



wwPDB EM Validation Summary Report ⓘ

Jun 1, 2026 – 07:15 PM EDT

PDB ID : 9YF4 / pdb_00009yf4
EMDB ID : EMD-72876
Title : N4 Full Virion C6 Tail
Authors : Bellis, N.F.; Cingolani, G.
Deposited on : 2025-09-25
Resolution : 3.28 Å(reported)

This is a wwPDB EM 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/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:

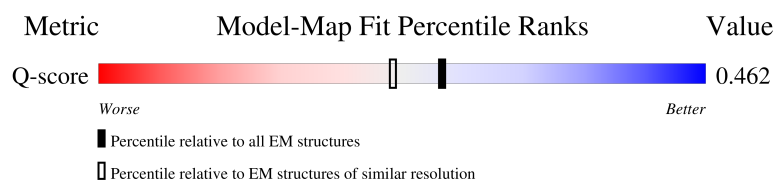
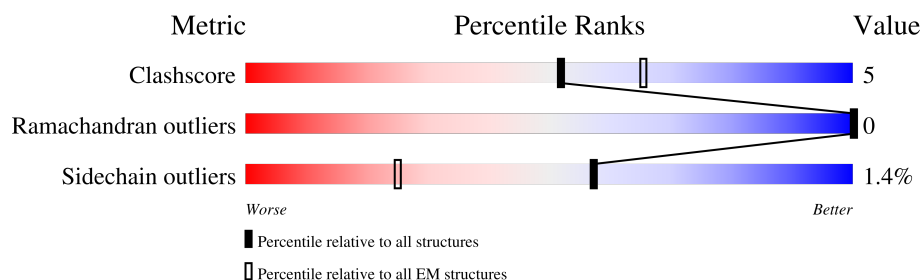
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.28 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.













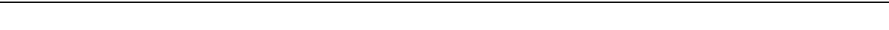

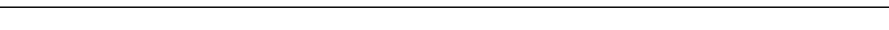
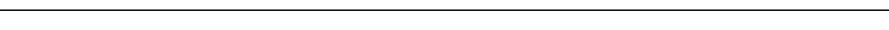











Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14492 (2.78 - 3.78)

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	AA	236	92% 8%
1	AB	236	87% 12% .
1	AC	236	92% 8%
1	AD	236	88% 11% .


























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Mol	Chain	Length	Quality of chain
1	AE	236	 91% 8%
1	AF	236	 88% 11%
1	AG	236	 92% 7%
1	AH	236	 87% 12%
1	AI	236	 92% 8%
1	AJ	236	 86% 13%
1	AK	236	 92% 8%
1	AL	236	 88% 11%
2	LA	1382	 71% 15% 15%
2	LB	1382	 70% 15% 15%
2	LC	1382	 71% 15% 15%
2	LD	1382	 70% 15% 15%
2	LE	1382	 71% 15% 15%
2	LF	1382	 70% 15% 15%
3	PA	763	 73% 16% 12%
3	PB	763	 72% 16% 12%
3	PC	763	 72% 16% 12%
3	PD	763	 73% 16% 12%
3	PE	763	 72% 16% 12%
3	PF	763	 73% 15% 12%
3	PG	763	 72% 16% 12%
3	PH	763	 72% 16% 12%
3	PI	763	 72% 16% 12%
3	PJ	763	 73% 15% 12%
3	PK	763	 72% 16% 12%


























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Mol	Chain	Length	Quality of chain
3	PL	763	 74%15%12%
4	SA	417	 83%16%
4	SB	417	 84%16%
4	SC	417	 83%16%
4	SD	417	 83%17%
4	SE	417	 83%16%
4	SF	417	 84%15%
5	TA	299	 89%11%
5	TB	299	 87%12%
5	TC	299	 89%11%
5	TD	299	 88%11%
5	TE	299	 88%11%
5	TF	299	 87%13%
5	TG	299	 89%11%
5	TH	299	 87%13%
5	TI	299	 88%11%
5	TJ	299	 88%12%
5	TK	299	 88%11%
5	TL	299	 87%12%
6	XA	556	 10%87%
6	XB	556	 11%87%
6	XC	556	 9%87%
6	XD	556	 11%87%
6	XE	556	 9%87%
6	XF	556	 11%87%


















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Mol	Chain	Length	Quality of chain	
6	XG	556		
6	XH	556		
6	XI	556		
6	XJ	556		
6	XK	556		
6	XL	556		
6	YA	556		
6	YB	556		
6	YC	556		
6	YD	556		
6	YE	556		
6	YF	556		
6	YG	556		
6	YH	556		
6	YI	556		
6	YJ	556		
6	YK	556		
6	YL	556		
6	ZA	556		
6	ZB	556		
6	ZC	556		
6	ZD	556		
6	ZE	556		
6	ZF	556		
6	ZG	556		

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Mol	Chain	Length	Quality of chain	
6	ZH	556		89%
6	ZI	556		89%
6	ZJ	556		89%
6	ZK	556		89%
6	ZL	556		89%
7	OA	150		91%
7	OB	150		91%
7	OC	150		91%
7	OD	150		91%
7	OE	150		91%
7	OF	150		91%
7	OG	150		91%
7	OH	150		91%
7	OI	150		91%
7	OJ	150		91%
7	OK	150		91%
7	OL	150		91%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 211500 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 30 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AB	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AC	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AD	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AE	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AF	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AG	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AH	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AI	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AJ	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AK	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AL	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		

- Molecule 2 is a protein called Non-contractile tail sheath.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LA	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LB	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LC	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	LD	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LE	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LF	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		

- Molecule 3 is a protein called Probable portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	PA	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PB	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PC	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PD	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PE	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PF	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PG	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PH	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PI	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PJ	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PK	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		
3	PL	675	Total	C	N	O	S	0	0
			5357	3358	943	1033	23		

- Molecule 4 is a protein called Gp64.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SA	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
4	SB	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
4	SD	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
4	SE	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		
4	SF	415	Total	C	N	O	S	0	0
			3383	2212	537	616	18		

- Molecule 5 is a protein called Gp54.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	TA	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TB	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TC	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TD	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TE	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TF	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TG	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TH	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TI	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TJ	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TK	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
5	TL	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		

- Molecule 6 is a protein called 60 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	XA	72	Total	C	N	O	S	0	0
			575	371	92	107	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	XB	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	YA	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	YB	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	ZA	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	ZB	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	XC	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	XD	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	YC	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	YD	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	ZC	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	ZD	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	XE	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	XF	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	YE	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	YF	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	ZE	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	ZF	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	XG	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	XH	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	YG	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	YH	68	Total	C	N	O	S	0	0
			543	355	89	96	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	ZG	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	ZH	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	XI	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	XJ	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	YI	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	YJ	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	ZI	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	ZJ	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	XK	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	XL	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
6	YK	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	YL	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
6	ZK	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
6	ZL	63	Total	C	N	O	S	0	0
			508	330	82	93	3		

- Molecule 7 is a protein called 16.5 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	OA	14	Total	C	N	O	S	0	0
			105	66	16	22	1		
7	OB	14	Total	C	N	O	S	0	0
			105	66	16	22	1		
7	OC	14	Total	C	N	O	S	0	0
			105	66	16	22	1		
7	OD	14	Total	C	N	O	S	0	0
			105	66	16	22	1		
7	OE	14	Total	C	N	O	S	0	0
			105	66	16	22	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	OF	14	Total 105	C 66	N 16	O 22	S 1	0	0
7	OG	14	Total 105	C 66	N 16	O 22	S 1	0	0
7	OH	14	Total 105	C 66	N 16	O 22	S 1	0	0
7	OI	14	Total 105	C 66	N 16	O 22	S 1	0	0
7	OJ	14	Total 105	C 66	N 16	O 22	S 1	0	0
7	OK	14	Total 105	C 66	N 16	O 22	S 1	0	0
7	OL	14	Total 105	C 66	N 16	O 22	S 1	0	0

3 Residue-property plots [i](#)

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: 30 kDa protein

Chain AA: 



- Molecule 1: 30 kDa protein

Chain AB: 



- Molecule 1: 30 kDa protein

Chain AC: 



- Molecule 1: 30 kDa protein

Chain AD: 




- Molecule 1: 30 kDa protein

Chain AE: 



- Molecule 1: 30 kDa protein

Chain AF:  88% 11%




- Molecule 1: 30 kDa protein

Chain AG:  92% 7%



- Molecule 1: 30 kDa protein

Chain AH:  87% 12%




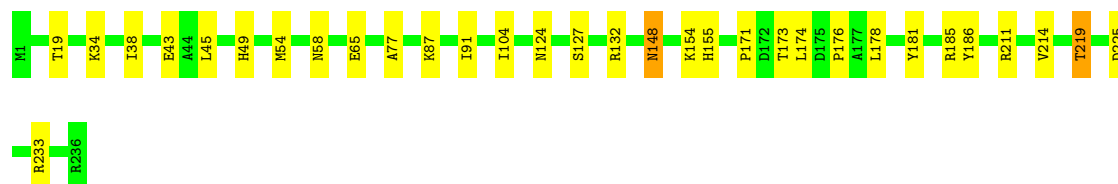
- Molecule 1: 30 kDa protein

Chain AI:  92% 8%



- Molecule 1: 30 kDa protein

Chain AJ:  86% 13%




- Molecule 1: 30 kDa protein

Chain AK:  92% 8%

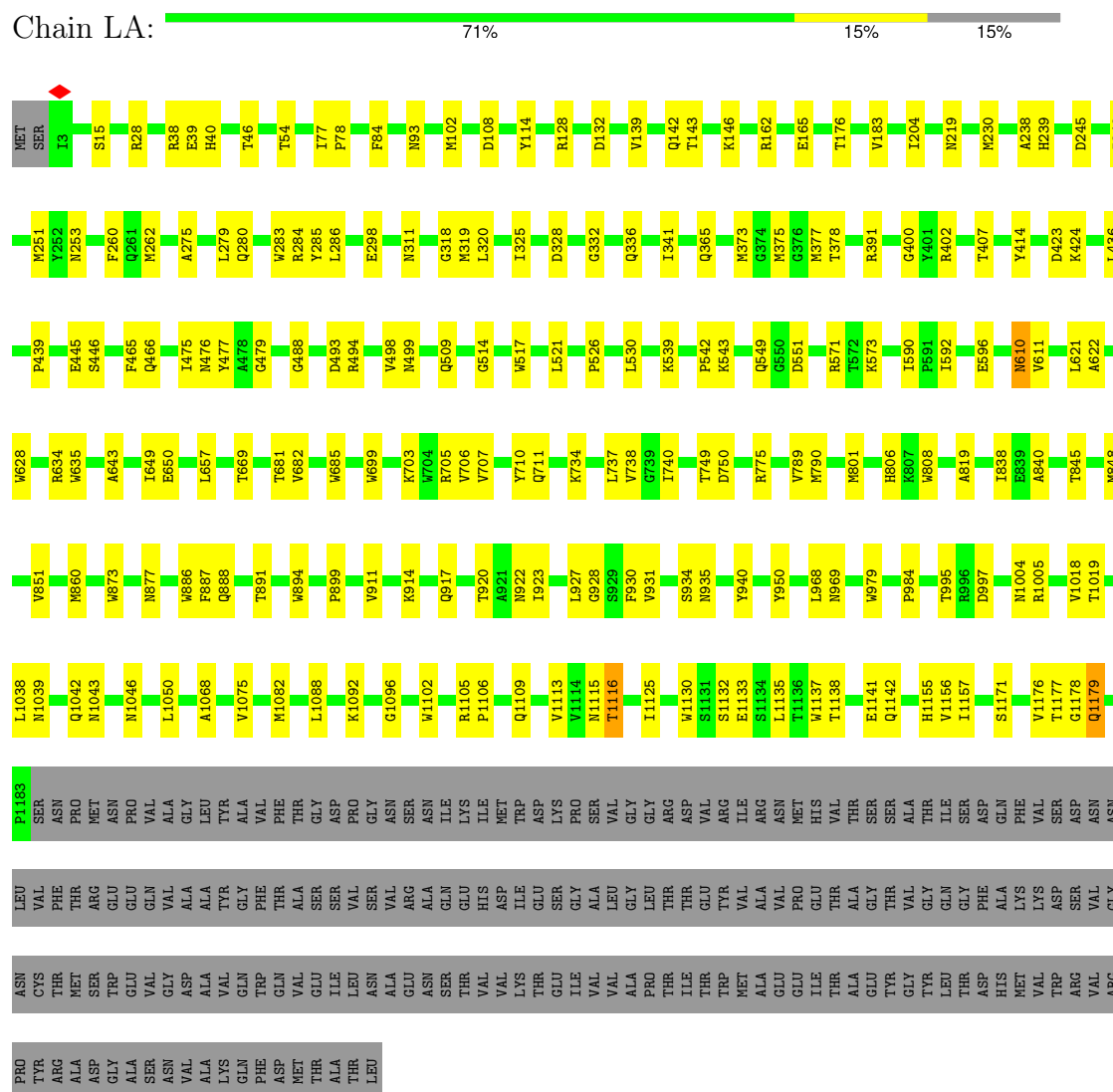


- Molecule 1: 30 kDa protein

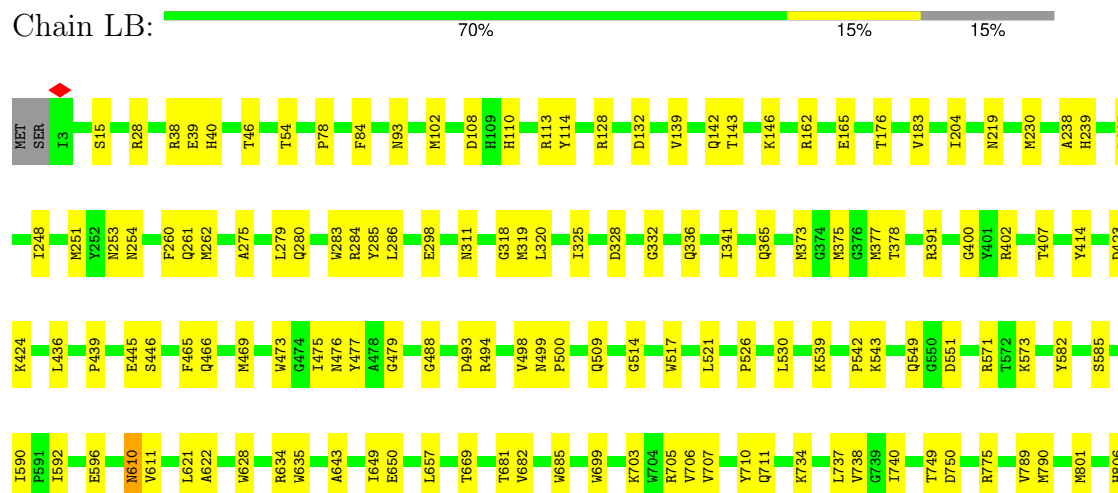
Chain AL:  88% 11%



- Molecule 2: Non-contractile tail sheath



- Molecule 2: Non-contractile tail sheath



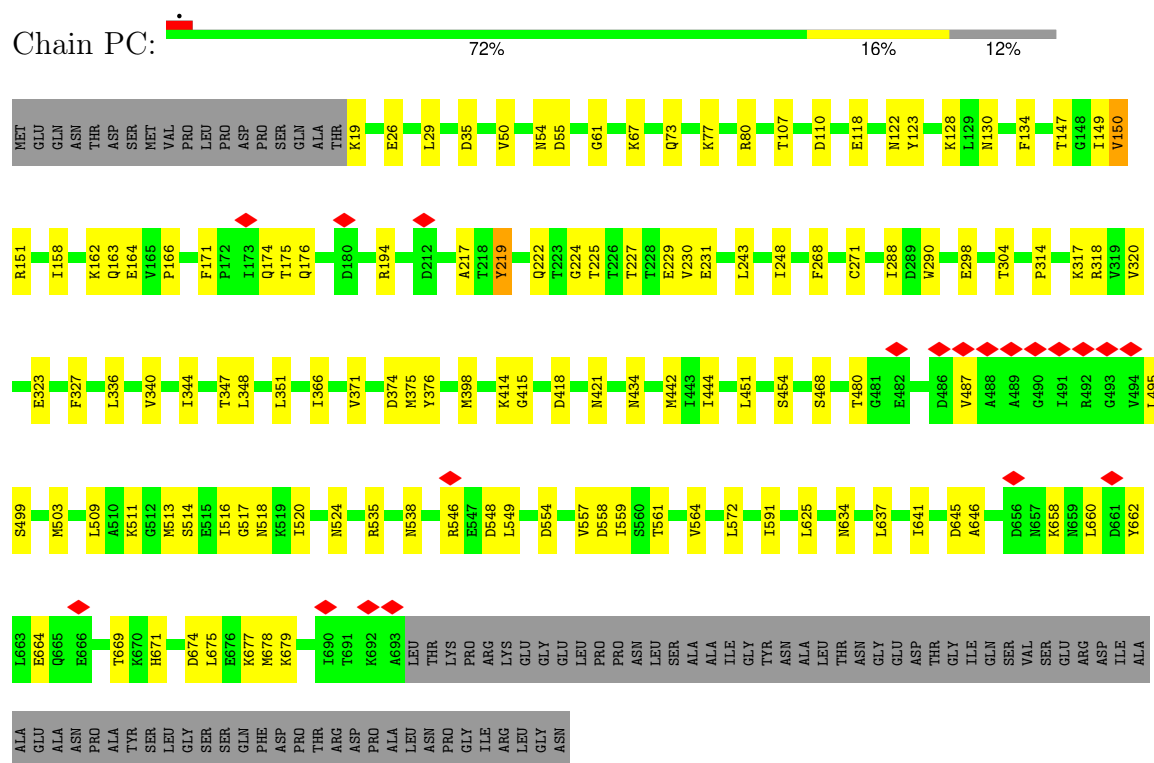
- Molecule 2: Non-contractile tail sheath

Chain LC:

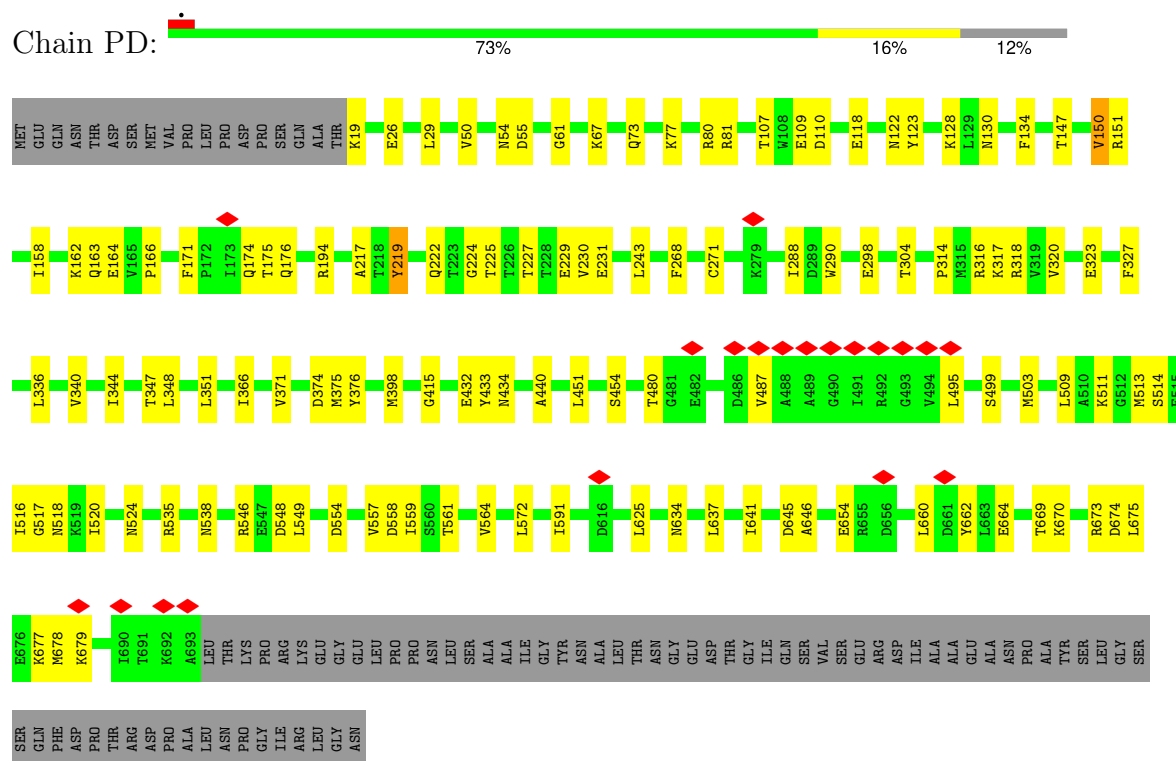




- Molecule 3: Probable portal protein

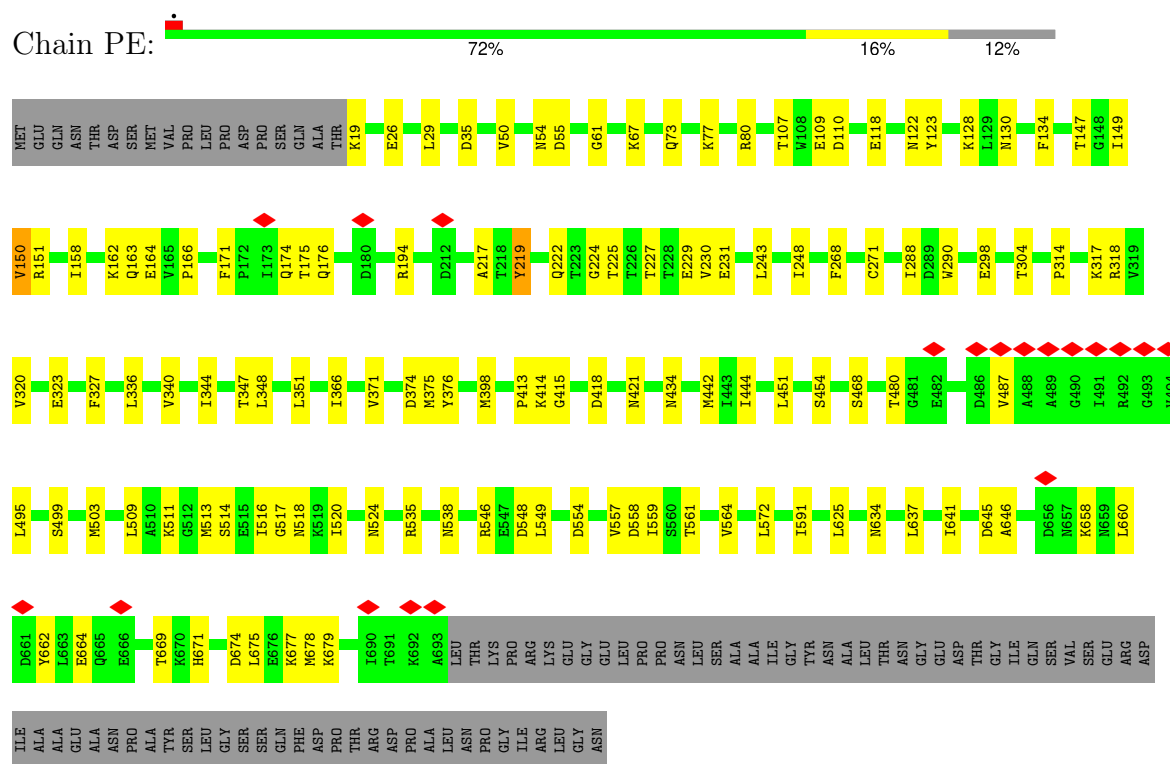


- Molecule 3: Probable portal protein



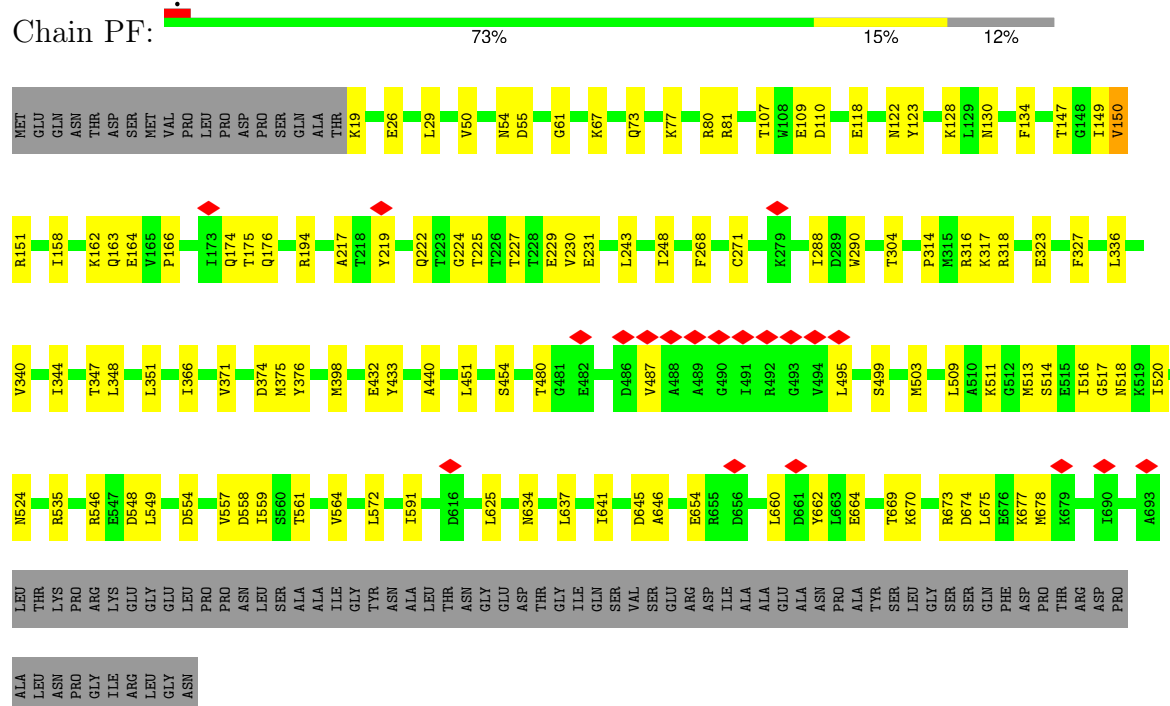
- Molecule 3: Probable portal protein

Chain PE:



- Molecule 3: Probable portal protein

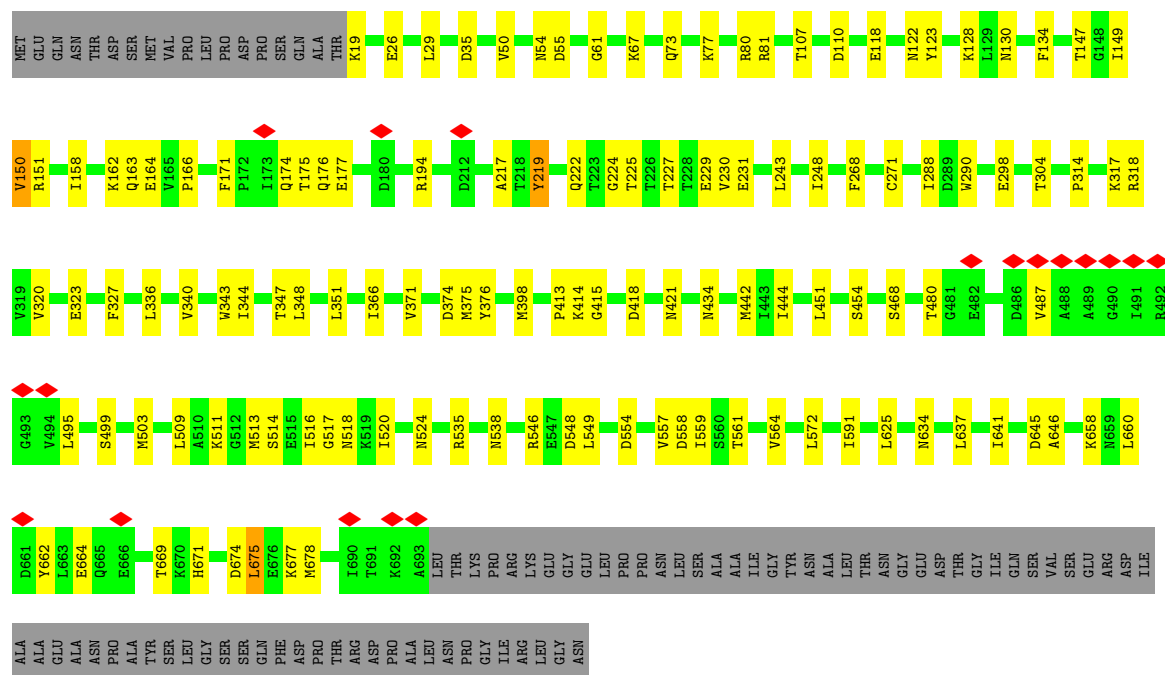
Chain PF:



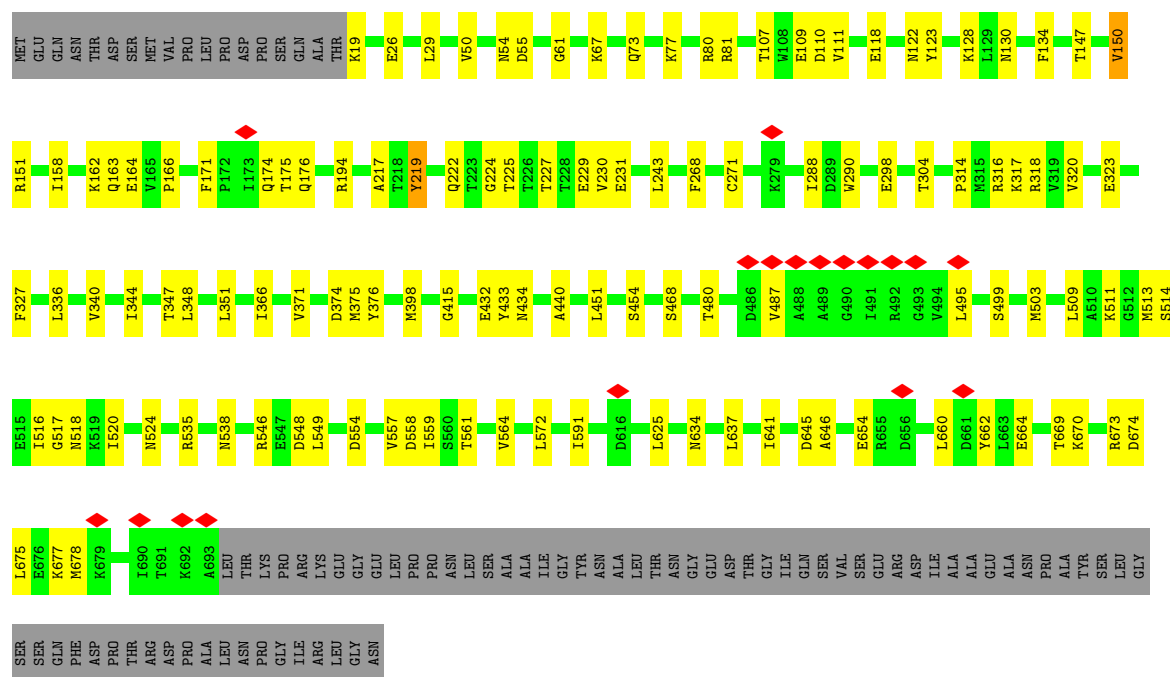
- Molecule 3: Probable portal protein

Chain PG:

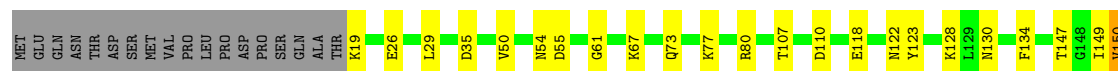




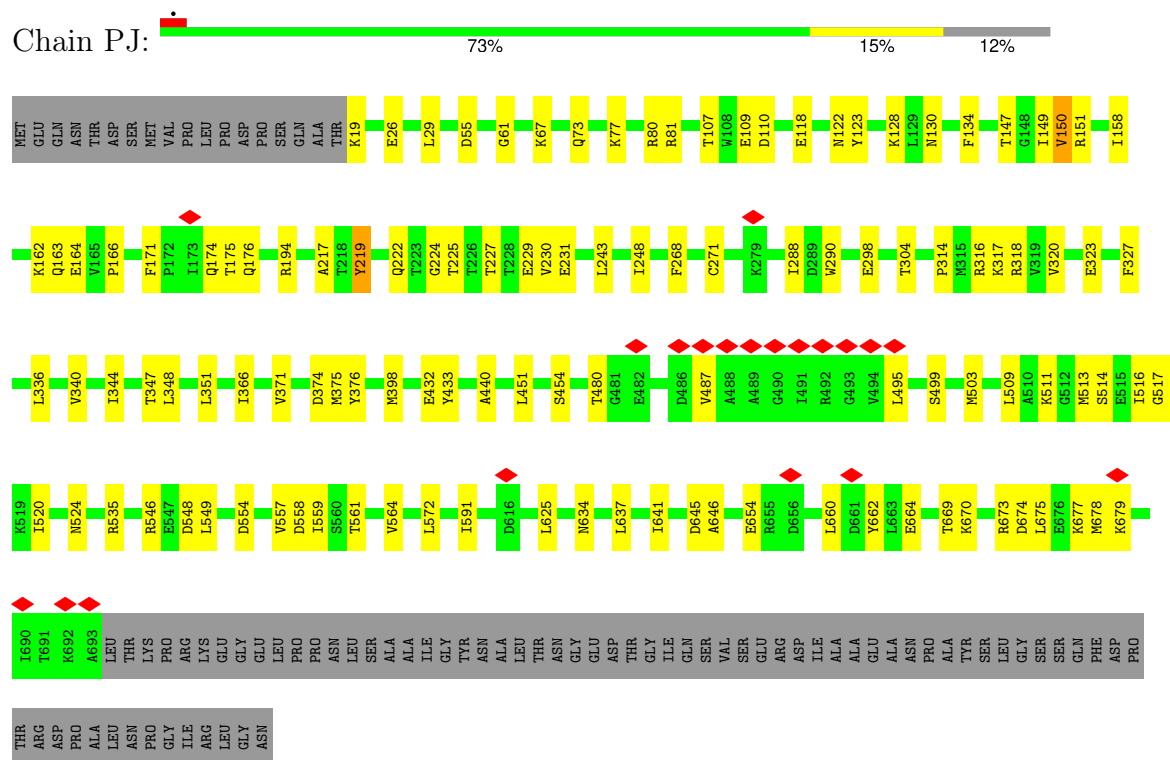
• Molecule 3: Probable portal protein



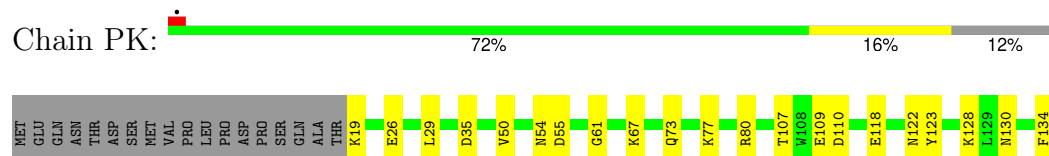
• Molecule 3: Probable portal protein

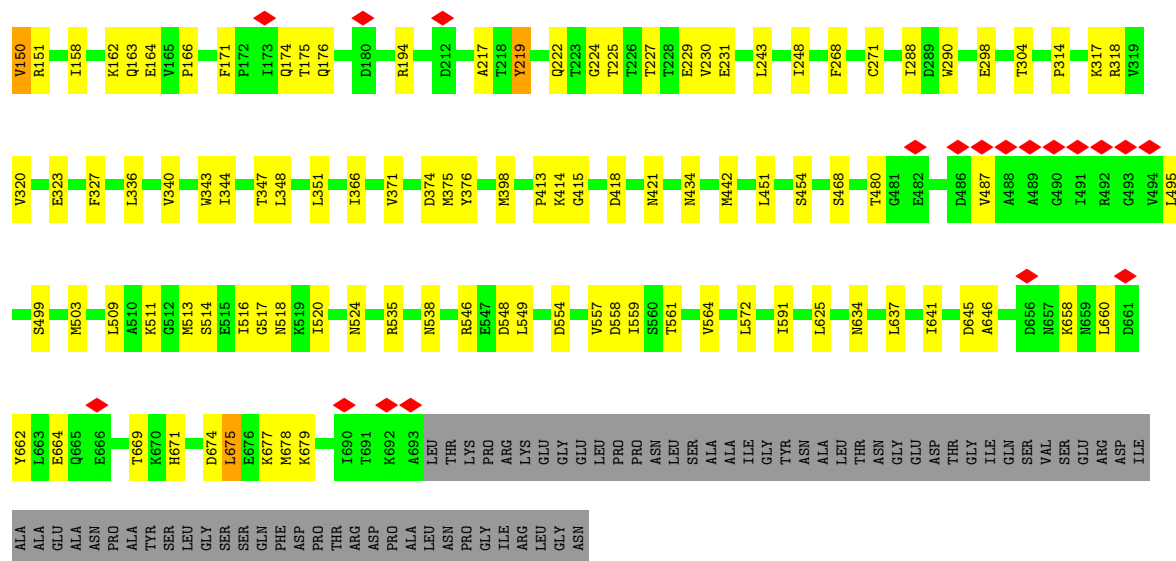


- Molecule 3: Probable portal protein



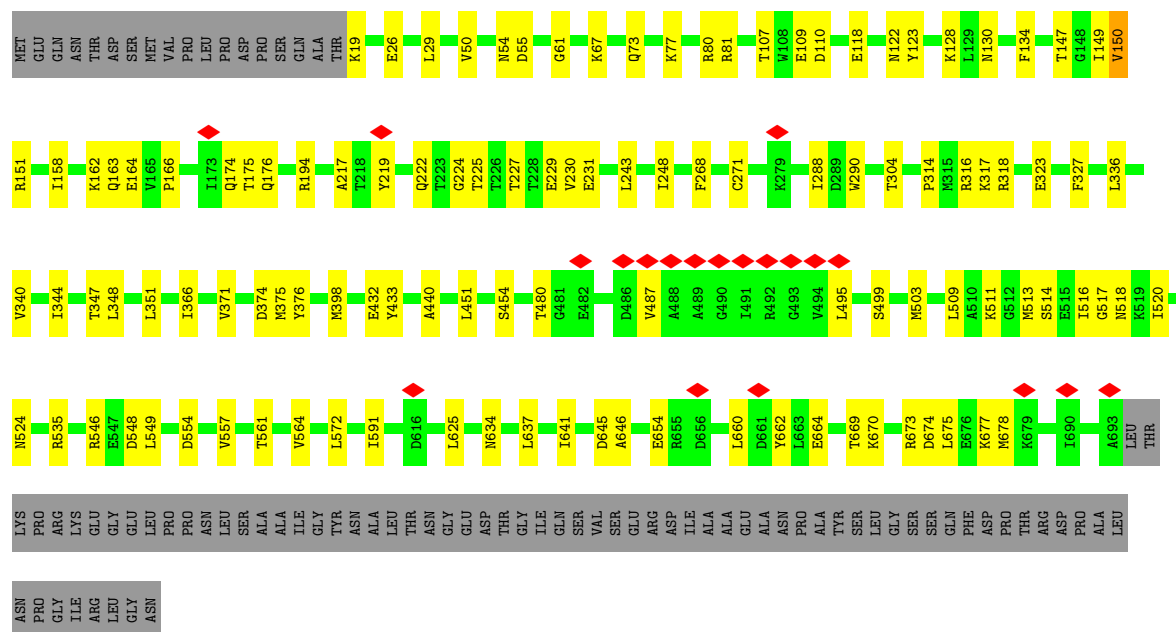
- Molecule 3: Probable portal protein





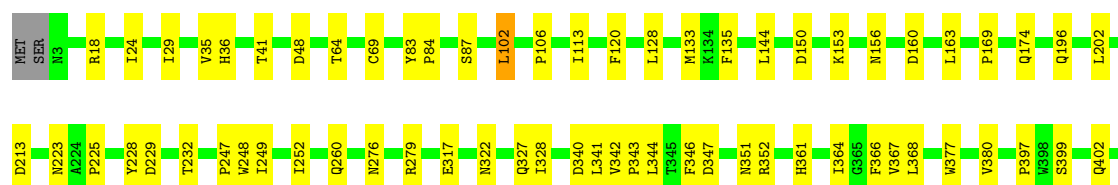
• Molecule 3: Probable portal protein

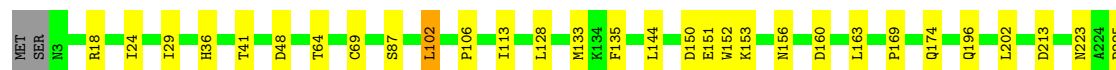
Chain PL: 74% 15% 12%

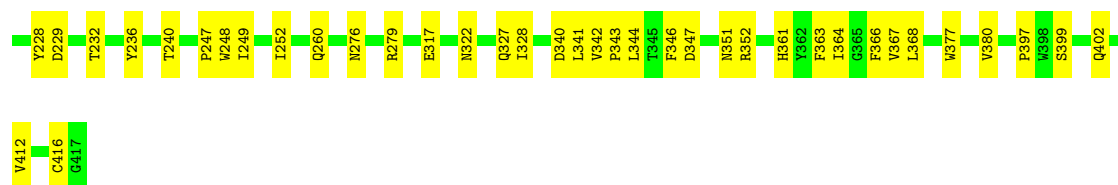


• Molecule 4: Gp64

Chain SA: 83% 16%

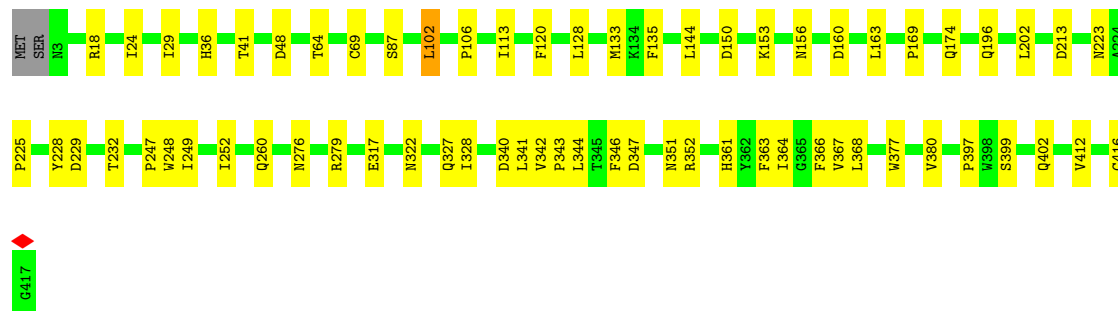






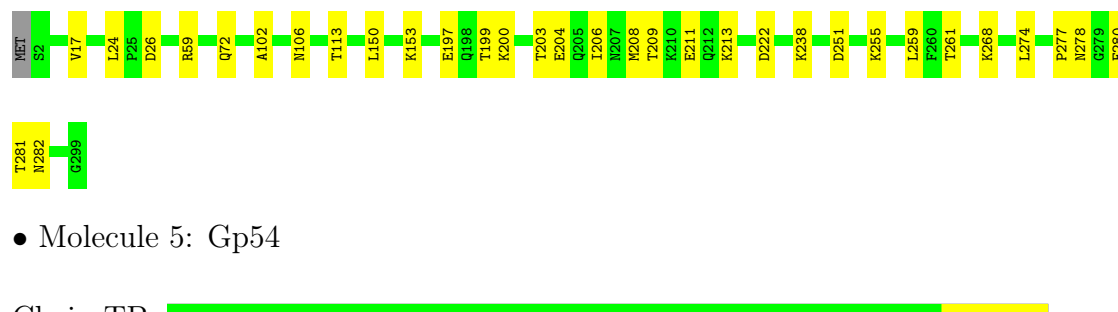
• Molecule 4: Gp64

Chain SF: 84% 15%



• Molecule 5: Gp54

Chain TA: 89% 11%



• Molecule 5: Gp54

Chain TB: 87% 12%



• Molecule 5: Gp54

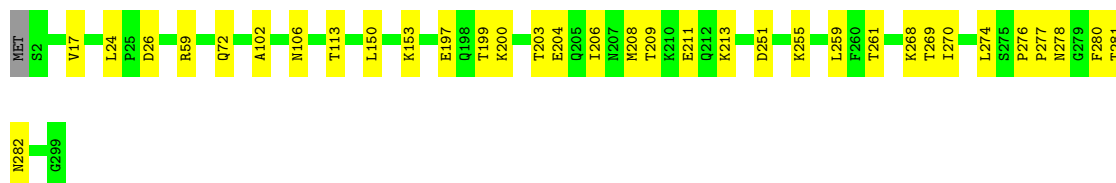
Chain TC: 89% 11%



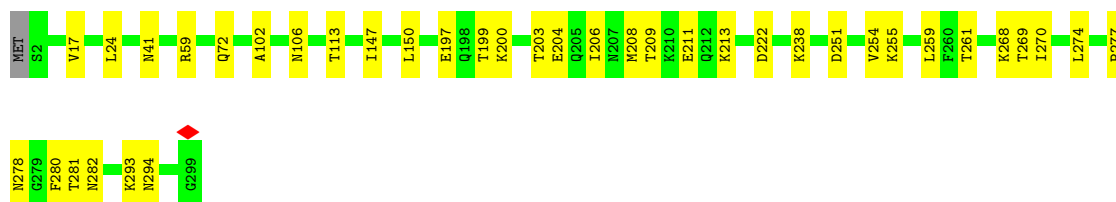
• Molecule 5: Gp54

Chain TD:  88% 11%

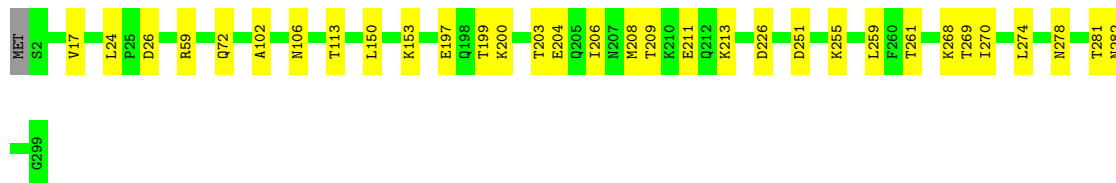
• Molecule 5: Gp54

Chain TE:  88% 11%

• Molecule 5: Gp54

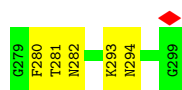
Chain TF:  87% 13%

• Molecule 5: Gp54

Chain TG:  89% 11%

• Molecule 5: Gp54

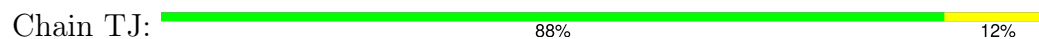
Chain TH:  87% 13%



- Molecule 5: Gp54



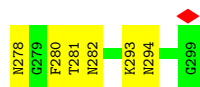
- Molecule 5: Gp54



- Molecule 5: Gp54



- Molecule 5: Gp54



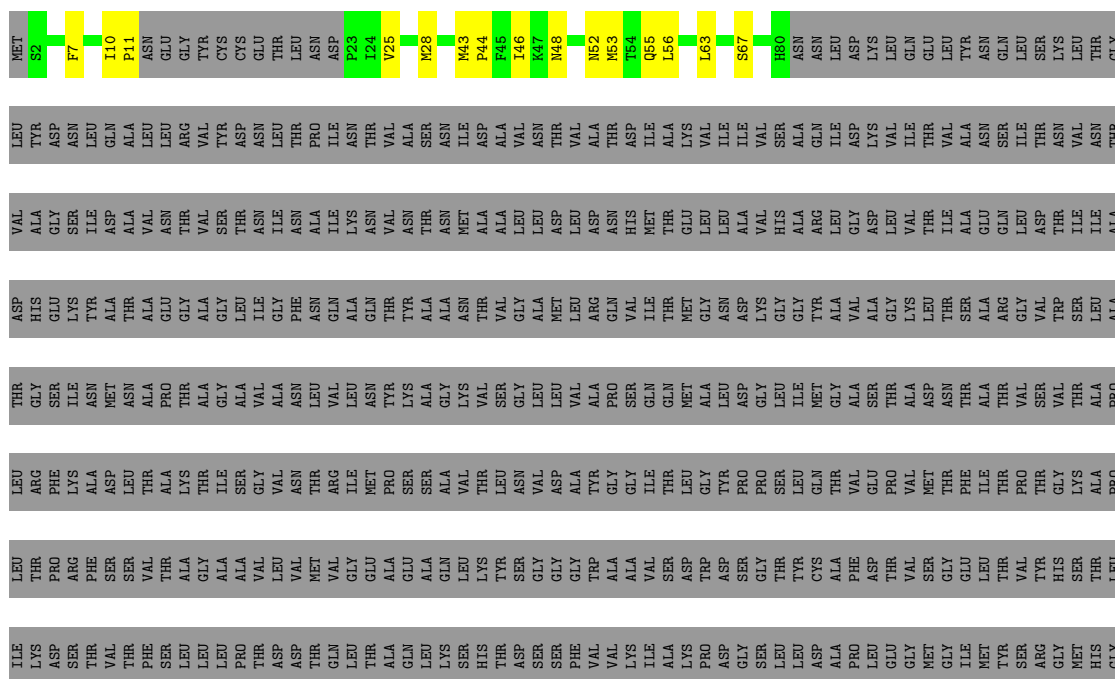
- Molecule 6: 60 kDa protein







- Molecule 6: 60 kDa protein



ASP	VAL	GLY	ARG	ASP	VAL	GLN	VAL	LYS	PHE	SER	GLU	PHE	GLU	ASN	THR	THR	GLU	GLY	ILE	SER	VAL	VAL	GLY	ILE	ASN	SER	ASN	ALA
LEU	PRO	THR	ASP	ASP	THR	GLN	LEU	LEU	THR	ALA	GLN	LEU	LYS	SER	HIS	THR	ASP	SER	SER	PHE	VAL	VAL	LYS	ILE	ALA	PRO	PRO	VAL

- Molecule 6: 60 kDa protein

Chain XC: 9% 1% 87%

[illegible]

- Molecule 6: 60 kDa protein

Chain XD: 11% . 87%

THR	ARG	VAL	LEU	ASN	ALA	PRO	MET
ILE	LEU	LEU	LEU	ALA	ILE	ILE	GLY
MET	MET	THR	GLN	ALA	ASN	THR	SER
PRO	PRO	TYR	THR	GLN	VAL	VAL	THR
SER	SER	LYS	TYR	TYR	ASN	ALA	PRO
SER	ALA	ALA	ALA	ALA	THR	SER	PHE
ALA	GLY	LEU	LEU	ALA	ASN	ASN	ASN
VAL	VAL	VAL	SER	VAL	MET	ILE	T9
THR	THR	VAL	SER	VAL	ALA	ASP	I10
LEU	LEU	LEU	GLY	GLY	LEU	VAL	M43
VAL	VAL	LEU	LEU	ALA	LEU	ASN	P44
ASP	ASP	LEU	VAL	MET	ASP	THR	
ALA	TYR	ALA	TYR	ARG	ASP	VAL	N52
GLY	GLY	PRO	PRO	GLN	ASN	THR	Q65
ILE	GLN	SER	ILE	VAL	HIS	ASP	
THR	GLN	GLN	THR	THR	MET	ILE	K62
LEU	LEU	MET	MET	GLU	THR	ALA	L63
GLY	ALA	ALA	ALA	GLY	LEU	VAL	T64
TYR	LEU	ASN	TYR	ALA	ILE	ILE	E65
PRO	ASP	ASP	ASP	LEU	ALA	ILE	L73
PRO	GLY	LEU	GLY	LYS	VAL	VAL	
SER	LEU	ILE	ILE	GLY	HIS	SER	H80
GLN	MET	TYR	TYR	ARG	ALA	ALA	ASN
THR	THR	ALA	ALA	VAL	GLY	ASP	LEU
VAL	VAL	ALA	ALA	VAL	GLY	LYS	ASP
GLU	SER	THR	THR	ALA	ASP	VAL	LYS
PRO	PRO	VAL	VAL	GLY	LEU	VAL	LEU
MET	MET	ALA	LEU	LYS	VAL	ILE	GLN
THR	ASP	THR	THR	THR	VAL	THR	GLU
PHE	THR	THR	ASN	ILE	ILE	VAL	LEU
ILE	ALA	ALA	SER	ALA	GLU	ALA	TYR
PRO	THR	THR	ARG	GLN	THR	ASN	ASN
PRO	VAL	VAL	VAL	GLY	LEU	ILE	GLM
GLY	SER	VAL	SER	VAL	ASP	THR	SER
LYS	THR	THR	SER	TRP	THR	ASN	LYS
ALA	ALA	ALA	LEU	LEU	ILE	VAL	LEU
PRO	PRO	PRO	PRO	ALA	ILE	ASN	THR
LEU	LEU	LEU	LEU	ASP	ALA	VAL	GLY
THR	THR	ARG	THR	HIS	GLY	ALA	TYR
PRO	PRO	PHE	PHE	SER	GLU	GLY	ASP
ARG	ARG	LYS	ILE	LYS	THR	SER	ASN
PHE	PHE	ALA	ASN	TYR	TYR	ILE	ASN
SER	SER	LEU	ASP	MET	ALA	ASP	GLM
SER	VAL	THR	THR	ALA	VAL	VAL	ALA
ALA	LYS	ALA	PRO	GLU	GLU	ASN	LEU
GLY	GLY	ILE	THR	GLY	GLY	THR	ARG
ALA	ILE	ALA	GLY	VAL	ALA	VAL	TYR
ALA	ALA	ALA	ALA	LEU	LEU	THR	ASP
VAL	VAL	GLY	VAL	VAL	ILE	ASN	ASN
LEU	LEU	VAL	ASN	ALA	PHE	ILE	THR
ALA	ASN	ASN	ASN	THR	THR	THR	LEU



[illegible]

- Molecule 6: 60 kDa protein

Chain ZC: 10% 1% 89%

PRO	THR	PHE	ALA	ASN	TYR	ILE	LEU	MET
TYR	VAL	SER	ASP	MET	ALA	THR	GLN	SER
GLY	THR	SER	SER	ASN	THR	THR	ALA	GLY
SER	PHE	VAL	THR	ALA	GLU	ALA	LEU	HIS
LEU	LEU	THR	ALA	PRO	THR	ASN	LEU	THR
ILE	LEU	ALA	LYS	THR	GLY	ALA	ARG	PRO
VAL	LEU	GLY	THR	ALA	ALA	VAL	VAL	PHE
ASP	LEU	ALA	ILE	GLY	GLY	SER	TYR	ASN
VAL	ASP	VAL	ASN	ASN	PHE	ASN	THR	ASN
GLN	THR	MET	THR	LEU	ASN	ALA	PRO	GLU
VAL	GLN	VAL	ARG	VAL	GLN	ILE	ILE	GLY
LYS	THR	GLY	ILE	LEU	ALA	LYS	ASN	TYR
PHE	THR	GLU	MET	ASN	GLN	ASN	THR	CYS
SER	ALA	ALA	PRO	TYR	THR	VAL	VAL	CYS
GLU	GLN	GLU	SER	LYS	TYR	ASN	ALA	E18
PHE	LEU	ALA	SER	SER	ALA	THR	SER	K37
ASN	LYS	GLN	ALA	GLY	ALA	ASN	ASN	L41
THR	SER	LEU	VAL	LYS	THR	ASN	ASP	M48
THR	HIS	LYS	THR	VAL	THR	ALA	VAL	M52
GLU	THR	THR	LEU	SER	VAL	ALA	ASN	M53
GLY	ASP	SER	VAL	GLY	GLY	THR	THR	H60
ILE	SER	GLY	VAL	LEU	ALA	LEU	ASP	M61
SER	SER	GLY	ASP	LEU	VAL	LEU	ASP	K62
VAL	PHE	GLY	TRP	VAL	TRP	THR	VAL	L63
VAL	VAL	GLY	TRP	ALA	GLY	GLY	VAL	L73
GLY	VAL	ALA	ALA	GLY	GLY	ASN	ILE	Q77
ASN	ILE	VAL	ILE	GLN	ILE	THR	ILE	H80
SER	ALA	SER	SER	SER	GLY	LYS	VAL	ASN
ASN	ALA	THR	THR	LEU	GLY	THR	SER	ASN
ALA	LYS	THR	THR	ILE	GLY	ARG	GLN	ASN
ASP	ASP	CYS	GLN	MET	TYR	THR	ILE	LEU
PRO	ALA	ALA	VAL	GLY	ALA	VAL	ASP	ASP
LEU	LEU	THR	GLU	SER	VAL	VAL	LYS	LYS
GLU	GLY	THR	VAL	THR	ALA	VAL	VAL	LEU
GLY	GLY	SER	VAL	ASP	LEU	THR	THR	GLU
GLY	GLY	GLY	GLY	ASN	THR	ILE	VAL	LEU
ILE	MET	LEU	ILE	THR	SER	ALA	ALA	TYR
TYR	TYR	THR	THR	THR	ALA	GLU	ASN	GLN
ARG	ARG	THR	VAL	SER	VAL	GLY	THR	SER
GLY	GLY	HIS	GLY	VAL	TRP	THR	ASN	LYS
MET	MET	SER	LYS	THR	SER	ILE	VAL	LEU
HIS	THR	THR	ALA	ALA	LEU	ILE	ASN	THR
ILE	ILE	LEU	PRO	PRO	ALA	ALA	VAL	GLY
ILE	ILE	ILE	LEU	LEU	THR	THR	VAL	LEU
TYR	TYR	LYS	THR	ARG	GLY	HIS	ALA	TYR
LYS	LYS	ASP	PRO	THR	SER	GLY	ASP	ASN
VAL	VAL	SER	ARG	LYS	THR	LYS	GLY	ASN

- Molecule 6: 60 kDa protein

Chain ZD:  10% 89%

[illegible]

[illegible]

- Molecule 6: 60 kDa protein

Chain XE: 9% 1% 87%

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

- Molecule 6: 60 kDa protein

Chain XF: 11% . 87%

[illegible]



[illegible]

- Molecule 6: 60 kDa protein

Chain ZE:  9% 89%

Lys	Val	Asp	Pro	Phe	Phe	Ser	Glu	Gly	Asn	Asp	Met
Pro	Pro	Ser	Arg	Phe	Lys	Ile	Lys	Ser	Lys	Ser	Gly
Gly	Tyr	Val	Ser	Ser	Asp	Met	Ala	Ala	Asn	Thr	His
Ser	Thr	Thr	Val	Thr	Thr	Ala	Ala	Ala	Val	Leu	Pro
Leu	Ser	Phe	Thr	Ala	Ala	Pro	Glu	Glu	Asn	Leu	Phe
Leu	Ile	Ser	Thr	Ala	Lys	Thr	Gly	Thr	Thr	Leu	Thr
Val	Val	Leu	Gly	Ala	Ile	Gly	Ala	Ala	Val	Val	Asn
Val	Asp	Leu	Ala	Thr	Thr	Gly	Gly	Ala	Ser	Tyr	Ile
Val	Pro	Pro	Ala	Ser	Ala	Val	Leu	Leu	Thr	Asp	Pro
Gly	Gly	Thr	Val	Gly	Val	Val	Ile	Ile	Asn	Asn	Asn
Arg	Arg	Asp	Leu	Val	Val	Ala	Gly	Ile	Ile	Leu	Glu
Val	Val	Asp	Val	Thr	Asn	Asn	Phe	Asn	Thr	Thr	Gly
Gln	Gln	Thr	Met	Thr	Thr	Leu	Asn	Ala	Pro	Pro	Tyr
Val	Val	Gln	Val	Arg	Ile	Val	Gln	Ile	Ile	Ile	Cys
Lys	Lys	Leu	Gly	Ile	Ile	Leu	Lys	Lys	Asn	Thr	E48
Phe	Phe	Thr	Glu	Ala	Met	Asn	Gln	Asn	Val	Val	K37
Ser	Ser	Ala	Ala	Gln	Pro	Tyr	Tyr	Asn	Ala	Ala	L41
Glu	Glu	Gln	Glu	Ala	Ser	Ala	Ala	Asn	Ser	Asn	N48
Asn	Asn	Lys	Gln	Ala	Ala	Gly	Asn	Met	Ile	Asp	N52
Thr	Thr	Ser	Lys	Thr	Leu	Ser	Val	Ala	Ala	Val	M53
Glu	Glu	Thr	Tyr	Tyr	Leu	Thr	Val	Thr	Val	Val	H60
Thr	Thr	His	Lys	Thr	Thr	Val	Leu	Leu	Ala	Ala	N61
Glu	Glu	Thr	Trp	Ala	Tyr	Ala	Arg	Asp	Thr	Thr	K62
Val	Val	Val	Ala	Gly	Gly	Pro	Gln	Asn	Ala	Asp	L63
Gly	Ile	Ile	Ala	Ile	Ile	Gln	Ile	His	Asp	Ile	T64
Asn	Asn	Ala	Ser	Thr	Thr	Gln	Thr	Thr	Ala	Ala	E65
Asn	Asn	Lys	Asp	Ala	Leu	Met	Met	Glu	Lys	Val	L73
Ala	Ala	Pro	Trp	Trp	Gly	Ala	Gly	Leu	Val	Ile	Q77
	Asp	Asp	Asp	Tyr	Tyr	Leu	Asn	Leu	Ile	Ile	H80
	Ser	Gly	Ser	Pro	Pro	Asp	Lys	Val	Val	Val	Asn
	Leu	Leu	Thr	Thr	Ser	Leu	Gly	His	Ser	Ala	Asn
	Asp	Asp	Cys	Ala	Gln	Met	Tyr	Arg	Gln	Gln	Asn
	Ala	Ala	Ala	Ala	Thr	Gly	Ala	Leu	Ile	Ile	Asn
	Pro	Pro	Phe	Phe	Val	Ala	Val	Gly	Leu	Leu	Leu
	Leu	Leu	Asp	Glu	Glu	Ser	Ala	Asp	Lys	Lys	Asp
	Glu	Glu	Thr	Pro	Val	Thr	Gly	Leu	Val	Val	Gln
	Gly	Gly	Val	Val	Val	Ala	Lys	Val	Ile	Ile	Glu
	Met	Met	Ser	Met	Met	Asp	Leu	Thr	Thr	Val	Leu
	Gly	Ile	Gly	Glu	Phe	Thr	Thr	Ile	Ala	Val	Leu
	Ile	Met	Leu	Leu	Ile	Ala	Ala	Glu	Asn	Ala	Tyr
	Tyr	Tyr	Thr	Thr	Thr	Thr	Arg	Gln	Ser	Ser	Gln
	Ser	Ser	Val	Pro	Pro	Val	Gly	Leu	Ile	Ile	Ser
	Arg	Arg	Tyr	Thr	Thr	Ser	Val	Asp	Thr	Thr	Lys
	Gly	Gly	His	Ser	Gly	Val	Trp	Thr	Asn	Val	Thr
	Met	Met	Ser	Thr	Lys	Thr	Ala	Ile	Val	Val	Leu
	His	His	Thr	Leu	Ala	Ala	Leu	Ile	Asn	Asn	Thr
	Gly	Gly	Leu	Leu	Pro	Pro	Ala	Ala	Thr	Thr	Gly
	Ile	Ile	Lys	Ile	Thr	Arg	Thr	Val	Val	Val	Leu
	Thr	Thr	Lys	Thr	Thr	Asp	Gly	His	Val	Val	Thr

- Molecule 6: 60 kDa protein

Chain ZF:  10% . 89%

Met	Ser	Gly	His	Pro	Phe	Asn	Thr	Leu	Pro	Pro	Ala	Glu	Gly	Trp	Cys	Cys	Leu	Asn	Met	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



- Molecule 6: 60 kDa protein



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

- Molecule 6: 60 kDa protein

Chain XJ: 11% 87%

[illegible]

- Molecule 6: 60 kDa protein

Chain YI: 11% • 88%

[illegible]

[illegible]

- Molecule 6: 60 kDa protein

Chain YJ: 10% 1% 88%

Lys	Val	Pro	Tyr	Gly	Ser	Leu	Leu	Val	Pro	Ala	Phe	Ser	Glu	Gly	Asp	Met
Val	Pro	Phe	Ser	Ser	Ser	Ser	Val	Thr	Thr	Ala	Ala	Ile	Lys	Arg	Ser	S2
Tyr	Val	Ser	Thr	Thr	Thr	Thr	Val	Thr	Ser	Thr	Thr	Met	Tyr	Ala	Asp	F7
Ser	Leu	Ser	Thr	Thr	Thr	Thr	Val	Thr	Val	Thr	Thr	Ala	Ala	Val	Leu	I10
Ser	Leu	Val	Thr	Thr	Thr	Thr	Val	Thr	Thr	Ala	Gly	Ala	Glu	Asn	Leu	P11
Ile	Val	Ala	Leu	Ala	Ala	Ala	Val	Ala	Ala	Thr	Lys	Pro	Glu	Arg	Leu	Asn
Val	Val	Ala	Leu	Ala	Ile	Ile	Ala	Gly	Gly	Val	Thr	Gly	Val	Tyr	Gly	Glu
Val	Val	Ala	Ala	Ala	Ala	Ser	Ala	Leu	Leu	Ser	Ala	Leu	Leu	Thr	Tyr	Tyr
Gly	Thr	Val	Thr	Thr	Gly	Gly	Val	Ile	Ile	Ala	Gly	Val	Ala	Asn	Cys	Cys
Arg	Val	Leu	Val	Val	Val	Val	Ala	Ala	Ala	Ala	Phe	Gly	Gly	Leu	Glu	Glu
Val	Val	Met	Thr	Thr	Thr	Thr	Asn	Asn	Asn	Asn	Asn	Leu	Thr	Thr	Pro	Thr
Val	Val	Val	Ala	Gly	Gly	Ile	Val	Ala	Ala	Ala	Gln	Lys	Asn	Asn	Asp	Asp
Phe	Thr	Glu	Thr	Thr	Thr	Met	Asn	Gln	Gln	Thr	Thr	Val	Val	Val	Val	P23
Ser	Ala	Ala	Ala	Ser	Ser	Ser	Lys	Tyr	Tyr	Tyr	Ala	Ala	Ala	Ala	Ala	I24
Glu	Gln	Glu	Leu	Leu	Leu	Ala	Gly	Ala	Ala	Gly	Ala	Ala	Ala	Asn	Ser	V26
Phe	Asn	Ala	Ser	Leu	Ser	Val	Val	Lys	Val	Lys	Met	Met	Ile	Ile	Thr	Met
Thr	Thr	Lys	His	Thr	Thr	Leu	Thr	Val	Ser	Val	Thr	Ala	Ala	Asp	Asp	M28
Glu	Thr	Tyr	Thr	Thr	Thr	Leu	Val	Thr	Val	Gln	Gln	Ala	Ala	Ala	Ala	M43
Gly	Gly	Ser	Asp	Ser	Ser	Asn	Gly	Gly	Gly	Ser	Val	His	His	Thr	Thr	P44
Ile	Ile	Gly	Ser	Gly	Gly	Val	Val	Ala	Ala	Ile	Ile	Met	Met	Ile	Ile	F45
Ser	Ser	Thr	Ala	Ser	Thr	Thr	Gln	Gln	Gln	Thr	Thr	Thr	Thr	Thr	Thr	I46
Val	Val	Gly	Phe	Thr	Thr	Ala	Val	Val	Val	Val	Leu	Leu	Val	Val	Val	K47
Val	Val	Trp	Val	Val	Val	Tyr	Thr	Thr	Ala	Ala	Arg	Asp	Asp	Ala	Ala	M48
Gly	Val	Ala	Val	Val	Ala	Gly	Ala	Gly	Pro	Gln	Gln	Asn	Asn	Thr	Thr	Asn
Ile	Ile	Ala	Lys	Lys	Ala	Gly	Thr	Thr	Ser	Val	Val	His	His	Ala	Ala	N52
Asn	Asn	Val	Ala	Ala	Ala	Ile	Val	Val	Gln	Ile	Ile	Met	Met	Ile	Ile	M53
Asn	Asn	Ser	Ser	Ser	Thr	Thr	Ser	Ser	Gln	Thr	Thr	Thr	Thr	Thr	Thr	T54
Ala	Ala	Asp	Lys	Lys	Ala	Leu	Asp	Ala	Ala	Met	Met	Glu	Glu	Lys	Val	Q55
		Trp	Pro	Trp	Trp	Gly	Trp	Thr	Ala	Ala	Gly	Leu	Leu	Val	Val	L56
		Asp	Pro	Asp	Asp	Tyr	Asp	Thr	Ala	Thr	Asn	Leu	Leu	Ile	Ile	
		Ser	Gly	Ser	Gly	Pro	Gly	Pro	Asp	Val	Lys	Val	Val	Ile	Ile	
		Leu	Leu	Leu	Leu	Ser	Ser	Thr	Ser	Lys	Gly	His	His	Ala	Ala	
		Thr	Thr	Thr	Thr	Leu	Thr	Gln	Ile	Gly	Gly	Arg	Arg	Gln	Gln	
		Cys	Ala	Ala	Ala	Thr	Met	Met	Met	Tyr	Tyr	Arg	Arg	Gln	Gln	
		Phe	Pro	Pro	Pro	Val	Val	Val	Gly	Ala	Val	Leu	Leu	Ile	Ile	
		Asp	Leu	Leu	Leu	Val	Ser	Ser	Asp	Val	Val	Gly	Asp	Asp	Asp	
		Thr	Glu	Glu	Glu	Val	Ser	Ser	Asp	Val	Val	Lys	Lys	Lys	Lys	
		Gly	Gly	Gly	Gly	Val	Val	Val	Ala	Lys	Lys	Val	Val	Ile	Ile	
		Met	Met	Met	Met	Met	Met	Met	Ala	Thr	Thr	Thr	Thr	Thr	Thr	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Ser	Arg	Ser	Arg	Val	Val	Val	Ser	Val	Val	Gly	Gly	Val	Val	
		His	Gly	His	Gly	His	His	His	Ser	His	His	His	His	His	His	
		Thr	Met	Thr	Met	Thr	Met	Thr	Val	Val	Val	Val	Val	Val	Val	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		Ile	Ile	Ile	Ile	Ile	Ile	Ile	Pro	Pro	Pro	Pro	Pro	Pro	Pro	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
		Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
		Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	Val	
		Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	
		Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
		His	His	His	His	His	His	His	His	His	His	His	His	His	His	
		Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn		

- Molecule 6: 60 kDa protein

Chain ZI: 9% . 89%

[illegible]

[illegible]

- Molecule 6: 60 kDa protein

Chain ZJ: 10% 89%

[illegible]

- Molecule 6: 60 kDa protein

Chain XK: 10% 87%

[illegible]

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

- Molecule 6: 60 kDa protein

Chain ZL:  10% . 89%

[illegible]

- Molecule 7: 16.5 kDa protein

Chain OA:  9% 91%

Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100	Q101	Q102	Q103	Q104	Q105	Q106	Q107	Q108	Q109	Q110	Q111	Q112	Q113	Q114	Q115	Q116	Q117	Q118	Q119	Q120	Q121	Q122	Q123	Q124	Q125	Q126	Q127	Q128	Q129	Q130	Q131	Q132	Q133	Q134	Q135	Q136	Q137	Q138	Q139	Q140	Q141	Q142	Q143	Q144	Q145	Q146	Q147	Q148	Q149	Q150	Q151	Q152	Q153	Q154	Q155	Q156	Q157	Q158	Q159	Q160	Q161	Q162	Q163	Q164	Q165	Q166	Q167	Q168	Q169	Q170	Q171	Q172	Q173	Q174	Q175	Q176	Q177	Q178	Q179	Q180	Q181	Q182	Q183	Q184	Q185	Q186	Q187	Q188	Q189	Q190	Q191	Q192	Q193	Q194	Q195	Q196	Q197	Q198	Q199	Q200	Q201	Q202	Q203	Q204	Q205	Q206	Q207	Q208	Q209	Q210	Q211	Q212	Q213	Q214	Q215	Q216	Q217	Q218	Q219	Q220	Q221	Q222	Q223	Q224	Q225	Q226	Q227	Q228	Q229	Q230	Q231	Q232	Q233	Q234	Q235	Q236	Q237	Q238	Q239	Q240	Q241	Q242	Q243	Q244	Q245	Q246	Q247	Q248	Q249	Q250	Q251	Q252	Q253	Q254	Q255	Q256	Q257	Q258	Q259	Q260	Q261	Q262	Q263	Q264	Q265	Q266	Q267	Q268	Q269	Q270	Q271	Q272	Q273	Q274	Q275	Q276	Q277	Q278	Q279	Q280	Q281	Q282	Q283	Q284	Q285	Q286	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299	Q300	Q301	Q302	Q303	Q304	Q305	Q306	Q307	Q308	Q309	Q310	Q311	Q312	Q313	Q314	Q315	Q316	Q317	Q318	Q319	Q320	Q321	Q322	Q323	Q324	Q325	Q326	Q327	Q328	Q329	Q330	Q331	Q332	Q333	Q334	Q335	Q336	Q337	Q338	Q339	Q340	Q341	Q342	Q343	Q344	Q345	Q346	Q347	Q348	Q349	Q350	Q351	Q352	Q353	Q354	Q355	Q356	Q357	Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416	Q417	Q418	Q419	Q420	Q421	Q422	Q423	Q424	Q425	Q426	Q427	Q428	Q429	Q430	Q431	Q432	Q433	Q434	Q435	Q436	Q437	Q438	Q439	Q440	Q441	Q442	Q443	Q444	Q445	Q446	Q447	Q448	Q449	Q450	Q451	Q452	Q453	Q454	Q455	Q456	Q457	Q458	Q459	Q460	Q461	Q462	Q463	Q464	Q465	Q466	Q467	Q468	Q469	Q470	Q471	Q472	Q473	Q474	Q475	Q476	Q477	Q478	Q479	Q480	Q481	Q482	Q483	Q484	Q485	Q486	Q487	Q488	Q489	Q490	Q491	Q492	Q493	Q494	Q495	Q496	Q497	Q498	Q499	Q500	Q501	Q502	Q503	Q504	Q505	Q506	Q507	Q508	Q509	Q510	Q511	Q512	Q513	Q514	Q515	Q516	Q517	Q518	Q519	Q520	Q521	Q522	Q523	Q524	Q525	Q526	Q527	Q528	Q529	Q530	Q531	Q532	Q533	Q534	Q535	Q536	Q537	Q538	Q539	Q540	Q541	Q542	Q543	Q544	Q545	Q546	Q547	Q548	Q549	Q550	Q551	Q552	Q553	Q554	Q555	Q556	Q557	Q558	Q559	Q560	Q561	Q562	Q563	Q564	Q565	Q566	Q567	Q568	Q569	Q570	Q571	Q572	Q573	Q574	Q575	Q576	Q577	Q578	Q579	Q580	Q581	Q582	Q583	Q584	Q585	Q586	Q587	Q588	Q589	Q590	Q591	Q592	Q593	Q594	Q595	Q596	Q597	Q598	Q599	Q600	Q601	Q602	Q603	Q604	Q605	Q606	Q607	Q608	Q609	Q610	Q611	Q612	Q613	Q614	Q615	Q616	Q617	Q618	Q619	Q620	Q621	Q622	Q623	Q624	Q625	Q626	Q627	Q628	Q629	Q630	Q631	Q632	Q633	Q634	Q635	Q636	Q637	Q638	Q639	Q640	Q641	Q642	Q643	Q644	Q645	Q646	Q647	Q648	Q649	Q650	Q651	Q652	Q653	Q654	Q655	Q656	Q657	Q658	Q659	Q660	Q661	Q662	Q663	Q664	Q665	Q666	Q667	Q668	Q669	Q670	Q671	Q672	Q673	Q674	Q675	Q676	Q677	Q678	Q679	Q680	Q681	Q682	Q683	Q684	Q685	Q686	Q687	Q688	Q689	Q690	Q691	Q692	Q693	Q694	Q695	Q696	Q697	Q698	Q699	Q700	Q701	Q702	Q703	Q704	Q705	Q706	Q707	Q708	Q709	Q710	Q711	Q712	Q713	Q714	Q715	Q716	Q717	Q718	Q719	Q720	Q721	Q722	Q723	Q724	Q725	Q726	Q727	Q728	Q729	Q730	Q731	Q732	Q733	Q734	Q735	Q736	Q737	Q738	Q739	Q740	Q741	Q742	Q743	Q744	Q745	Q746	Q747	Q748	Q749	Q750	Q751	Q752	Q753	Q754	Q755	Q756	Q757	Q758	Q759	Q760	Q761	Q762	Q763	Q764	Q765	Q766	Q767	Q768	Q769	Q770	Q771	Q772	Q773	Q774	Q775	Q776	Q777	Q778	Q779	Q780	Q781	Q782	Q783	Q784	Q785	Q786	Q787	Q788	Q789	Q790	Q791	Q792	Q793	Q794	Q795	Q796	Q797	Q798	Q799	Q800	Q801	Q802	Q803	Q804	Q805	Q806	Q807	Q808	Q809	Q810	Q811	Q812	Q813	Q814	Q815	Q816	Q817	Q818	Q819	Q820	Q821	Q822	Q823	Q824	Q825	Q826	Q827	Q828	Q829	Q830	Q831	Q832	Q833	Q834	Q835	Q836	Q837	Q838	Q839	Q840	Q841	Q842	Q843	Q844	Q845	Q846	Q847	Q848	Q849	Q850	Q851	Q852	Q853	Q854	Q855	Q856	Q857	Q858	Q859	Q860	Q861	Q862	Q863	Q864	Q865	Q866	Q867	Q868	Q869	Q870	Q871	Q872	Q873	Q874	Q875	Q876	Q877	Q878	Q879	Q880	Q881	Q882	Q883	Q884	Q885	Q886	Q887	Q888	Q889	Q890	Q891	Q892	Q893	Q894	Q895	Q896	Q897	Q898	Q899	Q900	Q901	Q902	Q903	Q904	Q905	Q906	Q907	Q908	Q909	Q910	Q911	Q912	Q913	Q914	Q915	Q916	Q917	Q918	Q919	Q920	Q921	Q922	Q923	Q924	Q925	Q926	Q927	Q928	Q929	Q930	Q931	Q932	Q933	Q934	Q935	Q936	Q937	Q938	Q939	Q940	Q941	Q942	Q943	Q944	Q945	Q946	Q947	Q948	Q949	Q950	Q951	Q952	Q953	Q954	Q955	Q956	Q957	Q958	Q959	Q960	Q961	Q962	Q963	Q964	Q965	Q966	Q967	Q968	Q969	Q970	Q971	Q972	Q973	Q974	Q975	Q976	Q977	Q978	Q979	Q980	Q981	Q982	Q983	Q984	Q985	Q986	Q987	Q988	Q989	Q990	Q991	Q992	Q993	Q994	Q995	Q996	Q997	Q998	Q999	Q1000
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THR	PHE	GLN	LEU	GLY	LEU	GLY	GLY	LEU	ASN	ALA	LEU	GLY	PHE	ASN	ILE	TYR	GLY	ALA	LEU	ASP	ARG	ALA	ARG	SER	ARG	ALA	PRO																									
HQ	Q12	S13	ASN	PHE	GLY	TYR	GLY	TYR	GLY	SER	PHE	ASN	THR	PRO	THR	MET	ASN	TYR	ASN	PRO	LEU	GLN	SER	GLY	ILE	LEU	SER	ASN	ASP	TRP	LEU	GLN	ASN	THR	GLY	GLY	ALA	THR	GLY	GLN	THR	GLN	GLY	LEU	THR	ASP	GLN	LEU	GLY	ASN	TLE	PRO

ALA
GLU
ASN
ARG
ASP
GLN
SER
THR
ALA
ALA
TYR
TLE
ALA
ALA
ASN
ARG
LEU
THR
ARG

● Molecule 7: 16.5 kDa protein

Chain OF: 9% 91%

NO
DI
S13
ASN
PHE
GLY
GLY
TYR
LEU
TYR
TYR
ALA
ALA
SER
PHE
ASN
THR
PRO
MET
ALA
MET
ASN
TYR
ASN
PRO
LEU
LEU
GLN
SER
GLY
ILE
LEU
GLN
SER
PHE
SER
ASN
ASP
TRP
LEU
GLN
ASN
THR
ILE
THR
GLY
GLY
ALA
ALA
THR
GLY
ASN
GLN
ASN
TLE
THR
GLY
GLY
TLE
THR
GLN
GLN
GLY
LEU
LEU
ASN
PRO
VAL

THR
PHE
GLN
LEU
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LEU
ASN
TYR
ALA
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ALA
TYR
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ALA
ASN
ARG
LEU
THR
ARG

● Molecule 7: 16.5 kDa protein

Chain OG: 9% 91%

NO
Q12
S13
ASN
PHE
GLY
TYR
GLY
TYR
GLY
ALA
ALA
GLY
SER
PHE
ASN
THR
PRO
MET
ASN
TYR
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ALA
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ARG

● Molecule 7: 16.5 kDa protein

Chain OH: 9% 91%

NO
DI
S13
ASN
PHE
GLY
GLY
TYR
LEU
TYR
TYR
ALA
ALA
SER
PHE
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GLY
ASN
GLY
ASN
GLN
TLE
THR
GLY
GLY
TLE
THR
GLN
GLN
THR
GLY
LEU
THR
ASP
ARG
GLN
LEU
GLY
LEU
ASN
TLE
PRO

THR
PHE
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ASN
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ALA
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ALA
THR
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ASP
ARG
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SER
ARG
TLE
VAL

ALA
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ARG
ASP
GLN
SER
THR
ALA
ASP
ALA
ALA
TYR
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ALA
ALA
ASN
ARG
LEU
THR
ARG

● Molecule 7: 16.5 kDa protein

Chain OI: 9% 91%

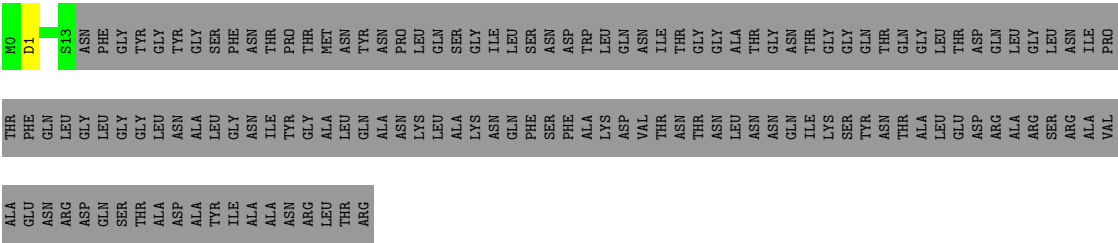
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Q12
S13
ASN
PHE
GLY
TYR
GLY
TYR
GLY
ALA
ALA
GLY
SER
PHE
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THR
PRO
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GLY
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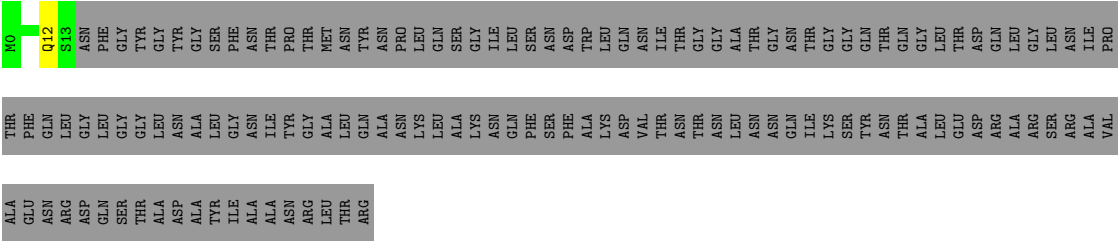
● Molecule 7: 16.5 kDa protein

Chain OJ: 9% . 91%



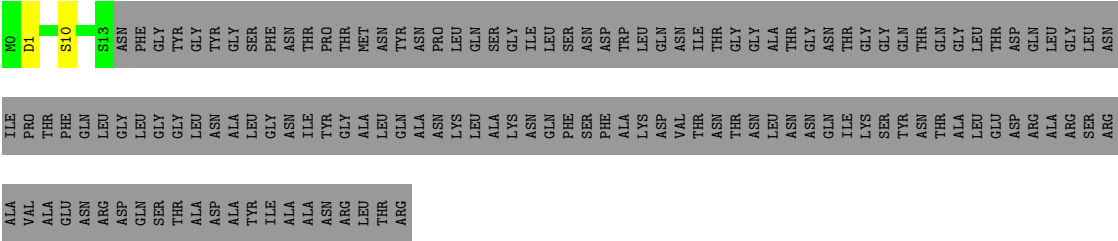
● Molecule 7: 16.5 kDa protein

Chain OK: 9% . 91%



● Molecule 7: 16.5 kDa protein

Chain OL: 8% . 91%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16320	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.694	Depositor
Minimum map value	-0.359	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.0693	Depositor
Map size (Å)	266.262, 265.068, 499.092	wwPDB
Map dimensions	418, 222, 223	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.194, 1.194, 1.194	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	AA	0.08	0/1953	0.19	0/2654
1	AB	0.09	0/1953	0.20	0/2654
1	AC	0.08	0/1953	0.19	0/2654
1	AD	0.09	0/1953	0.20	0/2654
1	AE	0.08	0/1953	0.19	0/2654
1	AF	0.09	0/1953	0.20	0/2654
1	AG	0.08	0/1953	0.19	0/2654
1	AH	0.09	0/1953	0.20	0/2654
1	AI	0.08	0/1953	0.19	0/2654
1	AJ	0.09	0/1953	0.20	0/2654
1	AK	0.08	0/1953	0.19	0/2654
1	AL	0.09	0/1953	0.20	0/2654
2	LA	0.07	0/9606	0.22	0/13093
2	LB	0.07	0/9606	0.22	0/13093
2	LC	0.07	0/9606	0.22	0/13093
2	LD	0.07	0/9606	0.22	0/13093
2	LE	0.07	0/9606	0.22	0/13093
2	LF	0.07	0/9606	0.22	0/13093
3	PA	0.07	0/5453	0.19	0/7377
3	PB	0.08	0/5453	0.19	0/7377
3	PC	0.07	0/5453	0.18	0/7377
3	PD	0.07	0/5453	0.19	0/7377
3	PE	0.07	0/5453	0.18	0/7377
3	PF	0.07	0/5453	0.19	0/7377
3	PG	0.07	0/5453	0.19	0/7377
3	PH	0.07	0/5453	0.19	0/7377
3	PI	0.07	0/5453	0.18	0/7377
3	PJ	0.07	0/5453	0.19	0/7377
3	PK	0.07	0/5453	0.18	0/7377
3	PL	0.07	0/5453	0.19	0/7377
4	SA	0.08	0/3498	0.22	0/4781
4	SB	0.08	0/3498	0.22	0/4781
4	SC	0.08	0/3498	0.22	0/4781
4	SD	0.08	0/3498	0.22	0/4781

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	SE	0.08	0/3498	0.22	0/4781
4	SF	0.08	0/3498	0.22	0/4781
5	TA	0.07	0/2290	0.18	0/3103
5	TB	0.07	0/2290	0.18	0/3103
5	TC	0.07	0/2290	0.18	0/3103
5	TD	0.07	0/2290	0.19	0/3103
5	TE	0.07	0/2290	0.17	0/3103
5	TF	0.07	0/2290	0.18	0/3103
5	TG	0.07	0/2290	0.18	0/3103
5	TH	0.07	0/2290	0.18	0/3103
5	TI	0.07	0/2290	0.18	0/3103
5	TJ	0.07	0/2290	0.19	0/3103
5	TK	0.07	0/2290	0.17	0/3103
5	TL	0.07	0/2290	0.18	0/3103
6	XA	0.09	0/585	0.23	0/794
6	XB	0.08	0/585	0.20	0/794
6	XC	0.09	0/585	0.23	0/794
6	XD	0.08	0/585	0.20	0/794
6	XE	0.08	0/585	0.23	0/794
6	XF	0.08	0/585	0.20	0/794
6	XG	0.09	0/585	0.23	0/794
6	XH	0.08	0/585	0.20	0/794
6	XI	0.09	0/585	0.23	0/794
6	XJ	0.08	0/585	0.20	0/794
6	XK	0.09	0/585	0.23	0/794
6	XL	0.08	0/585	0.20	0/794
6	YA	0.08	0/554	0.25	0/750
6	YB	0.08	0/554	0.22	0/750
6	YC	0.09	0/554	0.25	0/750
6	YD	0.08	0/554	0.22	0/750
6	YE	0.09	0/554	0.25	0/750
6	YF	0.07	0/554	0.21	0/750
6	YG	0.09	0/554	0.25	0/750
6	YH	0.08	0/554	0.22	0/750
6	YI	0.09	0/554	0.25	0/750
6	YJ	0.09	0/554	0.22	0/750
6	YK	0.09	0/554	0.25	0/750
6	YL	0.08	0/554	0.21	0/750
6	ZA	0.08	0/516	0.21	0/699
6	ZB	0.08	0/516	0.22	0/699
6	ZC	0.08	0/516	0.21	0/699
6	ZD	0.08	0/516	0.22	0/699
6	ZE	0.08	0/516	0.21	0/699

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	ZF	0.08	0/516	0.21	0/699
6	ZG	0.08	0/516	0.21	0/699
6	ZH	0.08	0/516	0.22	0/699
6	ZI	0.08	0/516	0.21	0/699
6	ZJ	0.08	0/516	0.22	0/699
6	ZK	0.08	0/516	0.21	0/699
6	ZL	0.08	0/516	0.21	0/699
7	OA	0.09	0/107	0.28	0/144
7	OB	0.10	0/107	0.26	0/144
7	OC	0.09	0/107	0.28	0/144
7	OD	0.11	0/107	0.26	0/144
7	OE	0.10	0/107	0.29	0/144
7	OF	0.11	0/107	0.26	0/144
7	OG	0.09	0/107	0.28	0/144
7	OH	0.10	0/107	0.26	0/144
7	OI	0.09	0/107	0.28	0/144
7	OJ	0.11	0/107	0.26	0/144
7	OK	0.09	0/107	0.28	0/144
7	OL	0.11	0/107	0.26	0/144
All	All	0.07	0/216120	0.20	0/293496

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](#)

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	AA	1912	0	1842	14	0
1	AB	1912	0	1843	23	0
1	AC	1912	0	1842	14	0
1	AD	1912	0	1843	22	0
1	AE	1912	0	1842	15	0
1	AF	1912	0	1843	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AG	1912	0	1842	13	0
1	AH	1912	0	1843	24	0
1	AI	1912	0	1842	14	0
1	AJ	1912	0	1843	23	0
1	AK	1912	0	1842	14	0
1	AL	1912	0	1843	22	0
2	LA	9341	0	8931	116	0
2	LB	9341	0	8931	123	0
2	LC	9341	0	8931	118	0
2	LD	9341	0	8931	118	0
2	LE	9341	0	8931	115	0
2	LF	9341	0	8931	120	0
3	PA	5357	0	5339	80	0
3	PB	5357	0	5339	77	0
3	PC	5357	0	5339	78	0
3	PD	5357	0	5339	80	0
3	PE	5357	0	5339	79	0
3	PF	5357	0	5339	73	0
3	PG	5357	0	5339	80	0
3	PH	5357	0	5339	77	0
3	PI	5357	0	5339	79	0
3	PJ	5357	0	5339	75	0
3	PK	5357	0	5339	79	0
3	PL	5357	0	5339	73	0
4	SA	3383	0	3269	42	0
4	SB	3383	0	3269	42	0
4	SC	3383	0	3269	43	0
4	SD	3383	0	3269	44	0
4	SE	3383	0	3269	43	0
4	SF	3383	0	3269	42	0
5	TA	2263	0	2258	23	0
5	TB	2263	0	2258	26	0
5	TC	2263	0	2258	22	0
5	TD	2263	0	2258	24	0
5	TE	2263	0	2258	24	0
5	TF	2263	0	2258	26	0
5	TG	2263	0	2258	23	0
5	TH	2263	0	2258	27	0
5	TI	2263	0	2258	23	0
5	TJ	2263	0	2258	25	0
5	TK	2263	0	2258	24	0
5	TL	2263	0	2258	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	XA	575	0	586	12	0
6	XB	575	0	586	9	0
6	XC	575	0	586	13	0
6	XD	575	0	586	8	0
6	XE	575	0	586	14	0
6	XF	575	0	586	7	0
6	XG	575	0	586	13	0
6	XH	575	0	586	7	0
6	XI	575	0	586	12	0
6	XJ	575	0	586	8	0
6	XK	575	0	586	13	0
6	XL	575	0	586	9	0
6	YA	543	0	563	6	0
6	YB	543	0	563	12	0
6	YC	543	0	563	5	0
6	YD	543	0	563	11	0
6	YE	543	0	563	6	0
6	YF	543	0	563	10	0
6	YG	543	0	563	6	0
6	YH	543	0	563	10	0
6	YI	543	0	563	6	0
6	YJ	543	0	563	12	0
6	YK	543	0	563	6	0
6	YL	543	0	563	13	0
6	ZA	508	0	528	8	0
6	ZB	508	0	528	5	0
6	ZC	508	0	528	8	0
6	ZD	508	0	528	4	0
6	ZE	508	0	528	9	0
6	ZF	508	0	528	5	0
6	ZG	508	0	528	9	0
6	ZH	508	0	528	5	0
6	ZI	508	0	528	9	0
6	ZJ	508	0	528	4	0
6	ZK	508	0	528	8	0
6	ZL	508	0	528	5	0
7	OA	105	0	97	0	0
7	OB	105	0	97	2	0
7	OC	105	0	97	0	0
7	OD	105	0	97	2	0
7	OE	105	0	97	0	0
7	OF	105	0	97	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	OG	105	0	97	0	0
7	OH	105	0	97	2	0
7	OI	105	0	97	0	0
7	OJ	105	0	97	1	0
7	OK	105	0	97	0	0
7	OL	105	0	97	3	0
All	All	211500	0	207762	2269	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 5.

The worst 5 of 2269 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)
2:LE:840:ALA:HA	2:LE:888:GLN:HB3	1.63	0.80
2:LF:840:ALA:HA	2:LF:888:GLN:HB3	1.63	0.79
2:LD:840:ALA:HA	2:LD:888:GLN:HB3	1.63	0.79
2:LA:840:ALA:HA	2:LA:888:GLN:HB3	1.63	0.79
2:LC:840:ALA:HA	2:LC:888:GLN:HB3	1.63	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	AA	234/236 (99%)	234 (100%)	0	0	100	100
1	AB	234/236 (99%)	232 (99%)	2 (1%)	0	100	100
1	AC	234/236 (99%)	234 (100%)	0	0	100	100
1	AD	234/236 (99%)	232 (99%)	2 (1%)	0	100	100
1	AE	234/236 (99%)	233 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AF	234/236 (99%)	232 (99%)	2 (1%)	0	100	100
1	AG	234/236 (99%)	234 (100%)	0	0	100	100
1	AH	234/236 (99%)	232 (99%)	2 (1%)	0	100	100
1	AI	234/236 (99%)	234 (100%)	0	0	100	100
1	AJ	234/236 (99%)	232 (99%)	2 (1%)	0	100	100
1	AK	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AL	234/236 (99%)	232 (99%)	2 (1%)	0	100	100
2	LA	1179/1382 (85%)	1150 (98%)	29 (2%)	0	100	100
2	LB	1179/1382 (85%)	1147 (97%)	32 (3%)	0	100	100
2	LC	1179/1382 (85%)	1147 (97%)	32 (3%)	0	100	100
2	LD	1179/1382 (85%)	1150 (98%)	29 (2%)	0	100	100
2	LE	1179/1382 (85%)	1147 (97%)	32 (3%)	0	100	100
2	LF	1179/1382 (85%)	1148 (97%)	31 (3%)	0	100	100
3	PA	673/763 (88%)	665 (99%)	8 (1%)	0	100	100
3	PB	673/763 (88%)	663 (98%)	10 (2%)	0	100	100
3	PC	673/763 (88%)	665 (99%)	8 (1%)	0	100	100
3	PD	673/763 (88%)	664 (99%)	9 (1%)	0	100	100
3	PE	673/763 (88%)	665 (99%)	8 (1%)	0	100	100
3	PF	673/763 (88%)	664 (99%)	9 (1%)	0	100	100
3	PG	673/763 (88%)	665 (99%)	8 (1%)	0	100	100
3	PH	673/763 (88%)	664 (99%)	9 (1%)	0	100	100
3	PI	673/763 (88%)	665 (99%)	8 (1%)	0	100	100
3	PJ	673/763 (88%)	664 (99%)	9 (1%)	0	100	100
3	PK	673/763 (88%)	665 (99%)	8 (1%)	0	100	100
3	PL	673/763 (88%)	664 (99%)	9 (1%)	0	100	100
4	SA	413/417 (99%)	404 (98%)	9 (2%)	0	100	100
4	SB	413/417 (99%)	403 (98%)	10 (2%)	0	100	100
4	SC	413/417 (99%)	404 (98%)	9 (2%)	0	100	100
4	SD	413/417 (99%)	404 (98%)	9 (2%)	0	100	100
4	SE	413/417 (99%)	403 (98%)	10 (2%)	0	100	100
4	SF	413/417 (99%)	404 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	TA	296/299 (99%)	292 (99%)	4 (1%)	0	100	100
5	TB	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	TC	296/299 (99%)	292 (99%)	4 (1%)	0	100	100
5	TD	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	TE	296/299 (99%)	292 (99%)	4 (1%)	0	100	100
5	TF	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	TG	296/299 (99%)	292 (99%)	4 (1%)	0	100	100
5	TH	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	TI	296/299 (99%)	292 (99%)	4 (1%)	0	100	100
5	TJ	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	TK	296/299 (99%)	292 (99%)	4 (1%)	0	100	100
5	TL	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
6	XA	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
6	XB	70/556 (13%)	68 (97%)	2 (3%)	0	100	100
6	XC	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
6	XD	70/556 (13%)	68 (97%)	2 (3%)	0	100	100
6	XE	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
6	XF	70/556 (13%)	68 (97%)	2 (3%)	0	100	100
6	XG	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
6	XH	70/556 (13%)	68 (97%)	2 (3%)	0	100	100
6	XI	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
6	XJ	70/556 (13%)	68 (97%)	2 (3%)	0	100	100
6	XK	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
6	XL	70/556 (13%)	68 (97%)	2 (3%)	0	100	100
6	YA	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YB	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YC	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YD	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YE	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YF	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YG	64/556 (12%)	63 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	YH	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YI	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YJ	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YK	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	YL	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
6	ZA	61/556 (11%)	61 (100%)	0	0	100	100
6	ZB	61/556 (11%)	61 (100%)	0	0	100	100
6	ZC	61/556 (11%)	61 (100%)	0	0	100	100
6	ZD	61/556 (11%)	61 (100%)	0	0	100	100
6	ZE	61/556 (11%)	61 (100%)	0	0	100	100
6	ZF	61/556 (11%)	61 (100%)	0	0	100	100
6	ZG	61/556 (11%)	61 (100%)	0	0	100	100
6	ZH	61/556 (11%)	61 (100%)	0	0	100	100
6	ZI	61/556 (11%)	61 (100%)	0	0	100	100
6	ZJ	61/556 (11%)	61 (100%)	0	0	100	100
6	ZK	61/556 (11%)	61 (100%)	0	0	100	100
6	ZL	61/556 (11%)	61 (100%)	0	0	100	100
7	OA	12/150 (8%)	12 (100%)	0	0	100	100
7	OB	12/150 (8%)	12 (100%)	0	0	100	100
7	OC	12/150 (8%)	12 (100%)	0	0	100	100
7	OD	12/150 (8%)	12 (100%)	0	0	100	100
7	OE	12/150 (8%)	12 (100%)	0	0	100	100
7	OF	12/150 (8%)	12 (100%)	0	0	100	100
7	OG	12/150 (8%)	12 (100%)	0	0	100	100
7	OH	12/150 (8%)	12 (100%)	0	0	100	100
7	OI	12/150 (8%)	12 (100%)	0	0	100	100
7	OJ	12/150 (8%)	12 (100%)	0	0	100	100
7	OK	12/150 (8%)	12 (100%)	0	0	100	100
7	OL	12/150 (8%)	12 (100%)	0	0	100	100
All	All	26472/48186 (55%)	26018 (98%)	454 (2%)	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	AA	209/209 (100%)	208 (100%)	1 (0%)	81	83
1	AB	209/209 (100%)	206 (99%)	3 (1%)	59	74
1	AC	209/209 (100%)	208 (100%)	1 (0%)	81	83
1	AD	209/209 (100%)	206 (99%)	3 (1%)	59	74
1	AE	209/209 (100%)	208 (100%)	1 (0%)	81	83
1	AF	209/209 (100%)	206 (99%)	3 (1%)	59	74
1	AG	209/209 (100%)	208 (100%)	1 (0%)	81	83
1	AH	209/209 (100%)	206 (99%)	3 (1%)	59	74
1	AI	209/209 (100%)	208 (100%)	1 (0%)	81	83
1	AJ	209/209 (100%)	206 (99%)	3 (1%)	59	74
1	AK	209/209 (100%)	208 (100%)	1 (0%)	81	83
1	AL	209/209 (100%)	206 (99%)	3 (1%)	59	74
2	LA	989/1155 (86%)	972 (98%)	17 (2%)	53	71
2	LB	989/1155 (86%)	972 (98%)	17 (2%)	53	71
2	LC	989/1155 (86%)	971 (98%)	18 (2%)	51	70
2	LD	989/1155 (86%)	972 (98%)	17 (2%)	53	71
2	LE	989/1155 (86%)	972 (98%)	17 (2%)	53	71
2	LF	989/1155 (86%)	971 (98%)	18 (2%)	51	70
3	PA	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PB	579/652 (89%)	568 (98%)	11 (2%)	50	69
3	PC	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PD	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PE	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PF	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PG	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PH	579/652 (89%)	571 (99%)	8 (1%)	59	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	PI	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PJ	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PK	579/652 (89%)	572 (99%)	7 (1%)	63	75
3	PL	579/652 (89%)	572 (99%)	7 (1%)	63	75
4	SA	369/371 (100%)	365 (99%)	4 (1%)	65	76
4	SB	369/371 (100%)	366 (99%)	3 (1%)	73	79
4	SC	369/371 (100%)	366 (99%)	3 (1%)	73	79
4	SD	369/371 (100%)	365 (99%)	4 (1%)	65	76
4	SE	369/371 (100%)	366 (99%)	3 (1%)	73	79
4	SF	369/371 (100%)	366 (99%)	3 (1%)	73	79
5	TA	243/244 (100%)	240 (99%)	3 (1%)	63	75
5	TB	243/244 (100%)	239 (98%)	4 (2%)	55	72
5	TC	243/244 (100%)	240 (99%)	3 (1%)	63	75
5	TD	243/244 (100%)	239 (98%)	4 (2%)	55	72
5	TE	243/244 (100%)	240 (99%)	3 (1%)	63	75
5	TF	243/244 (100%)	239 (98%)	4 (2%)	55	72
5	TG	243/244 (100%)	240 (99%)	3 (1%)	63	75
5	TH	243/244 (100%)	239 (98%)	4 (2%)	55	72
5	TI	243/244 (100%)	240 (99%)	3 (1%)	63	75
5	TJ	243/244 (100%)	239 (98%)	4 (2%)	55	72
5	TK	243/244 (100%)	240 (99%)	3 (1%)	63	75
5	TL	243/244 (100%)	239 (98%)	4 (2%)	55	72
6	XA	66/455 (14%)	64 (97%)	2 (3%)	36	61
6	XB	66/455 (14%)	65 (98%)	1 (2%)	57	73
6	XC	66/455 (14%)	64 (97%)	2 (3%)	36	61
6	XD	66/455 (14%)	65 (98%)	1 (2%)	57	73
6	XE	66/455 (14%)	64 (97%)	2 (3%)	36	61
6	XF	66/455 (14%)	65 (98%)	1 (2%)	57	73
6	XG	66/455 (14%)	64 (97%)	2 (3%)	36	61
6	XH	66/455 (14%)	65 (98%)	1 (2%)	57	73
6	XI	66/455 (14%)	64 (97%)	2 (3%)	36	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	XJ	66/455 (14%)	65 (98%)	1 (2%)	57	73
6	XK	66/455 (14%)	64 (97%)	2 (3%)	36	61
6	XL	66/455 (14%)	65 (98%)	1 (2%)	57	73
6	YA	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YB	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YC	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YD	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YE	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YF	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YG	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YH	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YI	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YJ	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YK	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	YL	62/455 (14%)	61 (98%)	1 (2%)	55	72
6	ZA	58/455 (13%)	58 (100%)	0	100	100
6	ZB	58/455 (13%)	56 (97%)	2 (3%)	32	59
6	ZC	58/455 (13%)	58 (100%)	0	100	100
6	ZD	58/455 (13%)	57 (98%)	1 (2%)	53	71
6	ZE	58/455 (13%)	58 (100%)	0	100	100
6	ZF	58/455 (13%)	57 (98%)	1 (2%)	53	71
6	ZG	58/455 (13%)	58 (100%)	0	100	100
6	ZH	58/455 (13%)	56 (97%)	2 (3%)	32	59
6	ZI	58/455 (13%)	58 (100%)	0	100	100
6	ZJ	58/455 (13%)	56 (97%)	2 (3%)	32	59
6	ZK	58/455 (13%)	58 (100%)	0	100	100
6	ZL	58/455 (13%)	56 (97%)	2 (3%)	32	59
7	OA	12/118 (10%)	11 (92%)	1 (8%)	10	35
7	OB	12/118 (10%)	12 (100%)	0	100	100
7	OC	12/118 (10%)	11 (92%)	1 (8%)	10	35
7	OD	12/118 (10%)	12 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	OE	12/118 (10%)	11 (92%)	1 (8%)	10	35
7	OF	12/118 (10%)	12 (100%)	0	100	100
7	OG	12/118 (10%)	11 (92%)	1 (8%)	10	35
7	OH	12/118 (10%)	12 (100%)	0	100	100
7	OI	12/118 (10%)	11 (92%)	1 (8%)	10	35
7	OJ	12/118 (10%)	12 (100%)	0	100	100
7	OK	12/118 (10%)	11 (92%)	1 (8%)	10	35
7	OL	12/118 (10%)	12 (100%)	0	100	100
All	All	22896/40212 (57%)	22571 (99%)	325 (1%)	57	74

5 of 325 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	LE	1116	THR
2	LF	1176	VAL
3	PI	340	VAL
3	PJ	487	VAL
5	TK	282	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 372 such sidechains are listed below:

Mol	Chain	Res	Type
3	PH	73	GLN
6	XI	12	ASN
3	PH	567	GLN
2	LE	311	ASN
3	PJ	567	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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.

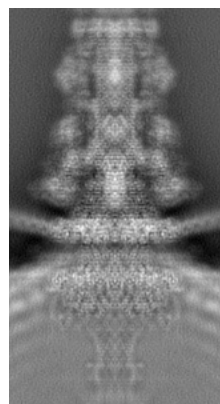
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72876. These allow visual inspection of the internal detail of the map and identification of artifacts.

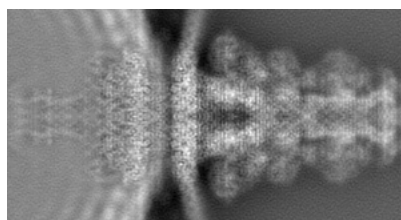
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

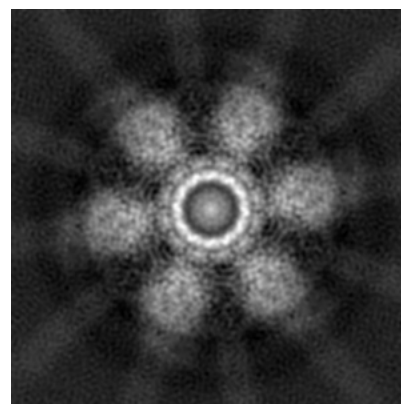
6.1.1 Primary map



X

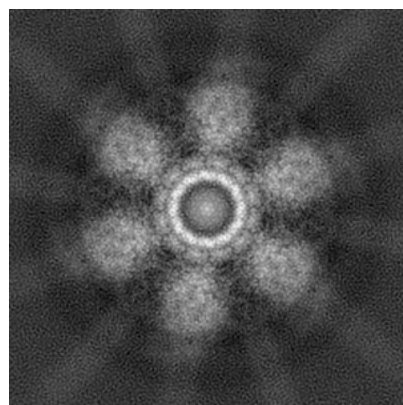


Y

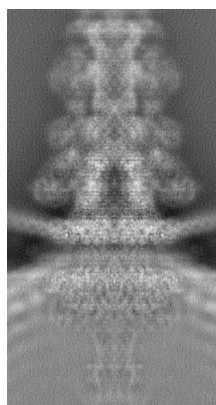


Z

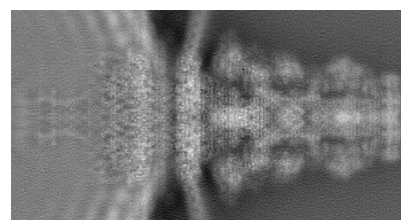
6.1.2 Raw map



X



Y

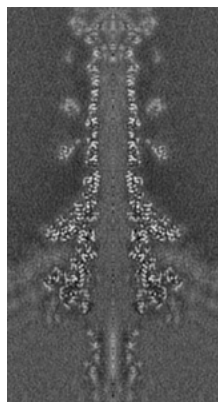


Z

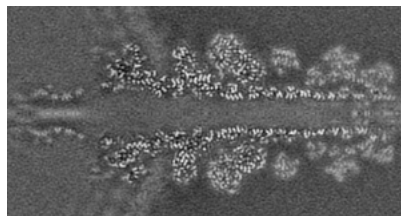
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

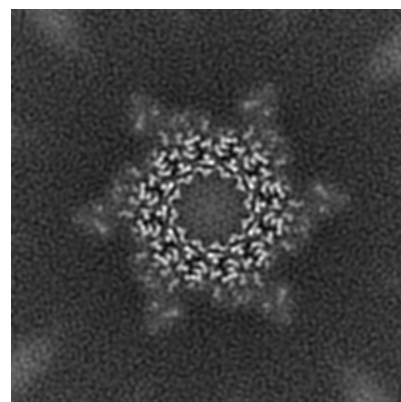
6.2.1 Primary map



X Index: 111

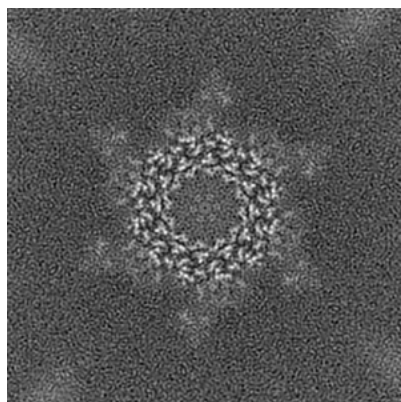


Y Index: 111

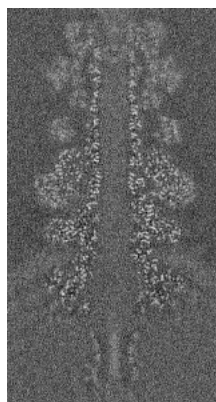


Z Index: 209

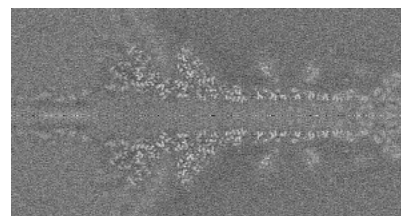
6.2.2 Raw map



X Index: 209



Y Index: 111

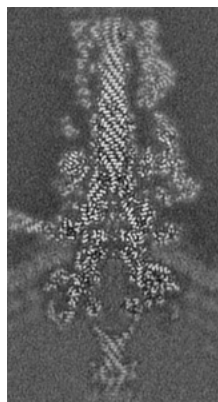


Z Index: 111

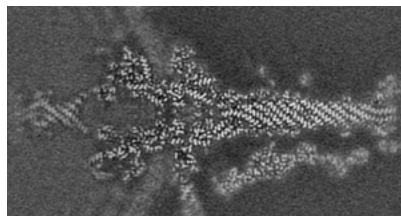
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

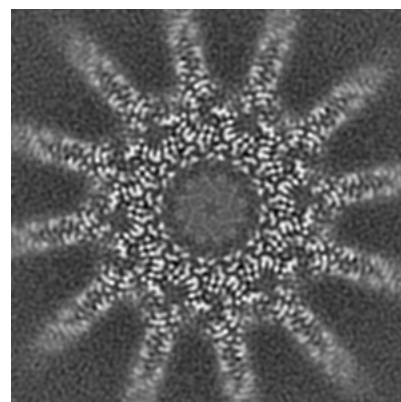
6.3.1 Primary map



X Index: 129

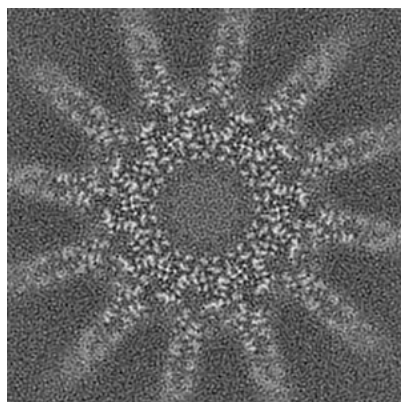


Y Index: 92

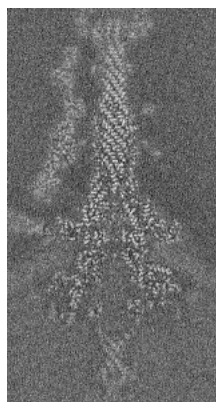


Z Index: 189

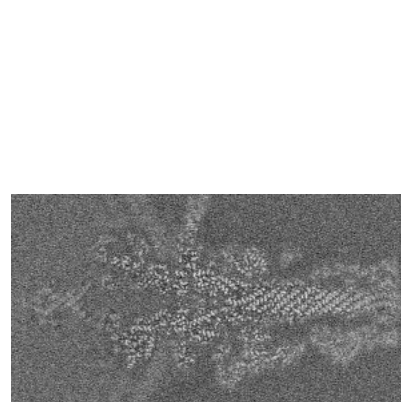
6.3.2 Raw map



X Index: 189



Y Index: 92

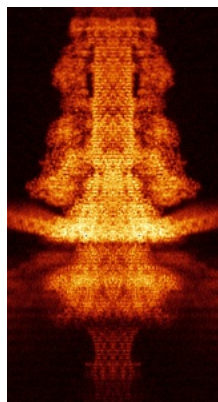


Z Index: 93

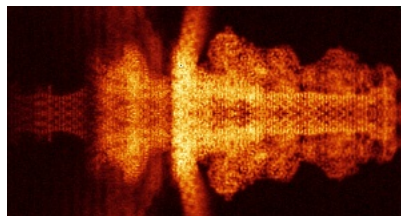
The images above show the largest variance slices of the map in three orthogonal directions.

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

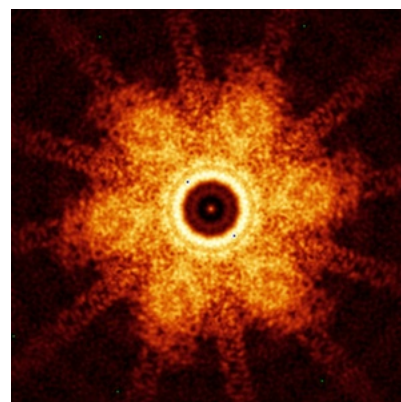
6.4.1 Primary map



X

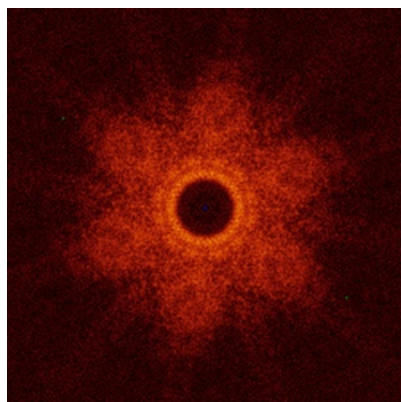


Y

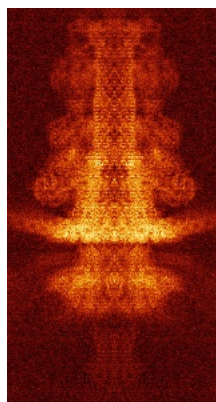


Z

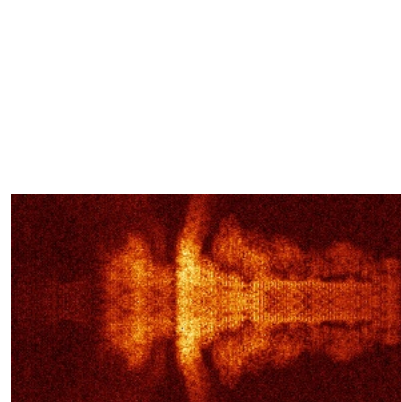
6.4.2 Raw map



X



Y



Z

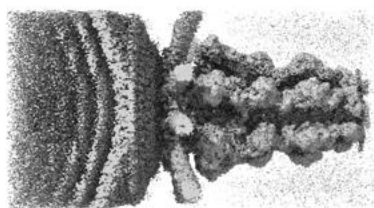
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

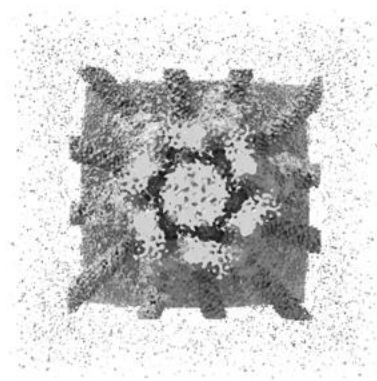
6.5.1 Primary map



X



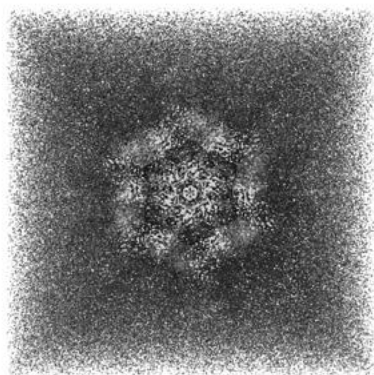
Y



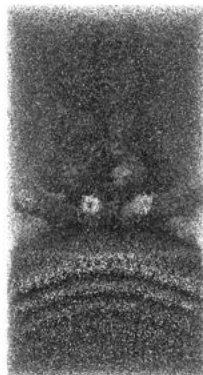
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0693. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

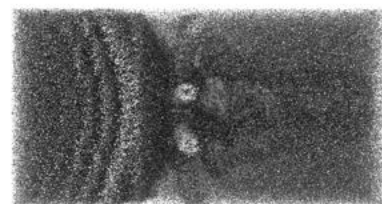
6.5.2 Raw map



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 shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

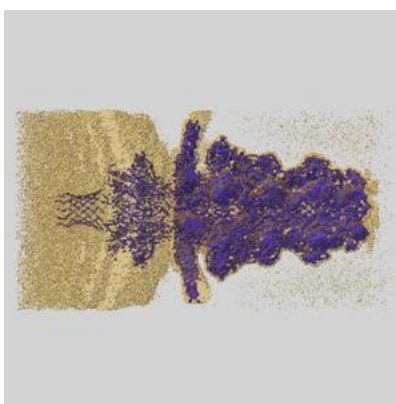
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

6.6.1 emd_72876_msk_1.map [i](#)



X



Y

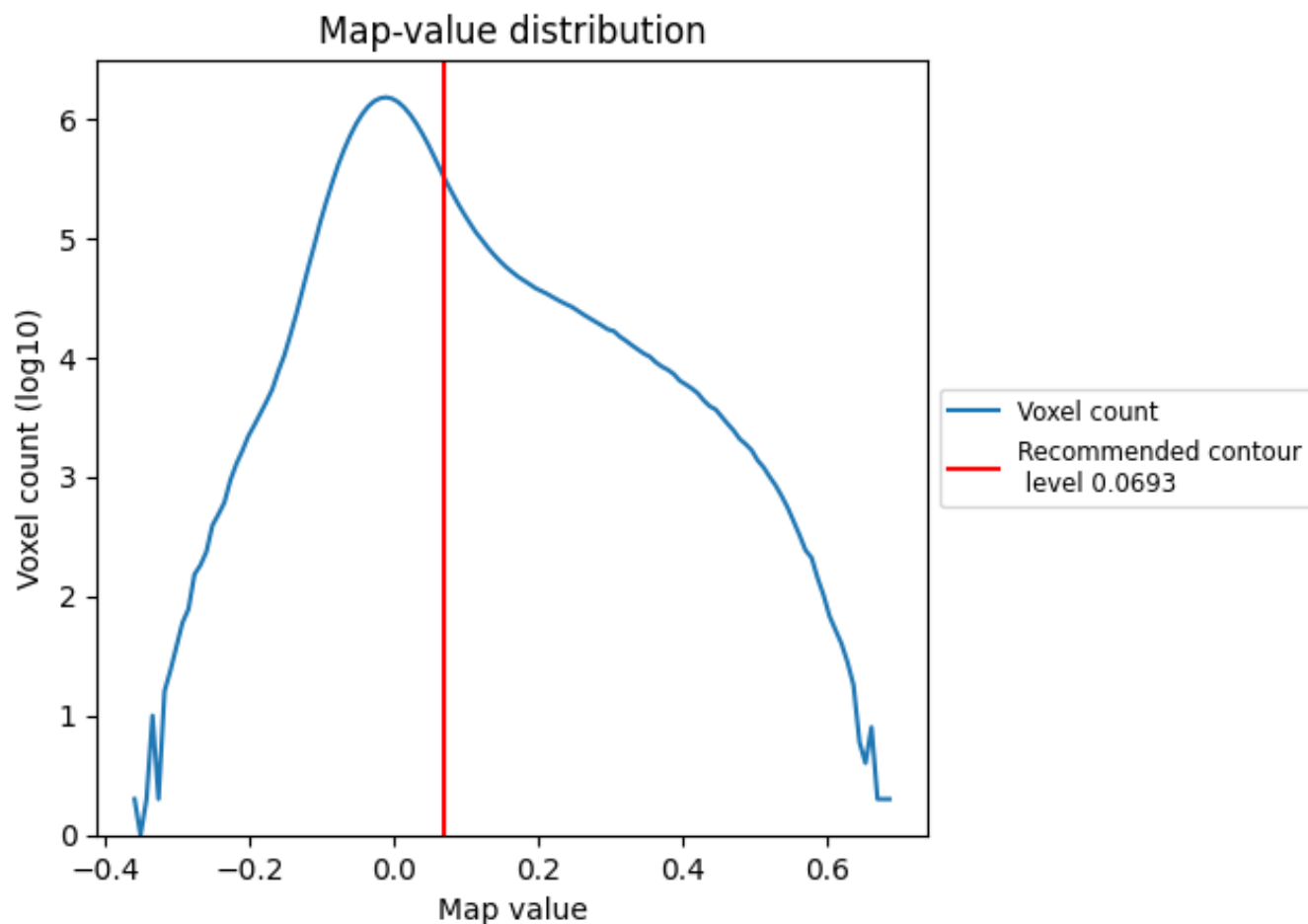


Z

7 Map analysis [i](#)

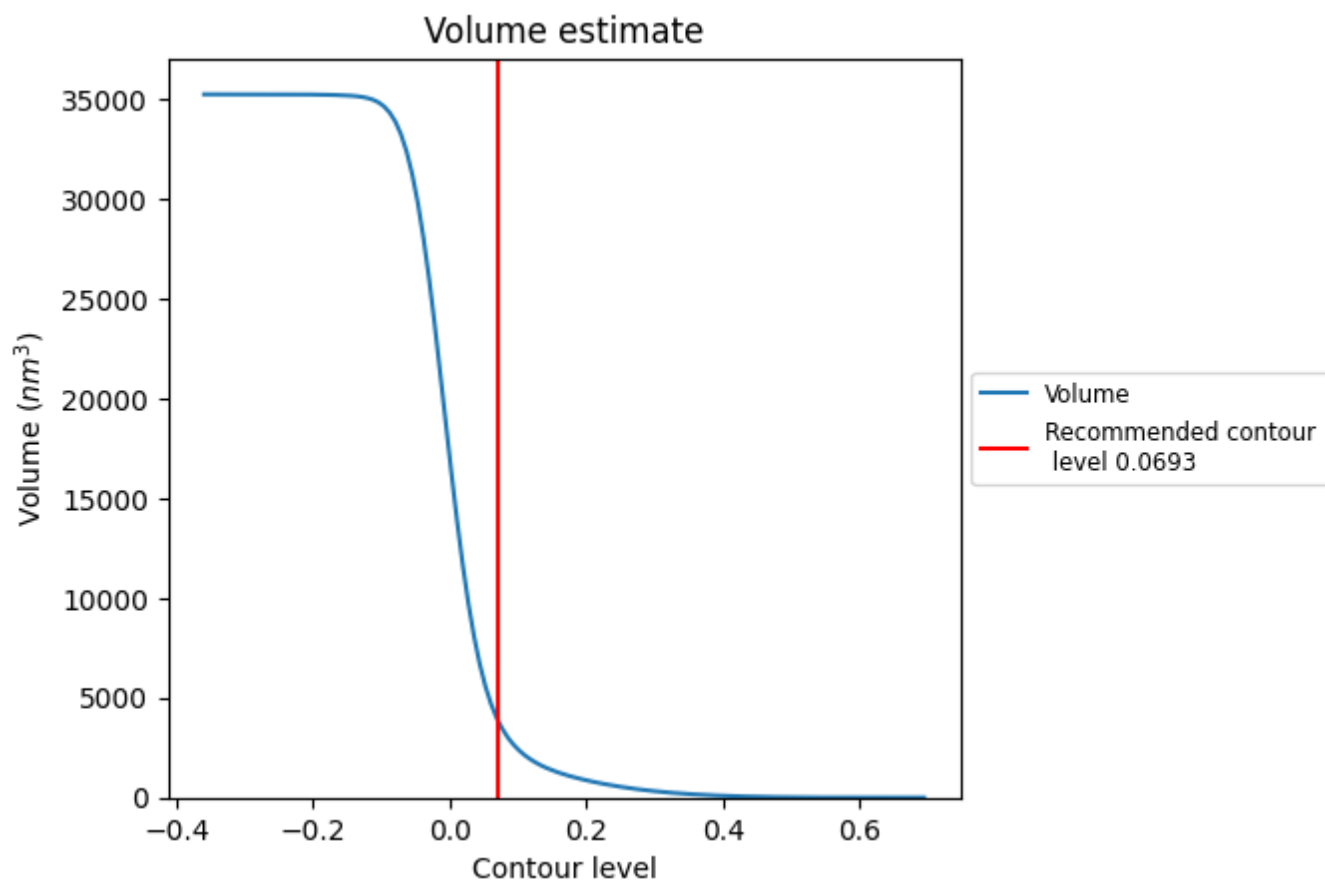
This section contains the results of statistical analysis of the map.

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 3953 nm³; this corresponds to an approximate mass of 3571 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

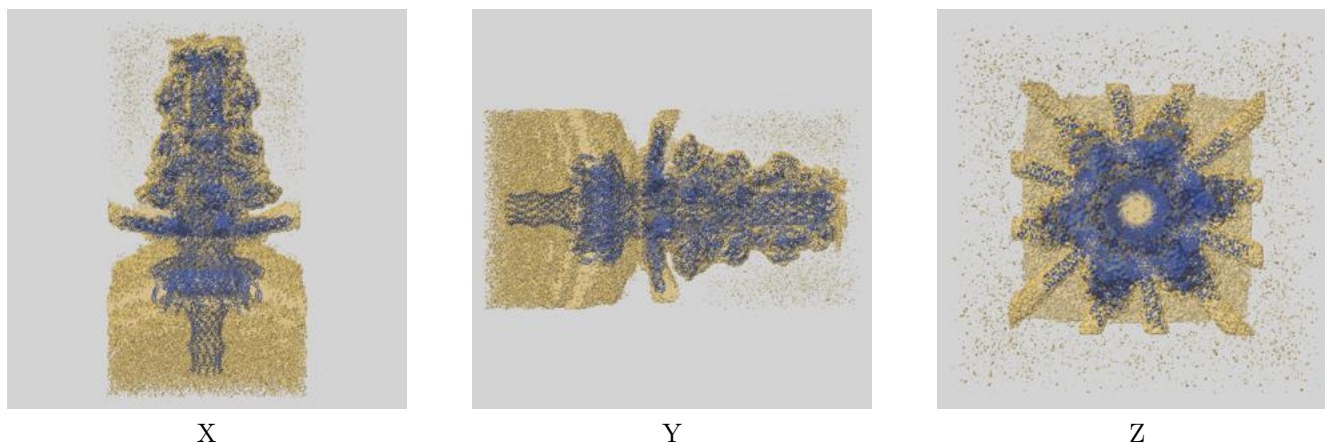
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

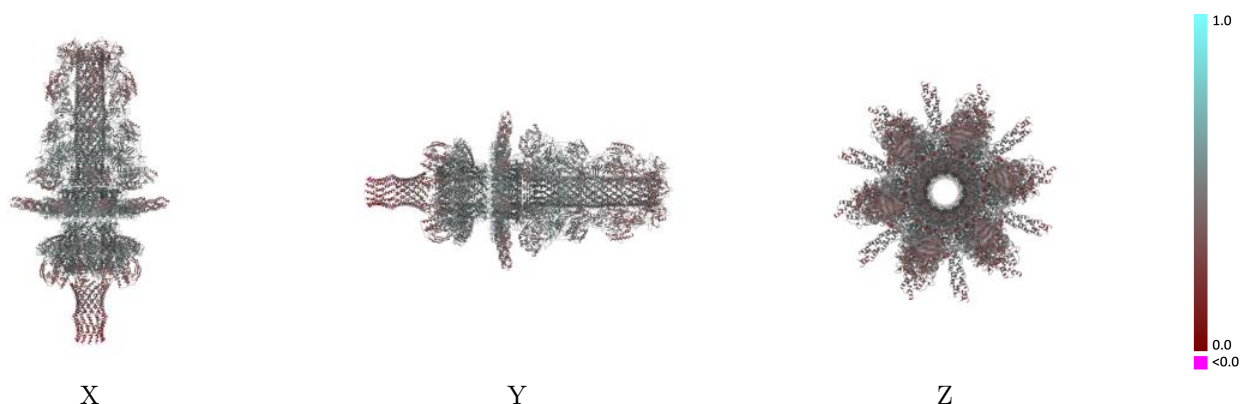
This section contains information regarding the fit between EMDB map EMD-72876 and PDB model 9YF4. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



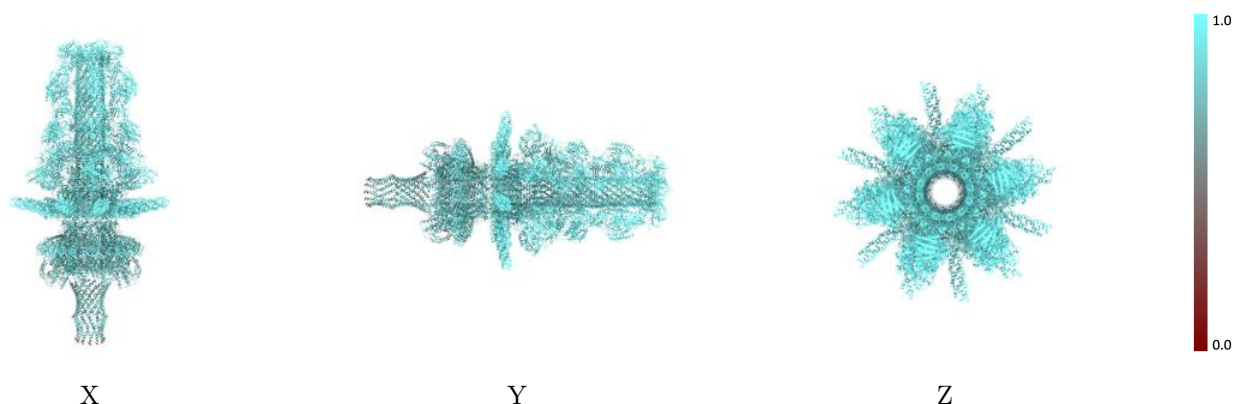
The images above show the 3D surface view of the map at the recommended contour level 0.0693 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



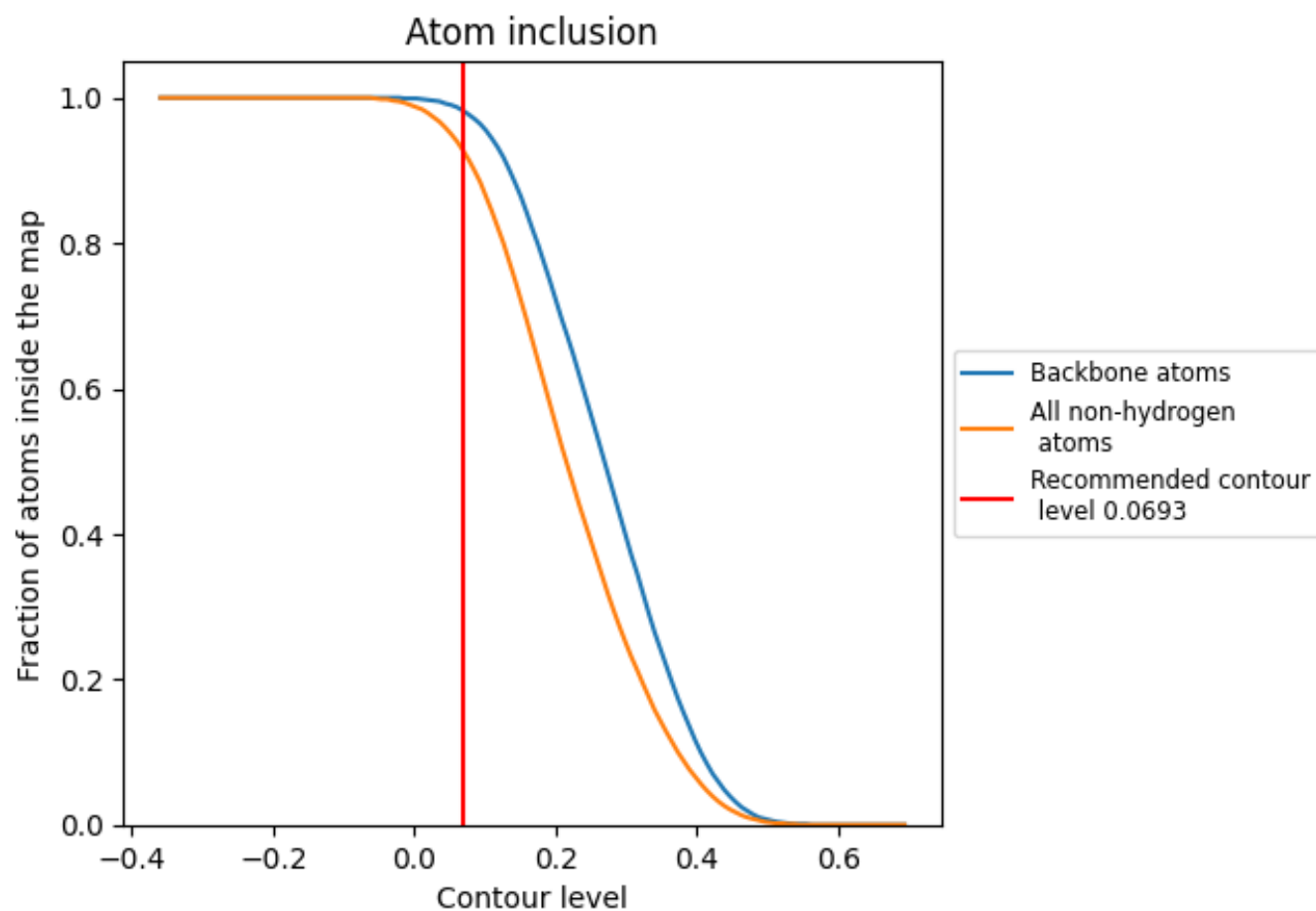
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0693).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% 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 (0.0693) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.4620
AA	 0.9570	 0.5230
AB	 0.9610	 0.5240
AC	 0.9560	 0.5220
AD	 0.9600	 0.5260
AE	 0.9570	 0.5210
AF	 0.9610	 0.5270
AG	 0.9570	 0.5230
AH	 0.9610	 0.5250
AI	 0.9560	 0.5210
AJ	 0.9600	 0.5270
AK	 0.9570	 0.5220
AL	 0.9610	 0.5270
LA	 0.9800	 0.4510
LB	 0.9810	 0.4510
LC	 0.9800	 0.4510
LD	 0.9800	 0.4520
LE	 0.9810	 0.4510
LF	 0.9800	 0.4500
OA	 0.9140	 0.5080
OB	 0.8670	 0.4740
OC	 0.8950	 0.4980
OD	 0.8670	 0.4740
OE	 0.9050	 0.5060
OF	 0.8670	 0.4720
OG	 0.9140	 0.5090
OH	 0.8670	 0.4750
OI	 0.8950	 0.5030
OJ	 0.8670	 0.4730
OK	 0.9050	 0.5030
OL	 0.8670	 0.4780
PA	 0.8270	 0.4580
PB	 0.8190	 0.4480
PC	 0.8240	 0.4570
PD	 0.8190	 0.4470











































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Chain	Atom inclusion	Q-score
PE	 0.8260	 0.4560
PF	 0.8180	 0.4450
PG	 0.8270	 0.4570
PH	 0.8190	 0.4460
PI	 0.8240	 0.4580
PJ	 0.8190	 0.4460
PK	 0.8260	 0.4580
PL	 0.8180	 0.4470
SA	 0.9810	 0.4550
SB	 0.9810	 0.4530
SC	 0.9810	 0.4530
SD	 0.9810	 0.4540
SE	 0.9810	 0.4530
SF	 0.9810	 0.4520
TA	 0.9680	 0.4790
TB	 0.9640	 0.4700
TC	 0.9690	 0.4790
TD	 0.9660	 0.4690
TE	 0.9690	 0.4780
TF	 0.9650	 0.4690
TG	 0.9680	 0.4780
TH	 0.9640	 0.4690
TI	 0.9690	 0.4780
TJ	 0.9660	 0.4710
TK	 0.9690	 0.4790
TL	 0.9650	 0.4710
XA	 0.9790	 0.4570
XB	 0.9600	 0.4390
XC	 0.9810	 0.4570
XD	 0.9610	 0.4450
XE	 0.9810	 0.4540
XF	 0.9600	 0.4440
XG	 0.9790	 0.4560
XH	 0.9600	 0.4420
XI	 0.9810	 0.4540
XJ	 0.9610	 0.4410
XK	 0.9810	 0.4540
XL	 0.9600	 0.4400
YA	 0.9850	 0.4590
YB	 0.9670	 0.4530
YC	 0.9870	 0.4620
YD	 0.9680	 0.4540

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Chain	Atom inclusion	Q-score
YE	 0.9810	 0.4610
YF	 0.9670	 0.4540
YG	 0.9850	 0.4590
YH	 0.9670	 0.4540
YI	 0.9870	 0.4600
YJ	 0.9680	 0.4500
YK	 0.9810	 0.4590
YL	 0.9670	 0.4520
ZA	 0.9800	 0.4370
ZB	 0.9820	 0.4310
ZC	 0.9800	 0.4360
ZD	 0.9800	 0.4320
ZE	 0.9800	 0.4420
ZF	 0.9800	 0.4310
ZG	 0.9800	 0.4370
ZH	 0.9820	 0.4340
ZI	 0.9800	 0.4370
ZJ	 0.9800	 0.4330
ZK	 0.9800	 0.4390
ZL	 0.9800	 0.4290