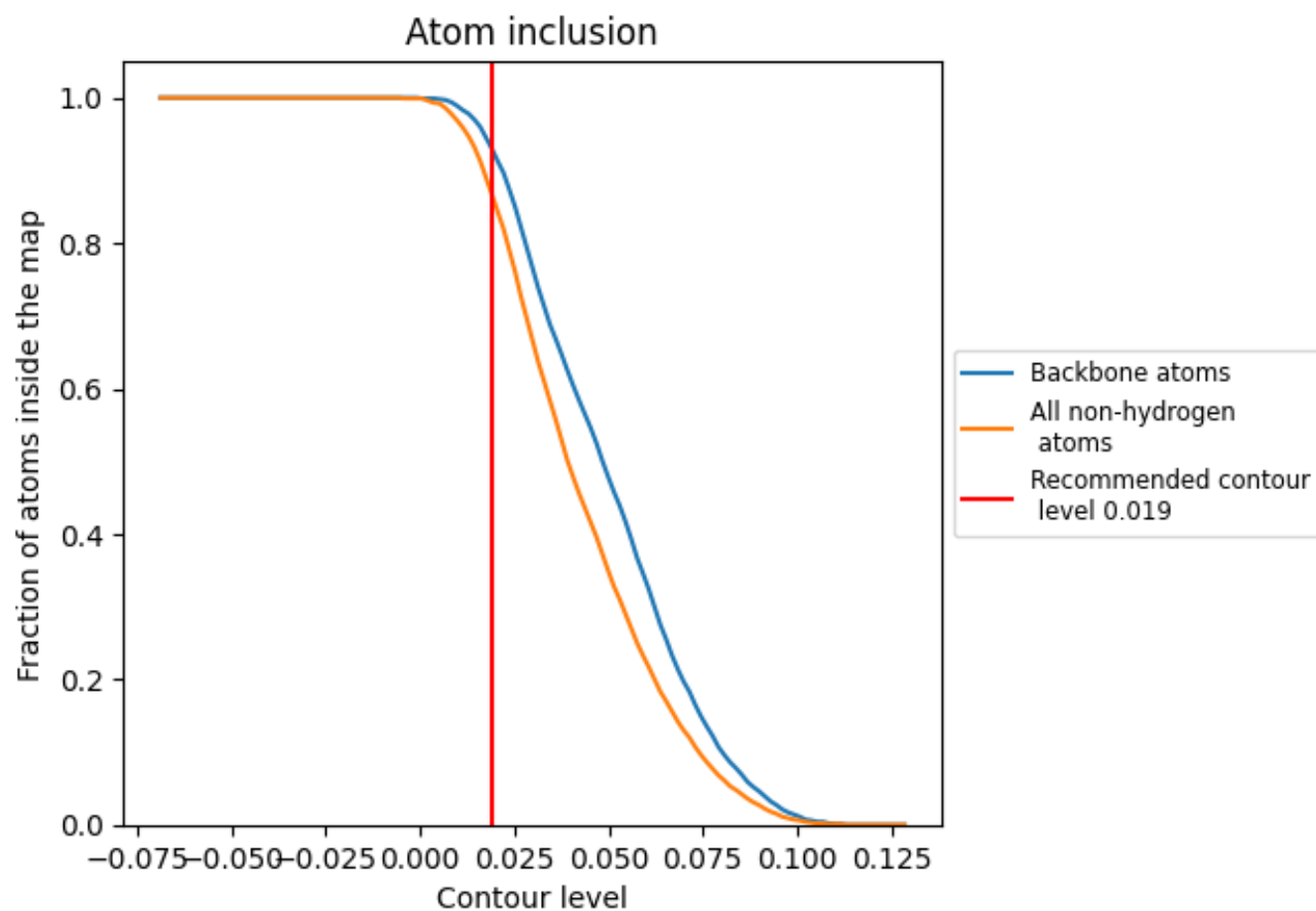
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.019).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ















The table lists the average atom inclusion at the recommended contour level (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8680	 0.4960
0	 0.8670	 0.4950
1	 0.8650	 0.4960
2	 0.8700	 0.5000
3	 0.8660	 0.4980
4	 0.8700	 0.4940
5	 0.8660	 0.4940
6	 0.8740	 0.4960
7	 0.8740	 0.4950
A	 0.8690	 0.4960
B	 0.8700	 0.4950
C	 0.8700	 0.4960
D	 0.8700	 0.4980
E	 0.8700	 0.4980
F	 0.8690	 0.4980
G	 0.8710	 0.4970
H	 0.8710	 0.4960
I	 0.8700	 0.4950
J	 0.8710	 0.4970
K	 0.8670	 0.4970
L	 0.8720	 0.4940
M	 0.8660	 0.4950
N	 0.8660	 0.4970
O	 0.8640	 0.4970
P	 0.8660	 0.4950
Q	 0.8620	 0.4960
R	 0.8710	 0.4930
S	 0.8670	 0.4980
T	 0.8660	 0.4980
U	 0.8700	 0.4940
V	 0.8720	 0.4950
W	 0.8720	 0.4950
X	 0.8690	 0.4970
Y	 0.8710	 0.4950
Z	 0.8630	 0.4950



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Chain	Atom inclusion	Q-score
a	 0.8660	 0.4950
b	 0.8640	 0.4980
c	 0.8720	 0.4980
d	 0.8710	 0.4950
e	 0.8670	 0.4950
f	 0.8650	 0.4930
g	 0.8660	 0.4940
h	 0.8650	 0.4990
i	 0.8670	 0.4940
j	 0.8640	 0.5010
k	 0.8690	 0.4950
l	 0.8670	 0.4960
m	 0.8650	 0.4930
n	 0.8630	 0.4950
o	 0.8660	 0.4990
p	 0.8690	 0.4970
q	 0.8710	 0.4980
r	 0.8730	 0.4950
s	 0.8700	 0.4960
t	 0.8690	 0.4990
u	 0.8670	 0.4970
v	 0.8670	 0.4960
w	 0.8650	 0.4930
x	 0.8630	 0.4990
y	 0.8740	 0.4960
z	 0.8700	 0.4960