Full wwPDB EM Validation Report (i)

Jun 23, 2024 – 05:19 PM EDT

PDB ID	:	6Q3G
EMDB ID	:	EMD-4459
Title	:	Structure of native bacteriophage P68
Authors	:	Dominik, H.; Karel, S.; Fuzik, T.; Plevka, P.
Deposited on	:	2018-12-04
Resolution	:	3.80 Å(reported)
Based on initial models	:	6IAT, 6IAW, 6IAB, 6IAC

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 (i) 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 (i)) were used in the production of this report:

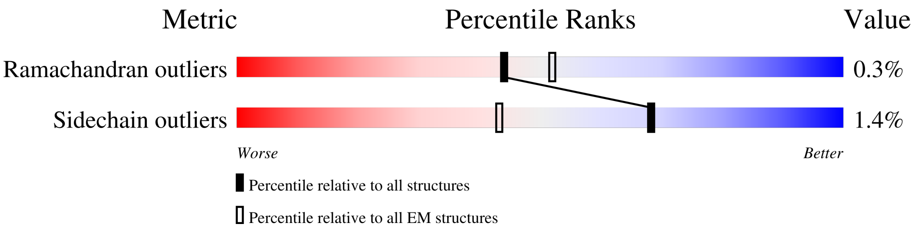
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	154571	4023
Sidechain outliers	154315	3826

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 <=5%

Mol	Chain	Length	Quality of chain
1	A1	408	93% • •
1	A3	408	93% • •
1	A4	408	93% • •
1	A6	408	93% • •
1	A7	408	93% • •
1	A8	408	93% • •
1	AD	408	82% • • 13%
1	AE	408	92% • 6%
1	AG	408	93% • •
1	AJ	408	82% • • 13%

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Mol	Chain	Length	Quality of chain
1	AK	408	82% • • 13%
1	AL	408	93% • •
1	AP	408	82% • • 13%
1	AQ	408	93% • •
1	AR	408	93% • •
1	AS	408	93% • •
1	B1	408	92% • 6%
1	B3	408	92% • 6%
1	B4	408	92% • 6%
1	B6	408	92% • 6%
1	B7	408	92% • 6%
1	B8	408	92% • 6%
1	BD	408	93% • •
1	BE	408	93% • •
1	BG	408	92% • 6%
1	BJ	408	93% • •
1	BK	408	93% • •
1	BL	408	92% • 6%
1	BP	408	93% • •
1	BQ	408	92% • 6%
1	BR	408	92% • 6%
1	BS	408	92% • 5%
1	C1	408	92% • 6%
1	C3	408	92% • 6%
1	C4	408	92% • 6%

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Mol	Chain	Length	Quality of chain
1	C6	408	92% • 6%
1	C7	408	92% • 6%
1	C8	408	92% • 6%
1	CD	408	92% • 5%
1	CE	408	92% • 6%
1	CG	408	92% • 6%
1	CJ	408	92% • 5%
1	CK	408	92% • 5%
1	CL	408	92% • 6%
1	CP	408	92% • 5%
1	CQ	408	92% • 6%
1	CR	408	92% • 6%
1	CS	408	91% • 5%
1	D1	408	95% • •
1	D3	408	95% • •
1	D4	408	95% • •
1	D6	408	95% • •
1	D7	408	95% • •
1	D8	408	95% • •
1	DD	408	91% • 5%
1	DE	408	95% • •
1	DG	408	95% • •
1	DJ	408	91% • 5%
1	DK	408	91% • 5%
1	DL	408	95% • •

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Mol	Chain	Length	Quality of chain
1	DP	408	91% • 5%
1	DQ	408	95% • •
1	DR	408	95% • •
1	FE	408	95% • •
1	I1	408	92% • 6%
1	I3	408	92% • 6%
1	I4	408	92% • 6%
1	I6	408	92% • 6%
1	I7	408	92% • 6%
1	I8	408	92% • 6%
1	IG	408	92% • 6%
1	IL	408	92% • 6%
1	IQ	408	92% • 6%
1	IR	408	92% • 6%
1	IS	408	82% • • 13%
1	J1	408	93% • •
1	J3	408	93% • •
1	J4	408	93% • •
1	J6	408	93% • •
1	J7	408	93% • •
1	J8	408	93% • •
1	JG	408	93% • •
1	JL	408	93% • •
1	JQ	408	93% • •
1	JR	408	93% • •

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Mol	Chain	Length	Quality of chain
1	JS	408	91% • 6%
1	K1	408	92% • 6%
1	K3	408	92% • 6%
1	K4	408	92% • 6%
1	K6	408	92% • 6%
1	K7	408	92% • 6%
1	K8	408	92% • 6%
1	KD	408	91% • 6%
1	KE	408	92% • 6%
1	KG	408	92% • 6%
1	KJ	408	91% • 6%
1	KK	408	91% • 6%
1	KL	408	92% • 6%
1	KP	408	91% • 6%
1	KQ	408	92% • 6%
1	KR	408	92% • 6%
1	KS	408	92% • 5%
1	L1	408	95% • •
1	L3	408	95% • •
1	L4	408	95% • •
1	L6	408	95% • •
1	L7	408	95% • •
1	L8	408	95% • •
1	LD	408	92% • 5%
1	LE	408	93% • •

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Mol	Chain	Length	Quality of chain
1	LG	408	95% • •
1	LJ	408	92% • 5%
1	LK	408	92% • 5%
1	LL	408	95% • •
1	LP	408	92% • 5%
1	LQ	408	95% • •
1	LR	408	95% • •
1	ME	408	92% • 6%
1	NE	408	95% • •
1	Q1	408	92% • 6%
1	Q3	408	92% • 6%
1	Q4	408	92% • 6%
1	Q6	408	92% • 6%
1	Q7	408	92% • 6%
1	Q8	408	92% • 6%
1	QG	408	92% • 6%
1	QL	408	92% • 6%
1	QQ	408	92% • 6%
1	QR	408	92% • 6%
1	R1	408	93% • •
1	R3	408	93% • •
1	R4	408	93% • •
1	R6	408	93% • •
1	R7	408	93% • •
1	R8	408	93% • •

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Mol	Chain	Length	Quality of chain
1	RG	408	93% • •
1	RL	408	93% • •
1	RQ	408	93% • •
1	RR	408	93% • •
1	S1	408	92% • 6%
1	S3	408	92% • 6%
1	S4	408	92% • 6%
1	S6	408	92% • 6%
1	S7	408	92% • 6%
1	S8	408	92% • 6%
1	SE	408	92% • 6%
1	SG	408	92% • 6%
1	SL	408	92% • 6%
1	SQ	408	92% • 6%
1	SR	408	92% • 6%
1	T1	408	95% • •
1	T3	408	95% • •
1	T4	408	95% • •
1	T6	408	95% • •
1	T7	408	95% • •
1	T8	408	95% • •
1	TE	408	93% • •
1	TG	408	95% • •
1	TL	408	95% • •
1	TQ	408	95% • •

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Mol	Chain	Length	Quality of chain
1	TR	408	95% • •
1	UE	408	92% • 6%
1	VE	408	95% • •
1	X1	408	92% • 6%
1	X4	408	92% • 6%
1	Y1	408	93% • •
1	Y3	408	95% • •
1	Y4	408	93% • •
1	Y6	408	92% • 6%
1	Y7	408	92% • 6%
1	Y8	408	92% • 6%
1	YG	408	92% • 6%
1	YL	408	92% • 6%
1	YQ	408	95% • •
1	YR	408	92% • 6%
1	Z1	408	92% • 6%
1	Z4	408	92% • 6%
1	Z6	408	93% • •
1	Z7	408	93% • •
1	Z8	408	93% • •
1	ZG	408	93% • •
1	ZL	408	93% • •
1	ZR	408	93% • •
1	a1	408	95% • •
1	a4	408	95% • •

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Mol	Chain	Length	Quality of chain
1	a6	408	92% • 6%
1	a7	408	92% • 6%
1	a8	408	92% • 6%
1	aE	408	92% • 6%
1	aG	408	92% • 6%
1	aL	408	92% • 6%
1	aR	408	92% • 6%
1	b3	408	95% • •
1	b6	408	95% • •
1	b7	408	95% • •
1	b8	408	95% • •
1	bE	408	93% • •
1	bG	408	95% • •
1	bL	408	95% • •
1	bQ	408	92% • 6%
1	bR	408	95% • •
1	cE	408	92% • 6%
1	cQ	408	93% • •
1	dE	408	95% • •
1	dQ	408	92% • 6%
1	eQ	408	95% • •
1	f1	408	92% • 6%
1	f4	408	92% • 6%
1	g1	408	93% • •
1	g4	408	93% • •

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Mol	Chain	Length	Quality of chain
1	g6	408	92% • 6%
1	g7	408	92% • 6%
1	g8	408	92% • 6%
1	gG	408	92% • 6%
1	gL	408	95% • •
1	gR	408	92% • 6%
1	h1	408	92% • 6%
1	h4	408	92% • 6%
1	h6	408	93% • •
1	h7	408	93% • •
1	h8	408	93% • •
1	hG	408	93% • •
1	hR	408	93% • •
1	i1	408	95% • •
1	i4	408	95% • •
1	i6	408	92% • 6%
1	i7	408	92% • 6%
1	i8	408	92% • 6%
1	iG	408	92% • 6%
1	iR	408	92% • 6%
1	j6	408	95% • •
1	j7	408	95% • •
1	j8	408	95% • •
1	jG	408	95% • •
1	jR	408	95% • •

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Mol	Chain	Length	Quality of chain
2	DS	60	85% 7% 8%
2	E1	60	78% 10% • 10%
2	E3	60	78% 10% • 10%
2	E4	60	78% 10% • 10%
2	E6	60	78% 10% • 10%
2	E7	60	78% 10% • 10%
2	E8	60	78% 10% • 10%
2	ED	60	85% 7% 8%
2	EE	60	78% 10% • 10%
2	EG	60	78% 10% • 10%
2	EJ	60	85% 7% 8%
2	EK	60	85% 7% 8%
2	EL	60	78% 10% • 10%
2	EP	60	85% 7% 8%
2	EQ	60	78% 10% • 10%
2	ER	60	78% 10% • 10%
2	ES	60	82% 8% • 8%
2	F1	60	83% 7% • 8%
2	F3	60	83% 7% • 8%
2	F4	60	83% 7% • 8%
2	F6	60	83% 7% • 8%
2	F7	60	83% 7% • 8%
2	F8	60	83% 7% • 8%
2	FD	60	82% 8% • 8%
2	FG	60	83% 7% • 8%

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Mol	Chain	Length	Quality of chain
2	FJ	60	82% 8% • 8%
2	FK	60	82% 8% • 8%
2	FL	60	83% 7% • 8%
2	FP	60	82% 8% • 8%
2	FQ	60	83% 7% • 8%
2	FR	60	83% 7% • 8%
2	FS	60	45% 5% 50%
2	G1	60	37% 8% 55%
2	G3	60	37% 8% 55%
2	G4	60	37% 8% 55%
2	G6	60	37% 8% 55%
2	G7	60	37% 8% 55%
2	G8	60	37% 8% 55%
2	GD	60	45% 5% 50%
2	GE	60	37% 8% 55%
2	GG	60	37% 8% 55%
2	GJ	60	45% 5% 50%
2	GK	60	45% 5% 50%
2	GL	60	37% 8% 55%
2	GP	60	45% 5% 50%
2	GQ	60	37% 8% 55%
2	GR	60	37% 8% 55%
2	GS	60	90% 10%
2	H1	60	87% 5% 8%
2	H3	60	87% 5% 8%

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Mol	Chain	Length	Quality of chain
2	H4	60	87% 5% 8%
2	H6	60	87% 5% 8%
2	H7	60	87% 5% 8%
2	H8	60	87% 5% 8%
2	HD	60	90% 10%
2	HE	60	83% 7% • 8%
2	HG	60	87% 5% 8%
2	HJ	60	90% 10%
2	HK	60	90% 10%
2	HL	60	87% 5% 8%
2	HP	60	90% 10%
2	HQ	60	87% 5% 8%
2	HR	60	87% 5% 8%
2	IE	60	37% 8% 55%
2	JE	60	87% 5% 8%
2	LS	60	83% 8% 8%
2	M1	60	78% 10% • 10%
2	M3	60	78% 10% • 10%
2	M4	60	78% 10% • 10%
2	M6	60	78% 10% • 10%
2	M7	60	78% 10% • 10%
2	M8	60	78% 10% • 10%
2	MD	60	83% 8% 8%
2	MG	60	78% 10% • 10%
2	MJ	60	83% 8% 8%

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Mol	Chain	Length	Quality of chain
2	MK	60	83% 8% 8%
2	ML	60	78% 10% • 10%
2	MP	60	83% 8% 8%
2	MQ	60	78% 10% • 10%
2	MR	60	78% 10% • 10%
2	MS	60	85% 5% • 8%
2	N1	60	83% 7% • 8%
2	N3	60	83% 7% • 8%
2	N4	60	83% 7% • 8%
2	N6	60	83% 7% • 8%
2	N7	60	83% 7% • 8%
2	N8	60	83% 7% • 8%
2	ND	60	85% 5% • 8%
2	NG	60	83% 7% • 8%
2	NJ	60	85% 5% • 8%
2	NK	60	85% 5% • 8%
2	NL	60	83% 7% • 8%
2	NP	60	85% 5% • 8%
2	NQ	60	83% 7% • 8%
2	NR	60	83% 7% • 8%
2	O1	60	37% 8% 55%
2	O3	60	37% 8% 55%
2	O4	60	37% 8% 55%
2	O6	60	37% 8% 55%
2	O7	60	37% 8% 55%

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Mol	Chain	Length	Quality of chain
2	O8	60	37% 8% 55%
2	OE	60	78% 10% • 10%
2	OG	60	37% 8% 55%
2	OL	60	37% 8% 55%
2	OQ	60	37% 8% 55%
2	OR	60	37% 8% 55%
2	P1	60	87% 5% 8%
2	P3	60	87% 5% 8%
2	P4	60	87% 5% 8%
2	P6	60	87% 5% 8%
2	P7	60	87% 5% 8%
2	P8	60	87% 5% 8%
2	PE	60	83% 7% • 8%
2	PG	60	87% 5% 8%
2	PL	60	87% 5% 8%
2	PQ	60	87% 5% 8%
2	PR	60	87% 5% 8%
2	QE	60	37% 8% 55%
2	RE	60	87% 5% 8%
2	U1	60	83% 7% • 8%
2	U3	60	78% 10% • 10%
2	U4	60	83% 7% • 8%
2	U6	60	78% 10% • 10%
2	U7	60	78% 10% • 10%
2	U8	60	78% 10% • 10%

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Mol	Chain	Length	Quality of chain
2	UG	60	78% 10% • 10%
2	UL	60	78% 10% • 10%
2	UQ	60	78% 10% • 10%
2	UR	60	78% 10% • 10%
2	V1	60	37% 8% 55%
2	V3	60	83% 7% • 8%
2	V4	60	37% 8% 55%
2	V6	60	83% 7% • 8%
2	V7	60	83% 7% • 8%
2	V8	60	83% 7% • 8%
2	VG	60	83% 7% • 8%
2	VL	60	83% 7% • 8%
2	VQ	60	83% 7% • 8%
2	VR	60	83% 7% • 8%
2	W1	60	87% 5% 8%
2	W3	60	37% 8% 55%
2	W4	60	87% 5% 8%
2	W6	60	37% 8% 55%
2	W7	60	37% 8% 55%
2	W8	60	37% 8% 55%
2	WE	60	78% 10% • 10%
2	WG	60	37% 8% 55%
2	WL	60	37% 8% 55%
2	WQ	60	37% 8% 55%
2	WR	60	37% 8% 55%

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Mol	Chain	Length	Quality of chain
2	X3	60	87% 5% 8%
2	X6	60	87% 5% 8%
2	X7	60	87% 5% 8%
2	X8	60	87% 5% 8%
2	XE	60	83% 7% • 8%
2	XG	60	87% 5% 8%
2	XL	60	87% 5% 8%
2	XQ	60	87% 5% 8%
2	XR	60	87% 5% 8%
2	YE	60	37% 8% 55%
2	Z3	60	78% 10% • 10%
2	ZE	60	87% 5% 8%
2	ZQ	60	78% 10% • 10%
2	a3	60	37% 8% 55%
2	aQ	60	37% 8% 55%
2	b1	60	78% 10% • 10%
2	b4	60	78% 10% • 10%
2	c1	60	83% 7% • 8%
2	c3	60	78% 10% • 10%
2	c4	60	83% 7% • 8%
2	c6	60	78% 10% • 10%
2	c7	60	78% 10% • 10%
2	c8	60	78% 10% • 10%
2	cG	60	78% 10% • 10%
2	cL	60	78% 10% • 10%

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Mol	Chain	Length	Quality of chain
2	cR	60	78% 10% • 10%
2	d1	60	37% 8% 55%
2	d3	60	37% 8% 55%
2	d4	60	37% 8% 55%
2	d6	60	83% 7% • 8%
2	d7	60	83% 7% • 8%
2	d8	60	83% 7% • 8%
2	dG	60	83% 7% • 8%
2	dL	60	83% 7% • 8%
2	dR	60	83% 7% • 8%
2	e1	60	87% 5% 8%
2	e4	60	87% 5% 8%
2	e6	60	37% 8% 55%
2	e7	60	37% 8% 55%
2	e8	60	37% 8% 55%
2	eE	60	78% 10% • 10%
2	eG	60	37% 8% 55%
2	eL	60	37% 8% 55%
2	eR	60	37% 8% 55%
2	f6	60	87% 5% 8%
2	f7	60	87% 5% 8%
2	f8	60	87% 5% 8%
2	fE	60	83% 7% • 8%
2	fG	60	87% 5% 8%
2	fL	60	87% 5% 8%

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Mol	Chain	Length	Quality of chain
2	fQ	60	78% 10% • 10%
2	fR	60	87% 5% 8%
2	gE	60	37% 8% 55%
2	gQ	60	83% 7% • 8%
2	hE	60	87% 5% 8%
2	hL	60	78% 10% • 10%
2	hQ	60	37% 8% 55%
2	iL	60	37% 8% 55%
2	iQ	60	87% 5% 8%
2	j1	60	78% 10% • 10%
2	j4	60	83% 7% • 8%
2	k1	60	83% 7% • 8%
2	k4	60	37% 8% 55%
2	k6	60	78% 10% • 10%
2	k7	60	78% 10% • 10%
2	k8	60	78% 10% • 10%
2	kG	60	78% 10% • 10%
2	kR	60	83% 7% • 8%
2	l1	60	37% 8% 55%
2	l4	60	87% 5% 8%
2	l6	60	83% 7% • 8%
2	l7	60	83% 7% • 8%
2	l8	60	83% 7% • 8%
2	lG	60	83% 7% • 8%
2	lR	60	37% 8% 55%

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Mol	Chain	Length	Quality of chain
2	m1	60	87% 5% 8%
2	m6	60	37% 8% 55%
2	m7	60	37% 8% 55%
2	m8	60	37% 8% 55%
2	mG	60	37% 8% 55%
2	mR	60	87% 5% 8%
2	n6	60	87% 5% 8%
2	n7	60	87% 5% 8%
2	n8	60	87% 5% 8%
2	nG	60	87% 5% 8%
3	A2	327	88% • 8%
3	A5	327	88% • 8%
3	A9	327	88% • 8%
3	AA	327	88% • 8%
3	AB	327	88% • 8%
3	AC	327	88% • 8%
3	AF	327	88% • 8%
3	AH	327	88% • 8%
3	AI	327	88% • 8%
3	AM	327	88% • 8%
3	AN	327	88% • 8%
3	AO	327	88% • 8%
4	B2	251	86% • 12%
4	B5	251	86% • 12%
4	B9	251	86% • 12%

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Mol	Chain	Length	Quality of chain
4	BA	251	86% • 12%
4	BB	251	86% • 12%
4	BC	251	86% • 12%
4	BF	251	86% • 12%
4	BH	251	86% • 12%
4	BI	251	86% • 12%
4	BM	251	86% • 12%
4	BN	251	86% • 12%
4	BO	251	86% • 12%
5	C2	647	77% 23%
5	C5	647	77% 23%
5	C9	647	77% 23%
5	CA	647	77% 23%
5	CB	647	77% 23%
5	CC	647	77% 23%
5	CF	647	77% 23%
5	CH	647	77% 23%
5	CI	647	77% 23%
5	CM	647	77% 23%
5	CN	647	77% 23%
5	CO	647	77% 23%
5	D2	647	20% 80%
5	D5	647	20% 80%
5	D9	647	20% 80%
5	DA	647	20% 80%

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Mol	Chain	Length	Quality of chain
5	DB	647	20% 80%
5	DC	647	20% 80%
5	DF	647	20% 80%
5	DH	647	20% 80%
5	DI	647	20% 80%
5	DM	647	20% 80%
5	DN	647	20% 80%
5	DO	647	20% 80%
5	E2	647	21% 79%
5	E5	647	21% 79%
5	E9	647	21% 79%
5	EA	647	21% 79%
5	EB	647	21% 79%
5	EC	647	21% 79%
5	EF	647	21% 79%
5	EH	647	21% 79%
5	EI	647	21% 79%
5	EM	647	21% 79%
5	EN	647	21% 79%
5	EO	647	21% 79%
5	F2	647	17% 83%
5	F5	647	17% 83%
5	F9	647	17% 83%
5	FA	647	17% 83%
5	FB	647	17% 83%

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Mol	Chain	Length	Quality of chain
5	FC	647	17% 83%
5	FF	647	17% 83%
5	FH	647	17% 83%
5	FI	647	17% 83%
5	FM	647	17% 83%
5	FN	647	17% 83%
5	FO	647	17% 83%
5	N2	647	77% 23%
5	N5	647	77% 23%
5	N9	647	77% 23%
5	NA	647	77% 23%
5	NB	647	77% 23%
5	NC	647	77% 23%
5	NF	647	77% 23%
5	NH	647	77% 23%
5	NI	647	77% 23%
5	NM	647	77% 23%
5	NN	647	77% 23%
5	NO	647	77% 23%
5	O2	647	77% 23%
5	O5	647	77% 23%
5	O9	647	77% 23%
5	OA	647	77% 23%
5	OB	647	77% 23%
5	OC	647	77% 23%

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Mol	Chain	Length	Quality of chain
5	OF	647	77% 23%
5	OH	647	77% 23%
5	OI	647	77% 23%
5	OM	647	77% 23%
5	ON	647	77% 23%
5	OO	647	77% 23%
6	G2	133	14% 86%
6	G5	133	14% 86%
6	G9	133	14% 86%
6	GA	133	14% 86%
6	GB	133	14% 86%
6	GC	133	14% 86%
6	GF	133	14% 86%
6	GH	133	14% 86%
6	GI	133	14% 86%
6	GM	133	14% 86%
6	GN	133	14% 86%
6	GO	133	14% 86%
6	H2	133	14% 86%
6	H5	133	14% 86%
6	H9	133	14% 86%
6	HA	133	14% 86%
6	HB	133	14% 86%
6	HC	133	14% 86%
6	HF	133	14% 86%

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Mol	Chain	Length	Quality of chain
6	HH	133	14% 86%
6	HI	133	14% 86%
6	HM	133	14% 86%
6	HN	133	14% 86%
6	HO	133	14% 86%
6	I2	133	18% 82%
6	I5	133	18% 82%
6	I9	133	18% 82%
6	IA	133	18% 82%
6	IB	133	18% 82%
6	IC	133	18% 82%
6	IF	133	18% 82%
6	IH	133	18% 82%
6	II	133	18% 82%
6	IM	133	18% 82%
6	IN	133	18% 82%
6	IO	133	18% 82%
6	J2	133	18% 82%
6	J5	133	18% 82%
6	J9	133	18% 82%
6	JA	133	18% 82%
6	JB	133	18% 82%
6	JC	133	18% 82%
6	JF	133	18% 82%
6	JH	133	18% 82%

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Mol	Chain	Length	Quality of chain
6	JI	133	18% 82%
6	JM	133	18% 82%
6	JN	133	18% 82%
6	JO	133	18% 82%
6	K2	133	17% 83%
6	K5	133	17% 83%
6	K9	133	17% 83%
6	KA	133	17% 83%
6	KB	133	17% 83%
6	KC	133	17% 83%
6	KF	133	17% 83%
6	KH	133	17% 83%
6	KI	133	17% 83%
6	KM	133	17% 83%
6	KN	133	17% 83%
6	KO	133	17% 83%
6	L2	133	18% 82%
6	L5	133	18% 82%
6	L9	133	18% 82%
6	LA	133	18% 82%
6	LB	133	18% 82%
6	LC	133	18% 82%
6	LF	133	18% 82%
6	LH	133	18% 82%
6	LI	133	18% 82%

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Mol	Chain	Length	Quality of chain
6	LM	133	18% 82%
6	LN	133	18% 82%
6	LO	133	18% 82%
7	HS	55	100%
7	ID	55	100%
7	IJ	55	100%
7	IK	55	100%
7	IP	55	100%
7	NS	55	100%
7	OD	55	100%
7	OJ	55	100%
7	OK	55	100%
7	OP	55	100%
7	SD	55	100%
7	SJ	55	100%
7	SK	55	100%
7	SP	55	100%
7	SS	55	100%
8	PD	17	100%
8	PJ	17	100%
8	PK	17	100%
8	PP	17	100%
8	PS	17	100%
8	QD	17	94% 6%
8	QJ	17	94% 6%

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Mol	Chain	Length	Quality of chain
8	QK	17	94% 6%
8	QP	17	94% 6%
8	QS	17	94% 6%
8	RD	17	71% 29%
8	RJ	17	71% 29%
8	RK	17	71% 29%
8	RP	17	71% 29%
8	RS	17	71% 29%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 1074183 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 Major head protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	A1	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	B1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	D1	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	I1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	J1	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	K1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	L1	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Q1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	R1	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	S1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	T1	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	X1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	Y1	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	Z1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	a1	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	f1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g1	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	h1	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	i1	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	C3	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	A3	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	B3	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	D3	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	I3	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	J3	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	K3	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	L3	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Q3	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	R3	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	S3	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	T3	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Y3	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	b3	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	C4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	A4	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	B4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	D4	393	Total 3190	C 2050	N 520	O 612	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	I4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	J4	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	K4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	L4	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Q4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	R4	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	S4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	T4	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	X4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	Y4	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	Z4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	a4	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	f4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	g4	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	h4	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	i4	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	C6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	A6	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	B6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	D6	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	I6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	J6	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	K6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	L6	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Q6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	R6	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	S6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	T6	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Y6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	Z6	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	a6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	b6	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	g6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	h6	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	i6	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	j6	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	C7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	A7	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	B7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	D7	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	I7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	J7	392	Total 3178	C 2044	N 518	O 608	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	K7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	L7	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Q7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	R7	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	S7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	T7	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Y7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	Z7	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	a7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	b7	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	g7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	h7	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	i7	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	j7	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	C8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	A8	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	B8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	D8	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	I8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	J8	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	K8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	L8	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Q8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	R8	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	S8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	T8	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	Y8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	Z8	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	a8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	b8	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	g8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	h8	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	i8	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	j8	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	AD	354	Total 2821	C 1810	N 463	O 541	S 7	0	0
1	BD	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	CD	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	DD	386	Total 3131	C 2017	N 510	O 596	S 8	0	0
1	KD	382	Total 3103	C 1997	N 505	O 593	S 8	0	0
1	LD	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	DE	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	AE	385	Total 3123	C 2013	N 508	O 594	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	BE	392	3178	2044	518	608	8	0	0
1	CE	385	3123	2013	508	594	8	0	0
1	FE	393	3190	2050	520	612	8	0	0
1	KE	385	3123	2013	508	594	8	0	0
1	LE	392	3178	2044	518	608	8	0	0
1	ME	385	3123	2013	508	594	8	0	0
1	NE	393	3190	2050	520	612	8	0	0
1	SE	385	3123	2013	508	594	8	0	0
1	TE	392	3178	2044	518	608	8	0	0
1	UE	385	3123	2013	508	594	8	0	0
1	VE	393	3190	2050	520	612	8	0	0
1	aE	385	3123	2013	508	594	8	0	0
1	bE	392	3178	2044	518	608	8	0	0
1	cE	385	3123	2013	508	594	8	0	0
1	dE	393	3190	2050	520	612	8	0	0
1	CG	385	3123	2013	508	594	8	0	0
1	AG	392	3178	2044	518	608	8	0	0
1	BG	385	3123	2013	508	594	8	0	0
1	DG	393	3190	2050	520	612	8	0	0
1	IG	385	3123	2013	508	594	8	0	0
1	JG	392	3178	2044	518	608	8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	KG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	LG	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	QG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	RG	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	SG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	TG	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	YG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	ZG	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	aG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	bG	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	gG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	hG	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	iG	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	jG	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	AJ	354	Total 2821	C 1810	N 463	O 541	S 7	0	0
1	BJ	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	CJ	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	DJ	386	Total 3131	C 2017	N 510	O 596	S 8	0	0
1	KJ	382	Total 3103	C 1997	N 505	O 593	S 8	0	0
1	LJ	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	AK	354	Total 2821	C 1810	N 463	O 541	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BK	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	CK	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	DK	386	Total 3131	C 2017	N 510	O 596	S 8	0	0
1	KK	382	Total 3103	C 1997	N 505	O 593	S 8	0	0
1	LK	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	CL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	AL	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	BL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	DL	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	IL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	JL	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	KL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	LL	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	QL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	RL	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	SL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	TL	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	YL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	ZL	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	aL	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	bL	393	Total 3190	C 2050	N 520	O 612	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	gL	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	AP	354	Total 2821	C 1810	N 463	O 541	S 7	0	0
1	BP	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	CP	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	DP	386	Total 3131	C 2017	N 510	O 596	S 8	0	0
1	KP	382	Total 3103	C 1997	N 505	O 593	S 8	0	0
1	LP	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	CQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	AQ	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	BQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	DQ	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	IQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	JQ	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	KQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	LQ	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	QQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	RQ	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	SQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	TQ	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	YQ	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	bQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	cQ	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	dQ	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	eQ	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	CR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	AR	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	BR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	DR	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	IR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	JR	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	KR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	LR	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	QR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	RR	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	SR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	TR	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	YR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	ZR	392	Total 3178	C 2044	N 518	O 608	S 8	0	0
1	aR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	bR	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	gR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	hR	392	Total 3178	C 2044	N 518	O 608	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	iR	385	Total 3123	C 2013	N 508	O 594	S 8	0	0
1	jR	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	AS	393	Total 3190	C 2050	N 520	O 612	S 8	0	0
1	BS	386	Total 3135	C 2019	N 510	O 598	S 8	0	0
1	CS	386	Total 3131	C 2017	N 510	O 596	S 8	0	0
1	IS	354	Total 2821	C 1810	N 463	O 541	S 7	0	0
1	JS	382	Total 3103	C 1997	N 505	O 593	S 8	0	0
1	KS	386	Total 3135	C 2019	N 510	O 598	S 8	0	0

- Molecule 2 is a protein called Arstotzka protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E1	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	F1	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	G1	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	H1	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	M1	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	N1	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	O1	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	P1	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	U1	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	V1	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	W1	55	Total 435	C 260	N 77	O 93	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	b1	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	c1	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	d1	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	e1	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	j1	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	k1	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	l1	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	m1	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	E3	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	F3	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	G3	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	H3	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	M3	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	N3	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	O3	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	P3	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	U3	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	V3	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	W3	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	X3	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	Z3	54	Total 432	C 258	N 76	O 93	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	a3	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	c3	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	d3	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	E4	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	F4	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	G4	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	H4	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	M4	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	N4	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	O4	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	P4	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	U4	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	V4	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	W4	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	b4	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	c4	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	d4	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	e4	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	j4	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	k4	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	l4	55	Total 435	C 260	N 77	O 93	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	E6	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	F6	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	G6	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	H6	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	M6	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	N6	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	O6	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	P6	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	U6	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	V6	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	W6	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	X6	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	c6	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	d6	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	e6	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	f6	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	k6	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	l6	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	m6	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	n6	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	E7	54	Total 432	C 258	N 76	O 93	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	F7	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	G7	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	H7	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	M7	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	N7	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	O7	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	P7	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	U7	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	V7	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	W7	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	X7	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	c7	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	d7	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	e7	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	f7	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	k7	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	l7	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	m7	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	n7	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	E8	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	F8	55	Total 436	C 260	N 77	O 94	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	G8	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	H8	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	M8	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	N8	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	O8	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	P8	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	U8	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	V8	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	W8	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	X8	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	c8	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	d8	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	e8	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	f8	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	k8	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	l8	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	m8	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	n8	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	ED	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	FD	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	GD	30	Total 237	C 143	N 39	O 54	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	HD	54	Total 433	C 258	N 76	O 94	S 5	0	0
2	MD	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	ND	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	EE	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	GE	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	HE	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	IE	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	JE	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	OE	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	PE	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	QE	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	RE	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	WE	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	XE	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	YE	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	ZE	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	eE	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	fE	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	gE	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	hE	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	EG	54	Total 432	C 258	N 76	O 93	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	FG	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	GG	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	HG	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	MG	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	NG	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	OG	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	PG	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	UG	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	VG	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	WG	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	XG	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	cG	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	dG	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	eG	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	fG	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	kG	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	lG	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	mG	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	nG	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	EJ	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	FJ	55	Total 437	C 260	N 77	O 95	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	GJ	30	Total 237	C 143	N 39	O 54	S 1	0	0
2	HJ	54	Total 433	C 258	N 76	O 94	S 5	0	0
2	MJ	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	NJ	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	EK	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	FK	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	GK	30	Total 237	C 143	N 39	O 54	S 1	0	0
2	HK	54	Total 433	C 258	N 76	O 94	S 5	0	0
2	MK	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	NK	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	EL	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	FL	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	GL	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	HL	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	ML	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	NL	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	OL	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	PL	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	UL	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	VL	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	WL	27	Total 221	C 130	N 41	O 46	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	XL	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	cL	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	dL	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	eL	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	fL	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	hL	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	iL	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	EP	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	FP	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	GP	30	Total 237	C 143	N 39	O 54	S 1	0	0
2	HP	54	Total 433	C 258	N 76	O 94	S 5	0	0
2	MP	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	NP	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	EQ	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	FQ	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	GQ	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	HQ	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	MQ	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	NQ	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	OQ	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	PQ	55	Total 435	C 260	N 77	O 93	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	UQ	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	VQ	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	WQ	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	XQ	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	ZQ	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	aQ	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	fQ	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	gQ	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	hQ	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	iQ	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	ER	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	FR	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	GR	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	HR	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	MR	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	NR	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	OR	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	PR	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	UR	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	VR	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	WR	27	Total 221	C 130	N 41	O 46	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	XR	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	cR	54	Total 432	C 258	N 76	O 93	S 5	0	0
2	dR	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	eR	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	fR	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	kR	55	Total 436	C 260	N 77	O 94	S 5	0	0
2	lR	27	Total 221	C 130	N 41	O 46	S 4	0	0
2	mR	55	Total 435	C 260	N 77	O 93	S 5	0	0
2	DS	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	ES	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	FS	30	Total 237	C 143	N 39	O 54	S 1	0	0
2	GS	54	Total 433	C 258	N 76	O 94	S 5	0	0
2	LS	55	Total 437	C 260	N 77	O 95	S 5	0	0
2	MS	55	Total 437	C 260	N 77	O 95	S 5	0	0

- Molecule 3 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	A5	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	A9	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AA	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AB	301	Total 2353	C 1486	N 398	O 460	S 9	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AF	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AH	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AI	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AM	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AN	301	Total 2353	C 1486	N 398	O 460	S 9	0	0
3	AO	301	Total 2353	C 1486	N 398	O 460	S 9	0	0

- Molecule 4 is a protein called Lower collar protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B2	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	B5	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	B9	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BA	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BB	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BC	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BF	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BH	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BI	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BM	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BN	220	Total 1763	C 1111	N 294	O 353	S 5	0	0
4	BO	220	Total 1763	C 1111	N 294	O 353	S 5	0	0

- Molecule 5 is a protein called Minor structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D2	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	E2	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	F2	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	C2	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	N2	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	O2	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	D5	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	E5	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	F5	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	C5	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	N5	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	O5	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	D9	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	E9	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	F9	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	C9	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	N9	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	O9	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DA	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EA	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FA	110	Total 927	C 595	N 155	O 174	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	CA	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NA	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OA	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DB	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EB	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FB	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CB	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NB	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OB	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DC	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EC	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FC	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CC	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NC	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OC	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DF	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EF	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FF	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CF	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NF	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OF	500	Total 4012	C 2539	N 688	O 770	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	DH	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EH	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FH	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CH	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NH	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OH	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DI	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EI	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FI	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CI	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NI	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OI	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DM	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EM	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FM	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CM	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NM	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OM	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DN	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EN	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FN	110	Total 927	C 595	N 155	O 174	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	CN	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NN	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	ON	500	Total 4012	C 2539	N 688	O 770	S 15	0	0
5	DO	132	Total 1107	C 718	N 178	O 208	S 3	0	0
5	EO	136	Total 1173	C 755	N 192	O 223	S 3	0	0
5	FO	110	Total 927	C 595	N 155	O 174	S 3	0	0
5	CO	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	NO	501	Total 4021	C 2545	N 690	O 771	S 15	0	0
5	OO	500	Total 4012	C 2539	N 688	O 770	S 15	0	0

- Molecule 6 is a protein called Tail fibre protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	G2	18	Total 90	C 54	N 18	O 18	0	0
6	H2	18	Total 90	C 54	N 18	O 18	0	0
6	I2	24	Total 120	C 72	N 24	O 24	0	0
6	J2	24	Total 120	C 72	N 24	O 24	0	0
6	K2	22	Total 112	C 67	N 22	O 23	0	0
6	L2	24	Total 120	C 72	N 24	O 24	0	0
6	G5	18	Total 90	C 54	N 18	O 18	0	0
6	H5	18	Total 90	C 54	N 18	O 18	0	0
6	I5	24	Total 120	C 72	N 24	O 24	0	0
6	J5	24	Total 120	C 72	N 24	O 24	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
6	K5	22	Total C N O 112 67 22 23	0	0
6	L5	24	Total C N O 120 72 24 24	0	0
6	G9	18	Total C N O 90 54 18 18	0	0
6	H9	18	Total C N O 90 54 18 18	0	0
6	I9	24	Total C N O 120 72 24 24	0	0
6	J9	24	Total C N O 120 72 24 24	0	0
6	K9	22	Total C N O 112 67 22 23	0	0
6	L9	24	Total C N O 120 72 24 24	0	0
6	GA	18	Total C N O 90 54 18 18	0	0
6	HA	18	Total C N O 90 54 18 18	0	0
6	IA	24	Total C N O 120 72 24 24	0	0
6	JA	24	Total C N O 120 72 24 24	0	0
6	KA	22	Total C N O 112 67 22 23	0	0
6	LA	24	Total C N O 120 72 24 24	0	0
6	GB	18	Total C N O 90 54 18 18	0	0
6	HB	18	Total C N O 90 54 18 18	0	0
6	IB	24	Total C N O 120 72 24 24	0	0
6	JB	24	Total C N O 120 72 24 24	0	0
6	KB	22	Total C N O 112 67 22 23	0	0
6	LB	24	Total C N O 120 72 24 24	0	0
6	GC	18	Total C N O 90 54 18 18	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
6	HC	18	Total C N O 90 54 18 18	0	0
6	IC	24	Total C N O 120 72 24 24	0	0
6	JC	24	Total C N O 120 72 24 24	0	0
6	KC	22	Total C N O 112 67 22 23	0	0
6	LC	24	Total C N O 120 72 24 24	0	0
6	GF	18	Total C N O 90 54 18 18	0	0
6	HF	18	Total C N O 90 54 18 18	0	0
6	IF	24	Total C N O 120 72 24 24	0	0
6	JF	24	Total C N O 120 72 24 24	0	0
6	KF	22	Total C N O 112 67 22 23	0	0
6	LF	24	Total C N O 120 72 24 24	0	0
6	GH	18	Total C N O 90 54 18 18	0	0
6	HH	18	Total C N O 90 54 18 18	0	0
6	IH	24	Total C N O 120 72 24 24	0	0
6	JH	24	Total C N O 120 72 24 24	0	0
6	KH	22	Total C N O 112 67 22 23	0	0
6	LH	24	Total C N O 120 72 24 24	0	0
6	GI	18	Total C N O 90 54 18 18	0	0
6	HI	18	Total C N O 90 54 18 18	0	0
6	II	24	Total C N O 120 72 24 24	0	0
6	JI	24	Total C N O 120 72 24 24	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
6	KI	22	Total C N O 112 67 22 23	0	0
6	LI	24	Total C N O 120 72 24 24	0	0
6	GM	18	Total C N O 90 54 18 18	0	0
6	HM	18	Total C N O 90 54 18 18	0	0
6	IM	24	Total C N O 120 72 24 24	0	0
6	JM	24	Total C N O 120 72 24 24	0	0
6	KM	22	Total C N O 112 67 22 23	0	0
6	LM	24	Total C N O 120 72 24 24	0	0
6	GN	18	Total C N O 90 54 18 18	0	0
6	HN	18	Total C N O 90 54 18 18	0	0
6	IN	24	Total C N O 120 72 24 24	0	0
6	JN	24	Total C N O 120 72 24 24	0	0
6	KN	22	Total C N O 112 67 22 23	0	0
6	LN	24	Total C N O 120 72 24 24	0	0
6	GO	18	Total C N O 90 54 18 18	0	0
6	HO	18	Total C N O 90 54 18 18	0	0
6	IO	24	Total C N O 120 72 24 24	0	0
6	JO	24	Total C N O 120 72 24 24	0	0
6	KO	22	Total C N O 112 67 22 23	0	0
6	LO	24	Total C N O 120 72 24 24	0	0

- Molecule 7 is a protein called Head fiber protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	ID	55	Total 275	C 165	N 55	O 55	0	0
7	OD	55	Total 275	C 165	N 55	O 55	0	0
7	SD	55	Total 275	C 165	N 55	O 55	0	0
7	IJ	55	Total 275	C 165	N 55	O 55	0	0
7	OJ	55	Total 275	C 165	N 55	O 55	0	0
7	SJ	55	Total 275	C 165	N 55	O 55	0	0
7	IK	55	Total 275	C 165	N 55	O 55	0	0
7	OK	55	Total 275	C 165	N 55	O 55	0	0
7	SK	55	Total 275	C 165	N 55	O 55	0	0
7	IP	55	Total 275	C 165	N 55	O 55	0	0
7	OP	55	Total 275	C 165	N 55	O 55	0	0
7	SP	55	Total 275	C 165	N 55	O 55	0	0
7	HS	55	Total 275	C 165	N 55	O 55	0	0
7	NS	55	Total 275	C 165	N 55	O 55	0	0
7	SS	55	Total 275	C 165	N 55	O 55	0	0

- Molecule 8 is a protein called Inner core protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	PD	17	Total 85	C 51	N 17	O 17	0	0
8	QD	16	Total 79	C 47	N 16	O 16	0	0
8	RD	12	Total 54	C 30	N 12	O 12	0	0
8	PJ	17	Total 85	C 51	N 17	O 17	0	0
8	QJ	16	Total 79	C 47	N 16	O 16	0	0

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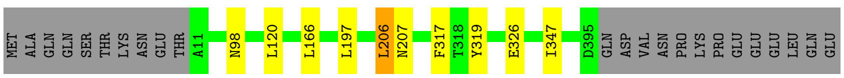
Mol	Chain	Residues	Atoms				AltConf	Trace
8	RJ	12	Total 54	C 30	N 12	O 12	0	0
8	PK	17	Total 85	C 51	N 17	O 17	0	0
8	QK	16	Total 79	C 47	N 16	O 16	0	0
8	RK	12	Total 54	C 30	N 12	O 12	0	0
8	PP	17	Total 85	C 51	N 17	O 17	0	0
8	QP	16	Total 79	C 47	N 16	O 16	0	0
8	RP	12	Total 54	C 30	N 12	O 12	0	0
8	PS	17	Total 85	C 51	N 17	O 17	0	0
8	QS	16	Total 79	C 47	N 16	O 16	0	0
8	RS	12	Total 54	C 30	N 12	O 12	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. 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. 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.

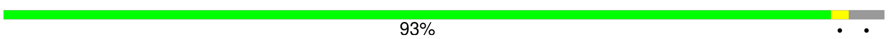
- Molecule 1: Major head protein

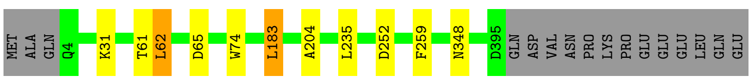
Chain C1:



- Molecule 1: Major head protein

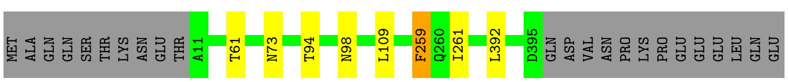
Chain A1:





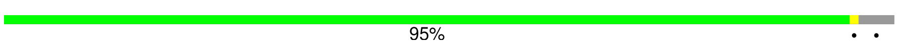
- Molecule 1: Major head protein

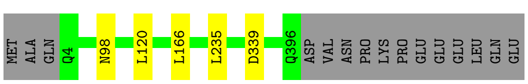
Chain B1:



- Molecule 1: Major head protein

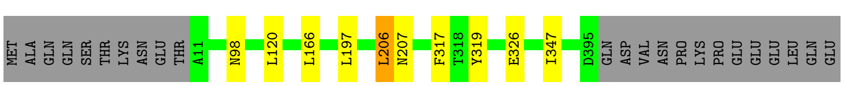
Chain D1:





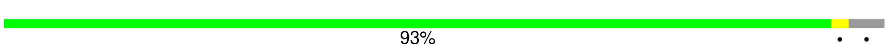
- Molecule 1: Major head protein

Chain I1:



- Molecule 1: Major head protein

Chain J1:



MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain K1: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain L1: 95% • •

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain Q1: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain R1: 93% • •

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain S1: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

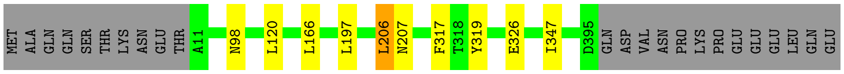
• Molecule 1: Major head protein

Chain T1: 95% • •

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

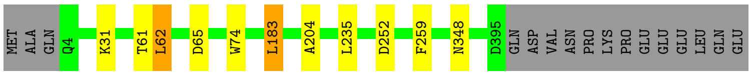
• Molecule 1: Major head protein

Chain X1: 92% • 6%



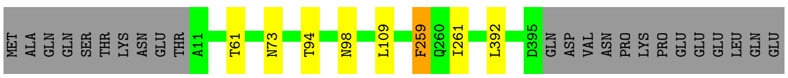
• Molecule 1: Major head protein

Chain Y1: 93%



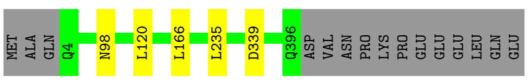
• Molecule 1: Major head protein

Chain Z1: 92% 6%



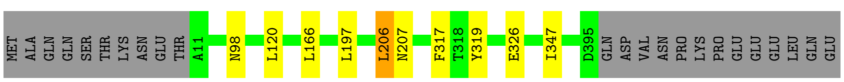
• Molecule 1: Major head protein

Chain a1: 95%



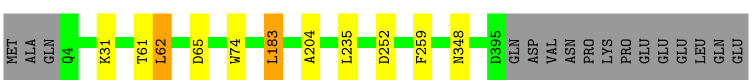
• Molecule 1: Major head protein

Chain f1: 92% 6%



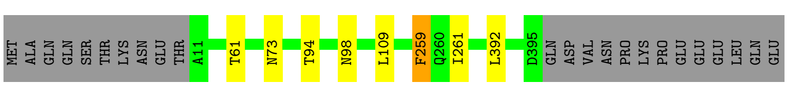
• Molecule 1: Major head protein

Chain g1: 93%



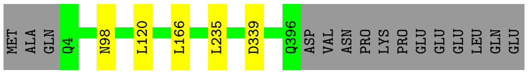
• Molecule 1: Major head protein

Chain h1: 92% 6%



• Molecule 1: Major head protein

Chain i1: 95%

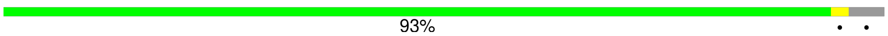


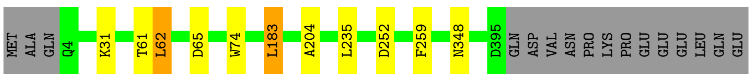
• Molecule 1: Major head protein

Chain C3:

• Molecule 1: Major head protein

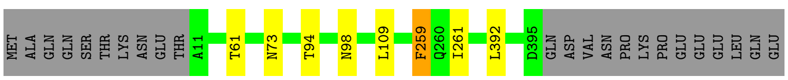
Chain A3:





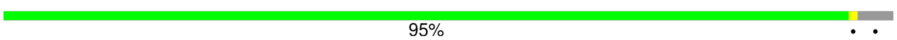
• Molecule 1: Major head protein

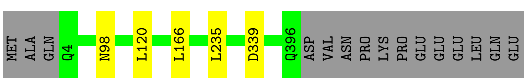
Chain B3:



• Molecule 1: Major head protein

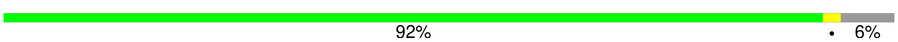
Chain D3:

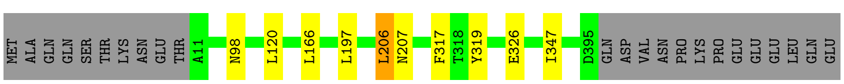




• Molecule 1: Major head protein

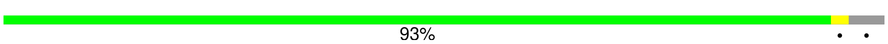
Chain I3:

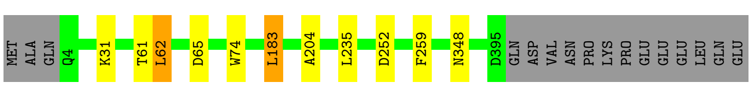




• Molecule 1: Major head protein

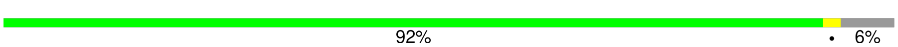
Chain J3:





• Molecule 1: Major head protein

Chain K3:



MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain L3: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain Q3: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain R3: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain S3: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain T3: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

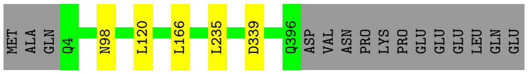
• Molecule 1: Major head protein

Chain Y3: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

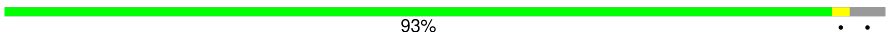
Chain b3: 95%

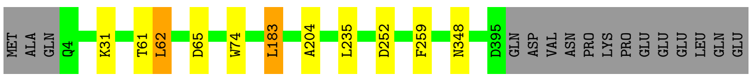


• Molecule 1: Major head protein

Chain C4:

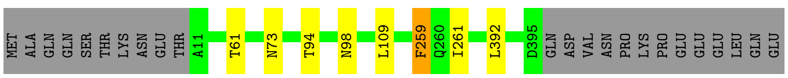

• Molecule 1: Major head protein

Chain A4:


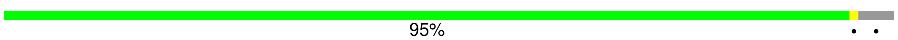


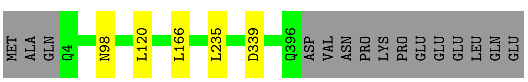
• Molecule 1: Major head protein

Chain B4:

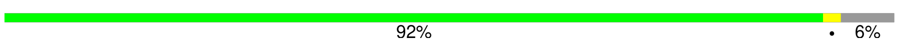



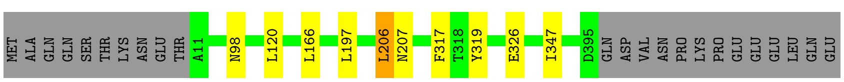
• Molecule 1: Major head protein

Chain D4:


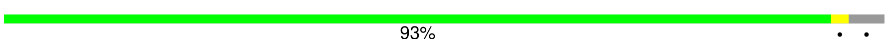


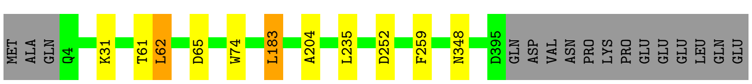
• Molecule 1: Major head protein

Chain I4:




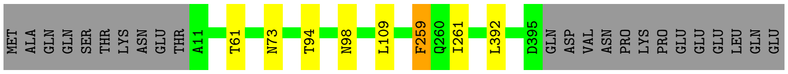
• Molecule 1: Major head protein

Chain J4:




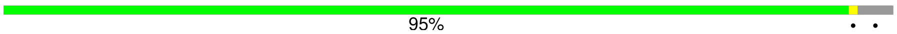
• Molecule 1: Major head protein

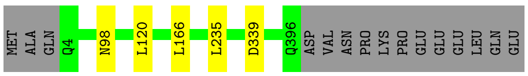
Chain K4:

• Molecule 1: Major head protein

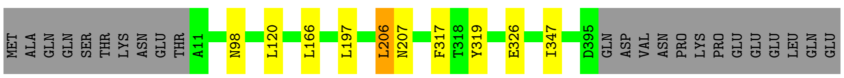
Chain L4:





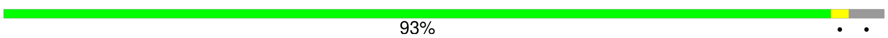
• Molecule 1: Major head protein

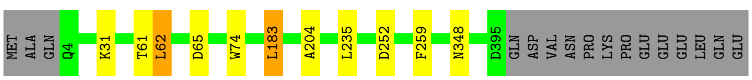
Chain Q4:



• Molecule 1: Major head protein

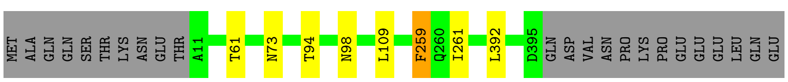
Chain R4:





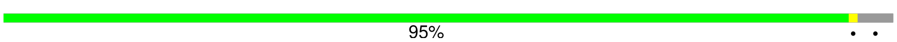
• Molecule 1: Major head protein

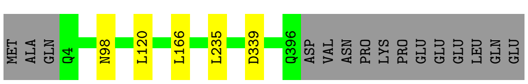
Chain S4:



• Molecule 1: Major head protein

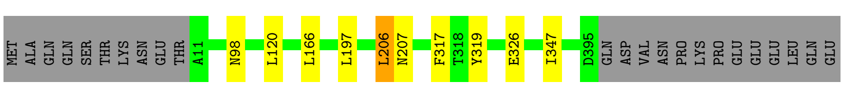
Chain T4:





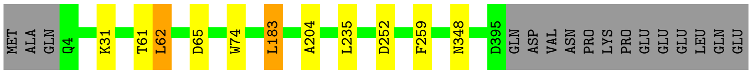
• Molecule 1: Major head protein

Chain X4:



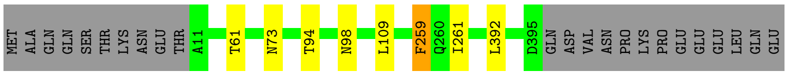
• Molecule 1: Major head protein

Chain Y4:



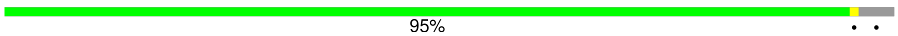
• Molecule 1: Major head protein

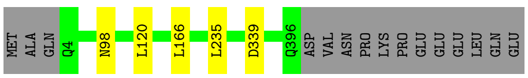
Chain Z4:



• Molecule 1: Major head protein

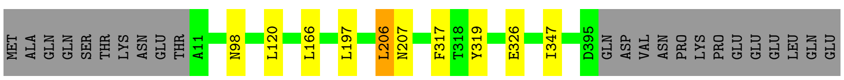
Chain a4:





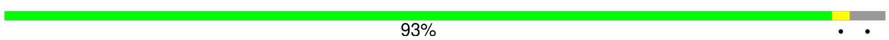
• Molecule 1: Major head protein

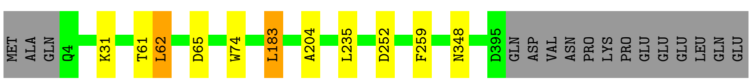
Chain f4:



• Molecule 1: Major head protein

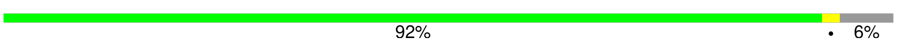
Chain g4:

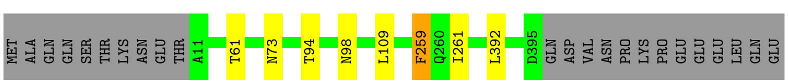




• Molecule 1: Major head protein

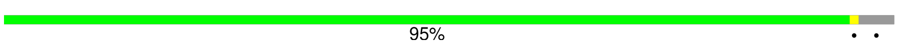
Chain h4:

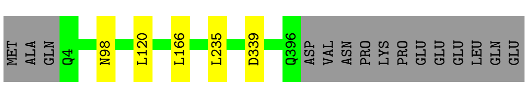




• Molecule 1: Major head protein

Chain i4:





• Molecule 1: Major head protein

Chain C6:

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain A6: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain B6: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain D6: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain I6: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain J6: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

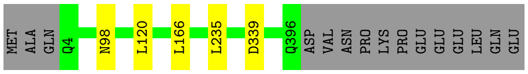
• Molecule 1: Major head protein

Chain K6: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

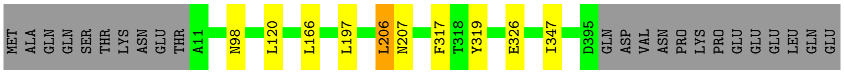
• Molecule 1: Major head protein

Chain L6: 95%



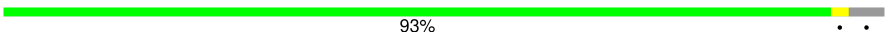
• Molecule 1: Major head protein

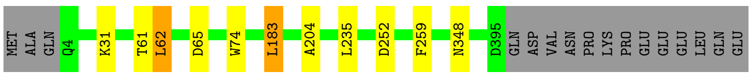
Chain Q6:



• Molecule 1: Major head protein

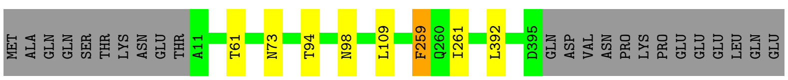
Chain R6:





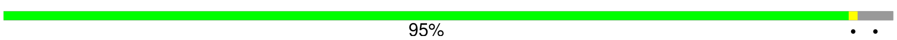
• Molecule 1: Major head protein

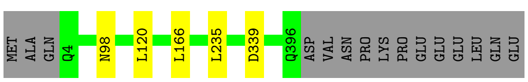
Chain S6:



• Molecule 1: Major head protein

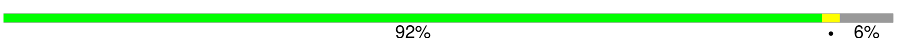
Chain T6:

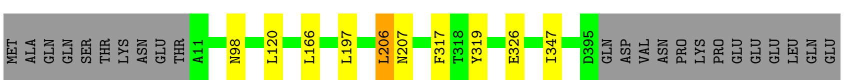




• Molecule 1: Major head protein

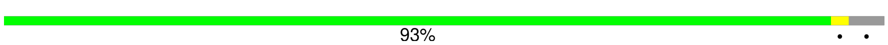
Chain Y6:

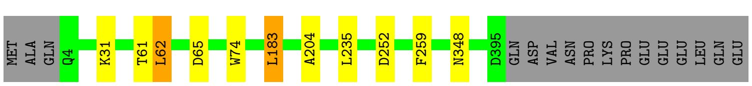




• Molecule 1: Major head protein

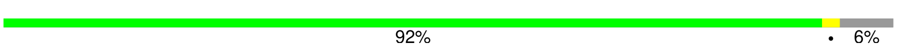
Chain Z6:





• Molecule 1: Major head protein

Chain a6:



MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain b6: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain g6: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain h6: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain i6: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain j6: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain C7: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain A7: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain B7: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain D7: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain I7: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain J7: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain K7: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

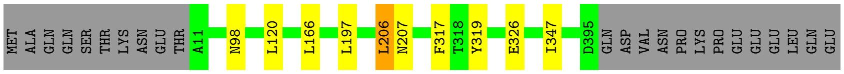
- Molecule 1: Major head protein

Chain L7: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

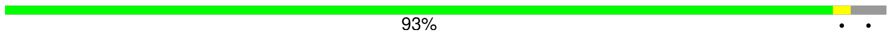
- Molecule 1: Major head protein

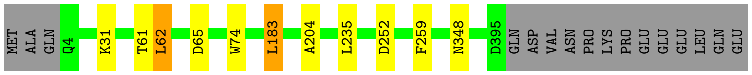
Chain Q7: 92% 6%



• Molecule 1: Major head protein

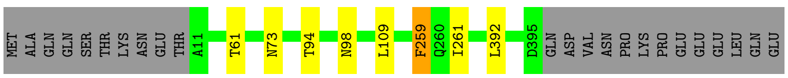
Chain R7:





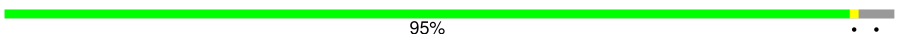
• Molecule 1: Major head protein

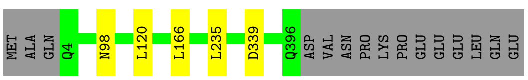
Chain S7:



• Molecule 1: Major head protein

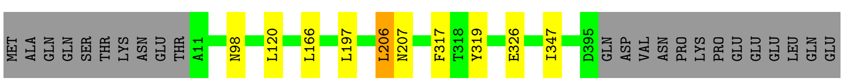
Chain T7:





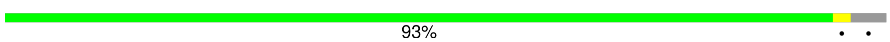
• Molecule 1: Major head protein

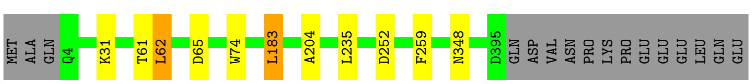
Chain Y7:



• Molecule 1: Major head protein

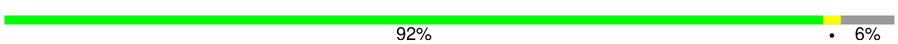
Chain Z7:

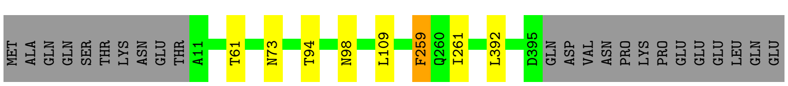




• Molecule 1: Major head protein

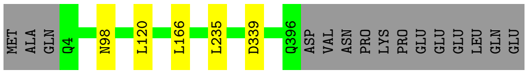
Chain a7:





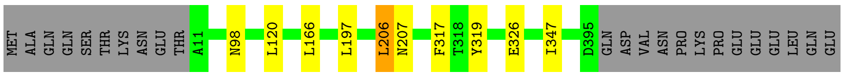
• Molecule 1: Major head protein

Chain b7:



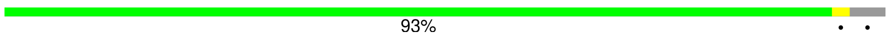
• Molecule 1: Major head protein

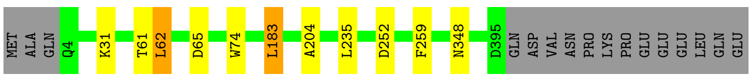
Chain g7:



• Molecule 1: Major head protein

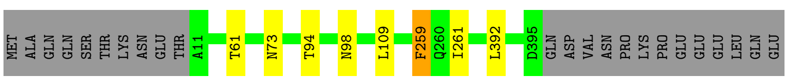
Chain h7:





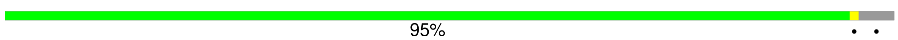
• Molecule 1: Major head protein

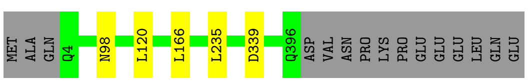
Chain i7:



• Molecule 1: Major head protein

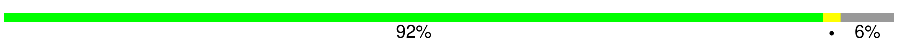
Chain j7:

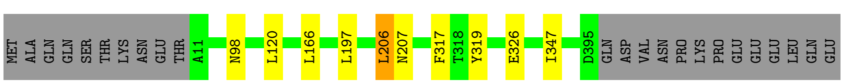




• Molecule 1: Major head protein

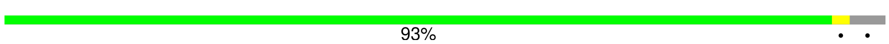
Chain C8:

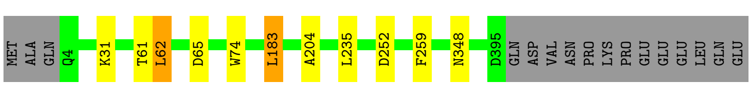




• Molecule 1: Major head protein

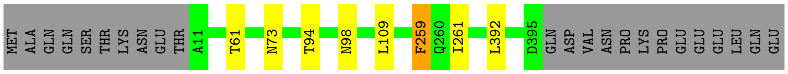
Chain A8:





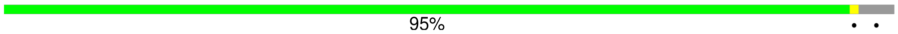
• Molecule 1: Major head protein

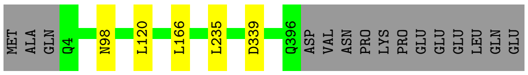
Chain B8:



• Molecule 1: Major head protein

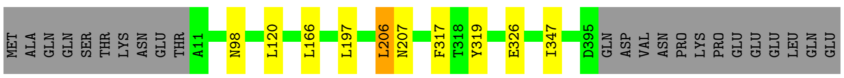
Chain D8:





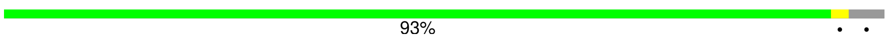
• Molecule 1: Major head protein

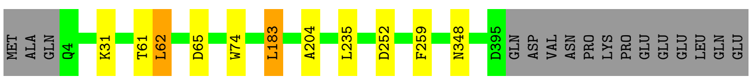
Chain I8:



• Molecule 1: Major head protein

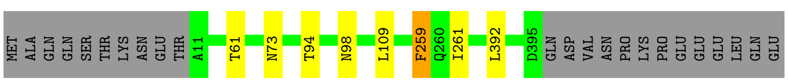
Chain J8:





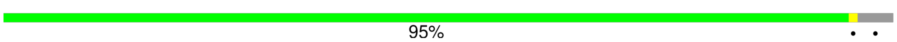
• Molecule 1: Major head protein

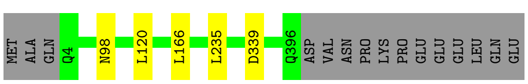
Chain K8:



• Molecule 1: Major head protein

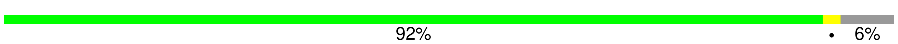
Chain L8:

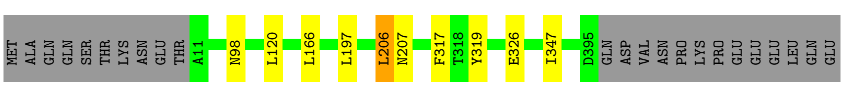




• Molecule 1: Major head protein

Chain Q8:





• Molecule 1: Major head protein

Chain R8:

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain S8: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain T8: 95% • •

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain Y8: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain Z8: 93% • •

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

- Molecule 1: Major head protein

Chain a8: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

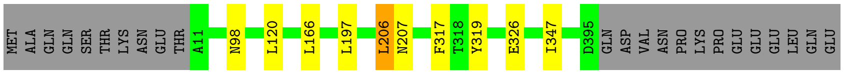
- Molecule 1: Major head protein

Chain b8: 95% • •

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

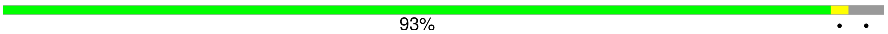
- Molecule 1: Major head protein

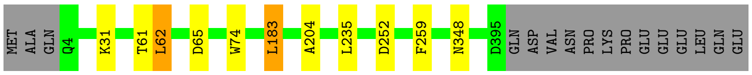
Chain g8: 92% • 6%



• Molecule 1: Major head protein

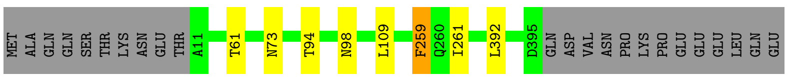
Chain h8:





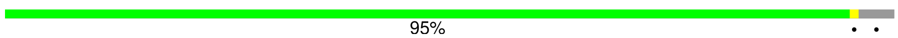
• Molecule 1: Major head protein

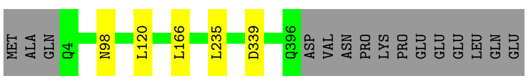
Chain i8:



• Molecule 1: Major head protein

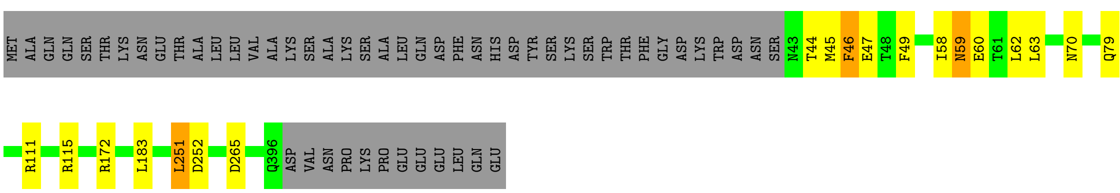
Chain j8:





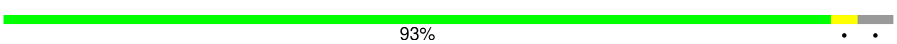
• Molecule 1: Major head protein

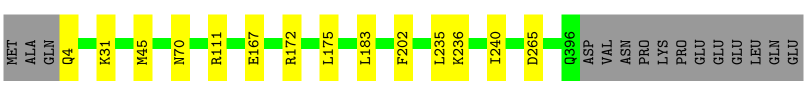
Chain AD:



• Molecule 1: Major head protein

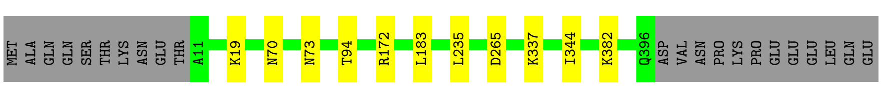
Chain BD:





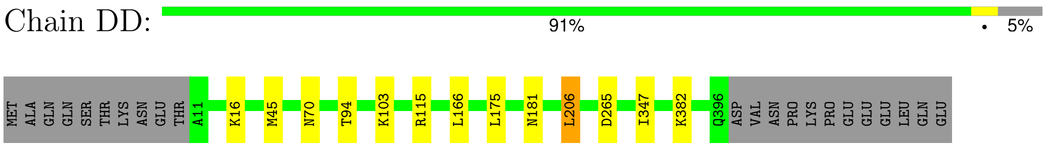
• Molecule 1: Major head protein

Chain CD:



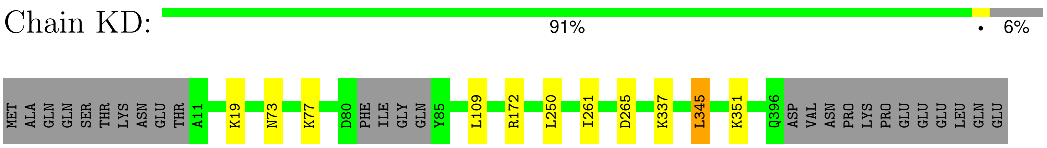
• Molecule 1: Major head protein

Chain DD:



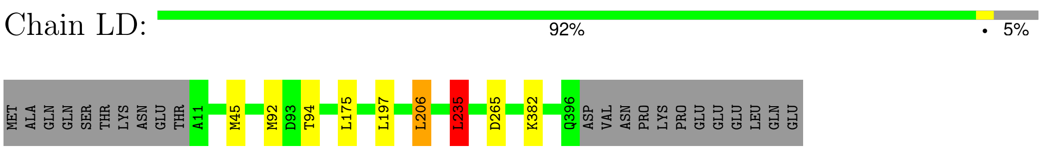
• Molecule 1: Major head protein

Chain KD:



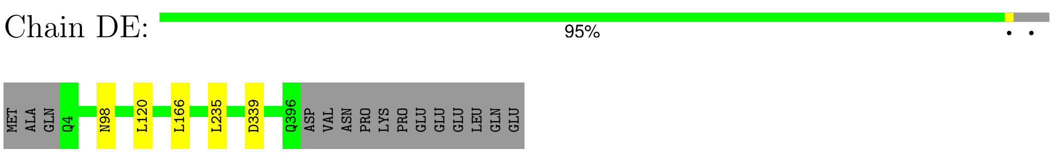
• Molecule 1: Major head protein

Chain LD:



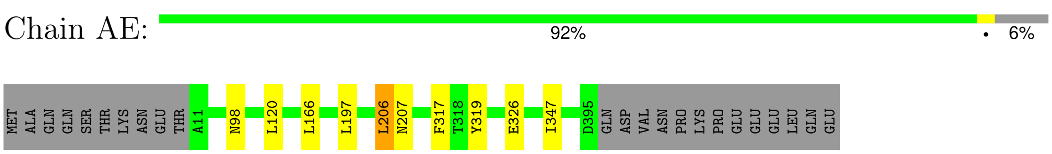
• Molecule 1: Major head protein

Chain DE:



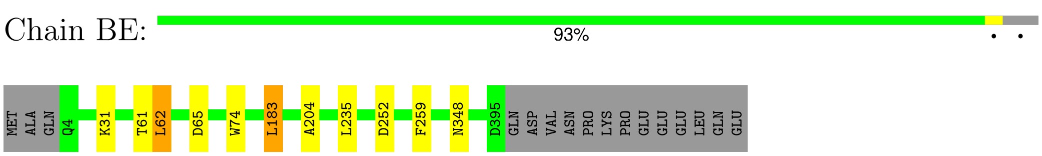
• Molecule 1: Major head protein

Chain AE:



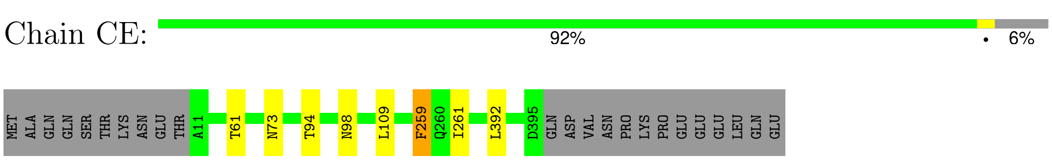
• Molecule 1: Major head protein

Chain BE:



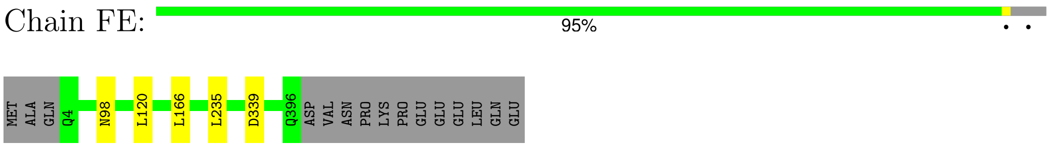
• Molecule 1: Major head protein

Chain CE:



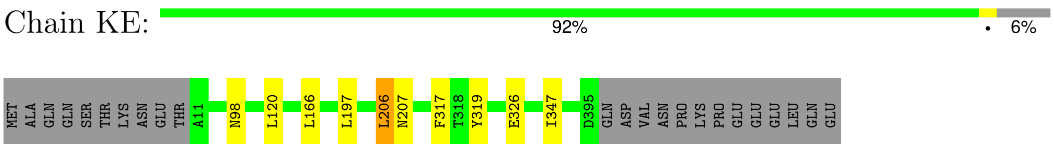
• Molecule 1: Major head protein

Chain FE:



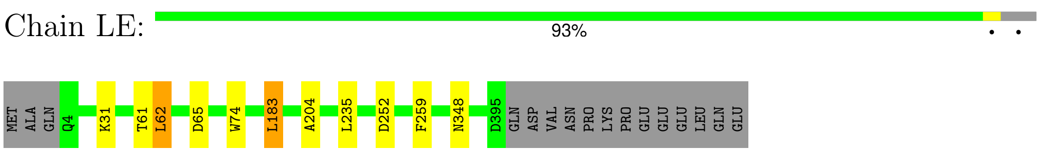
• Molecule 1: Major head protein

Chain KE:



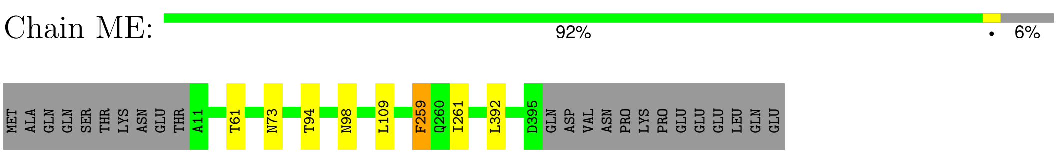
• Molecule 1: Major head protein

Chain LE:



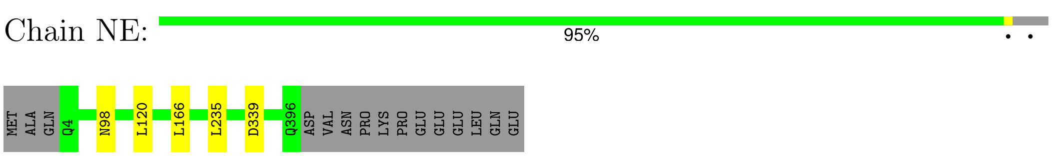
• Molecule 1: Major head protein

Chain ME:



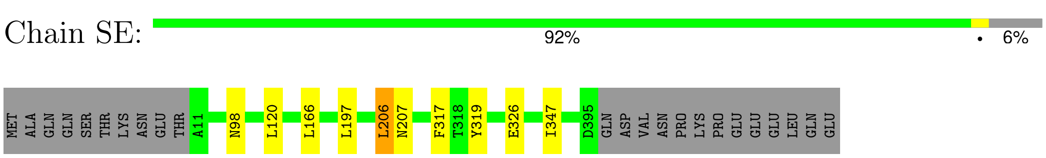
• Molecule 1: Major head protein

Chain NE:



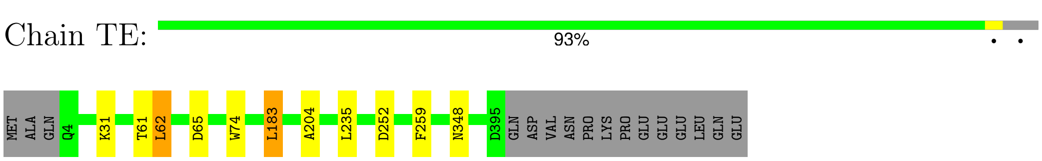
• Molecule 1: Major head protein

Chain SE:



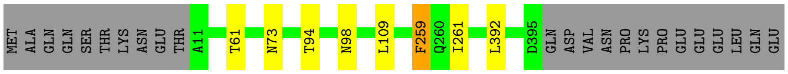
• Molecule 1: Major head protein

Chain TE:



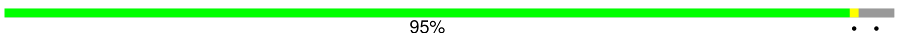
• Molecule 1: Major head protein

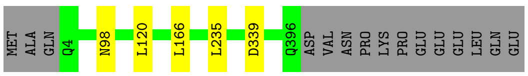
Chain UE:



• Molecule 1: Major head protein

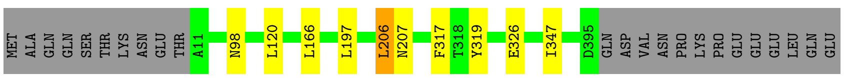
Chain VE:





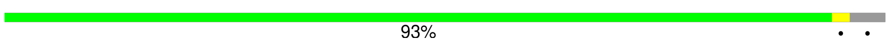
• Molecule 1: Major head protein

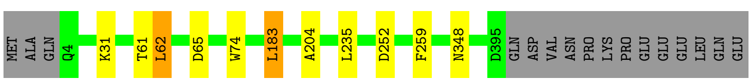
Chain aE:



• Molecule 1: Major head protein

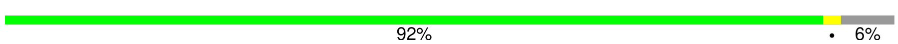
Chain bE:

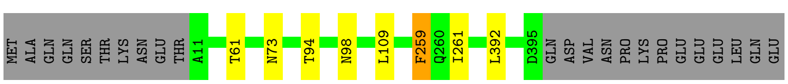




• Molecule 1: Major head protein

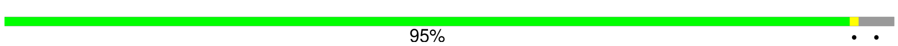
Chain cE:

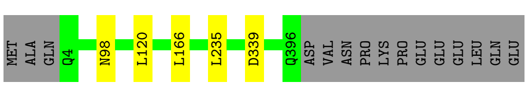




• Molecule 1: Major head protein

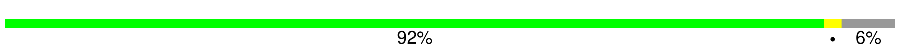
Chain dE:

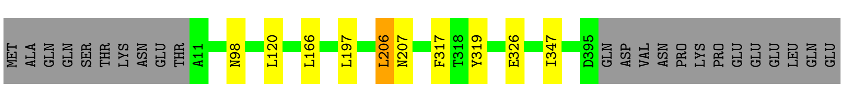




• Molecule 1: Major head protein

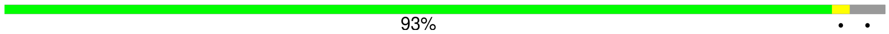
Chain CG:

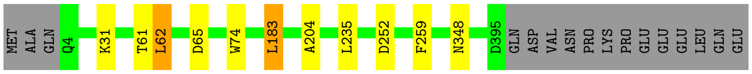




• Molecule 1: Major head protein

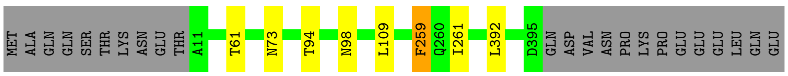
Chain AG:





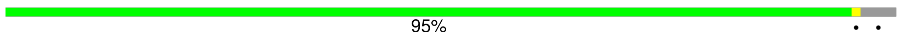
• Molecule 1: Major head protein

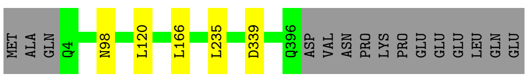
Chain BG:



• Molecule 1: Major head protein

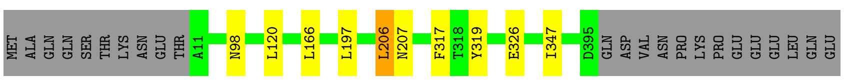
Chain DG:





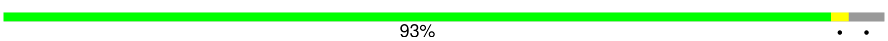
• Molecule 1: Major head protein

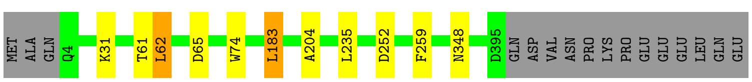
Chain IG:



• Molecule 1: Major head protein

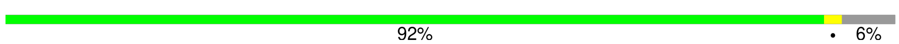
Chain JG:

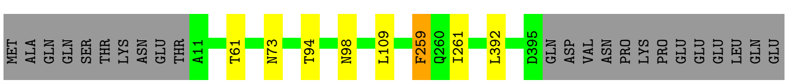




• Molecule 1: Major head protein

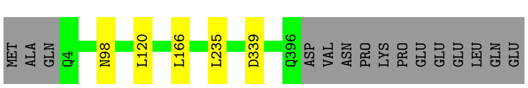
Chain KG:





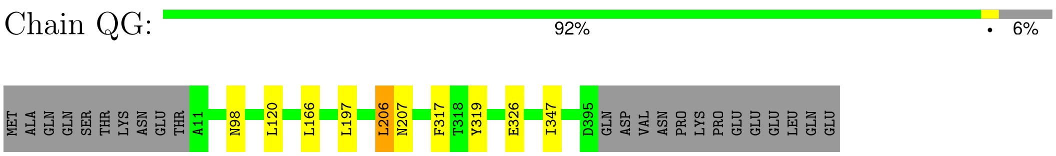
• Molecule 1: Major head protein

Chain LG:



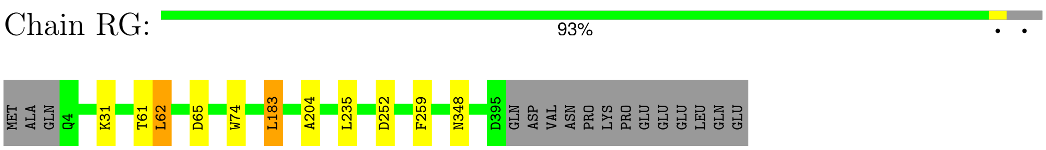
• Molecule 1: Major head protein

Chain QG:



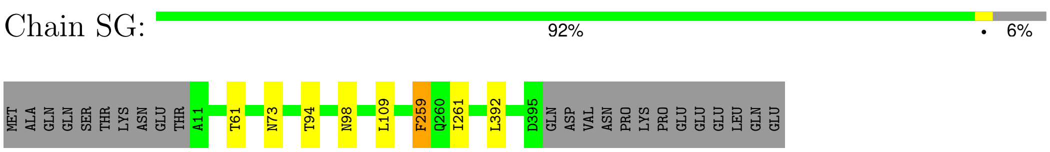
• Molecule 1: Major head protein

Chain RG:



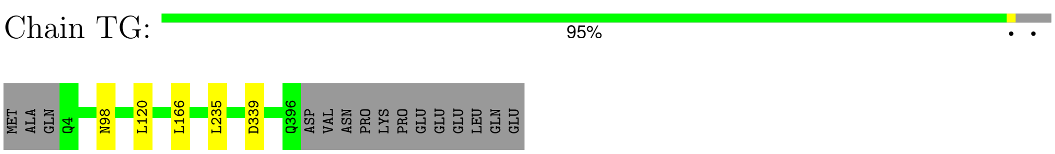
• Molecule 1: Major head protein

Chain SG:



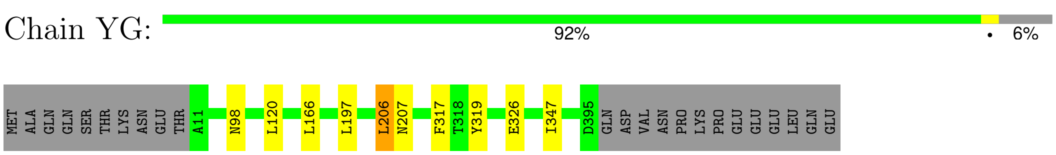
• Molecule 1: Major head protein

Chain TG:



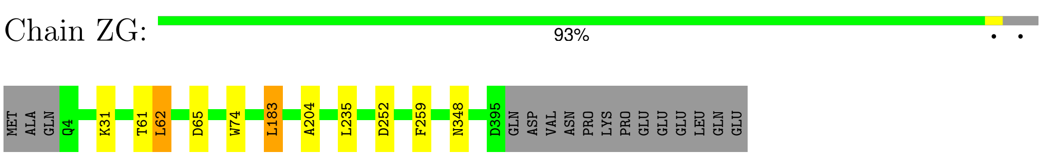
• Molecule 1: Major head protein

Chain YG:



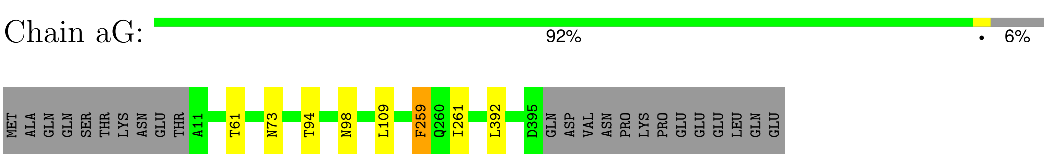
• Molecule 1: Major head protein

Chain ZG:



• Molecule 1: Major head protein

Chain aG:



• Molecule 1: Major head protein

Chain bG: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain gG: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain hG: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain iG: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain jG: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain AJ: 82% 13%

MET ALA GLN GLN SER THR LYS ASN GLU THR ALA LEU LEU VAL ALA LYS SER ALA LYS SER ALA LEU GLN ASP PHE ASN HIS ASP TYR SER LYS SER TRP THR PHE GLY ASP LYS TRP ASP ASN SER N43 T44 M45 F46 E47 T48 F49 I58 N59 E60 T61 L62 L63 N70 Q79 R111 R115 R172 L183 L251 D252 D265 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

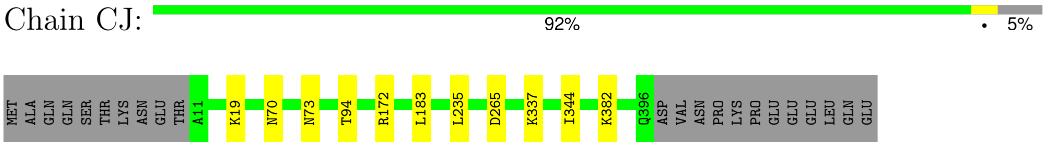
• Molecule 1: Major head protein

Chain BJ: 93%

MET ALA GLN Q4 K31 M45 N70 R111 E167 R172 L175 L183 F202 L235 K236 I240 D265 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

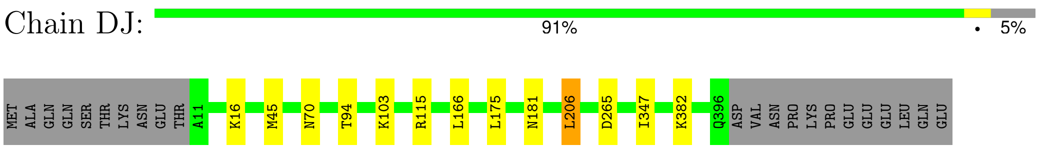
- Molecule 1: Major head protein

Chain CJ:



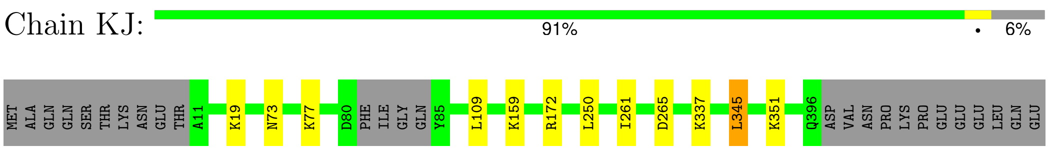
- Molecule 1: Major head protein

Chain DJ:



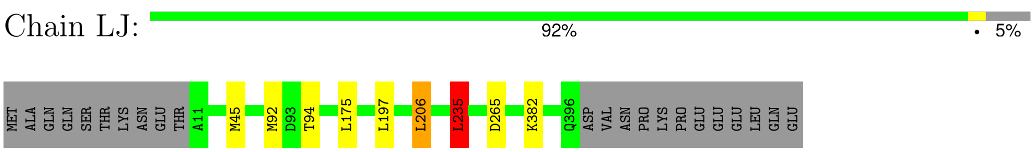
- Molecule 1: Major head protein

Chain KJ:



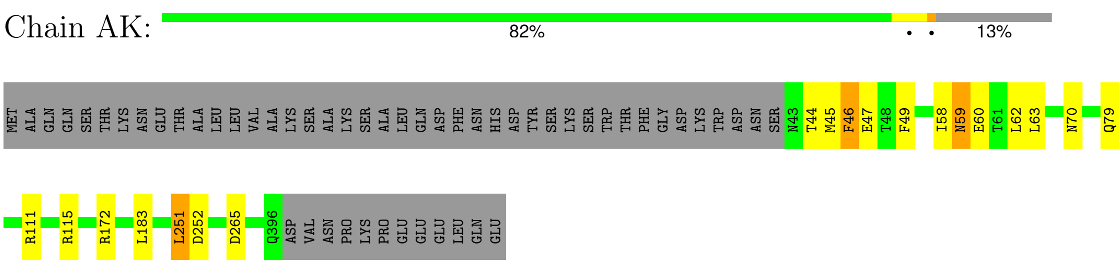
- Molecule 1: Major head protein

Chain LJ:



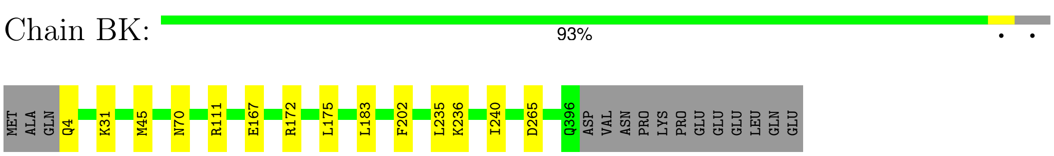
- Molecule 1: Major head protein

Chain AK:



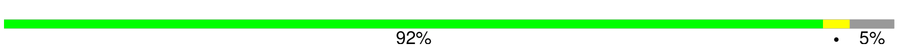
- Molecule 1: Major head protein

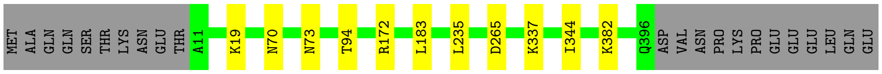
Chain BK:



- Molecule 1: Major head protein

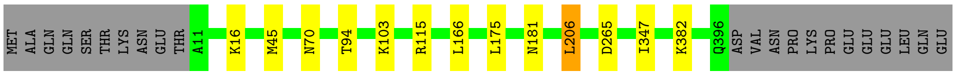
Chain CK:





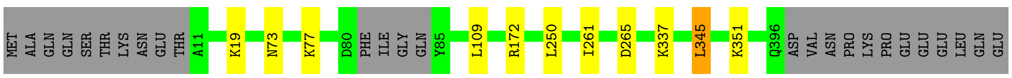
• Molecule 1: Major head protein

Chain DK:

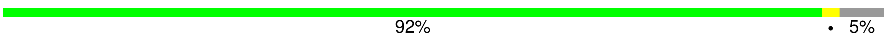



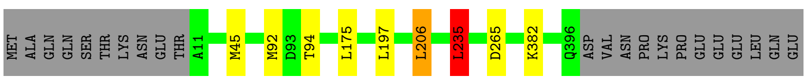
• Molecule 1: Major head protein

Chain KK:

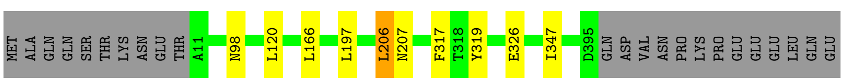
• Molecule 1: Major head protein

Chain LK:


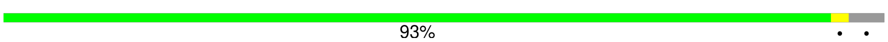


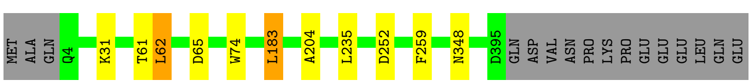
• Molecule 1: Major head protein

Chain CL:

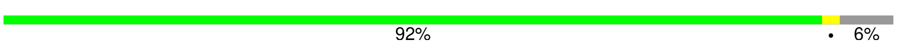



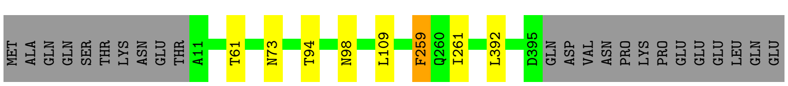
• Molecule 1: Major head protein

Chain AL:




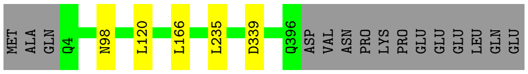
• Molecule 1: Major head protein

Chain BL:




• Molecule 1: Major head protein

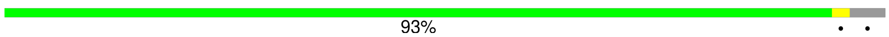
Chain DL:

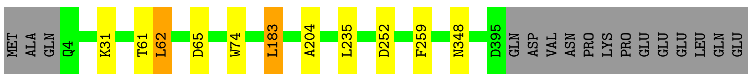


• Molecule 1: Major head protein

Chain IL:

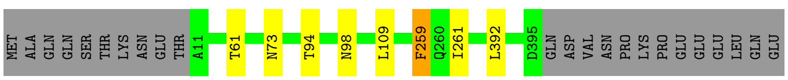

• Molecule 1: Major head protein

Chain JL:


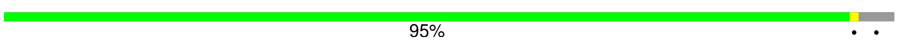


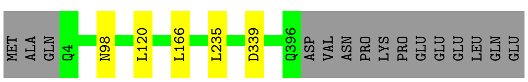
• Molecule 1: Major head protein

Chain KL:

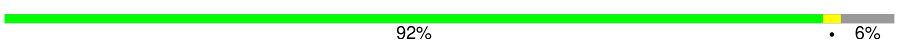



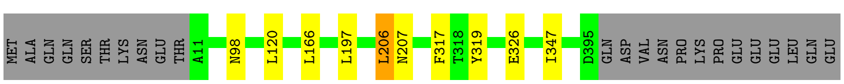
• Molecule 1: Major head protein

Chain LL:


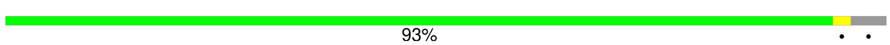


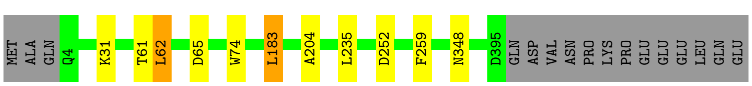
• Molecule 1: Major head protein

Chain QL:


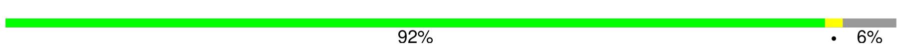


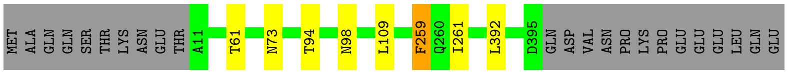
• Molecule 1: Major head protein

Chain RL:




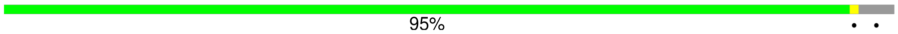
• Molecule 1: Major head protein

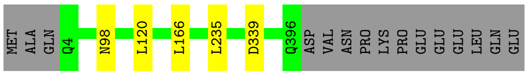
Chain SL:




• Molecule 1: Major head protein

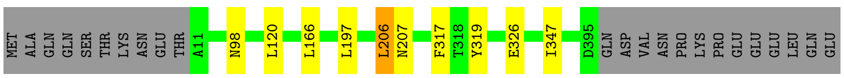
Chain TL:





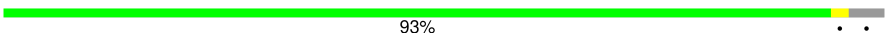
• Molecule 1: Major head protein

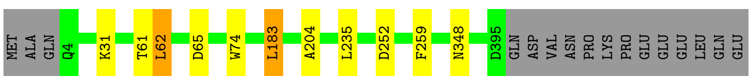
Chain YL:



• Molecule 1: Major head protein

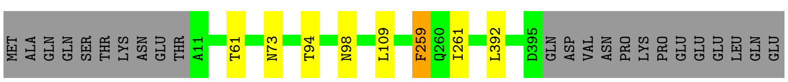
Chain ZL:





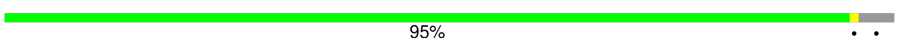
• Molecule 1: Major head protein

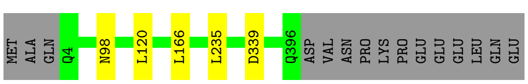
Chain aL:



• Molecule 1: Major head protein

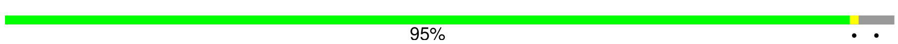
Chain bL:

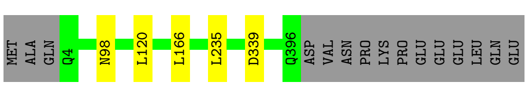




• Molecule 1: Major head protein

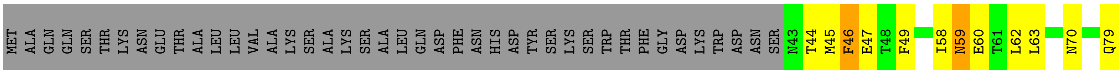
Chain gL:

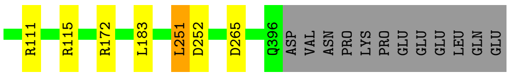




• Molecule 1: Major head protein

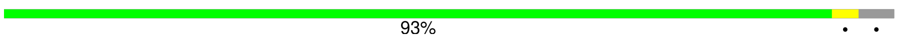
Chain AP:

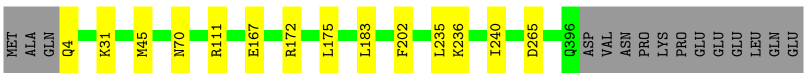




• Molecule 1: Major head protein

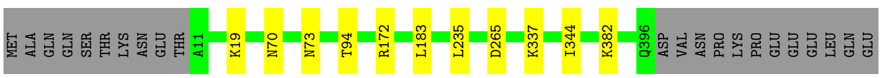
Chain BP:





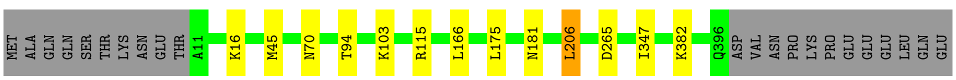
• Molecule 1: Major head protein

Chain CP:



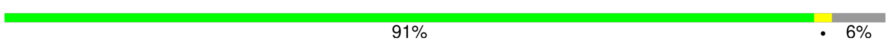
• Molecule 1: Major head protein

Chain DP:



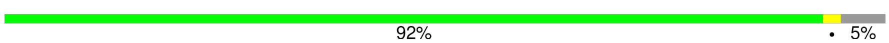
• Molecule 1: Major head protein

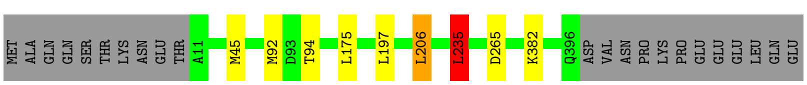
Chain KP:



• Molecule 1: Major head protein

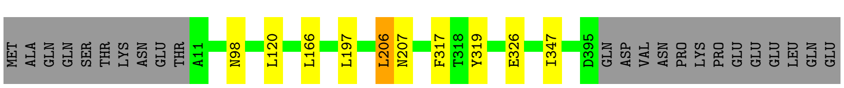
Chain LP:





• Molecule 1: Major head protein

Chain CQ:



• Molecule 1: Major head protein

Chain AQ: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain BQ: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain DQ: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain IQ: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain JQ: 93%

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain KQ: 92% 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain LQ: 95%

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain QQ: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain RQ: 93% • •

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain SQ: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 T61 N73 T94 N98 L109 F259 Q260 I261 L392 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain TQ: 95% • •

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain YQ: 95% • •

MET ALA GLN Q4 N98 L120 L166 L235 D339 Q396 ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

• Molecule 1: Major head protein

Chain bQ: 92% • 6%

MET ALA GLN GLN SER THR LYS ASN GLU THR A11 N98 L120 L166 L197 L206 N207 F317 T318 Y319 E326 I347 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

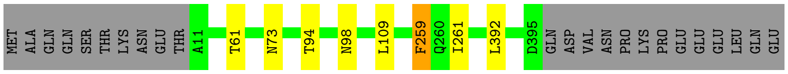
• Molecule 1: Major head protein

Chain cQ: 93% • •

MET ALA GLN Q4 K31 T61 L62 D65 W74 L183 A204 L235 D252 F259 N348 D395 GLN ASP VAL ASN PRO LYS PRO GLU GLU GLU LEU GLN GLU

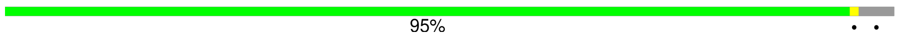
• Molecule 1: Major head protein

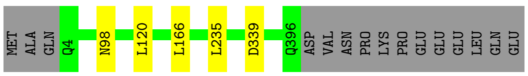
Chain dQ:



• Molecule 1: Major head protein

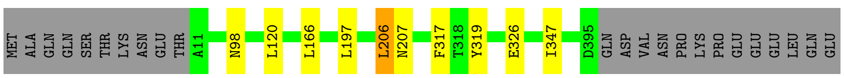
Chain eQ:





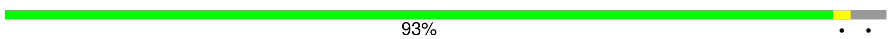
• Molecule 1: Major head protein

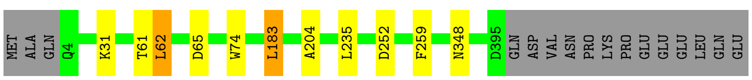
Chain CR:



• Molecule 1: Major head protein

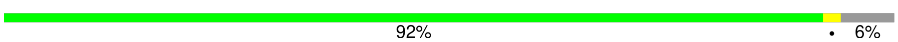
Chain AR:

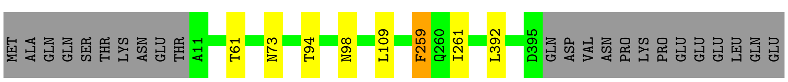




• Molecule 1: Major head protein

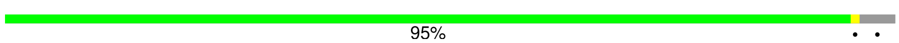
Chain BR:

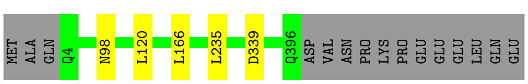




• Molecule 1: Major head protein

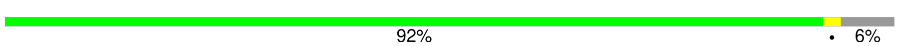
Chain DR:

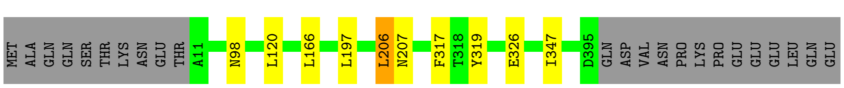




• Molecule 1: Major head protein

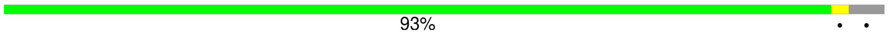
Chain IR:

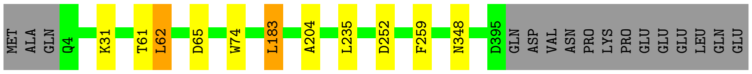




• Molecule 1: Major head protein

Chain JR:



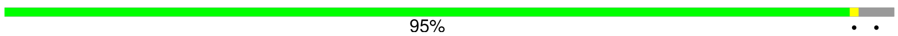


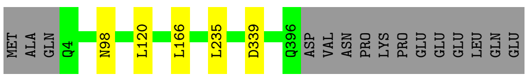
• Molecule 1: Major head protein

Chain KR:

• Molecule 1: Major head protein

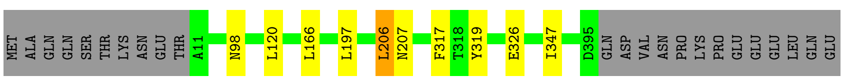
Chain LR:





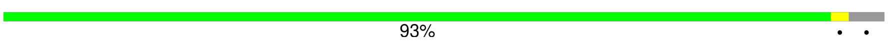
• Molecule 1: Major head protein

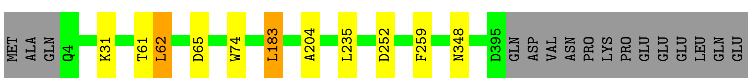
Chain QR:



• Molecule 1: Major head protein

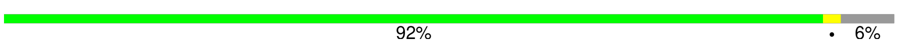
Chain RR:

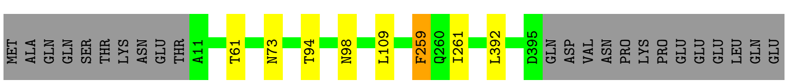




• Molecule 1: Major head protein

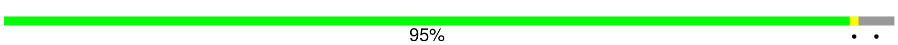
Chain SR:

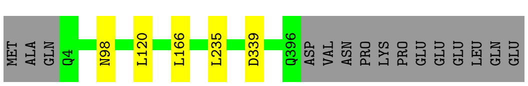




• Molecule 1: Major head protein

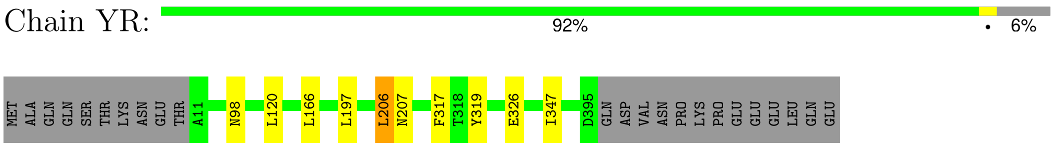
Chain TR:





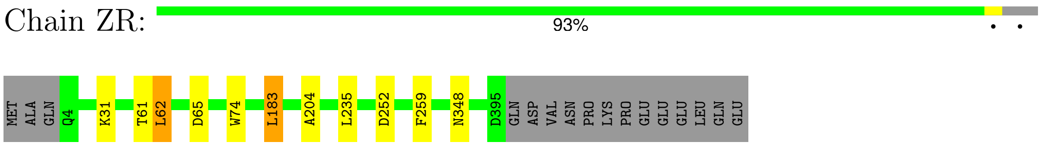
• Molecule 1: Major head protein

Chain YR:



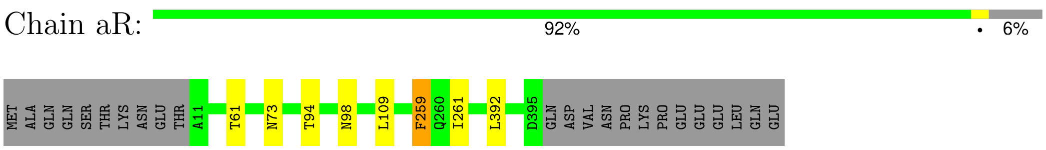
• Molecule 1: Major head protein

Chain ZR:



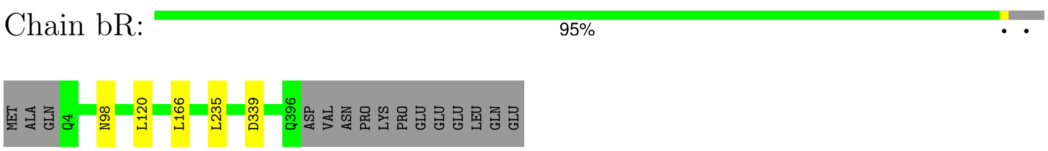
• Molecule 1: Major head protein

Chain aR:



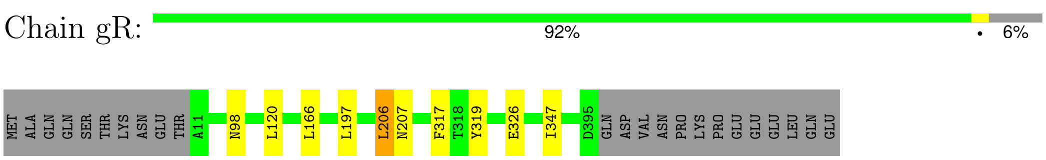
• Molecule 1: Major head protein

Chain bR:



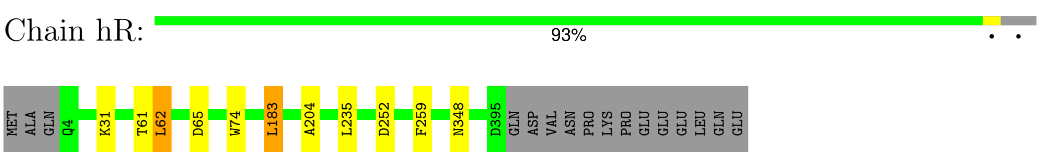
• Molecule 1: Major head protein

Chain gR:



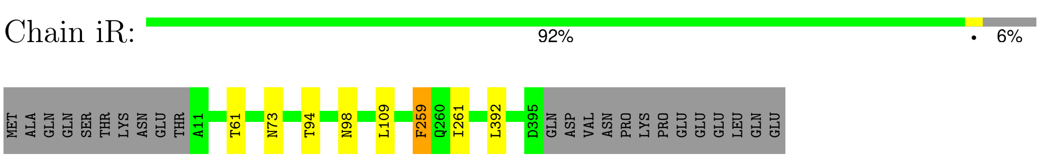
• Molecule 1: Major head protein

Chain hR:



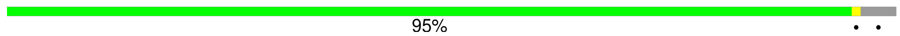
• Molecule 1: Major head protein

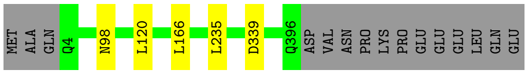
Chain iR:



• Molecule 1: Major head protein

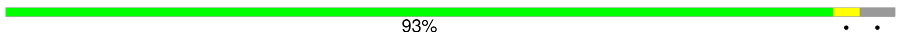
Chain jR:

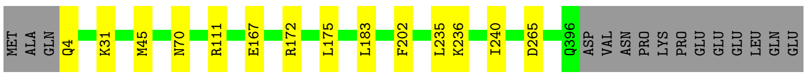




• Molecule 1: Major head protein

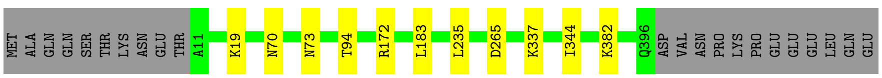
Chain AS:





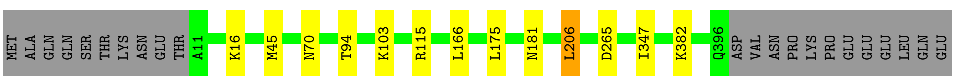
• Molecule 1: Major head protein

Chain BS:



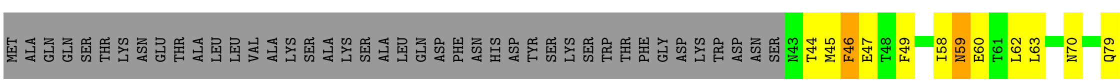
• Molecule 1: Major head protein

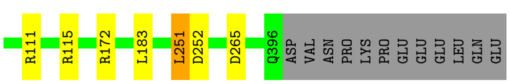
Chain CS:



• Molecule 1: Major head protein

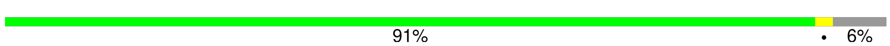
Chain IS:

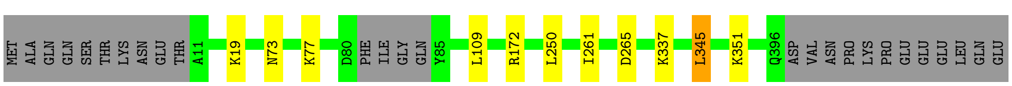




• Molecule 1: Major head protein

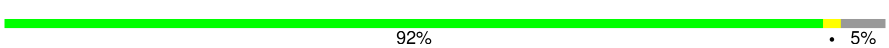
Chain JS:

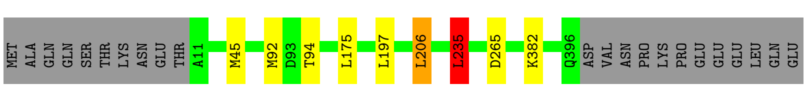




• Molecule 1: Major head protein

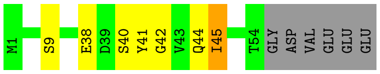
Chain KS:





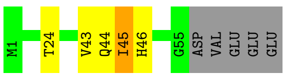
- Molecule 2: Arstotzka protein

Chain E1:



- Molecule 2: Arstotzka protein

Chain F1:

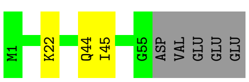


- Molecule 2: Arstotzka protein

Chain G1:

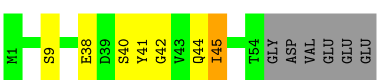
- Molecule 2: Arstotzka protein

Chain H1:



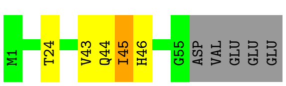
- Molecule 2: Arstotzka protein

Chain M1:



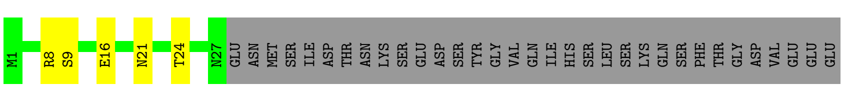
- Molecule 2: Arstotzka protein

Chain N1:



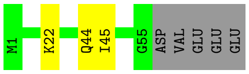
- Molecule 2: Arstotzka protein

Chain O1:



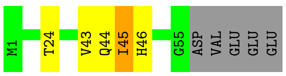
- Molecule 2: Arstotzka protein

Chain P1:



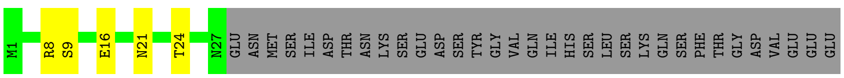
• Molecule 2: Arstotzka protein

Chain U1:



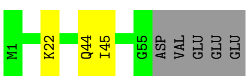
• Molecule 2: Arstotzka protein

Chain V1:



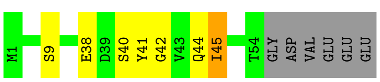
• Molecule 2: Arstotzka protein

Chain W1:



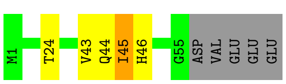
• Molecule 2: Arstotzka protein

Chain b1:



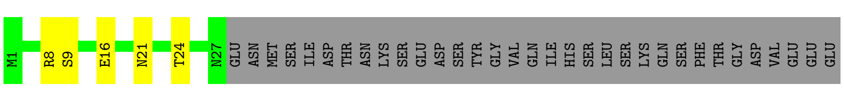
• Molecule 2: Arstotzka protein

Chain c1:



• Molecule 2: Arstotzka protein

Chain d1:



• Molecule 2: Arstotzka protein

Chain e1: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain j1: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain k1: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain l1: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain m1: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain E3: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain F3: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain G3: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

- Molecule 2: Arstotzka protein

Chain H3: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

- Molecule 2: Arstotzka protein

Chain M3: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

- Molecule 2: Arstotzka protein

Chain N3: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

- Molecule 2: Arstotzka protein

Chain O3: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

- Molecule 2: Arstotzka protein

Chain P3: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

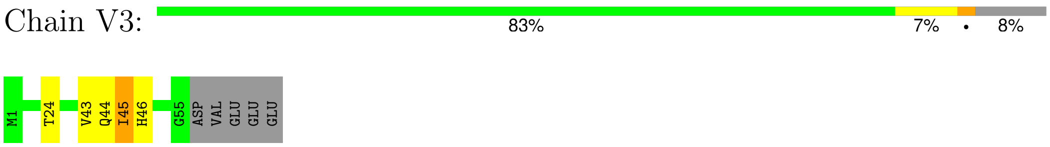
- Molecule 2: Arstotzka protein

Chain U3: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

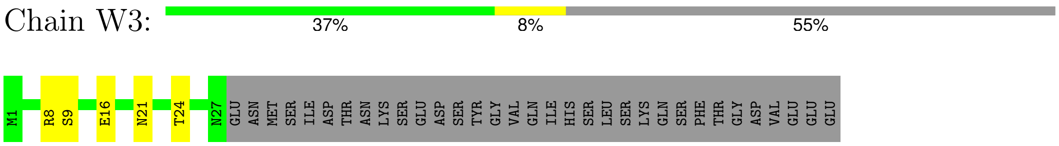
- Molecule 2: Arstotzka protein

Chain V3:



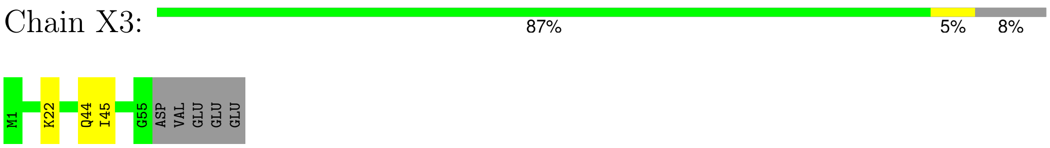
• Molecule 2: Arstotzka protein

Chain W3:



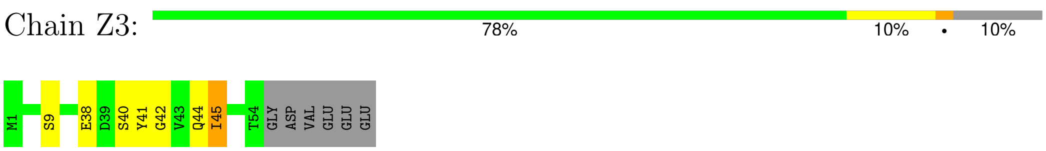
• Molecule 2: Arstotzka protein

Chain X3:



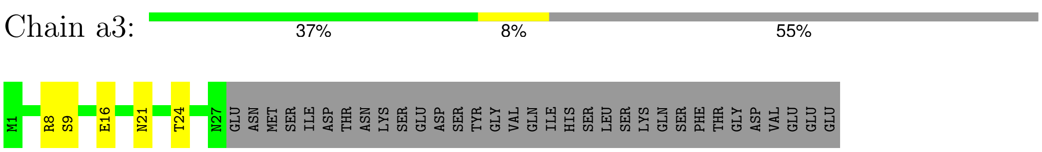
• Molecule 2: Arstotzka protein

Chain Z3:



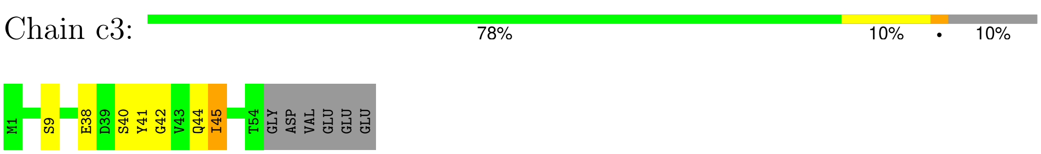
• Molecule 2: Arstotzka protein

Chain a3:



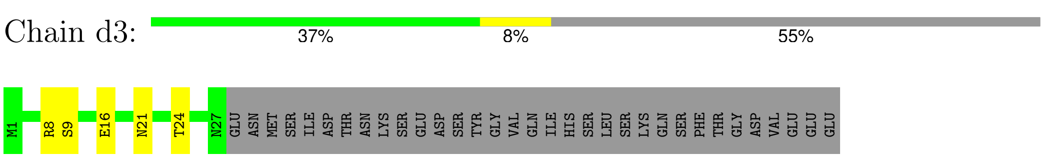
• Molecule 2: Arstotzka protein

Chain c3:



• Molecule 2: Arstotzka protein

Chain d3:



• Molecule 2: Arstotzka protein

Chain E4: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain F4: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain G4: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain H4: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain M4: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain N4: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

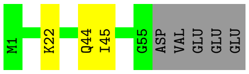
• Molecule 2: Arstotzka protein

Chain O4: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

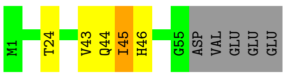
• Molecule 2: Arstotzka protein

Chain P4:



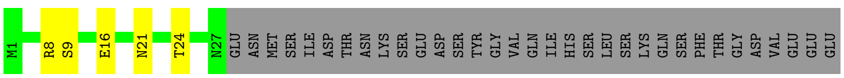
• Molecule 2: Arstotzka protein

Chain U4:



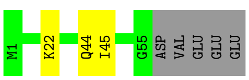
• Molecule 2: Arstotzka protein

Chain V4:



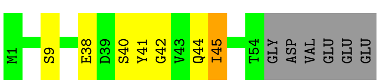
• Molecule 2: Arstotzka protein

Chain W4:



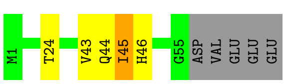
• Molecule 2: Arstotzka protein

Chain b4:



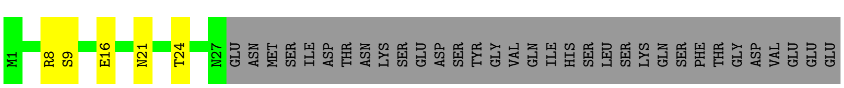
• Molecule 2: Arstotzka protein

Chain c4:



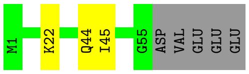
• Molecule 2: Arstotzka protein

Chain d4:



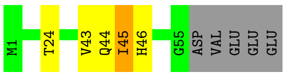
• Molecule 2: Arstotzka protein

Chain e4:



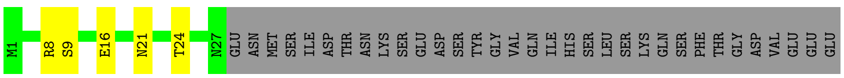
• Molecule 2: Arstotzka protein

Chain j4:



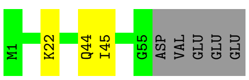
• Molecule 2: Arstotzka protein

Chain k4:



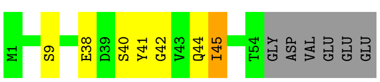
• Molecule 2: Arstotzka protein

Chain l4:



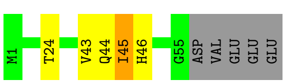
• Molecule 2: Arstotzka protein

Chain E6:



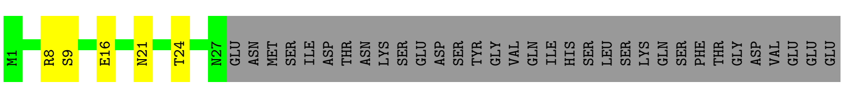
• Molecule 2: Arstotzka protein

Chain F6:



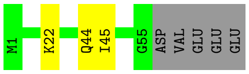
• Molecule 2: Arstotzka protein

Chain G6:



• Molecule 2: Arstotzka protein

Chain H6:

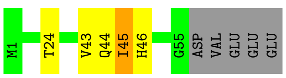


• Molecule 2: Arstotzka protein

Chain M6:

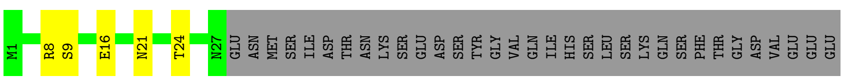
• Molecule 2: Arstotzka protein

Chain N6:



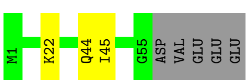
• Molecule 2: Arstotzka protein

Chain O6:



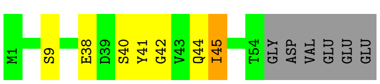
• Molecule 2: Arstotzka protein

Chain P6:



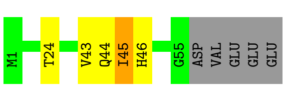
• Molecule 2: Arstotzka protein

Chain U6:



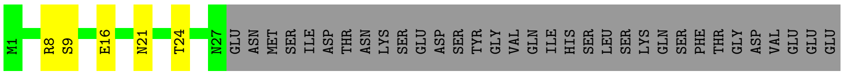
• Molecule 2: Arstotzka protein

Chain V6:



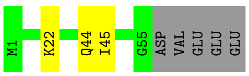
• Molecule 2: Arstotzka protein

Chain W6:



• Molecule 2: Arstotzka protein

Chain X6:

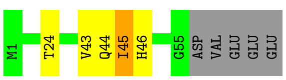


• Molecule 2: Arstotzka protein

Chain c6:

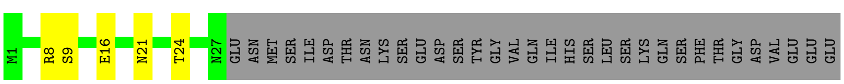
• Molecule 2: Arstotzka protein

Chain d6:



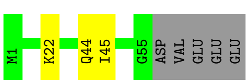
• Molecule 2: Arstotzka protein

Chain e6:



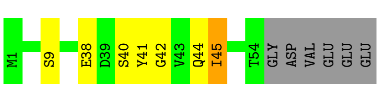
• Molecule 2: Arstotzka protein

Chain f6:



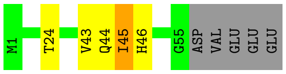
• Molecule 2: Arstotzka protein

Chain k6:



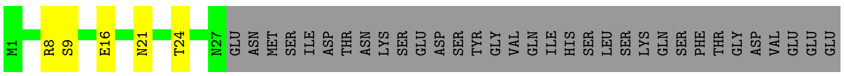
• Molecule 2: Arstotzka protein

Chain l6:



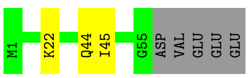
• Molecule 2: Arstotzka protein

Chain m6:



• Molecule 2: Arstotzka protein

Chain n6:

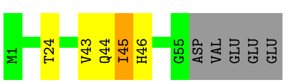


• Molecule 2: Arstotzka protein

Chain E7:

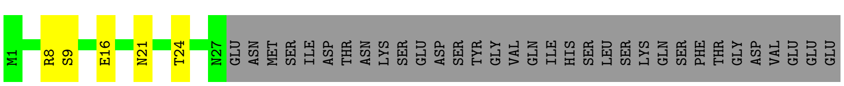
• Molecule 2: Arstotzka protein

Chain F7:



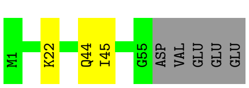
• Molecule 2: Arstotzka protein

Chain G7:



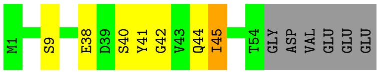
• Molecule 2: Arstotzka protein

Chain H7:



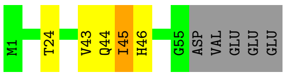
• Molecule 2: Arstotzka protein

Chain M7:



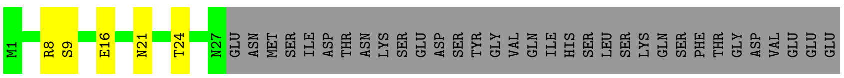
• Molecule 2: Arstotzka protein

Chain N7:



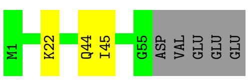
• Molecule 2: Arstotzka protein

Chain O7:



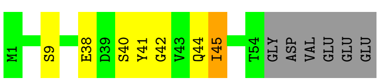
• Molecule 2: Arstotzka protein

Chain P7:



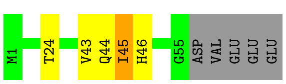
• Molecule 2: Arstotzka protein

Chain U7:



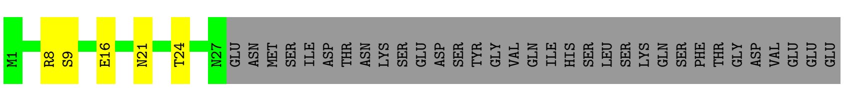
• Molecule 2: Arstotzka protein

Chain V7:



• Molecule 2: Arstotzka protein

Chain W7:



• Molecule 2: Arstotzka protein

Chain X7: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain c7: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain d7: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain e7: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain f7: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain k7: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

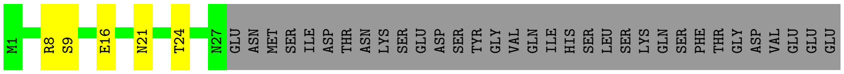
• Molecule 2: Arstotzka protein

Chain l7: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

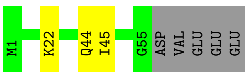
• Molecule 2: Arstotzka protein

Chain m7:



• Molecule 2: Arstotzka protein

Chain n7:

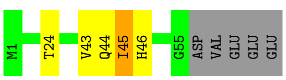


• Molecule 2: Arstotzka protein

Chain E8:

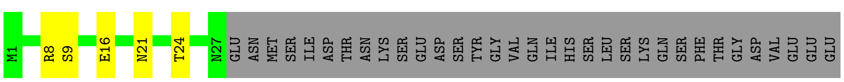
• Molecule 2: Arstotzka protein

Chain F8:



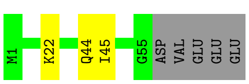
• Molecule 2: Arstotzka protein

Chain G8:



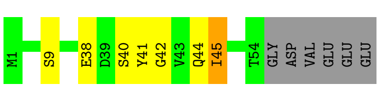
• Molecule 2: Arstotzka protein

Chain H8:



• Molecule 2: Arstotzka protein

Chain M8:



• Molecule 2: Arstotzka protein

Chain N8: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain O8: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain P8: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain U8: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain V8: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain W8: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain X8: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain c8: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain d8: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain e8: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain f8: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain k8: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain l8: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

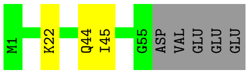
• Molecule 2: Arstotzka protein

Chain m8: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

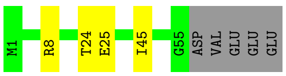
• Molecule 2: Arstotzka protein

Chain n8:



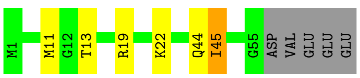
• Molecule 2: Arstotzka protein

Chain ED:



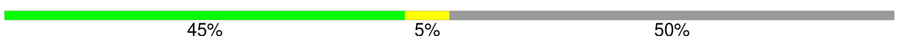
• Molecule 2: Arstotzka protein

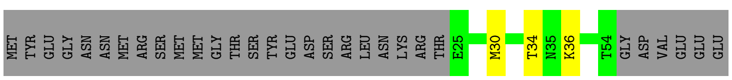
Chain FD:



• Molecule 2: Arstotzka protein

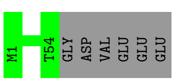
Chain GD:





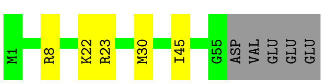
• Molecule 2: Arstotzka protein

Chain HD:



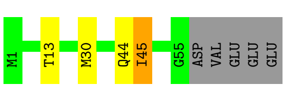
• Molecule 2: Arstotzka protein

Chain MD:



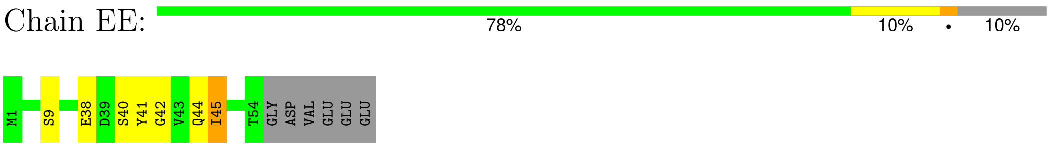
• Molecule 2: Arstotzka protein

Chain ND:



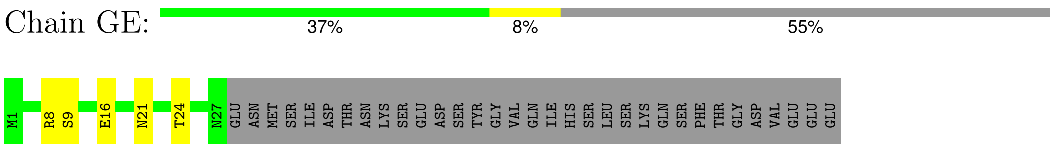
• Molecule 2: Arstotzka protein

Chain EE:



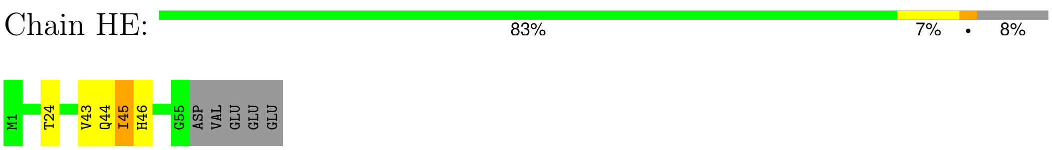
• Molecule 2: Arstotzka protein

Chain GE:



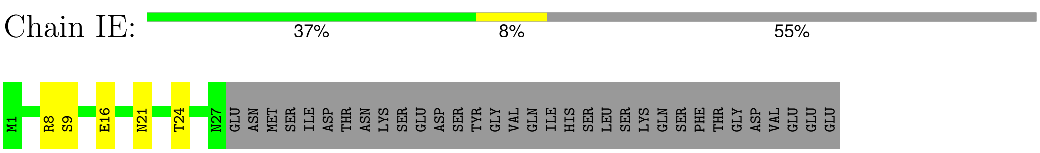
• Molecule 2: Arstotzka protein

Chain HE:



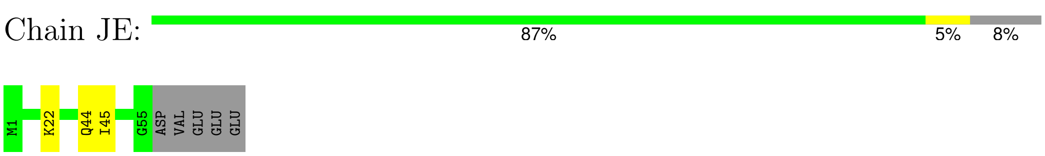
• Molecule 2: Arstotzka protein

Chain IE:



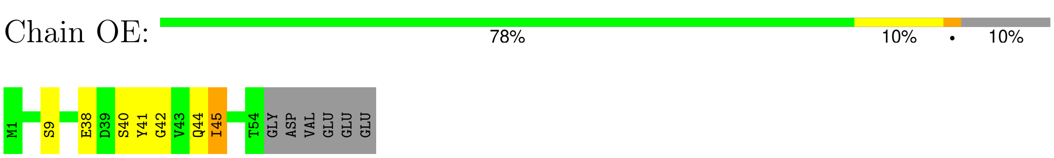
• Molecule 2: Arstotzka protein

Chain JE:



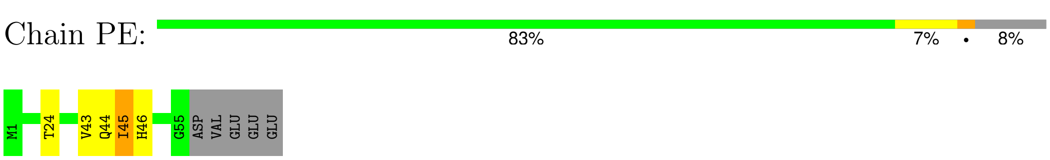
• Molecule 2: Arstotzka protein

Chain OE:



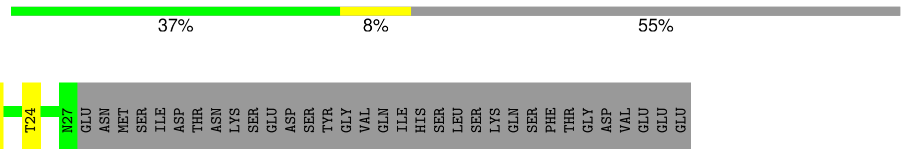
• Molecule 2: Arstotzka protein

Chain PE:



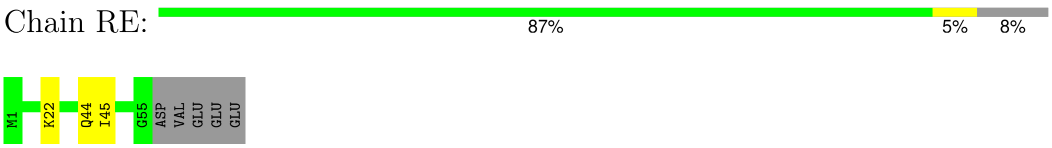
• Molecule 2: Arstotzka protein

Chain QE:



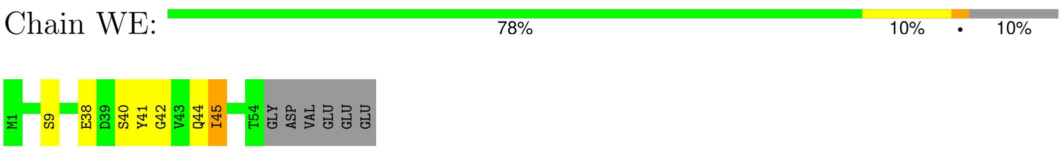
• Molecule 2: Arstotzka protein

Chain RE:



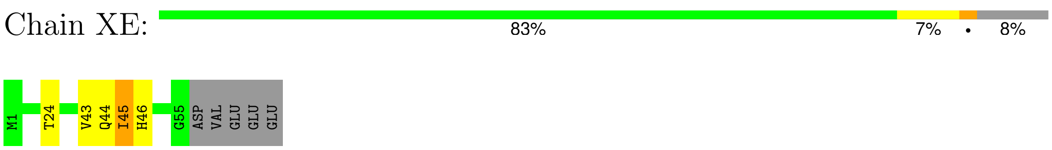
• Molecule 2: Arstotzka protein

Chain WE:



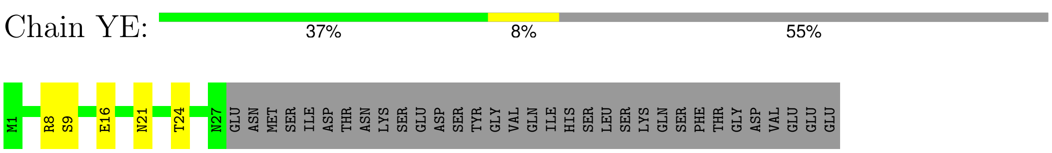
• Molecule 2: Arstotzka protein

Chain XE:



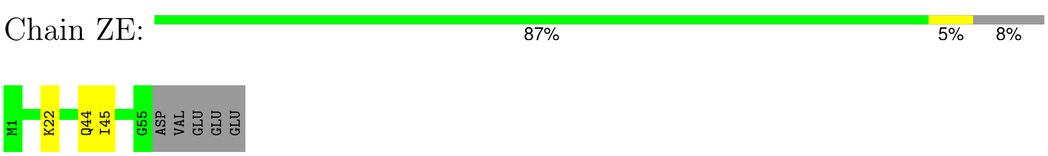
• Molecule 2: Arstotzka protein

Chain YE:



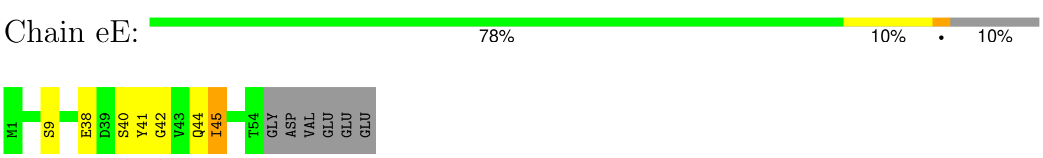
• Molecule 2: Arstotzka protein

Chain ZE:



• Molecule 2: Arstotzka protein

Chain eE:



• Molecule 2: Arstotzka protein

Chain fE: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain gE: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain hE: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain EG: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain FG: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain GG: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain HG: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain MG: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain NG: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain OG: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain PG: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain UG: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain VG: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

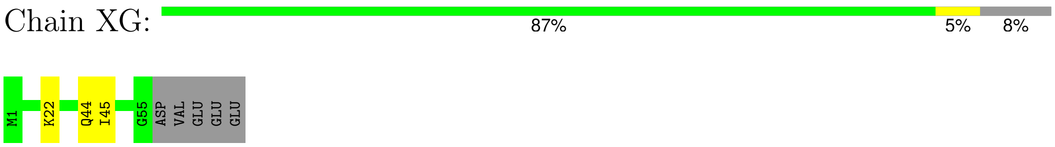
• Molecule 2: Arstotzka protein

Chain WG: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

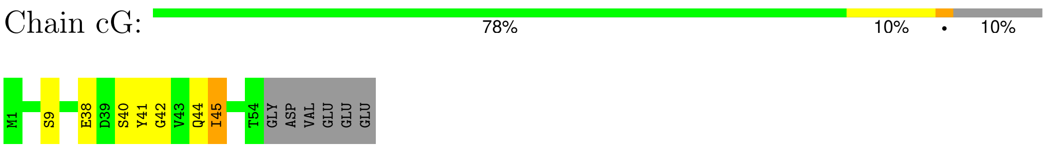
• Molecule 2: Arstotzka protein

Chain XG:



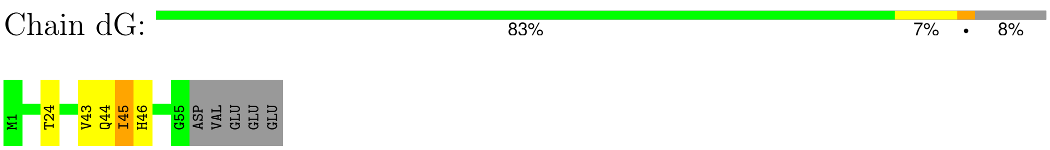
• Molecule 2: Arstotzka protein

Chain cG:



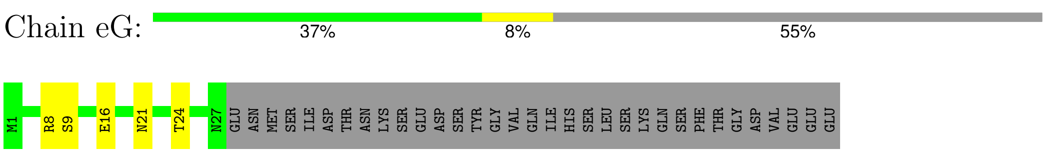
• Molecule 2: Arstotzka protein

Chain dG:



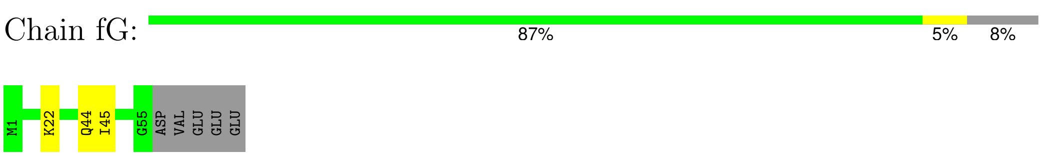
• Molecule 2: Arstotzka protein

Chain eG:



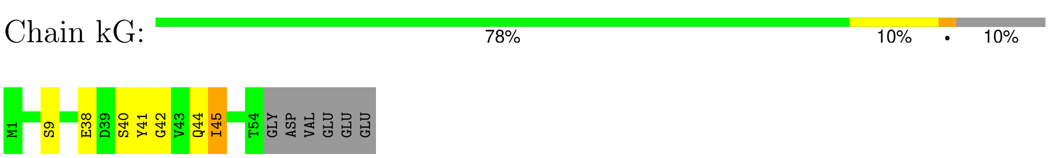
• Molecule 2: Arstotzka protein

Chain fG:



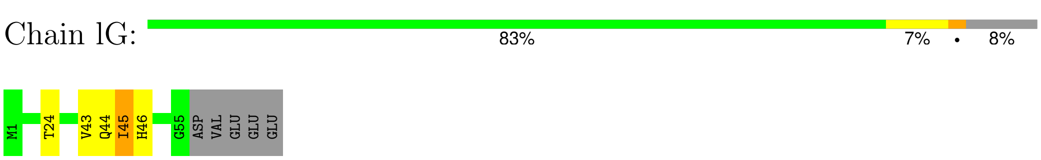
• Molecule 2: Arstotzka protein

Chain kG:



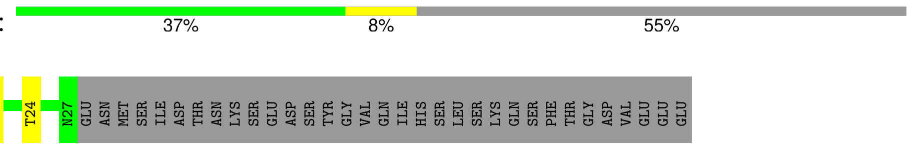
• Molecule 2: Arstotzka protein

Chain lG:



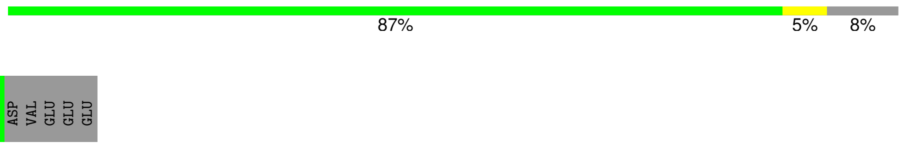
• Molecule 2: Arstotzka protein

Chain mG:



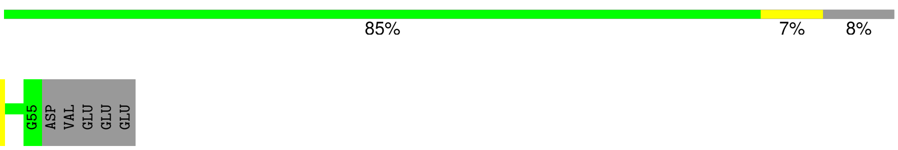
• Molecule 2: Arstotzka protein

Chain nG:



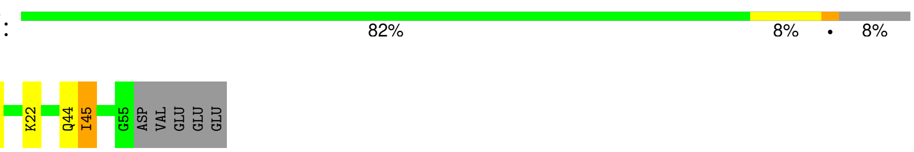
• Molecule 2: Arstotzka protein

Chain EJ:



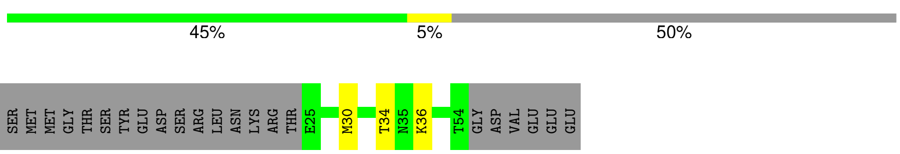
• Molecule 2: Arstotzka protein

Chain FJ:



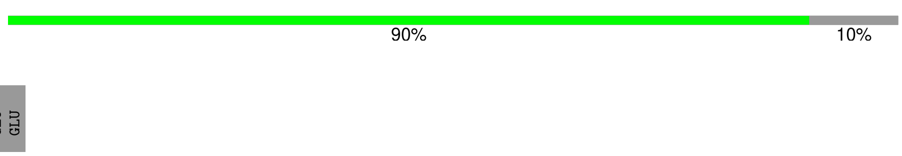
• Molecule 2: Arstotzka protein

Chain GJ:



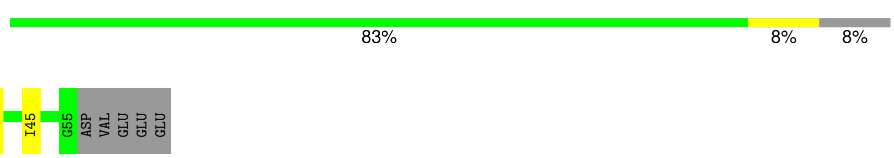
• Molecule 2: Arstotzka protein

Chain HJ:



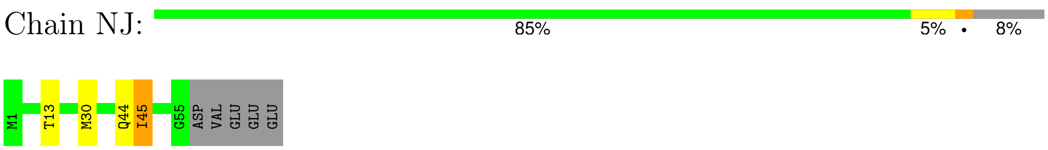
• Molecule 2: Arstotzka protein

Chain MJ:



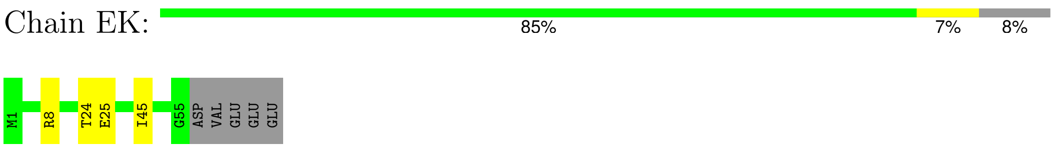
• Molecule 2: Arstotzka protein

Chain NJ:



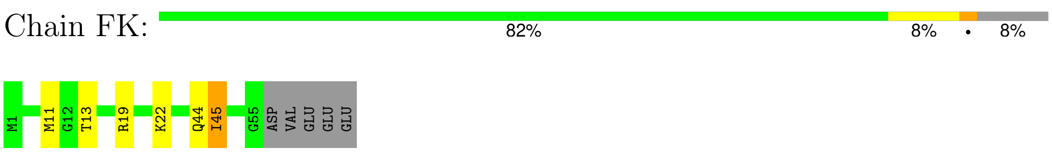
• Molecule 2: Arstotzka protein

Chain EK:



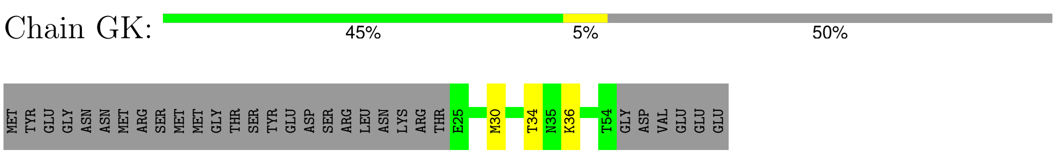
• Molecule 2: Arstotzka protein

Chain FK:



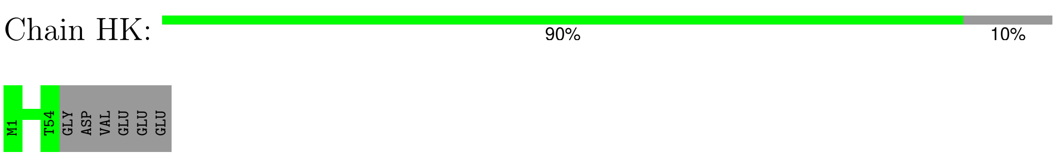
• Molecule 2: Arstotzka protein

Chain GK:



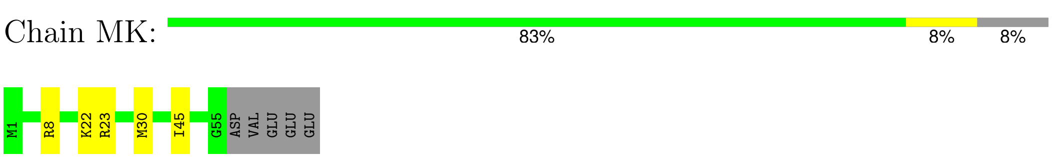
• Molecule 2: Arstotzka protein

Chain HK:



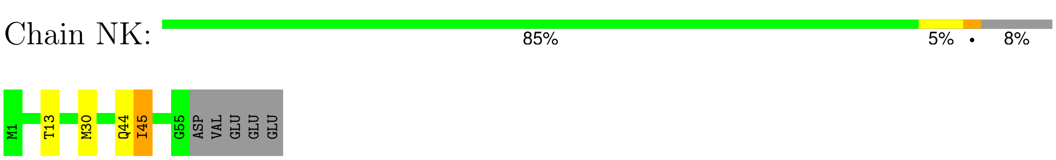
• Molecule 2: Arstotzka protein

Chain MK:



• Molecule 2: Arstotzka protein

Chain NK:



• Molecule 2: Arstotzka protein

Chain EL: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain FL: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain GL: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain HL: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain ML: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain NL: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain OL: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain PL: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain UL: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain VL: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain WL: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain XL: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain cL: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain dL: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain eL: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain fL: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain hL: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain iL: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain EP: 85% 7% 8%

M1 R8 T24 E25 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain FP: 82% 8% • 8%

M1 M11 G12 T13 R19 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

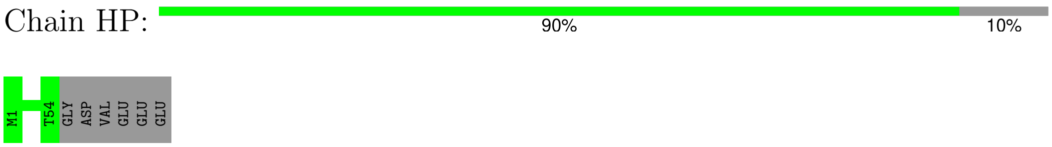
• Molecule 2: Arstotzka protein

Chain GP: 45% 5% 50%

MET TYR GLU GLY ASN ASN MET ARG SER MET GLY THR SER TYR GLU ASP SER ARG LEU ASN LYS ARG THR E25 M30 T34 N35 K36 T54 GLY ASP VAL GLU GLU GLU

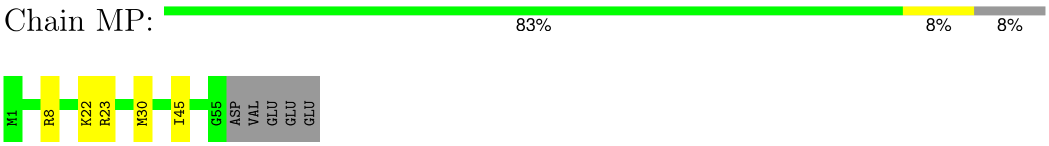
• Molecule 2: Arstotzka protein

Chain HP:



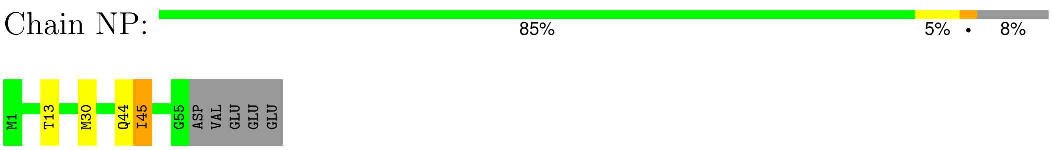
• Molecule 2: Arstotzka protein

Chain MP:



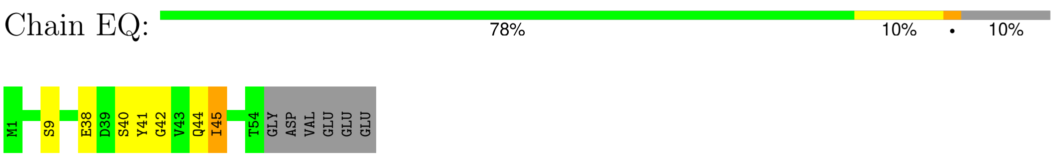
• Molecule 2: Arstotzka protein

Chain NP:



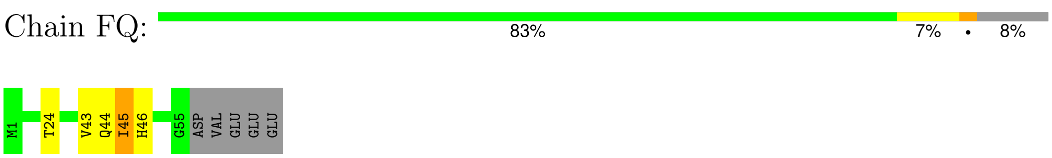
• Molecule 2: Arstotzka protein

Chain EQ:



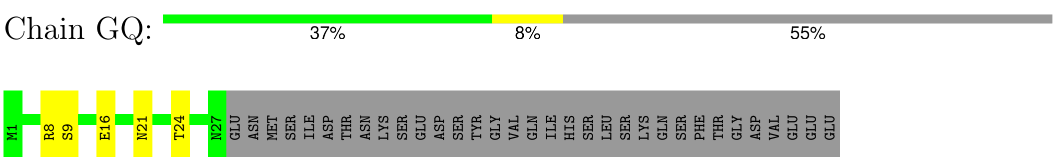
• Molecule 2: Arstotzka protein

Chain FQ:



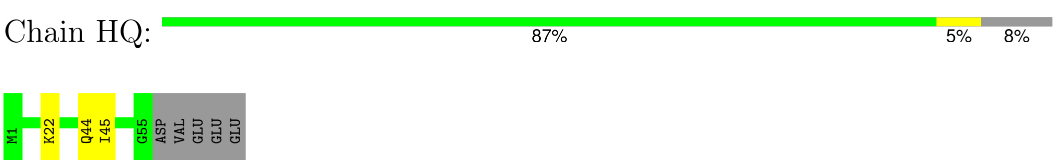
• Molecule 2: Arstotzka protein

Chain GQ:



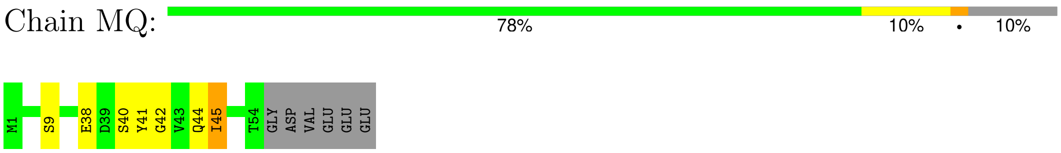
• Molecule 2: Arstotzka protein

Chain HQ:



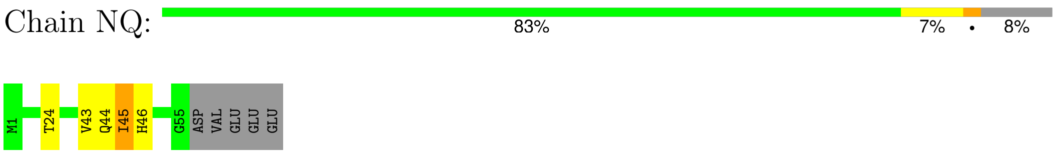
• Molecule 2: Arstotzka protein

Chain MQ:



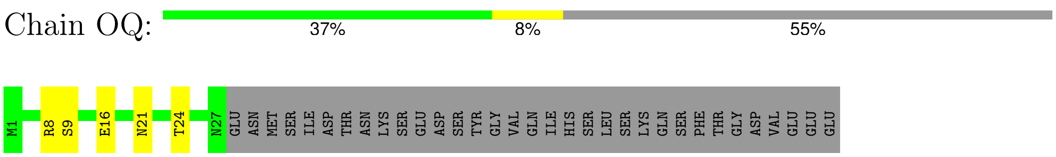
• Molecule 2: Arstotzka protein

Chain NQ:



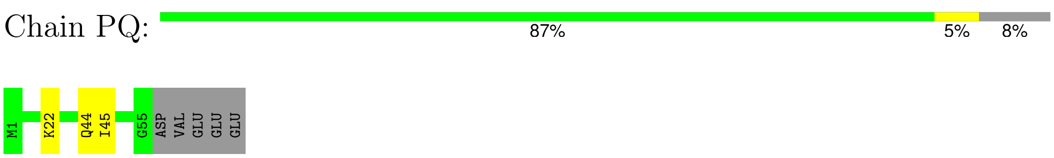
• Molecule 2: Arstotzka protein

Chain OQ:



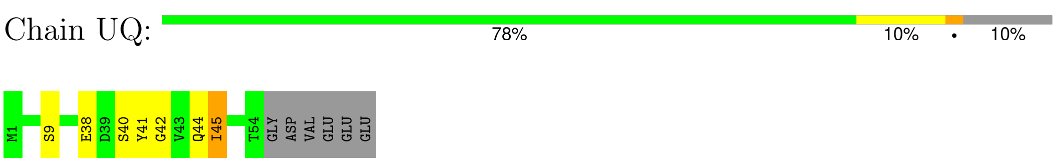
• Molecule 2: Arstotzka protein

Chain PQ:



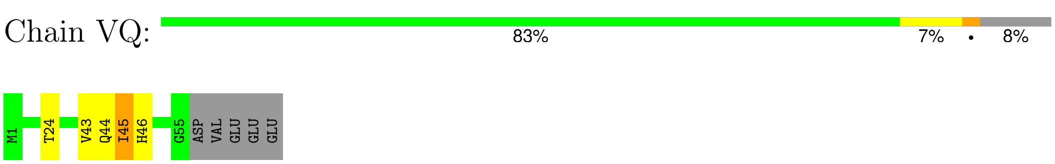
• Molecule 2: Arstotzka protein

Chain UQ:



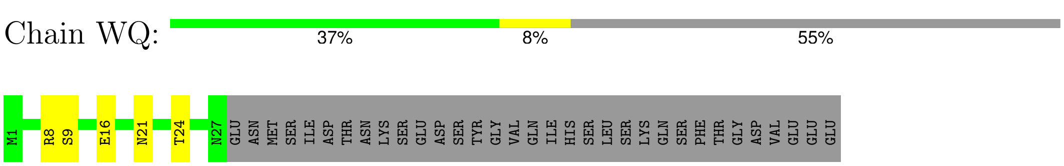
• Molecule 2: Arstotzka protein

Chain VQ:



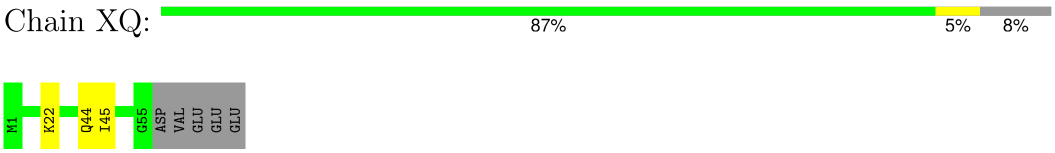
• Molecule 2: Arstotzka protein

Chain WQ:



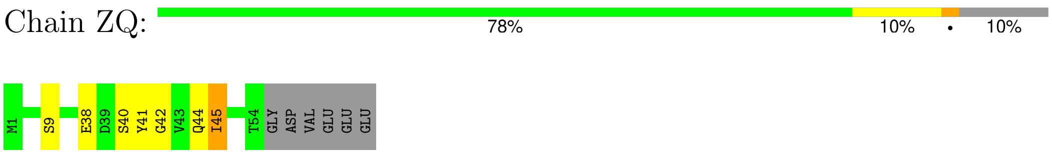
• Molecule 2: Arstotzka protein

Chain XQ:



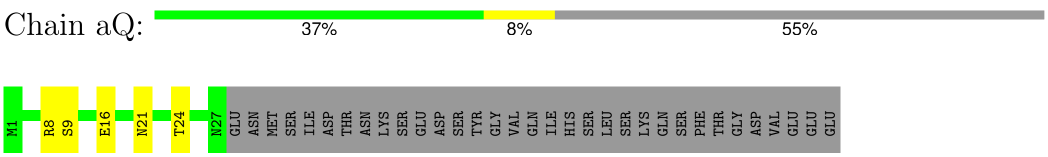
• Molecule 2: Arstotzka protein

Chain ZQ:



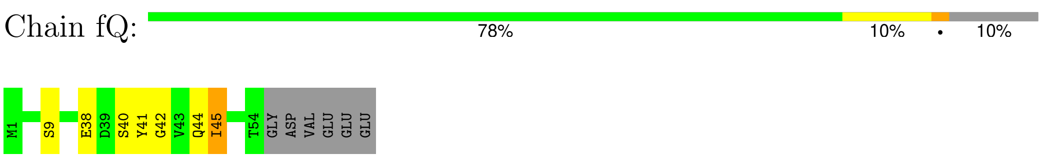
• Molecule 2: Arstotzka protein

Chain aQ:



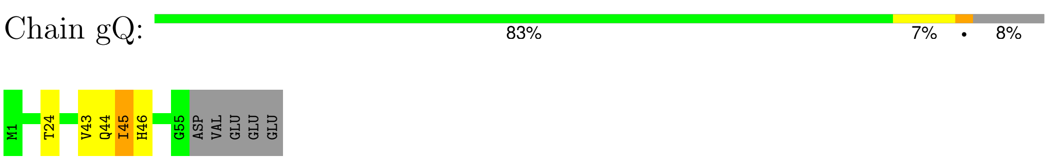
• Molecule 2: Arstotzka protein

Chain fQ:



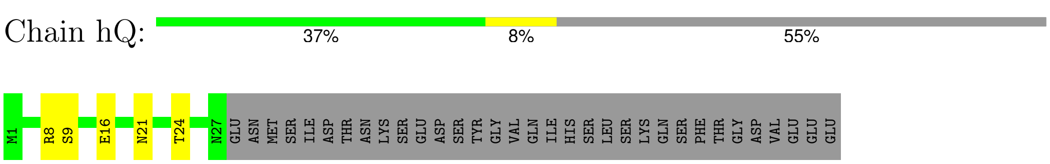
• Molecule 2: Arstotzka protein

Chain gQ:



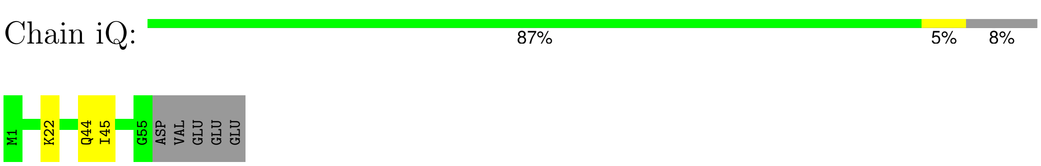
• Molecule 2: Arstotzka protein

Chain hQ:



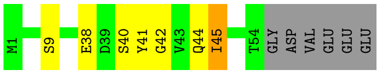
• Molecule 2: Arstotzka protein

Chain iQ:



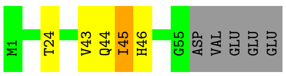
• Molecule 2: Arstotzka protein

Chain ER:



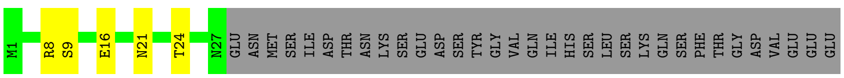
• Molecule 2: Arstotzka protein

Chain FR:



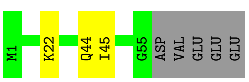
• Molecule 2: Arstotzka protein

Chain GR:



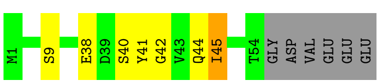
• Molecule 2: Arstotzka protein

Chain HR:



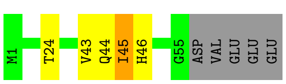
• Molecule 2: Arstotzka protein

Chain MR:



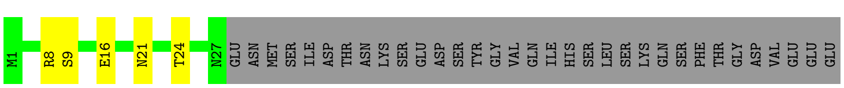
• Molecule 2: Arstotzka protein

Chain NR:



• Molecule 2: Arstotzka protein

Chain OR:



• Molecule 2: Arstotzka protein

Chain PR: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain UR: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain VR: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain WR: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain XR: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain cR: 78% 10% • 10%

M1 S9 E38 D39 S40 Y41 G42 V43 Q44 I45 T54 GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain dR: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain eR: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain fR: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain kR: 83% 7% • 8%

M1 T24 V43 Q44 I45 H46 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain lR: 37% 8% 55%

M1 R8 S9 E16 N21 T24 N27 GLU ASN MET SER ILE ASP THR ASN LYS SER GLU ASP SER TYR GLY VAL GLN ILE HIS SER LEU SER LYS GLN SER PHE THR GLY ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain mR: 87% 5% 8%

M1 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

• Molecule 2: Arstotzka protein

Chain DS: 85% 7% 8%

M1 R8 T24 E25 I45 G55 ASP VAL GLU GLU GLU

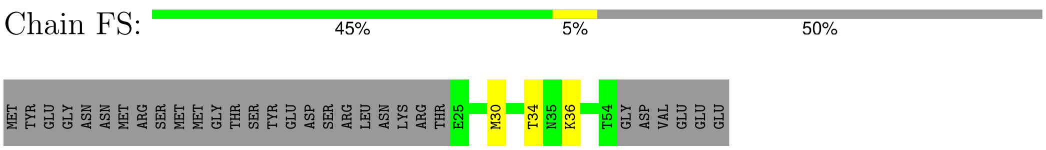
• Molecule 2: Arstotzka protein

Chain ES: 82% 8% • 8%

M1 M11 G12 T13 R19 K22 Q44 I45 G55 ASP VAL GLU GLU GLU

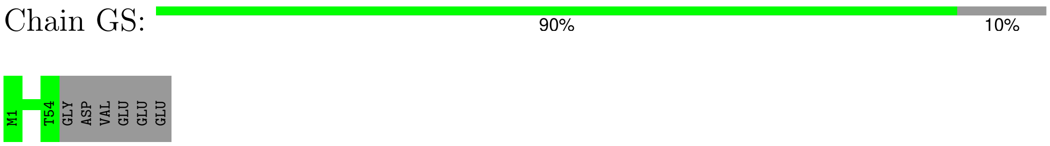
• Molecule 2: Arstotzka protein

Chain FS:



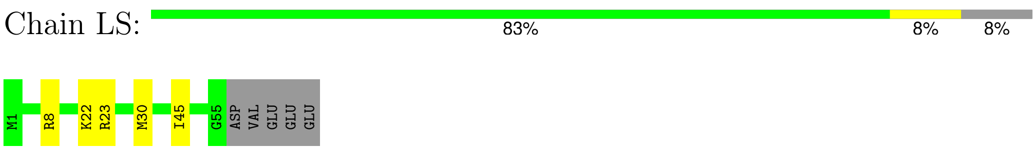
• Molecule 2: Arstotzka protein

Chain GS:



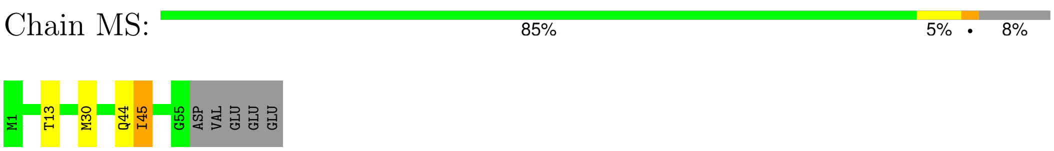
• Molecule 2: Arstotzka protein

Chain LS:



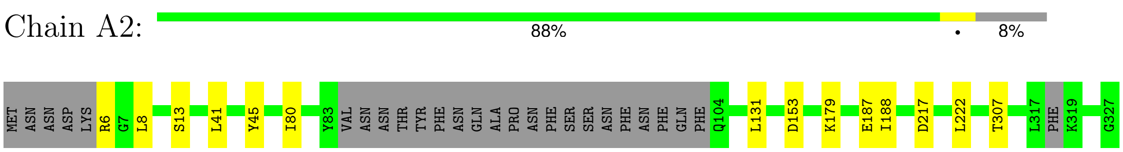
• Molecule 2: Arstotzka protein

Chain MS:



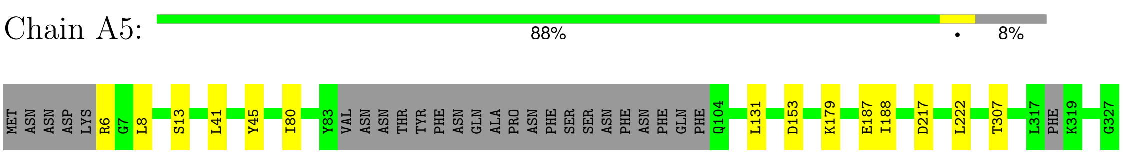
• Molecule 3: Portal protein

Chain A2:



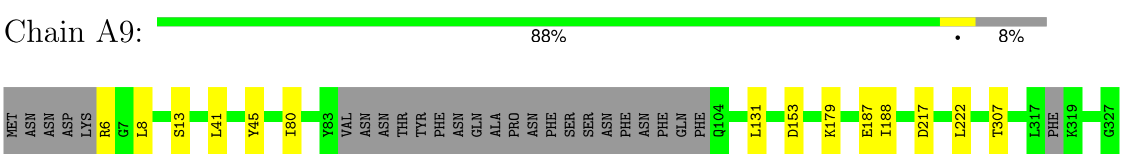
• Molecule 3: Portal protein

Chain A5:



• Molecule 3: Portal protein

Chain A9:



• Molecule 3: Portal protein

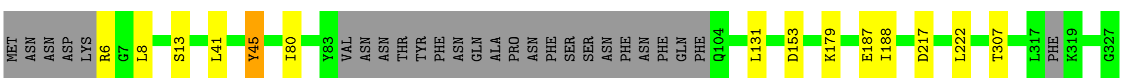
Chain AA:

• Molecule 3: Portal protein

Chain AB:

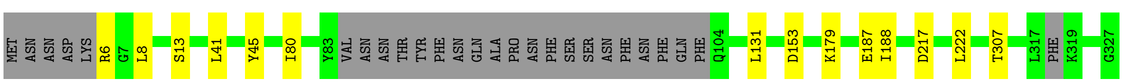
• Molecule 3: Portal protein

Chain AC:



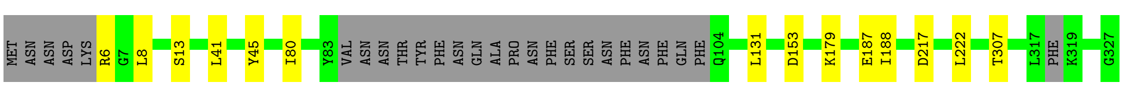
• Molecule 3: Portal protein

Chain AF:



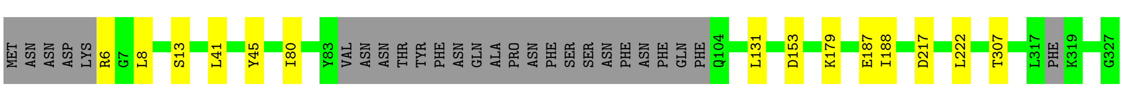
• Molecule 3: Portal protein

Chain AH:



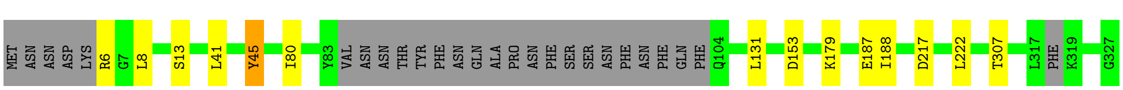
• Molecule 3: Portal protein

Chain AI:



• Molecule 3: Portal protein

Chain AM:



• Molecule 3: Portal protein

Chain AN: 88% • 8%

MET ASN ASN ASP LYS R6 G7 L8 S13 L41 Y45 I80 Y83 VAL ASN ASN THR TYR PHE ASN GLN ALA PRO ASN PHE SER SER ASN PHE ASN PHE GLN PHE Q104 L131 D153 K179 E187 I188 D217 L222 T307 L317 PHE K319 G327

• Molecule 3: Portal protein

Chain AO: 88% • 8%

MET ASN ASN ASP LYS R6 G7 L8 S13 L41 Y45 I80 Y83 VAL ASN ASN THR TYR PHE ASN GLN ALA PRO ASN PHE SER SER ASN PHE ASN PHE GLN PHE Q104 L131 D153 K179 E187 I188 D217 L222 T307 L317 PHE K319 G327

• Molecule 4: Lower collar protein

Chain B2: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain B5: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain B9: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BA: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BB: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BC: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BF: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BH: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BI: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BM: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BN: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 4: Lower collar protein

Chain BO: 86% • 12%

MET ALA R3 Y113 S114 G154 MET THR ALA ASN ARG ASN ALA TYR VAL SER LEU PRO GLN SER GLU VAL ASN ILE ASP VAL ASP ASN THR THR LEU ARG PHE ALA ASP N184 T220 L224 W251

• Molecule 5: Minor structural protein

Chain D2: 20% 80%

MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

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

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

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

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

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

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

• Molecule 5: Minor structural protein

Chain E2: 21% 79%

MET ALA TYR ASN E5 E108 D140 LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER THR GLN SER ASP

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

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

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

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

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

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

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

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

• Molecule 5: Minor structural protein

Chain F2: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

• Molecule 5: Minor structural protein

Chain C2: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain N2: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain O2: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain D5: 20% 80%

MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain E5: 21% 79%

MET ALA TYR ASN E5 E108 D140 LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER THR GLN SER ASP

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain F5: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain C5: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain N5: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain O5: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain D9: 20% 80%

MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain E9: 21% 79%

MET ALA TYR ASN E5 E108 D140 LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER THR GLN SER ASP

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain F9: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain C9: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain N9: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain O9: 77% 23%

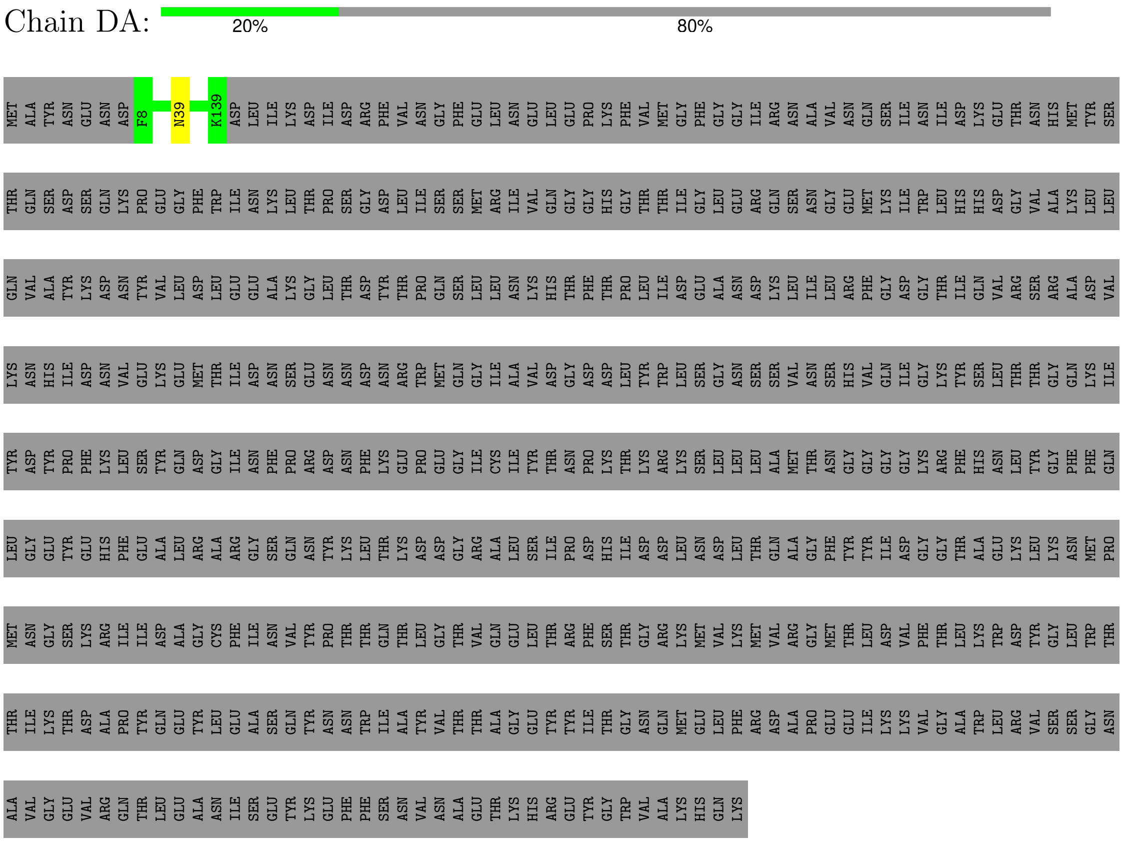
MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS THR ARG GLU ARG TYR THR PRO PHE TYR ASP ASP ARG ALA ASP TYR ASN THR ASN SER LYS SER TYR TYR ASP TYR ILE SER ARG LEU SER LYS LEU ILE GLU VAL LEU ALA

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

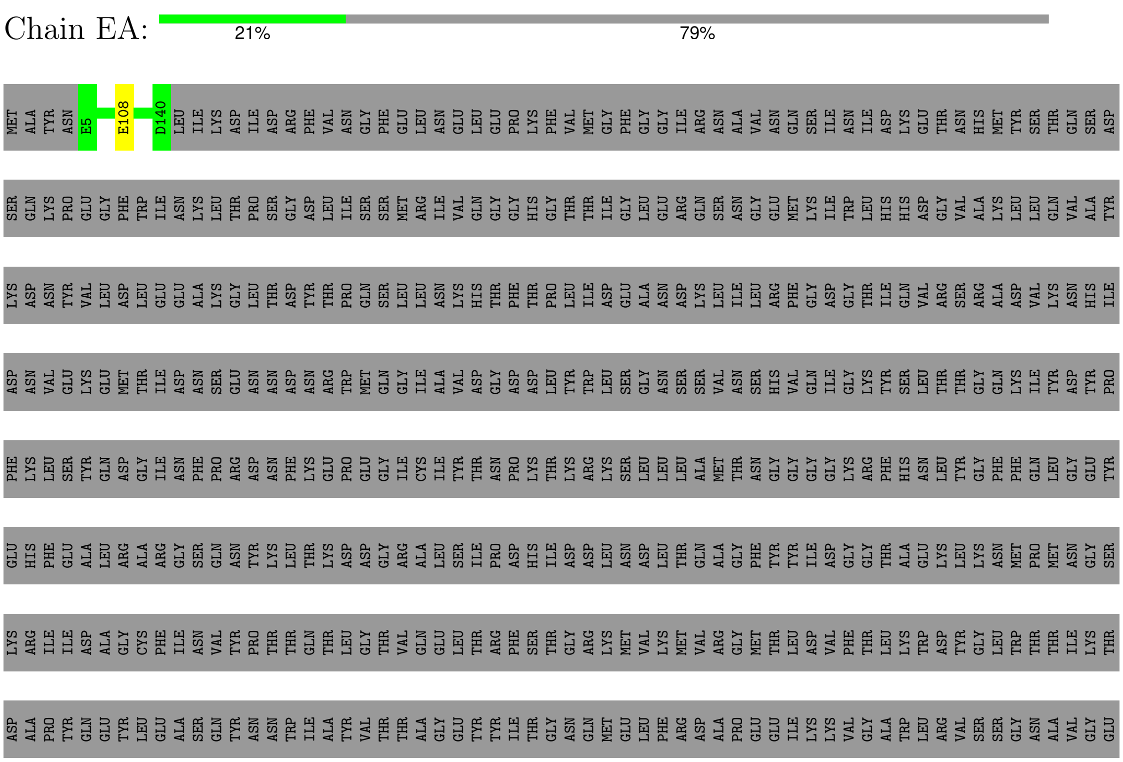
• Molecule 5: Minor structural protein

Chain DA:



• Molecule 5: Minor structural protein

Chain EA:



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

• Molecule 5: Minor structural protein

Chain FA: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

• Molecule 5: Minor structural protein

Chain CA: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain NA: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain OA: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain DB: 20% 80%

MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

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

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

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

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

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

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

• Molecule 5: Minor structural protein

Chain EB: 21% 79%

MET ALA TYR ASN E5 E108 D140 LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER THR GLN SER ASP

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain FB: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain CB: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain NB: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain OB: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain DC: 20% 80%

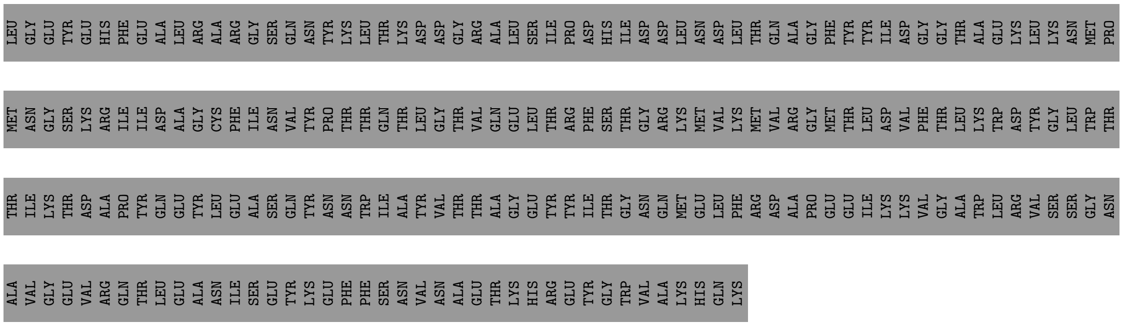
MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

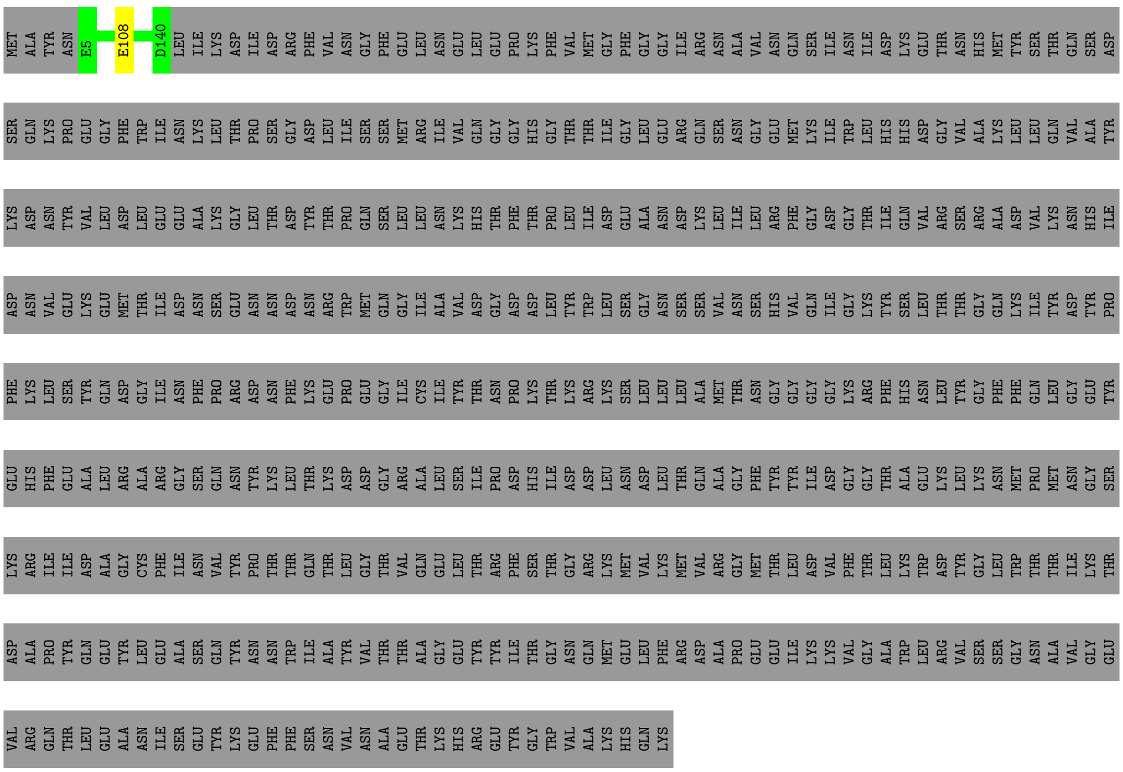
LYS ASN HIS ILE ASP ASN VAL GLU LYS GLU MET THR ILE ASP ASN SER GLU ASN ASN ASP ASN ARG TRP MET GLN GLY ILE ALA VAL ASP GLY ASP ASP LEU TYR TRP LEU SER GLY ASN SER SER VAL ASN SER HIS VAL GLN ILE GLY LYS TYR SER LEU THR THR GLY GLN LYS ILE

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



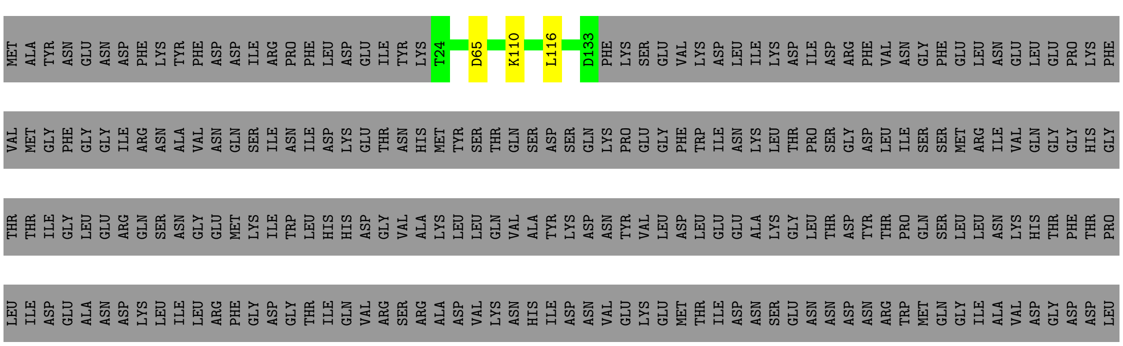
- Molecule 5: Minor structural protein

Chain EC:



- Molecule 5: Minor structural protein

Chain FC:



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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain CC: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain NC: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

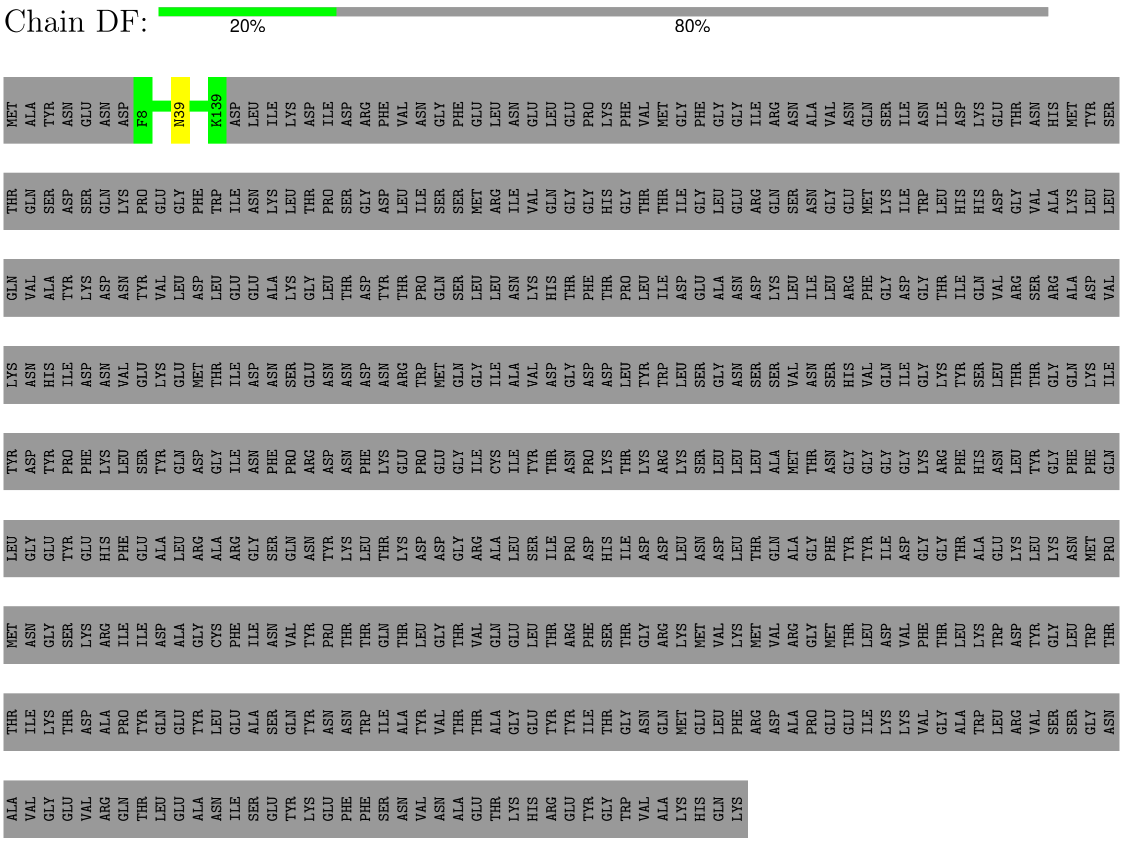
Chain OC: 77% 23%

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

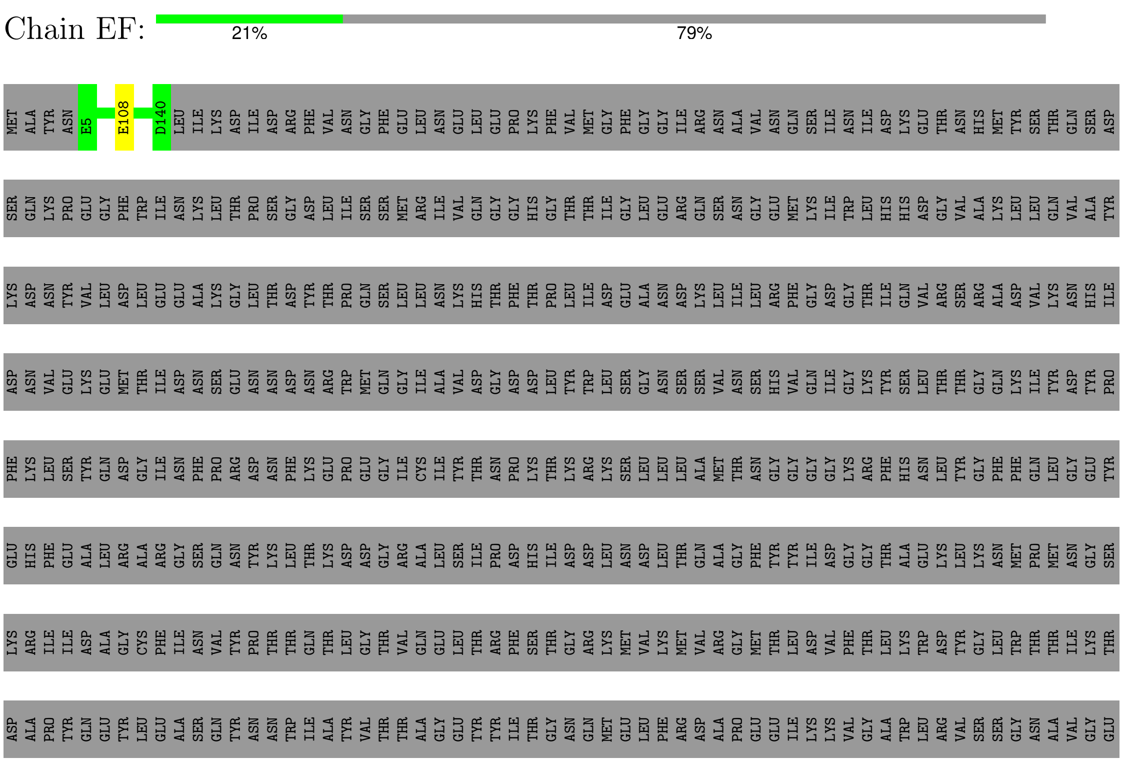
ARG ARG ILE TRP ASP TYR ASP ASN GLU LEU LYS LYS ARG PHE LYS ASN TRP ASP ASP LEU MET LYS ALA PHE PRO GLU GLN ALA LYS ASP LEU PHE ARG GLY TRP LEU ASN ASP GLY THR ILE ASP SER ILE ILE HIS ASP GLU PHE LYS LYS TYR SER ALA GLY LEU THR SER ALA PHE

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein



• Molecule 5: Minor structural protein



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

• Molecule 5: Minor structural protein

Chain FF: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

• Molecule 5: Minor structural protein

Chain CF: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain NF: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain OF: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain DH: 20% 80%

MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

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

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

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

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

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

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

• Molecule 5: Minor structural protein

Chain EH: 21% 79%

MET ALA TYR ASN E5 E108 D140 LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER THR GLN SER ASP

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain FH: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain CH: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain NH: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain OH: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain DI: 20% 80%

MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain EI: 21% 79%

MET ALA TYR ASN E5 E108 D140 LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER THR GLN SER ASP

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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain FI: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain CI: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain NI: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

Chain OI: 77% 23%

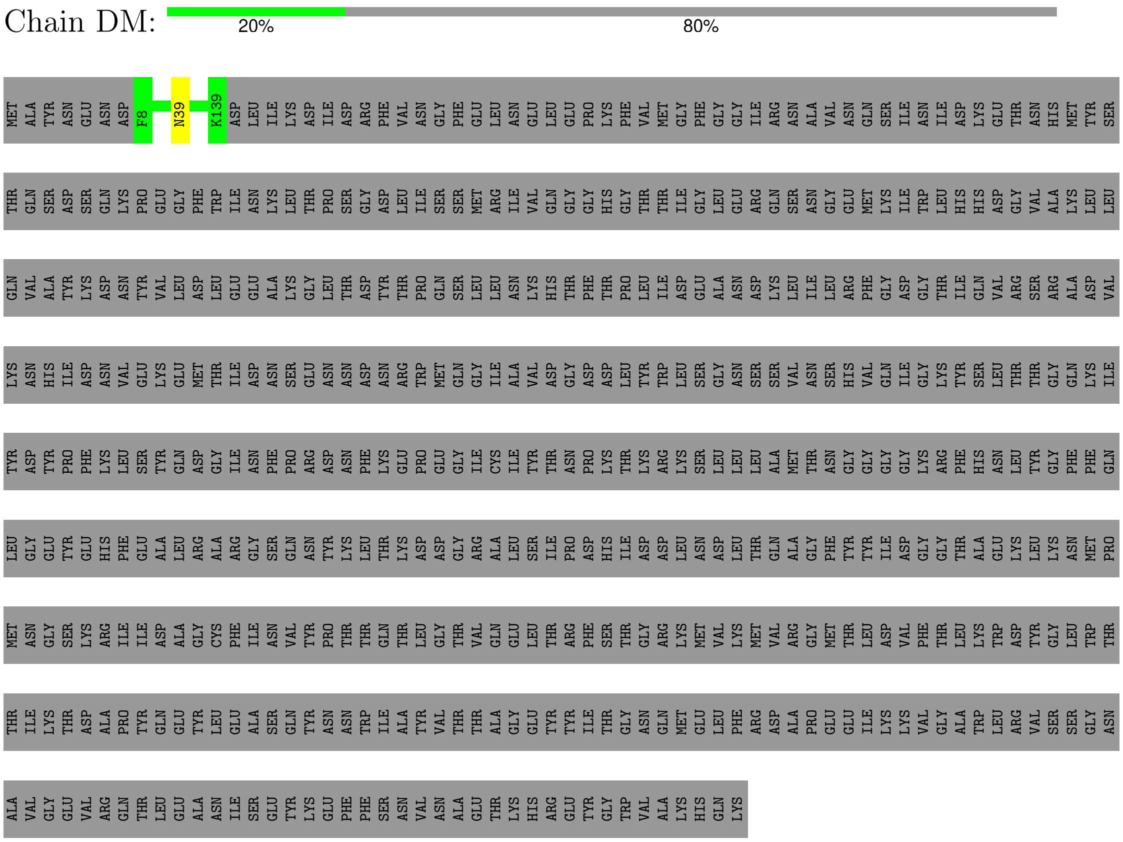
MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS THR ARG GLU ARG TYR THR PRO PHE TYR ASP ASP ARG ALA ASP TYR ASN THR ASN SER LYS SER TYR TYR ASP TYR ILE SER ARG LEU SER LYS LEU ILE GLU VAL LEU ALA

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

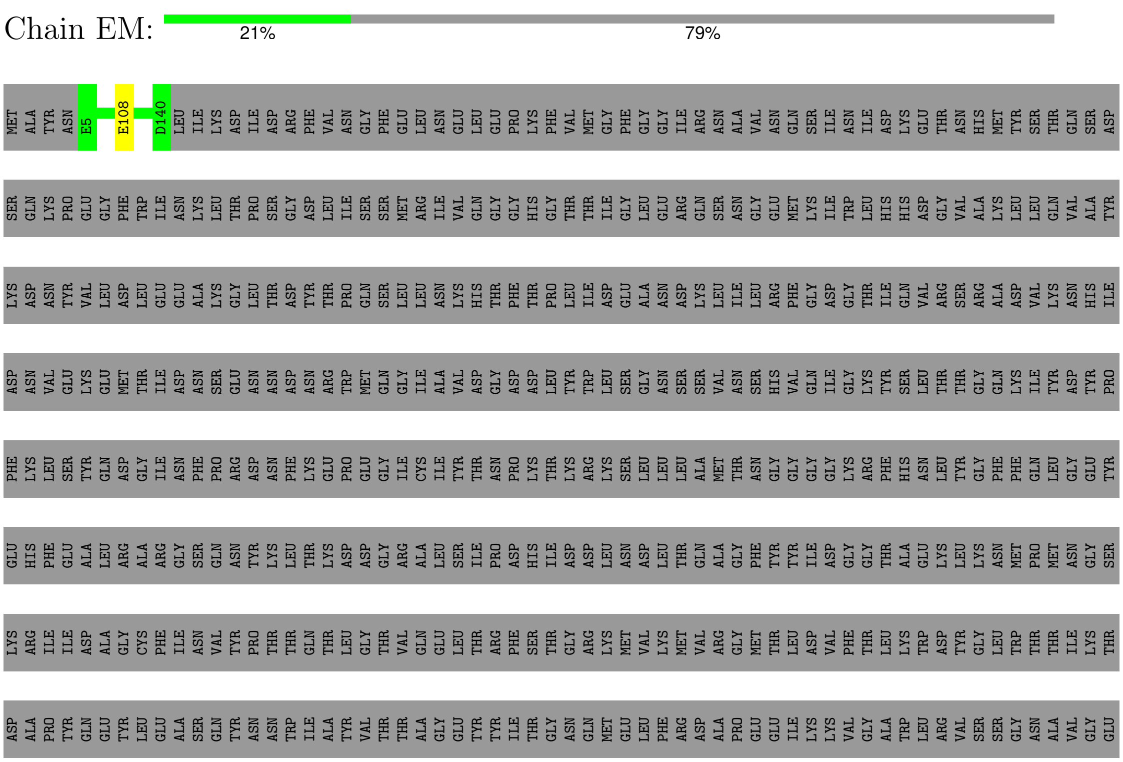
- Molecule 5: Minor structural protein

Chain DM:



- Molecule 5: Minor structural protein

Chain EM:



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

- Molecule 5: Minor structural protein

Chain FM: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain CM: 77% 23%

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

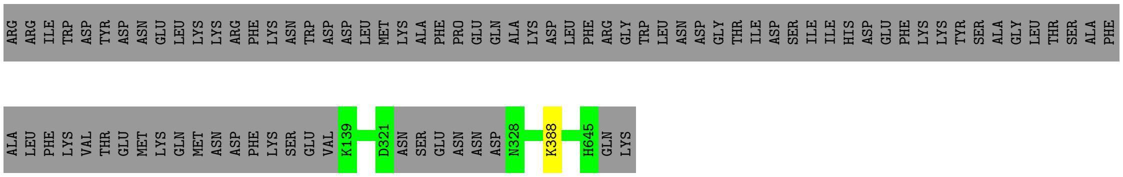
ARG ARG ILE TRP ASP TYR ASP ASN GLU LEU LYS LYS ARG PHE LYS ASN TRP ASP ASP LEU MET LYS ALA PHE PRO GLU GLN ALA LYS ASP LEU PHE ARG GLY TRP LEU ASN ASP GLY THR ILE ASP SER ILE ILE HIS ASP GLU PHE LYS LYS TYR SER ALA GLY LEU THR SER ALA PHE

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

- Molecule 5: Minor structural protein

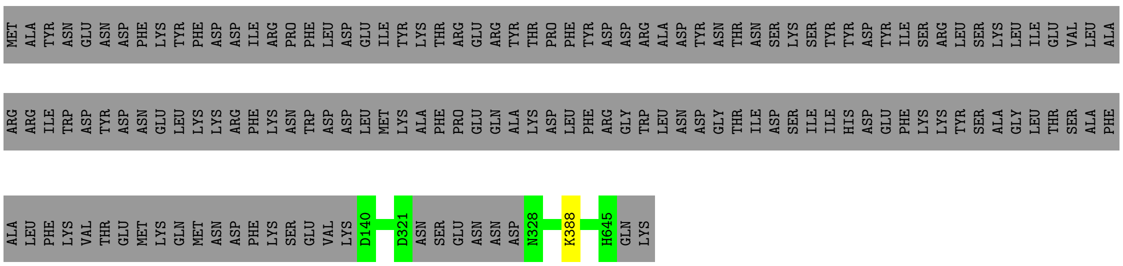
Chain NM: 77% 23%

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



• Molecule 5: Minor structural protein

Chain OM:

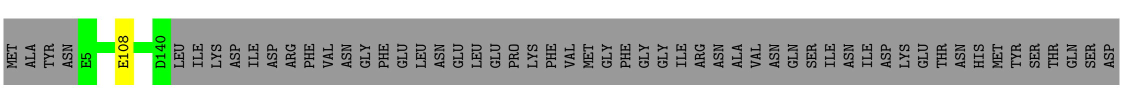


• Molecule 5: Minor structural protein

Chain DN:

• Molecule 5: Minor structural protein

Chain EN:



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

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

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

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

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

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

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

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

- Molecule 5: Minor structural protein

Chain FN: 17% 83%

MET ALA TYR ASN GLU ASN ASP PHE LYS TYR PHE ASP ASP ILE ARG PRO PHE LEU ASP GLU ILE TYR LYS T24 D65 K110 L116 D133 PHE LYS SER GLU VAL LYS ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE

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

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

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

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

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

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

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

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

VAL ALA LYS HIS GLN LYS

- Molecule 5: Minor structural protein

Chain CN: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain NN: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain ON: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain DO: 20% 80%

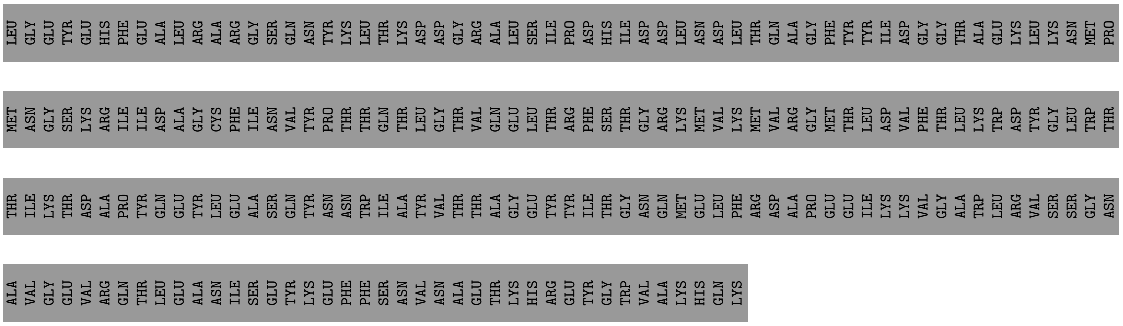
MET ALA TYR ASN GLU ASN ASP F8 N39 K139 ASP LEU ILE LYS ASP ILE ASP ARG PHE VAL ASN GLY PHE GLU LEU ASN GLU LEU GLU PRO LYS PHE VAL MET GLY PHE GLY GLY ILE ARG ASN ALA VAL ASN GLN SER ILE ASN ILE ASP LYS GLU THR ASN HIS MET TYR SER

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

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

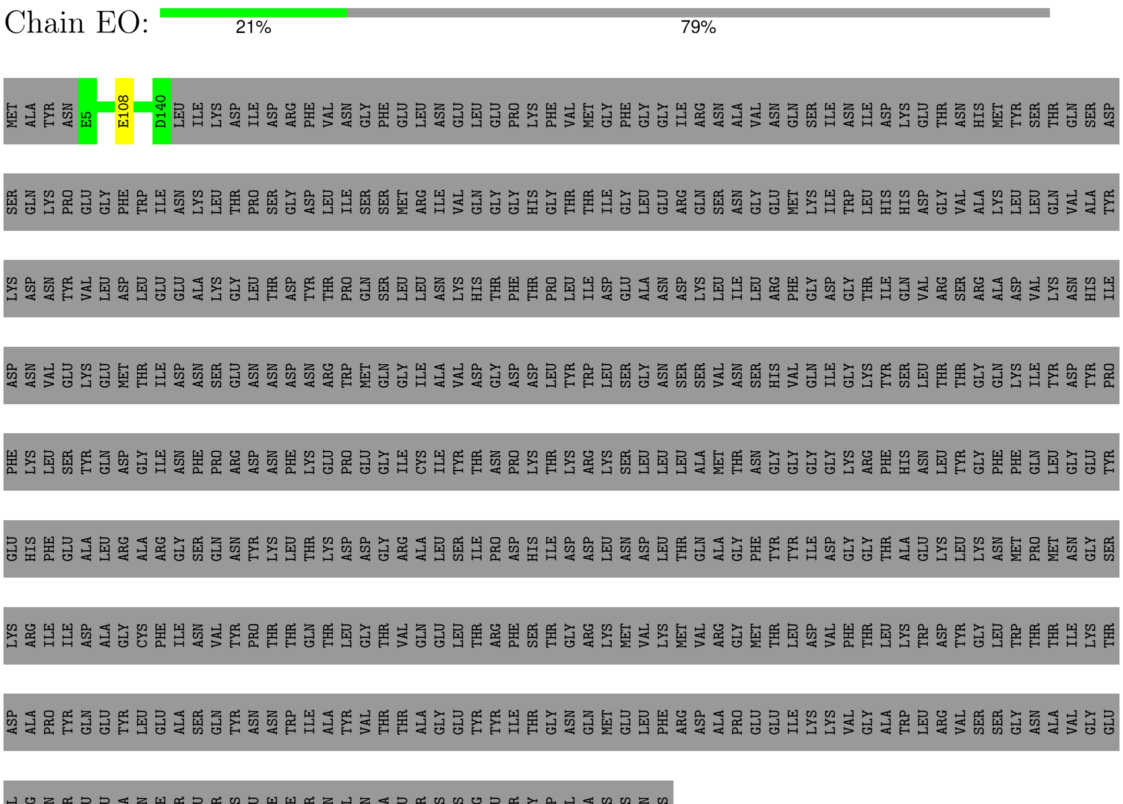
LYS ASN HIS ILE ASP ASN VAL GLU LYS GLU MET THR ILE ASP ASN SER GLU ASN ASN ASP ASN ARG TRP MET GLN GLY ILE ALA VAL ASP GLY ASP ASP LEU TYR TRP LEU SER GLY ASN SER SER VAL ASN SER HIS VAL GLN ILE GLY LYS TYR SER LEU THR THR GLY GLN LYS ILE

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



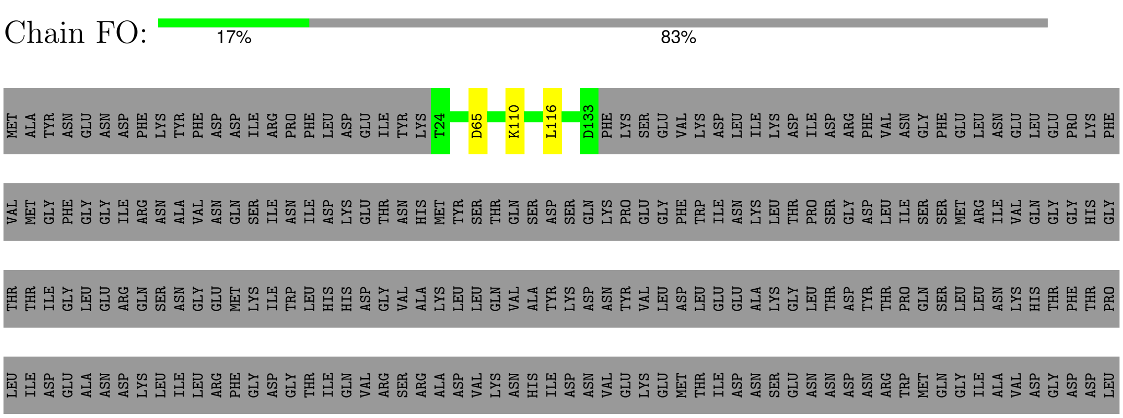
- Molecule 5: Minor structural protein

Chain EO:



- Molecule 5: Minor structural protein

Chain FO:



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

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

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

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

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

VAL ALA LYS HIS GLN LYS

• Molecule 5: Minor structural protein

Chain CO: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain NO: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL K139 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 5: Minor structural protein

Chain OO: 77% 23%

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

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

ALA LEU PHE LYS VAL THR GLU MET LYS GLN MET ASN ASP PHE LYS SER GLU VAL LYS D140 D321 ASN SER GLU ASN ASN ASP N328 K388 H645 GLN LYS

• Molecule 6: Tail fibre protein

Chain G2: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain H2: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain I2: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain J2: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain K2: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain L2: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain G5: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain H5: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain I5: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain J5: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain K5: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain L5: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain G9: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain H9: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain I9: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

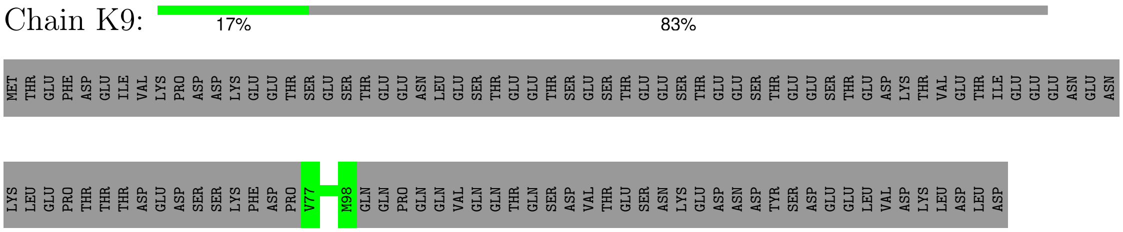
- Molecule 6: Tail fibre protein

Chain J9: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

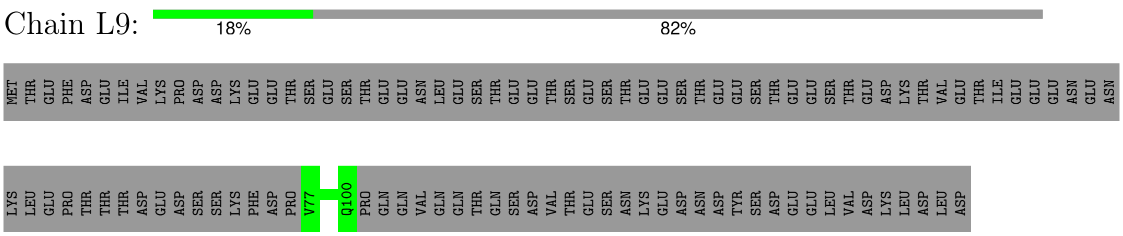
- Molecule 6: Tail fibre protein

Chain K9:



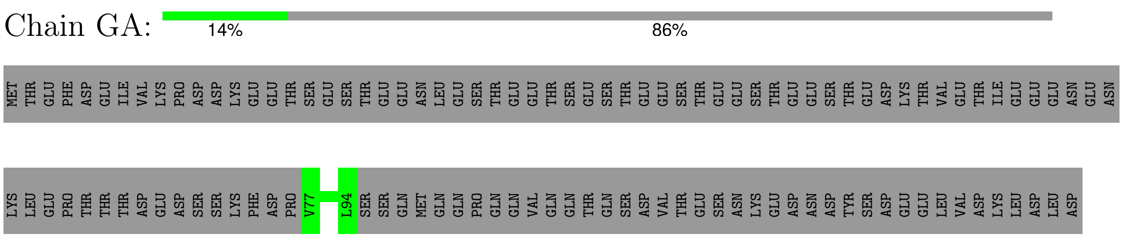
- Molecule 6: Tail fibre protein

Chain L9:



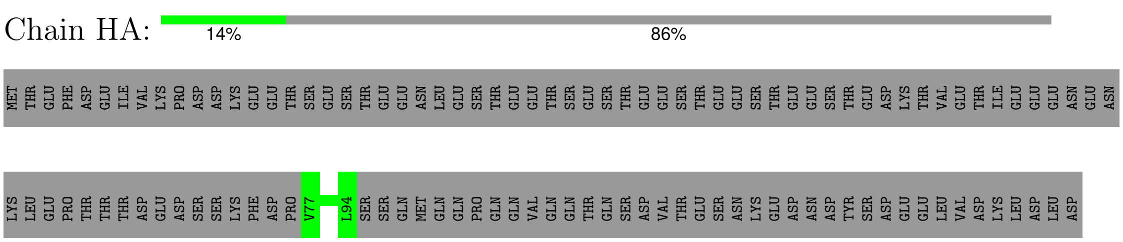
- Molecule 6: Tail fibre protein

Chain GA:



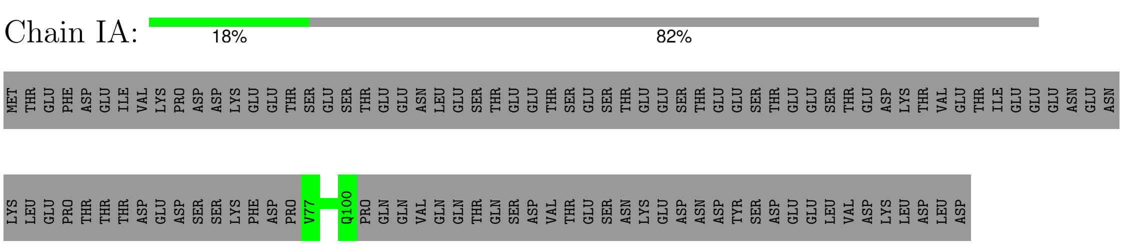
- Molecule 6: Tail fibre protein

Chain HA:



- Molecule 6: Tail fibre protein

Chain IA:



• Molecule 6: Tail fibre protein

Chain JA: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain KA: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain LA: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain GB: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain HB: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain IB: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain JB: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain KB: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN PRO GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain LB: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain GC: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain HC: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain IC: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain JC: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain KC: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain LC: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain GF: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain HF: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain IF: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain JF: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain KF: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

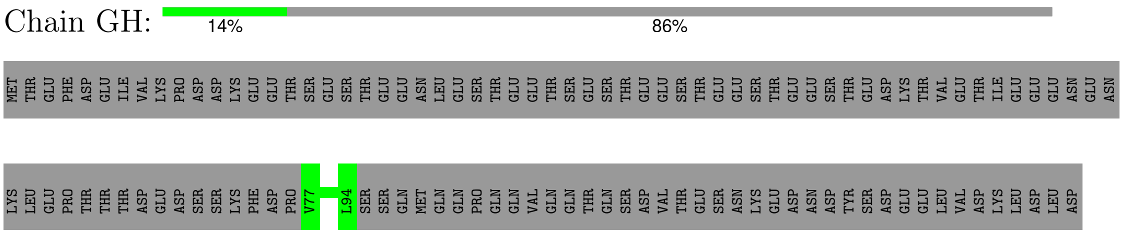
Chain LF: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

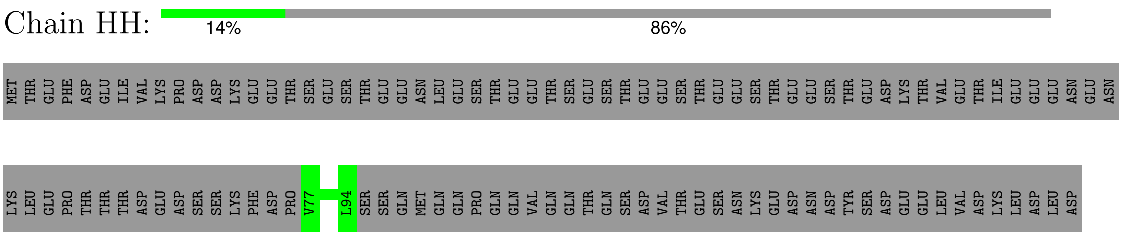
• Molecule 6: Tail fibre protein

Chain GH:



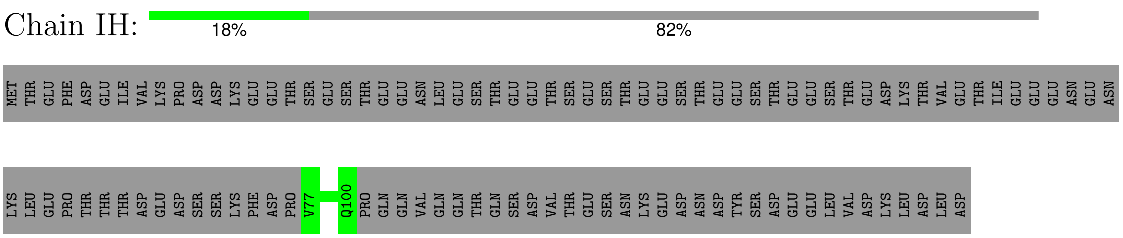
• Molecule 6: Tail fibre protein

Chain HH:



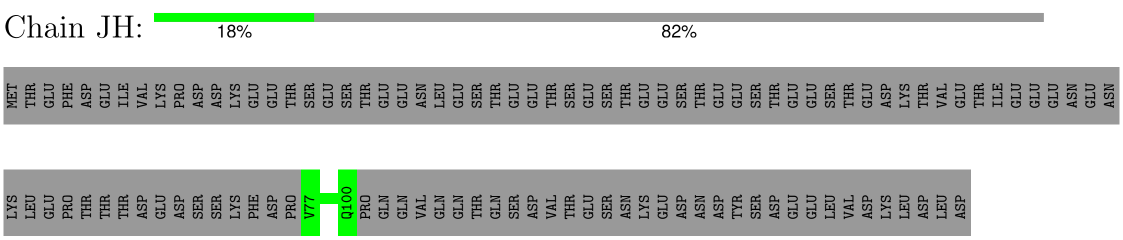
• Molecule 6: Tail fibre protein

Chain IH:



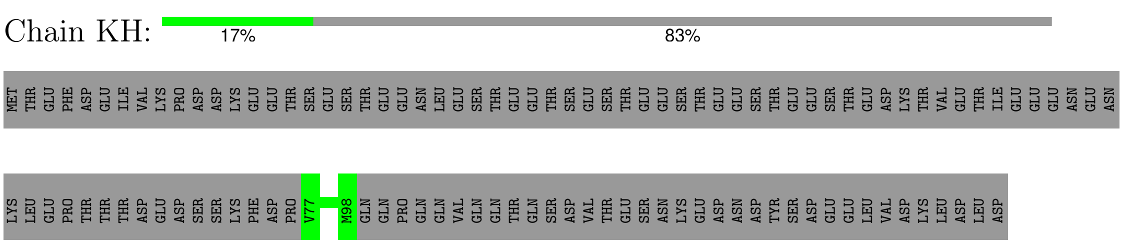
• Molecule 6: Tail fibre protein

Chain JH:



• Molecule 6: Tail fibre protein

Chain KH:



• Molecule 6: Tail fibre protein

Chain LH: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain GI: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain HI: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain II: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain JI: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain KI: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain LI: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain GM: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain HM: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain IM: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain JM: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain KM: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain LM: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain GN: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain HN: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

• Molecule 6: Tail fibre protein

Chain IN: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain JN: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain KN: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain LN: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain GO: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain HO: 14% 86%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 L94 SER SER GLN MET GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain IO: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain JO: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain KO: 17% 83%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 M98 GLN GLN PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 6: Tail fibre protein

Chain LO: 18% 82%

MET THR GLU PHE ASP GLU ILE VAL LYS PRO ASP ASP LYS GLU GLU THR SER GLU SER THR GLU GLU ASN LEU GLU SER THR GLU GLU THR SER GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU GLU SER THR GLU ASP LYS THR VAL GLU THR ILE GLU GLU GLU ASN GLU ASN

LYS LEU GLU PRO THR THR THR ASP GLU ASP SER SER LYS PHE ASP PRO V77 Q100 PRO GLN GLN VAL GLN GLN THR GLN SER ASP VAL THR GLU SER ASN LYS GLU ASP ASN ASP TYR SER ASP GLU GLU LEU VAL ASP LYS LEU ASP LEU ASP

- Molecule 7: Head fiber protein

Chain ID: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain OD: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain SD: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain IJ: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain OJ: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain SJ: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain IK: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain OK: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain SK: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain IP: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain OP: 100%

There are no outlier residues recorded for this chain.

- Molecule 7: Head fiber protein

Chain SP: 100%

There are no outlier residues recorded for this chain.

• Molecule 7: Head fiber protein

Chain HS: 100%

There are no outlier residues recorded for this chain.

• Molecule 7: Head fiber protein

Chain NS: 100%

There are no outlier residues recorded for this chain.

• Molecule 7: Head fiber protein

Chain SS: 100%

There are no outlier residues recorded for this chain.

• Molecule 8: Inner core protein

Chain PD: 100%

There are no outlier residues recorded for this chain.

• Molecule 8: Inner core protein

Chain QD: 94% 6%

A109 A124 ALA

• Molecule 8: Inner core protein

Chain RD: 71% 29%

A112 A123 ALA ALA ALA ALA ALA

• Molecule 8: Inner core protein

Chain PJ: 100%

There are no outlier residues recorded for this chain.

• Molecule 8: Inner core protein

Chain QJ: 94% 6%

A109 A124 ALA

- Molecule 8: Inner core protein

Chain RJ: 71% 29%

A112 A123 ALA ALA ALA ALA ALA

- Molecule 8: Inner core protein

Chain PK: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Inner core protein

Chain QK: 94% 6%

A109 A124 ALA

- Molecule 8: Inner core protein

Chain RK: 71% 29%

A112 A123 ALA ALA ALA ALA ALA

- Molecule 8: Inner core protein

Chain PP: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Inner core protein

Chain QP: 94% 6%

A109 A124 ALA

- Molecule 8: Inner core protein

Chain RP: 71% 29%

A112 A123 ALA ALA ALA ALA ALA

- Molecule 8: Inner core protein

Chain PS: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Inner core protein

Chain QS: 94% 6%

A109 A124 ALA

- Molecule 8: Inner core protein

Chain RS: 71% 29%

A112 A123 ALA ALA ALA ALA ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	33612	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 $(e^-/\text{Å}^2)$	21	Depositor
Minimum defocus (nm)	1.0	Depositor
Maximum defocus (nm)	3.0	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	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	A1	0.46	0/3244	0.66	4/4381 (0.1%)
1	A3	0.46	0/3244	0.66	4/4381 (0.1%)
1	A4	0.46	0/3244	0.66	4/4381 (0.1%)
1	A6	0.46	0/3244	0.66	4/4381 (0.1%)
1	A7	0.46	0/3244	0.66	4/4381 (0.1%)
1	A8	0.46	0/3244	0.66	4/4381 (0.1%)
1	AD	0.53	2/2875 (0.1%)	0.80	10/3887 (0.3%)
1	AE	0.47	0/3190	0.66	6/4310 (0.1%)
1	AG	0.46	0/3244	0.66	4/4381 (0.1%)
1	AJ	0.53	2/2875 (0.1%)	0.80	10/3887 (0.3%)
1	AK	0.53	2/2875 (0.1%)	0.80	10/3887 (0.3%)
1	AL	0.46	0/3244	0.66	4/4381 (0.1%)
1	AP	0.53	2/2875 (0.1%)	0.80	10/3887 (0.3%)
1	AQ	0.46	0/3244	0.66	4/4381 (0.1%)
1	AR	0.46	0/3244	0.66	4/4381 (0.1%)
1	AS	0.44	0/3257	0.69	3/4400 (0.1%)
1	B1	0.43	0/3190	0.62	2/4310 (0.0%)
1	B3	0.43	0/3190	0.62	2/4310 (0.0%)
1	B4	0.43	0/3190	0.62	2/4310 (0.0%)
1	B6	0.43	0/3190	0.62	2/4310 (0.0%)
1	B7	0.43	0/3190	0.62	2/4310 (0.0%)
1	B8	0.43	0/3190	0.62	2/4310 (0.0%)
1	BD	0.45	0/3257	0.69	3/4400 (0.1%)
1	BE	0.46	0/3244	0.66	4/4381 (0.1%)
1	BG	0.43	0/3190	0.62	2/4310 (0.0%)
1	BJ	0.45	0/3257	0.69	3/4400 (0.1%)
1	BK	0.45	0/3257	0.69	3/4400 (0.1%)
1	BL	0.43	0/3190	0.62	2/4310 (0.0%)
1	BP	0.45	0/3257	0.69	3/4400 (0.1%)
1	BQ	0.43	0/3190	0.62	2/4310 (0.0%)
1	BR	0.43	0/3190	0.62	2/4310 (0.0%)
1	BS	0.43	0/3202	0.67	4/4326 (0.1%)
1	C1	0.47	0/3190	0.66	6/4310 (0.1%)
1	C3	0.47	0/3190	0.66	6/4310 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	C4	0.47	0/3190	0.66	6/4310 (0.1%)
1	C6	0.47	0/3190	0.66	6/4310 (0.1%)
1	C7	0.47	0/3190	0.66	6/4310 (0.1%)
1	C8	0.47	0/3190	0.66	6/4310 (0.1%)
1	CD	0.43	0/3202	0.67	4/4326 (0.1%)
1	CE	0.43	0/3190	0.62	2/4310 (0.0%)
1	CG	0.47	0/3190	0.66	6/4310 (0.1%)
1	CJ	0.43	0/3202	0.67	4/4326 (0.1%)
1	CK	0.43	0/3202	0.67	4/4326 (0.1%)
1	CL	0.47	0/3190	0.66	6/4310 (0.1%)
1	CP	0.43	0/3202	0.67	4/4326 (0.1%)
1	CQ	0.47	0/3190	0.66	6/4310 (0.1%)
1	CR	0.47	0/3190	0.66	6/4310 (0.1%)
1	CS	0.44	0/3198	0.66	2/4321 (0.0%)
1	D1	0.41	0/3257	0.61	2/4400 (0.0%)
1	D3	0.41	0/3257	0.61	2/4400 (0.0%)
1	D4	0.41	0/3257	0.61	2/4400 (0.0%)
1	D6	0.41	0/3257	0.61	2/4400 (0.0%)
1	D7	0.41	0/3257	0.61	2/4400 (0.0%)
1	D8	0.41	0/3257	0.61	2/4400 (0.0%)
1	DD	0.44	0/3198	0.66	2/4321 (0.0%)
1	DE	0.41	0/3257	0.61	2/4400 (0.0%)
1	DG	0.41	0/3257	0.61	2/4400 (0.0%)
1	DJ	0.44	0/3198	0.66	2/4321 (0.0%)
1	DK	0.44	0/3198	0.66	2/4321 (0.0%)
1	DL	0.41	0/3257	0.61	2/4400 (0.0%)
1	DP	0.44	0/3198	0.66	2/4321 (0.0%)
1	DQ	0.41	0/3257	0.61	2/4400 (0.0%)
1	DR	0.41	0/3257	0.61	2/4400 (0.0%)
1	FE	0.41	0/3257	0.61	2/4400 (0.0%)
1	I1	0.47	0/3190	0.66	6/4310 (0.1%)
1	I3	0.47	0/3190	0.66	6/4310 (0.1%)
1	I4	0.47	0/3190	0.66	6/4310 (0.1%)
1	I6	0.47	0/3190	0.66	6/4310 (0.1%)
1	I7	0.47	0/3190	0.66	6/4310 (0.1%)
1	I8	0.47	0/3190	0.66	6/4310 (0.1%)
1	IG	0.47	0/3190	0.66	6/4310 (0.1%)
1	IL	0.47	0/3190	0.66	6/4310 (0.1%)
1	IQ	0.47	0/3190	0.66	6/4310 (0.1%)
1	IR	0.47	0/3190	0.66	6/4310 (0.1%)
1	IS	0.53	2/2875 (0.1%)	0.80	10/3887 (0.3%)
1	J1	0.46	0/3244	0.66	4/4381 (0.1%)
1	J3	0.46	0/3244	0.66	4/4381 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	J4	0.46	0/3244	0.66	4/4381 (0.1%)
1	J6	0.46	0/3244	0.66	4/4381 (0.1%)
1	J7	0.46	0/3244	0.66	4/4381 (0.1%)
1	J8	0.46	0/3244	0.66	4/4381 (0.1%)
1	JG	0.46	0/3244	0.66	4/4381 (0.1%)
1	JL	0.46	0/3244	0.66	4/4381 (0.1%)
1	JQ	0.46	0/3244	0.66	4/4381 (0.1%)
1	JR	0.46	0/3244	0.66	4/4381 (0.1%)
1	JS	0.42	0/3168	0.70	4/4279 (0.1%)
1	K1	0.43	0/3190	0.62	2/4310 (0.0%)
1	K3	0.43	0/3190	0.62	2/4310 (0.0%)
1	K4	0.43	0/3190	0.62	2/4310 (0.0%)
1	K6	0.43	0/3190	0.62	2/4310 (0.0%)
1	K7	0.43	0/3190	0.62	2/4310 (0.0%)
1	K8	0.43	0/3190	0.62	2/4310 (0.0%)
1	KD	0.42	0/3168	0.70	4/4279 (0.1%)
1	KE	0.47	0/3190	0.66	6/4310 (0.1%)
1	KG	0.43	0/3190	0.62	2/4310 (0.0%)
1	KJ	0.42	0/3168	0.70	4/4279 (0.1%)
1	KK	0.42	0/3168	0.70	4/4279 (0.1%)
1	KL	0.43	0/3190	0.62	2/4310 (0.0%)
1	KP	0.42	0/3168	0.70	4/4279 (0.1%)
1	KQ	0.43	0/3190	0.62	2/4310 (0.0%)
1	KR	0.43	0/3190	0.62	2/4310 (0.0%)
1	KS	0.43	0/3202	0.67	4/4326 (0.1%)
1	L1	0.41	0/3257	0.61	2/4400 (0.0%)
1	L3	0.41	0/3257	0.61	2/4400 (0.0%)
1	L4	0.41	0/3257	0.61	2/4400 (0.0%)
1	L6	0.41	0/3257	0.61	2/4400 (0.0%)
1	L7	0.41	0/3257	0.61	2/4400 (0.0%)
1	L8	0.41	0/3257	0.61	2/4400 (0.0%)
1	LD	0.44	0/3202	0.67	4/4326 (0.1%)
1	LE	0.46	0/3244	0.66	4/4381 (0.1%)
1	LG	0.41	0/3257	0.61	2/4400 (0.0%)
1	LJ	0.43	0/3202	0.67	4/4326 (0.1%)
1	LK	0.44	0/3202	0.67	4/4326 (0.1%)
1	LL	0.41	0/3257	0.61	2/4400 (0.0%)
1	LP	0.44	0/3202	0.67	4/4326 (0.1%)
1	LQ	0.41	0/3257	0.61	2/4400 (0.0%)
1	LR	0.41	0/3257	0.61	2/4400 (0.0%)
1	ME	0.43	0/3190	0.62	2/4310 (0.0%)
1	NE	0.41	0/3257	0.61	2/4400 (0.0%)
1	Q1	0.47	0/3190	0.66	6/4310 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	Q3	0.47	0/3190	0.66	6/4310 (0.1%)
1	Q4	0.47	0/3190	0.66	6/4310 (0.1%)
1	Q6	0.47	0/3190	0.66	6/4310 (0.1%)
1	Q7	0.47	0/3190	0.66	6/4310 (0.1%)
1	Q8	0.47	0/3190	0.66	6/4310 (0.1%)
1	QG	0.47	0/3190	0.66	6/4310 (0.1%)
1	QL	0.47	0/3190	0.66	6/4310 (0.1%)
1	QQ	0.47	0/3190	0.66	6/4310 (0.1%)
1	QR	0.47	0/3190	0.66	6/4310 (0.1%)
1	R1	0.46	0/3244	0.66	4/4381 (0.1%)
1	R3	0.46	0/3244	0.66	4/4381 (0.1%)
1	R4	0.46	0/3244	0.66	4/4381 (0.1%)
1	R6	0.46	0/3244	0.66	4/4381 (0.1%)
1	R7	0.46	0/3244	0.66	4/4381 (0.1%)
1	R8	0.46	0/3244	0.66	4/4381 (0.1%)
1	RG	0.46	0/3244	0.66	4/4381 (0.1%)
1	RL	0.46	0/3244	0.66	4/4381 (0.1%)
1	RQ	0.46	0/3244	0.66	4/4381 (0.1%)
1	RR	0.46	0/3244	0.66	4/4381 (0.1%)
1	S1	0.43	0/3190	0.62	2/4310 (0.0%)
1	S3	0.43	0/3190	0.62	2/4310 (0.0%)
1	S4	0.43	0/3190	0.62	2/4310 (0.0%)
1	S6	0.43	0/3190	0.62	2/4310 (0.0%)
1	S7	0.43	0/3190	0.62	2/4310 (0.0%)
1	S8	0.43	0/3190	0.62	2/4310 (0.0%)
1	SE	0.47	0/3190	0.66	6/4310 (0.1%)
1	SG	0.43	0/3190	0.62	2/4310 (0.0%)
1	SL	0.43	0/3190	0.62	2/4310 (0.0%)
1	SQ	0.43	0/3190	0.62	2/4310 (0.0%)
1	SR	0.43	0/3190	0.62	2/4310 (0.0%)
1	T1	0.41	0/3257	0.61	2/4400 (0.0%)
1	T3	0.41	0/3257	0.61	2/4400 (0.0%)
1	T4	0.41	0/3257	0.61	2/4400 (0.0%)
1	T6	0.41	0/3257	0.61	2/4400 (0.0%)
1	T7	0.41	0/3257	0.61	2/4400 (0.0%)
1	T8	0.41	0/3257	0.61	2/4400 (0.0%)
1	TE	0.46	0/3244	0.66	4/4381 (0.1%)
1	TG	0.41	0/3257	0.61	2/4400 (0.0%)
1	TL	0.41	0/3257	0.61	2/4400 (0.0%)
1	TQ	0.41	0/3257	0.61	2/4400 (0.0%)
1	TR	0.41	0/3257	0.61	2/4400 (0.0%)
1	UE	0.43	0/3190	0.62	2/4310 (0.0%)
1	VE	0.41	0/3257	0.61	2/4400 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	X1	0.47	0/3190	0.66	6/4310 (0.1%)
1	X4	0.47	0/3190	0.66	6/4310 (0.1%)
1	Y1	0.46	0/3244	0.66	4/4381 (0.1%)
1	Y3	0.41	0/3257	0.61	2/4400 (0.0%)
1	Y4	0.46	0/3244	0.66	4/4381 (0.1%)
1	Y6	0.47	0/3190	0.66	6/4310 (0.1%)
1	Y7	0.47	0/3190	0.66	6/4310 (0.1%)
1	Y8	0.47	0/3190	0.66	6/4310 (0.1%)
1	YG	0.47	0/3190	0.66	6/4310 (0.1%)
1	YL	0.47	0/3190	0.66	6/4310 (0.1%)
1	YQ	0.41	0/3257	0.61	2/4400 (0.0%)
1	YR	0.47	0/3190	0.66	6/4310 (0.1%)
1	Z1	0.43	0/3190	0.62	2/4310 (0.0%)
1	Z4	0.43	0/3190	0.62	2/4310 (0.0%)
1	Z6	0.46	0/3244	0.66	4/4381 (0.1%)
1	Z7	0.46	0/3244	0.66	4/4381 (0.1%)
1	Z8	0.46	0/3244	0.66	4/4381 (0.1%)
1	ZG	0.46	0/3244	0.66	4/4381 (0.1%)
1	ZL	0.46	0/3244	0.66	4/4381 (0.1%)
1	ZR	0.46	0/3244	0.66	4/4381 (0.1%)
1	a1	0.41	0/3257	0.61	2/4400 (0.0%)
1	a4	0.41	0/3257	0.61	2/4400 (0.0%)
1	a6	0.43	0/3190	0.62	2/4310 (0.0%)
1	a7	0.43	0/3190	0.62	2/4310 (0.0%)
1	a8	0.43	0/3190	0.62	2/4310 (0.0%)
1	aE	0.47	0/3190	0.66	6/4310 (0.1%)
1	aG	0.43	0/3190	0.62	2/4310 (0.0%)
1	aL	0.43	0/3190	0.62	2/4310 (0.0%)
1	aR	0.43	0/3190	0.62	2/4310 (0.0%)
1	b3	0.41	0/3257	0.61	2/4400 (0.0%)
1	b6	0.41	0/3257	0.61	2/4400 (0.0%)
1	b7	0.41	0/3257	0.61	2/4400 (0.0%)
1	b8	0.41	0/3257	0.61	2/4400 (0.0%)
1	bE	0.46	0/3244	0.66	4/4381 (0.1%)
1	bG	0.41	0/3257	0.61	2/4400 (0.0%)
1	bL	0.41	0/3257	0.61	2/4400 (0.0%)
1	bQ	0.47	0/3190	0.66	6/4310 (0.1%)
1	bR	0.41	0/3257	0.61	2/4400 (0.0%)
1	cE	0.43	0/3190	0.62	2/4310 (0.0%)
1	cQ	0.46	0/3244	0.66	4/4381 (0.1%)
1	dE	0.41	0/3257	0.61	2/4400 (0.0%)
1	dQ	0.43	0/3190	0.62	2/4310 (0.0%)
1	eQ	0.41	0/3257	0.61	2/4400 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	f1	0.47	0/3190	0.66	6/4310 (0.1%)
1	f4	0.47	0/3190	0.66	6/4310 (0.1%)
1	g1	0.46	0/3244	0.66	4/4381 (0.1%)
1	g4	0.46	0/3244	0.66	4/4381 (0.1%)
1	g6	0.47	0/3190	0.66	6/4310 (0.1%)
1	g7	0.47	0/3190	0.66	6/4310 (0.1%)
1	g8	0.47	0/3190	0.66	6/4310 (0.1%)
1	gG	0.47	0/3190	0.66	6/4310 (0.1%)
1	gL	0.41	0/3257	0.61	2/4400 (0.0%)
1	gR	0.47	0/3190	0.66	6/4310 (0.1%)
1	h1	0.43	0/3190	0.62	2/4310 (0.0%)
1	h4	0.43	0/3190	0.62	2/4310 (0.0%)
1	h6	0.46	0/3244	0.66	4/4381 (0.1%)
1	h7	0.46	0/3244	0.66	4/4381 (0.1%)
1	h8	0.46	0/3244	0.66	4/4381 (0.1%)
1	hG	0.46	0/3244	0.66	4/4381 (0.1%)
1	hR	0.46	0/3244	0.66	4/4381 (0.1%)
1	i1	0.41	0/3257	0.61	2/4400 (0.0%)
1	i4	0.41	0/3257	0.61	2/4400 (0.0%)
1	i6	0.43	0/3190	0.62	2/4310 (0.0%)
1	i7	0.43	0/3190	0.62	2/4310 (0.0%)
1	i8	0.43	0/3190	0.62	2/4310 (0.0%)
1	iG	0.43	0/3190	0.62	2/4310 (0.0%)
1	iR	0.43	0/3190	0.62	2/4310 (0.0%)
1	j6	0.41	0/3257	0.61	2/4400 (0.0%)
1	j7	0.41	0/3257	0.61	2/4400 (0.0%)
1	j8	0.41	0/3257	0.61	2/4400 (0.0%)
1	jG	0.41	0/3257	0.61	2/4400 (0.0%)
1	jR	0.41	0/3257	0.61	2/4400 (0.0%)
2	DS	0.37	0/441	0.72	0/587
2	E1	0.56	0/436	1.03	3/581 (0.5%)
2	E3	0.56	0/436	1.03	3/581 (0.5%)
2	E4	0.56	0/436	1.03	3/581 (0.5%)
2	E6	0.56	0/436	1.03	3/581 (0.5%)
2	E7	0.56	0/436	1.03	3/581 (0.5%)
2	E8	0.56	0/436	1.03	3/581 (0.5%)
2	ED	0.37	0/441	0.71	0/587
2	EE	0.56	0/436	1.03	3/581 (0.5%)
2	EG	0.56	0/436	1.03	3/581 (0.5%)
2	EJ	0.37	0/441	0.71	0/587
2	EK	0.37	0/441	0.72	0/587
2	EL	0.56	0/436	1.03	3/581 (0.5%)
2	EP	0.37	0/441	0.72	0/587

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	EQ	0.56	0/436	1.03	3/581 (0.5%)
2	ER	0.56	0/436	1.03	3/581 (0.5%)
2	ES	0.36	0/441	0.93	1/587 (0.2%)
2	F1	0.39	0/440	0.79	1/586 (0.2%)
2	F3	0.39	0/440	0.79	1/586 (0.2%)
2	F4	0.39	0/440	0.79	1/586 (0.2%)
2	F6	0.39	0/440	0.79	1/586 (0.2%)
2	F7	0.39	0/440	0.79	1/586 (0.2%)
2	F8	0.39	0/440	0.79	1/586 (0.2%)
2	FD	0.36	0/441	0.93	1/587 (0.2%)
2	FG	0.39	0/440	0.79	1/586 (0.2%)
2	FJ	0.36	0/441	0.93	1/587 (0.2%)
2	FK	0.36	0/441	0.93	1/587 (0.2%)
2	FL	0.39	0/440	0.79	1/586 (0.2%)
2	FP	0.36	0/441	0.93	1/587 (0.2%)
2	FQ	0.39	0/440	0.79	1/586 (0.2%)
2	FR	0.39	0/440	0.79	1/586 (0.2%)
2	FS	0.40	0/239	0.78	0/320
2	G1	0.33	0/222	0.69	0/293
2	G3	0.33	0/222	0.68	0/293
2	G4	0.33	0/222	0.69	0/293
2	G6	0.33	0/222	0.69	0/293
2	G7	0.33	0/222	0.69	0/293
2	G8	0.33	0/222	0.68	0/293
2	GD	0.40	0/239	0.78	0/320
2	GE	0.33	0/222	0.69	0/293
2	GG	0.33	0/222	0.69	0/293
2	GJ	0.40	0/239	0.78	0/320
2	GK	0.40	0/239	0.78	0/320
2	GL	0.33	0/222	0.69	0/293
2	GP	0.40	0/239	0.78	0/320
2	GQ	0.33	0/222	0.69	0/293
2	GR	0.33	0/222	0.68	0/293
2	GS	0.35	0/437	0.82	0/582
2	H1	0.41	0/439	0.76	0/585
2	H3	0.41	0/439	0.76	0/585
2	H4	0.41	0/439	0.76	0/585
2	H6	0.41	0/439	0.76	0/585
2	H7	0.41	0/439	0.76	0/585
2	H8	0.41	0/439	0.76	0/585
2	HD	0.36	0/437	0.82	0/582
2	HE	0.39	0/440	0.79	1/586 (0.2%)
2	HG	0.41	0/439	0.76	0/585

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	HJ	0.36	0/437	0.82	0/582
2	HK	0.36	0/437	0.82	0/582
2	HL	0.41	0/439	0.76	0/585
2	HP	0.36	0/437	0.82	0/582
2	HQ	0.41	0/439	0.76	0/585
2	HR	0.41	0/439	0.76	0/585
2	IE	0.33	0/222	0.68	0/293
2	JE	0.41	0/439	0.76	0/585
2	LS	0.37	0/441	0.79	0/587
2	M1	0.56	0/436	1.03	3/581 (0.5%)
2	M3	0.56	0/436	1.03	3/581 (0.5%)
2	M4	0.56	0/436	1.03	3/581 (0.5%)
2	M6	0.56	0/436	1.03	3/581 (0.5%)
2	M7	0.56	0/436	1.03	3/581 (0.5%)
2	M8	0.56	0/436	1.03	3/581 (0.5%)
2	MD	0.37	0/441	0.79	0/587
2	MG	0.56	0/436	1.03	3/581 (0.5%)
2	MJ	0.37	0/441	0.79	0/587
2	MK	0.37	0/441	0.79	0/587
2	ML	0.56	0/436	1.03	3/581 (0.5%)
2	MP	0.37	0/441	0.79	0/587
2	MQ	0.56	0/436	1.03	3/581 (0.5%)
2	MR	0.56	0/436	1.03	3/581 (0.5%)
2	MS	0.40	0/441	0.88	1/587 (0.2%)
2	N1	0.39	0/440	0.79	1/586 (0.2%)
2	N3	0.39	0/440	0.79	1/586 (0.2%)
2	N4	0.39	0/440	0.79	1/586 (0.2%)
2	N6	0.39	0/440	0.79	1/586 (0.2%)
2	N7	0.39	0/440	0.79	1/586 (0.2%)
2	N8	0.39	0/440	0.79	1/586 (0.2%)
2	ND	0.40	0/441	0.88	1/587 (0.2%)
2	NG	0.39	0/440	0.79	1/586 (0.2%)
2	NJ	0.40	0/441	0.88	1/587 (0.2%)
2	NK	0.40	0/441	0.88	1/587 (0.2%)
2	NL	0.39	0/440	0.79	1/586 (0.2%)
2	NP	0.40	0/441	0.88	1/587 (0.2%)
2	NQ	0.39	0/440	0.79	1/586 (0.2%)
2	NR	0.39	0/440	0.79	1/586 (0.2%)
2	O1	0.33	0/222	0.68	0/293
2	O3	0.33	0/222	0.69	0/293
2	O4	0.33	0/222	0.68	0/293
2	O6	0.33	0/222	0.69	0/293
2	O7	0.33	0/222	0.69	0/293

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	O8	0.33	0/222	0.68	0/293
2	OE	0.56	0/436	1.03	3/581 (0.5%)
2	OG	0.33	0/222	0.68	0/293
2	OL	0.33	0/222	0.69	0/293
2	OQ	0.33	0/222	0.68	0/293
2	OR	0.33	0/222	0.69	0/293
2	P1	0.41	0/439	0.76	0/585
2	P3	0.41	0/439	0.76	0/585
2	P4	0.41	0/439	0.76	0/585
2	P6	0.41	0/439	0.76	0/585
2	P7	0.41	0/439	0.76	0/585
2	P8	0.41	0/439	0.76	0/585
2	PE	0.39	0/440	0.79	1/586 (0.2%)
2	PG	0.41	0/439	0.76	0/585
2	PL	0.41	0/439	0.76	0/585
2	PQ	0.41	0/439	0.76	0/585
2	PR	0.41	0/439	0.76	0/585
2	QE	0.33	0/222	0.68	0/293
2	RE	0.41	0/439	0.76	0/585
2	U1	0.39	0/440	0.79	1/586 (0.2%)
2	U3	0.56	0/436	1.03	3/581 (0.5%)
2	U4	0.39	0/440	0.79	1/586 (0.2%)
2	U6	0.56	0/436	1.03	3/581 (0.5%)
2	U7	0.56	0/436	1.03	3/581 (0.5%)
2	U8	0.56	0/436	1.03	3/581 (0.5%)
2	UG	0.56	0/436	1.03	3/581 (0.5%)
2	UL	0.56	0/436	1.03	3/581 (0.5%)
2	UQ	0.56	0/436	1.03	3/581 (0.5%)
2	UR	0.56	0/436	1.03	3/581 (0.5%)
2	V1	0.33	0/222	0.69	0/293
2	V3	0.39	0/440	0.79	1/586 (0.2%)
2	V4	0.33	0/222	0.69	0/293
2	V6	0.39	0/440	0.79	1/586 (0.2%)
2	V7	0.39	0/440	0.79	1/586 (0.2%)
2	V8	0.39	0/440	0.79	1/586 (0.2%)
2	VG	0.39	0/440	0.79	1/586 (0.2%)
2	VL	0.39	0/440	0.79	1/586 (0.2%)
2	VQ	0.39	0/440	0.79	1/586 (0.2%)
2	VR	0.39	0/440	0.79	1/586 (0.2%)
2	W1	0.41	0/439	0.76	0/585
2	W3	0.33	0/222	0.68	0/293
2	W4	0.41	0/439	0.76	0/585
2	W6	0.33	0/222	0.69	0/293

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	W7	0.33	0/222	0.69	0/293
2	W8	0.33	0/222	0.69	0/293
2	WE	0.56	0/436	1.03	3/581 (0.5%)
2	WG	0.33	0/222	0.69	0/293
2	WL	0.33	0/222	0.69	0/293
2	WQ	0.33	0/222	0.69	0/293
2	WR	0.33	0/222	0.69	0/293
2	X3	0.41	0/439	0.76	0/585
2	X6	0.41	0/439	0.76	0/585
2	X7	0.41	0/439	0.76	0/585
2	X8	0.41	0/439	0.76	0/585
2	XE	0.39	0/440	0.79	1/586 (0.2%)
2	XG	0.41	0/439	0.76	0/585
2	XL	0.41	0/439	0.76	0/585
2	XQ	0.41	0/439	0.76	0/585
2	XR	0.41	0/439	0.76	0/585
2	YE	0.33	0/222	0.68	0/293
2	Z3	0.56	0/436	1.03	3/581 (0.5%)
2	ZE	0.41	0/439	0.76	0/585
2	ZQ	0.56	0/436	1.03	3/581 (0.5%)
2	a3	0.33	0/222	0.68	0/293
2	aQ	0.33	0/222	0.69	0/293
2	b1	0.56	0/436	1.03	3/581 (0.5%)
2	b4	0.56	0/436	1.03	3/581 (0.5%)
2	c1	0.39	0/440	0.79	1/586 (0.2%)
2	c3	0.56	0/436	1.03	3/581 (0.5%)
2	c4	0.39	0/440	0.79	1/586 (0.2%)
2	c6	0.56	0/436	1.03	3/581 (0.5%)
2	c7	0.56	0/436	1.03	3/581 (0.5%)
2	c8	0.56	0/436	1.03	3/581 (0.5%)
2	cG	0.56	0/436	1.03	3/581 (0.5%)
2	cL	0.56	0/436	1.03	3/581 (0.5%)
2	cR	0.56	0/436	1.03	3/581 (0.5%)
2	d1	0.33	0/222	0.69	0/293
2	d3	0.33	0/222	0.68	0/293
2	d4	0.33	0/222	0.68	0/293
2	d6	0.39	0/440	0.79	1/586 (0.2%)
2	d7	0.39	0/440	0.79	1/586 (0.2%)
2	d8	0.39	0/440	0.79	1/586 (0.2%)
2	dG	0.39	0/440	0.79	1/586 (0.2%)
2	dL	0.39	0/440	0.79	1/586 (0.2%)
2	dR	0.39	0/440	0.79	1/586 (0.2%)
2	e1	0.41	0/439	0.76	0/585

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	e4	0.41	0/439	0.76	0/585
2	e6	0.33	0/222	0.68	0/293
2	e7	0.33	0/222	0.69	0/293
2	e8	0.33	0/222	0.68	0/293
2	eE	0.56	0/436	1.03	3/581 (0.5%)
2	eG	0.33	0/222	0.68	0/293
2	eL	0.33	0/222	0.69	0/293
2	eR	0.33	0/222	0.69	0/293
2	f6	0.41	0/439	0.76	0/585
2	f7	0.41	0/439	0.76	0/585
2	f8	0.41	0/439	0.76	0/585
2	fE	0.39	0/440	0.79	1/586 (0.2%)
2	fG	0.41	0/439	0.76	0/585
2	fL	0.41	0/439	0.76	0/585
2	fQ	0.56	0/436	1.03	3/581 (0.5%)
2	fR	0.41	0/439	0.76	0/585
2	gE	0.33	0/222	0.68	0/293
2	gQ	0.39	0/440	0.79	1/586 (0.2%)
2	hE	0.41	0/439	0.76	0/585
2	hL	0.56	0/436	1.03	3/581 (0.5%)
2	hQ	0.33	0/222	0.69	0/293
2	iL	0.33	0/222	0.69	0/293
2	iQ	0.41	0/439	0.76	0/585
2	j1	0.56	0/436	1.03	3/581 (0.5%)
2	j4	0.39	0/440	0.79	1/586 (0.2%)
2	k1	0.39	0/440	0.79	1/586 (0.2%)
2	k4	0.33	0/222	0.68	0/293
2	k6	0.56	0/436	1.03	3/581 (0.5%)
2	k7	0.56	0/436	1.03	3/581 (0.5%)
2	k8	0.56	0/436	1.03	3/581 (0.5%)
2	kG	0.56	0/436	1.03	3/581 (0.5%)
2	kR	0.39	0/440	0.79	1/586 (0.2%)
2	l1	0.33	0/222	0.69	0/293
2	l4	0.41	0/439	0.76	0/585
2	l6	0.39	0/440	0.79	1/586 (0.2%)
2	l7	0.39	0/440	0.79	1/586 (0.2%)
2	l8	0.39	0/440	0.79	1/586 (0.2%)
2	lG	0.39	0/440	0.79	1/586 (0.2%)
2	lR	0.33	0/222	0.69	0/293
2	m1	0.41	0/439	0.76	0/585
2	m6	0.33	0/222	0.68	0/293
2	m7	0.33	0/222	0.68	0/293
2	m8	0.33	0/222	0.69	0/293

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	mG	0.33	0/222	0.69	0/293
2	mR	0.41	0/439	0.76	0/585
2	n6	0.41	0/439	0.76	0/585
2	n7	0.41	0/439	0.76	0/585
2	n8	0.41	0/439	0.76	0/585
2	nG	0.41	0/439	0.76	0/585
3	A2	0.55	0/2386	0.81	8/3223 (0.2%)
3	A5	0.55	0/2386	0.81	8/3223 (0.2%)
3	A9	0.55	0/2386	0.81	8/3223 (0.2%)
3	AA	0.55	0/2386	0.81	8/3223 (0.2%)
3	AB	0.55	0/2386	0.81	8/3223 (0.2%)
3	AC	0.55	0/2386	0.81	7/3223 (0.2%)
3	AF	0.55	0/2386	0.81	8/3223 (0.2%)
3	AH	0.55	0/2386	0.81	7/3223 (0.2%)
3	AI	0.55	0/2386	0.81	7/3223 (0.2%)
3	AM	0.55	0/2386	0.81	7/3223 (0.2%)
3	AN	0.55	0/2386	0.81	7/3223 (0.2%)
3	AO	0.55	0/2386	0.81	8/3223 (0.2%)
4	B2	0.48	0/1791	0.70	1/2411 (0.0%)
4	B5	0.48	0/1791	0.70	1/2411 (0.0%)
4	B9	0.48	0/1791	0.70	1/2411 (0.0%)
4	BA	0.48	0/1791	0.70	1/2411 (0.0%)
4	BB	0.48	0/1791	0.69	1/2411 (0.0%)
4	BC	0.48	0/1791	0.70	1/2411 (0.0%)
4	BF	0.48	0/1791	0.70	1/2411 (0.0%)
4	BH	0.48	0/1791	0.70	1/2411 (0.0%)
4	BI	0.48	0/1791	0.70	1/2411 (0.0%)
4	BM	0.48	0/1791	0.70	1/2411 (0.0%)
4	BN	0.48	0/1791	0.70	1/2411 (0.0%)
4	BO	0.48	0/1791	0.70	1/2411 (0.0%)
5	C2	0.26	0/4109	0.48	0/5550
5	C5	0.26	0/4109	0.48	0/5550
5	C9	0.26	0/4109	0.48	0/5550
5	CA	0.26	0/4109	0.48	0/5550
5	CB	0.26	0/4109	0.48	0/5550
5	CC	0.26	0/4109	0.48	0/5550
5	CF	0.26	0/4109	0.48	0/5550
5	CH	0.26	0/4109	0.48	0/5550
5	CI	0.26	0/4109	0.48	0/5550
5	CM	0.26	0/4109	0.48	0/5550
5	CN	0.26	0/4109	0.48	0/5550
5	CO	0.26	0/4109	0.48	0/5550
5	D2	0.48	0/1135	0.65	0/1529

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	D5	0.48	0/1135	0.65	0/1529
5	D9	0.47	0/1135	0.65	0/1529
5	DA	0.47	0/1135	0.65	0/1529
5	DB	0.47	0/1135	0.65	0/1529
5	DC	0.48	0/1135	0.65	0/1529
5	DF	0.47	0/1135	0.65	0/1529
5	DH	0.48	0/1135	0.65	0/1529
5	DI	0.48	0/1135	0.65	0/1529
5	DM	0.48	0/1135	0.65	0/1529
5	DN	0.48	0/1135	0.65	0/1529
5	DO	0.47	0/1135	0.65	0/1529
5	E2	0.49	0/1203	0.68	0/1617
5	E5	0.48	0/1203	0.68	0/1617
5	E9	0.48	0/1203	0.68	0/1617
5	EA	0.48	0/1203	0.68	0/1617
5	EB	0.49	0/1203	0.68	0/1617
5	EC	0.49	0/1203	0.68	0/1617
5	EF	0.48	0/1203	0.68	0/1617
5	EH	0.49	0/1203	0.68	0/1617
5	EI	0.48	0/1203	0.68	0/1617
5	EM	0.48	0/1203	0.68	0/1617
5	EN	0.49	0/1203	0.68	0/1617
5	EO	0.49	0/1203	0.68	0/1617
5	F2	0.55	0/950	0.73	2/1279 (0.2%)
5	F5	0.55	0/950	0.73	2/1279 (0.2%)
5	F9	0.55	0/950	0.73	2/1279 (0.2%)
5	FA	0.55	0/950	0.73	2/1279 (0.2%)
5	FB	0.55	0/950	0.73	2/1279 (0.2%)
5	FC	0.55	0/950	0.73	2/1279 (0.2%)
5	FF	0.55	0/950	0.73	2/1279 (0.2%)
5	FH	0.55	0/950	0.73	2/1279 (0.2%)
5	FI	0.55	0/950	0.73	2/1279 (0.2%)
5	FM	0.55	0/950	0.73	2/1279 (0.2%)
5	FN	0.55	0/950	0.73	2/1279 (0.2%)
5	FO	0.55	0/950	0.73	2/1279 (0.2%)
5	N2	0.26	0/4109	0.48	0/5550
5	N5	0.26	0/4109	0.48	0/5550
5	N9	0.26	0/4109	0.48	0/5550
5	NA	0.26	0/4109	0.48	0/5550
5	NB	0.26	0/4109	0.48	0/5550
5	NC	0.26	0/4109	0.48	0/5550
5	NF	0.26	0/4109	0.48	0/5550
5	NH	0.26	0/4109	0.48	0/5550

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	NI	0.26	0/4109	0.48	0/5550
5	NM	0.26	0/4109	0.48	0/5550
5	NN	0.26	0/4109	0.48	0/5550
5	NO	0.26	0/4109	0.48	0/5550
5	O2	0.26	0/4100	0.48	0/5539
5	O5	0.26	0/4100	0.48	0/5539
5	O9	0.26	0/4100	0.48	0/5539
5	OA	0.26	0/4100	0.48	0/5539
5	OB	0.26	0/4100	0.48	0/5539
5	OC	0.26	0/4100	0.48	0/5539
5	OF	0.26	0/4100	0.48	0/5539
5	OH	0.26	0/4100	0.48	0/5539
5	OI	0.26	0/4100	0.48	0/5539
5	OM	0.26	0/4100	0.48	0/5539
5	ON	0.26	0/4100	0.48	0/5539
5	OO	0.26	0/4100	0.48	0/5539
6	G2	0.24	0/89	0.38	0/123
6	G5	0.24	0/89	0.38	0/123
6	G9	0.24	0/89	0.38	0/123
6	GA	0.24	0/89	0.38	0/123
6	GB	0.24	0/89	0.38	0/123
6	GC	0.24	0/89	0.38	0/123
6	GF	0.24	0/89	0.38	0/123
6	GH	0.24	0/89	0.38	0/123
6	GI	0.24	0/89	0.38	0/123
6	GM	0.24	0/89	0.38	0/123
6	GN	0.24	0/89	0.38	0/123
6	GO	0.23	0/89	0.38	0/123
6	H2	0.24	0/89	0.38	0/123
6	H5	0.25	0/89	0.38	0/123
6	H9	0.24	0/89	0.38	0/123
6	HA	0.25	0/89	0.38	0/123
6	HB	0.24	0/89	0.38	0/123
6	HC	0.24	0/89	0.38	0/123
6	HF	0.25	0/89	0.38	0/123
6	HH	0.24	0/89	0.38	0/123
6	HI	0.24	0/89	0.38	0/123
6	HM	0.24	0/89	0.38	0/123
6	HN	0.25	0/89	0.38	0/123
6	HO	0.24	0/89	0.38	0/123
6	I2	0.24	0/119	0.42	0/165
6	I5	0.24	0/119	0.42	0/165
6	I9	0.24	0/119	0.42	0/165

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
6	IA	0.24	0/119	0.42	0/165
6	IB	0.24	0/119	0.42	0/165
6	IC	0.24	0/119	0.42	0/165
6	IF	0.24	0/119	0.42	0/165
6	IH	0.24	0/119	0.42	0/165
6	II	0.24	0/119	0.42	0/165
6	IM	0.24	0/119	0.42	0/165
6	IN	0.24	0/119	0.42	0/165
6	IO	0.24	0/119	0.42	0/165
6	J2	0.26	0/119	0.41	0/165
6	J5	0.26	0/119	0.41	0/165
6	J9	0.26	0/119	0.41	0/165
6	JA	0.26	0/119	0.41	0/165
6	JB	0.25	0/119	0.41	0/165
6	JC	0.26	0/119	0.41	0/165
6	JF	0.26	0/119	0.41	0/165
6	JH	0.26	0/119	0.41	0/165
6	JI	0.26	0/119	0.41	0/165
6	JM	0.26	0/119	0.41	0/165
6	JN	0.26	0/119	0.41	0/165
6	JO	0.25	0/119	0.41	0/165
6	K2	0.21	0/111	0.44	0/154
6	K5	0.21	0/111	0.45	0/154
6	K9	0.21	0/111	0.45	0/154
6	KA	0.21	0/111	0.45	0/154
6	KB	0.21	0/111	0.45	0/154
6	KC	0.21	0/111	0.45	0/154
6	KF	0.21	0/111	0.45	0/154
6	KH	0.21	0/111	0.45	0/154
6	KI	0.21	0/111	0.45	0/154
6	KM	0.21	0/111	0.45	0/154
6	KN	0.21	0/111	0.45	0/154
6	KO	0.21	0/111	0.45	0/154
6	L2	0.25	0/119	0.40	0/165
6	L5	0.25	0/119	0.40	0/165
6	L9	0.25	0/119	0.40	0/165
6	LA	0.25	0/119	0.40	0/165
6	LB	0.25	0/119	0.40	0/165
6	LC	0.25	0/119	0.40	0/165
6	LF	0.25	0/119	0.40	0/165
6	LH	0.25	0/119	0.40	0/165
6	LI	0.25	0/119	0.40	0/165
6	LM	0.25	0/119	0.40	0/165

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
6	LN	0.25	0/119	0.40	0/165
6	LO	0.25	0/119	0.40	0/165
7	HS	0.31	0/274	0.58	0/382
7	ID	0.31	0/274	0.58	0/382
7	IJ	0.31	0/274	0.58	0/382
7	IK	0.31	0/274	0.58	0/382
7	IP	0.31	0/274	0.58	0/382
7	NS	0.31	0/274	0.58	0/382
7	OD	0.30	0/274	0.58	0/382
7	OJ	0.31	0/274	0.58	0/382
7	OK	0.31	0/274	0.58	0/382
7	OP	0.31	0/274	0.58	0/382
7	SD	0.31	0/274	0.58	0/382
7	SJ	0.31	0/274	0.58	0/382
7	SK	0.31	0/274	0.58	0/382
7	SP	0.31	0/274	0.58	0/382
7	SS	0.31	0/274	0.58	0/382
8	PD	0.27	0/84	0.47	0/116
8	PJ	0.27	0/84	0.47	0/116
8	PK	0.27	0/84	0.47	0/116
8	PP	0.27	0/84	0.47	0/116
8	PS	0.27	0/84	0.47	0/116
8	QD	0.26	0/78	0.49	0/107
8	QJ	0.26	0/78	0.49	0/107
8	QK	0.26	0/78	0.49	0/107
8	QP	0.25	0/78	0.49	0/107
8	QS	0.25	0/78	0.49	0/107
8	RD	0.27	0/53	0.57	0/69
8	RJ	0.27	0/53	0.57	0/69
8	RK	0.27	0/53	0.57	0/69
8	RP	0.27	0/53	0.57	0/69
8	RS	0.27	0/53	0.57	0/69
All	All	0.43	10/1095338 (0.0%)	0.65	1182/1478016 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A1	0	2
1	A3	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	A4	0	2
1	A6	0	2
1	A7	0	2
1	A8	0	2
1	AD	0	1
1	AE	0	1
1	AG	0	2
1	AJ	0	1
1	AK	0	1
1	AL	0	2
1	AP	0	1
1	AQ	0	2
1	AR	0	2
1	AS	0	2
1	B1	0	1
1	B3	0	1
1	B4	0	1
1	B6	0	1
1	B7	0	1
1	B8	0	1
1	BD	0	2
1	BE	0	2
1	BG	0	1
1	BJ	0	2
1	BK	0	2
1	BL	0	1
1	BP	0	2
1	BQ	0	1
1	BR	0	1
1	C1	0	1
1	C3	0	1
1	C4	0	1
1	C6	0	1
1	C7	0	1
1	C8	0	1
1	CE	0	1
1	CG	0	1
1	CL	0	1
1	CQ	0	1
1	CR	0	1
1	CS	0	2
1	DD	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	DJ	0	2
1	DK	0	2
1	DP	0	2
1	I1	0	1
1	I3	0	1
1	I4	0	1
1	I6	0	1
1	I7	0	1
1	I8	0	1
1	IG	0	1
1	IL	0	1
1	IQ	0	1
1	IR	0	1
1	IS	0	1
1	J1	0	2
1	J3	0	2
1	J4	0	2
1	J6	0	2
1	J7	0	2
1	J8	0	2
1	JG	0	2
1	JL	0	2
1	JQ	0	2
1	JR	0	2
1	JS	0	1
1	K1	0	1
1	K3	0	1
1	K4	0	1
1	K6	0	1
1	K7	0	1
1	K8	0	1
1	KD	0	1
1	KE	0	1
1	KG	0	1
1	KJ	0	2
1	KK	0	1
1	KL	0	1
1	KP	0	1
1	KQ	0	1
1	KR	0	1
1	KS	0	1
1	LD	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	LE	0	2
1	LJ	0	1
1	LK	0	1
1	LP	0	1
1	ME	0	1
1	Q1	0	1
1	Q3	0	1
1	Q4	0	1
1	Q6	0	1
1	Q7	0	1
1	Q8	0	1
1	QG	0	1
1	QL	0	1
1	QQ	0	1
1	QR	0	1
1	R1	0	2
1	R3	0	2
1	R4	0	2
1	R6	0	2
1	R7	0	2
1	R8	0	2
1	RG	0	2
1	RL	0	2
1	RQ	0	2
1	RR	0	2
1	S1	0	1
1	S3	0	1
1	S4	0	1
1	S6	0	1
1	S7	0	1
1	S8	0	1
1	SE	0	1
1	SG	0	1
1	SL	0	1
1	SQ	0	1
1	SR	0	1
1	TE	0	2
1	UE	0	1
1	X1	0	1
1	X4	0	1
1	Y1	0	2
1	Y4	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Y6	0	1
1	Y7	0	1
1	Y8	0	1
1	YG	0	1
1	YL	0	1
1	YR	0	1
1	Z1	0	1
1	Z4	0	1
1	Z6	0	2
1	Z7	0	2
1	Z8	0	2
1	ZG	0	2
1	ZL	0	2
1	ZR	0	2
1	a6	0	1
1	a7	0	1
1	a8	0	1
1	aE	0	1
1	aG	0	1
1	aL	0	1
1	aR	0	1
1	bE	0	2
1	bQ	0	1
1	cE	0	1
1	cQ	0	2
1	dQ	0	1
1	f1	0	1
1	f4	0	1
1	g1	0	2
1	g4	0	2
1	g6	0	1
1	g7	0	1
1	g8	0	1
1	gG	0	1
1	gR	0	1
1	h1	0	1
1	h4	0	1
1	h6	0	2
1	h7	0	2
1	h8	0	2
1	hG	0	2
1	hR	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	i6	0	1
1	i7	0	1
1	i8	0	1
1	iG	0	1
1	iR	0	1
2	DS	0	3
2	E1	0	1
2	E3	0	1
2	E4	0	1
2	E6	0	1
2	E7	0	1
2	E8	0	1
2	ED	0	3
2	EE	0	1
2	EG	0	1
2	EJ	0	3
2	EK	0	3
2	EL	0	1
2	EP	0	3
2	EQ	0	1
2	ER	0	1
2	ES	0	2
2	F1	0	2
2	F3	0	2
2	F4	0	2
2	F6	0	2
2	F7	0	2
2	F8	0	2
2	FD	0	2
2	FG	0	2
2	FJ	0	2
2	FK	0	2
2	FL	0	2
2	FP	0	2
2	FQ	0	2
2	FR	0	2
2	G1	0	3
2	G3	0	3
2	G4	0	3
2	G6	0	3
2	G7	0	3
2	G8	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	GE	0	3
2	GG	0	3
2	GL	0	3
2	GQ	0	3
2	GR	0	3
2	H1	0	1
2	H3	0	1
2	H4	0	1
2	H6	0	1
2	H7	0	1
2	H8	0	1
2	HE	0	2
2	HG	0	1
2	HL	0	1
2	HQ	0	1
2	HR	0	1
2	IE	0	3
2	JE	0	1
2	LS	0	1
2	M1	0	1
2	M3	0	1
2	M4	0	1
2	M6	0	1
2	M7	0	1
2	M8	0	1
2	MD	0	1
2	MG	0	1
2	MJ	0	1
2	MK	0	1
2	ML	0	1
2	MP	0	1
2	MQ	0	1
2	MR	0	1
2	MS	0	1
2	N1	0	2
2	N3	0	2
2	N4	0	2
2	N6	0	2
2	N7	0	2
2	N8	0	2
2	ND	0	1
2	NG	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	NJ	0	1
2	NK	0	1
2	NL	0	2
2	NP	0	1
2	NQ	0	2
2	NR	0	2
2	O1	0	3
2	O3	0	3
2	O4	0	3
2	O6	0	3
2	O7	0	3
2	O8	0	3
2	OE	0	1
2	OG	0	3
2	OL	0	3
2	OQ	0	3
2	OR	0	3
2	P1	0	1
2	P3	0	1
2	P4	0	1
2	P6	0	1
2	P7	0	1
2	P8	0	1
2	PE	0	2
2	PG	0	1
2	PL	0	1
2	PQ	0	1
2	PR	0	1
2	QE	0	3
2	RE	0	1
2	U1	0	2
2	U3	0	1
2	U4	0	2
2	U6	0	1
2	U7	0	1
2	U8	0	1
2	UG	0	1
2	UL	0	1
2	UQ	0	1
2	UR	0	1
2	V1	0	3
2	V3	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	V4	0	3
2	V6	0	2
2	V7	0	2
2	V8	0	2
2	VG	0	2
2	VL	0	2
2	VQ	0	2
2	VR	0	2
2	W1	0	1
2	W3	0	3
2	W4	0	1
2	W6	0	3
2	W7	0	3
2	W8	0	3
2	WE	0	1
2	WG	0	3
2	WL	0	3
2	WQ	0	3
2	WR	0	3
2	X3	0	1
2	X6	0	1
2	X7	0	1
2	X8	0	1
2	XE	0	2
2	XG	0	1
2	XL	0	1
2	XQ	0	1
2	XR	0	1
2	YE	0	3
2	Z3	0	1
2	ZE	0	1
2	ZQ	0	1
2	a3	0	3
2	aQ	0	3
2	b1	0	1
2	b4	0	1
2	c1	0	2
2	c3	0	1
2	c4	0	2
2	c6	0	1
2	c7	0	1
2	c8	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	cG	0	1
2	cL	0	1
2	cR	0	1
2	d1	0	3
2	d3	0	3
2	d4	0	3
2	d6	0	2
2	d7	0	2
2	d8	0	2
2	dG	0	2
2	dL	0	2
2	dR	0	2
2	e1	0	1
2	e4	0	1
2	e6	0	3
2	e7	0	3
2	e8	0	3
2	eE	0	1
2	eG	0	3
2	eL	0	3
2	eR	0	3
2	f6	0	1
2	f7	0	1
2	f8	0	1
2	fE	0	2
2	fG	0	1
2	fL	0	1
2	fQ	0	1
2	fR	0	1
2	gE	0	3
2	gQ	0	2
2	hE	0	1
2	hL	0	1
2	hQ	0	3
2	iL	0	3
2	iQ	0	1
2	j1	0	1
2	j4	0	2
2	k1	0	2
2	k4	0	3
2	k6	0	1
2	k7	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	k8	0	1
2	kG	0	1
2	kR	0	2
2	l1	0	3
2	l4	0	1
2	l6	0	2
2	l7	0	2
2	l8	0	2
2	lG	0	2
2	lR	0	3
2	m1	0	1
2	m6	0	3
2	m7	0	3
2	m8	0	3
2	mG	0	3
2	mR	0	1
2	n6	0	1
2	n7	0	1
2	n8	0	1
2	nG	0	1
3	A2	0	5
3	A5	0	5
3	A9	0	5
3	AA	0	5
3	AB	0	5
3	AC	0	5
3	AF	0	5
3	AH	0	5
3	AI	0	5
3	AM	0	5
3	AN	0	5
3	AO	0	5
4	B2	0	2
4	B5	0	2
4	B9	0	2
4	BA	0	2
4	BB	0	2
4	BC	0	2
4	BF	0	2
4	BH	0	2
4	BI	0	2
4	BM	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	BN	0	2
4	BO	0	2
5	F2	0	1
5	F5	0	1
5	F9	0	1
5	FA	0	1
5	FB	0	1
5	FC	0	1
5	FF	0	1
5	FH	0	1
5	FI	0	1
5	FM	0	1
5	FN	0	1
5	FO	0	1
All	All	0	732

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AD	49	PHE	CA-C	-7.83	1.32	1.52
1	AJ	49	PHE	CA-C	-7.82	1.32	1.52
1	IS	49	PHE	CA-C	-7.81	1.32	1.52
1	AP	49	PHE	CA-C	-7.81	1.32	1.52
1	AK	49	PHE	CA-C	-7.79	1.32	1.52
1	AD	47	GLU	CA-C	-5.47	1.38	1.52
1	AP	47	GLU	CA-C	-5.45	1.38	1.52
1	IS	47	GLU	CA-C	-5.44	1.38	1.52
1	AJ	47	GLU	CA-C	-5.44	1.38	1.52
1	AK	47	GLU	CA-C	-5.43	1.38	1.52

All (1182) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A1	62	LEU	N-CA-C	9.00	135.31	111.00
1	J3	62	LEU	N-CA-C	9.00	135.31	111.00
1	A4	62	LEU	N-CA-C	9.00	135.31	111.00
1	R4	62	LEU	N-CA-C	9.00	135.31	111.00
1	A6	62	LEU	N-CA-C	9.00	135.31	111.00
1	Z7	62	LEU	N-CA-C	9.00	135.31	111.00
1	R8	62	LEU	N-CA-C	9.00	135.31	111.00
1	h8	62	LEU	N-CA-C	9.00	135.31	111.00
1	RG	62	LEU	N-CA-C	9.00	135.31	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	JR	62	LEU	N-CA-C	9.00	135.31	111.00
1	A3	62	LEU	N-CA-C	9.00	135.29	111.00
1	J4	62	LEU	N-CA-C	9.00	135.29	111.00
1	g4	62	LEU	N-CA-C	9.00	135.29	111.00
1	J6	62	LEU	N-CA-C	9.00	135.29	111.00
1	R6	62	LEU	N-CA-C	9.00	135.29	111.00
1	h6	62	LEU	N-CA-C	9.00	135.29	111.00
1	J7	62	LEU	N-CA-C	9.00	135.29	111.00
1	R7	62	LEU	N-CA-C	9.00	135.29	111.00
1	J8	62	LEU	N-CA-C	9.00	135.29	111.00
1	Z8	62	LEU	N-CA-C	9.00	135.29	111.00
1	LE	62	LEU	N-CA-C	9.00	135.29	111.00
1	bE	62	LEU	N-CA-C	9.00	135.29	111.00
1	JG	62	LEU	N-CA-C	9.00	135.29	111.00
1	AL	62	LEU	N-CA-C	9.00	135.29	111.00
1	ZL	62	LEU	N-CA-C	9.00	135.29	111.00
1	AQ	62	LEU	N-CA-C	9.00	135.29	111.00
1	JQ	62	LEU	N-CA-C	9.00	135.29	111.00
1	RR	62	LEU	N-CA-C	9.00	135.29	111.00
1	ZR	62	LEU	N-CA-C	9.00	135.29	111.00
1	hR	62	LEU	N-CA-C	9.00	135.29	111.00
1	J1	62	LEU	N-CA-C	8.99	135.27	111.00
1	R3	62	LEU	N-CA-C	8.99	135.27	111.00
1	Y4	62	LEU	N-CA-C	8.99	135.27	111.00
1	Z6	62	LEU	N-CA-C	8.99	135.27	111.00
1	h7	62	LEU	N-CA-C	8.99	135.27	111.00
1	A8	62	LEU	N-CA-C	8.99	135.27	111.00
1	BE	62	LEU	N-CA-C	8.99	135.27	111.00
1	TE	62	LEU	N-CA-C	8.99	135.27	111.00
1	ZG	62	LEU	N-CA-C	8.99	135.27	111.00
1	AR	62	LEU	N-CA-C	8.99	135.27	111.00
1	R1	62	LEU	N-CA-C	8.98	135.25	111.00
1	Y1	62	LEU	N-CA-C	8.98	135.25	111.00
1	g1	62	LEU	N-CA-C	8.98	135.25	111.00
1	A7	62	LEU	N-CA-C	8.98	135.25	111.00
1	AG	62	LEU	N-CA-C	8.98	135.25	111.00
1	hG	62	LEU	N-CA-C	8.98	135.25	111.00
1	JL	62	LEU	N-CA-C	8.98	135.25	111.00
1	RL	62	LEU	N-CA-C	8.98	135.25	111.00
1	RQ	62	LEU	N-CA-C	8.98	135.25	111.00
1	cQ	62	LEU	N-CA-C	8.98	135.25	111.00
1	CP	183	LEU	CA-CB-CG	8.52	134.90	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CJ	183	LEU	CA-CB-CG	8.52	134.90	115.30
1	CK	183	LEU	CA-CB-CG	8.51	134.87	115.30
1	BS	183	LEU	CA-CB-CG	8.51	134.87	115.30
1	CD	183	LEU	CA-CB-CG	8.50	134.85	115.30
4	BC	224	LEU	CA-CB-CG	8.26	134.29	115.30
4	BF	224	LEU	CA-CB-CG	8.24	134.25	115.30
4	BO	224	LEU	CA-CB-CG	8.24	134.25	115.30
4	B5	224	LEU	CA-CB-CG	8.24	134.24	115.30
4	BI	224	LEU	CA-CB-CG	8.23	134.24	115.30
4	BM	224	LEU	CA-CB-CG	8.23	134.23	115.30
4	B9	224	LEU	CA-CB-CG	8.23	134.23	115.30
4	BA	224	LEU	CA-CB-CG	8.23	134.22	115.30
4	BH	224	LEU	CA-CB-CG	8.23	134.22	115.30
4	BN	224	LEU	CA-CB-CG	8.23	134.22	115.30
4	B2	224	LEU	CA-CB-CG	8.22	134.22	115.30
4	BB	224	LEU	CA-CB-CG	8.21	134.19	115.30
1	DJ	206	LEU	CA-CB-CG	7.86	133.38	115.30
1	DP	206	LEU	CA-CB-CG	7.86	133.37	115.30
1	DD	206	LEU	CA-CB-CG	7.85	133.36	115.30
1	CS	206	LEU	CA-CB-CG	7.85	133.36	115.30
1	DK	206	LEU	CA-CB-CG	7.85	133.35	115.30
1	KS	206	LEU	CA-CB-CG	7.79	133.22	115.30
1	LK	206	LEU	CA-CB-CG	7.79	133.21	115.30
1	LJ	206	LEU	CA-CB-CG	7.77	133.18	115.30
1	LD	206	LEU	CA-CB-CG	7.77	133.18	115.30
1	LP	206	LEU	CA-CB-CG	7.76	133.15	115.30
2	FP	45	ILE	CG1-CB-CG2	-7.70	94.46	111.40
2	ES	45	ILE	CG1-CB-CG2	-7.70	94.46	111.40
2	FJ	45	ILE	CG1-CB-CG2	-7.69	94.48	111.40
2	FD	45	ILE	CG1-CB-CG2	-7.69	94.48	111.40
2	FK	45	ILE	CG1-CB-CG2	-7.67	94.52	111.40
1	IS	45	MET	C-N-CA	7.07	139.36	121.70
1	AD	45	MET	C-N-CA	7.06	139.36	121.70
1	AJ	45	MET	C-N-CA	7.06	139.36	121.70
1	AP	45	MET	C-N-CA	7.06	139.35	121.70
1	AK	45	MET	C-N-CA	7.05	139.32	121.70
3	AC	8	LEU	CA-CB-CG	7.01	131.43	115.30
3	AF	8	LEU	CA-CB-CG	7.01	131.42	115.30
3	AB	8	LEU	CA-CB-CG	7.00	131.41	115.30
3	AN	8	LEU	CA-CB-CG	7.00	131.40	115.30
3	AO	8	LEU	CA-CB-CG	7.00	131.40	115.30
3	A2	8	LEU	CA-CB-CG	7.00	131.40	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A9	8	LEU	CA-CB-CG	7.00	131.39	115.30
3	AH	8	LEU	CA-CB-CG	7.00	131.39	115.30
3	AM	8	LEU	CA-CB-CG	7.00	131.39	115.30
3	AI	8	LEU	CA-CB-CG	6.99	131.38	115.30
3	AA	8	LEU	CA-CB-CG	6.99	131.38	115.30
3	A5	8	LEU	CA-CB-CG	6.98	131.36	115.30
3	AI	217	ASP	CB-CG-OD1	6.98	124.58	118.30
3	A2	217	ASP	CB-CG-OD1	6.96	124.57	118.30
3	A9	217	ASP	CB-CG-OD1	6.96	124.56	118.30
3	AO	217	ASP	CB-CG-OD1	6.94	124.55	118.30
3	A5	217	ASP	CB-CG-OD1	6.93	124.54	118.30
3	AM	217	ASP	CB-CG-OD1	6.93	124.54	118.30
3	AB	217	ASP	CB-CG-OD1	6.92	124.53	118.30
3	AH	217	ASP	CB-CG-OD1	6.91	124.52	118.30
3	AF	217	ASP	CB-CG-OD1	6.91	124.52	118.30
5	FB	65	ASP	CB-CG-OD1	6.90	124.51	118.30
5	FH	65	ASP	CB-CG-OD1	6.89	124.50	118.30
3	AA	217	ASP	CB-CG-OD1	6.89	124.50	118.30
5	FN	65	ASP	CB-CG-OD1	6.89	124.50	118.30
3	AN	217	ASP	CB-CG-OD1	6.89	124.50	118.30
3	AC	217	ASP	CB-CG-OD1	6.88	124.49	118.30
5	F5	65	ASP	CB-CG-OD1	6.88	124.49	118.30
5	FA	65	ASP	CB-CG-OD1	6.87	124.48	118.30
5	F9	65	ASP	CB-CG-OD1	6.86	124.47	118.30
5	FF	65	ASP	CB-CG-OD1	6.86	124.47	118.30
5	FC	65	ASP	CB-CG-OD1	6.85	124.47	118.30
1	AD	183	LEU	CA-CB-CG	6.83	131.02	115.30
1	AJ	183	LEU	CA-CB-CG	6.83	131.00	115.30
5	FM	65	ASP	CB-CG-OD1	6.82	124.44	118.30
1	AK	183	LEU	CA-CB-CG	6.82	130.99	115.30
1	AP	183	LEU	CA-CB-CG	6.82	130.98	115.30
1	IS	183	LEU	CA-CB-CG	6.82	130.98	115.30
5	FO	65	ASP	CB-CG-OD1	6.82	124.43	118.30
5	F2	65	ASP	CB-CG-OD1	6.80	124.42	118.30
5	FI	65	ASP	CB-CG-OD1	6.79	124.42	118.30
1	I6	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	Q6	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	I7	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	Q7	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	CL	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	YL	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	CQ	197	LEU	CA-CB-CG	6.66	130.61	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	QR	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	YR	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	gR	197	LEU	CA-CB-CG	6.66	130.61	115.30
1	I1	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	Q3	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	X4	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	Y6	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	g7	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	C8	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	AE	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	SE	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	YG	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	CR	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	C3	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	I4	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	f4	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	g6	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	I8	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	Y8	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	KE	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	aE	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	IG	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	IQ	197	LEU	CA-CB-CG	6.65	130.60	115.30
1	C1	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	I3	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	C4	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	Q4	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	C6	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	Y7	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	Q8	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	g8	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	QG	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	IR	197	LEU	CA-CB-CG	6.64	130.58	115.30
1	Q1	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	X1	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	f1	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	C7	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	CG	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	gG	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	IL	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	QL	197	LEU	CA-CB-CG	6.64	130.57	115.30
1	QQ	197	LEU	CA-CB-CG	6.64	130.57	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bQ	197	LEU	CA-CB-CG	6.64	130.57	115.30
2	NJ	45	ILE	CG1-CB-CG2	-6.63	96.82	111.40
2	NP	45	ILE	CG1-CB-CG2	-6.62	96.84	111.40
2	MS	45	ILE	CG1-CB-CG2	-6.61	96.85	111.40
2	ND	45	ILE	CG1-CB-CG2	-6.61	96.86	111.40
2	NK	45	ILE	CG1-CB-CG2	-6.60	96.87	111.40
1	I6	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	Q6	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	I7	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	Q7	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	CL	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	YL	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	CQ	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	QR	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	YR	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	gR	206	LEU	CA-CB-CG	6.60	130.47	115.30
1	I1	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	Q1	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	X1	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	f1	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	Q3	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	X4	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	Y6	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	C7	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	g7	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	C8	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	AE	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	SE	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	CG	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	YG	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	gG	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	IL	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	QL	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	QQ	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	bQ	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	CR	206	LEU	CA-CB-CG	6.59	130.46	115.30
1	C1	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	I3	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	C4	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	Q4	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	C6	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	Y7	206	LEU	CA-CB-CG	6.58	130.44	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q8	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	g8	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	QG	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	IR	206	LEU	CA-CB-CG	6.58	130.44	115.30
1	C3	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	I4	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	f4	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	g6	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	I8	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	Y8	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	KE	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	aE	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	IG	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	IQ	206	LEU	CA-CB-CG	6.58	130.43	115.30
1	KD	261	ILE	CG1-CB-CG2	-6.39	97.33	111.40
1	JS	261	ILE	CG1-CB-CG2	-6.39	97.34	111.40
1	KP	261	ILE	CG1-CB-CG2	-6.38	97.36	111.40
1	KK	261	ILE	CG1-CB-CG2	-6.38	97.36	111.40
1	KJ	261	ILE	CG1-CB-CG2	-6.38	97.37	111.40
1	Q1	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	X1	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	f1	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	C7	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	CG	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	gG	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	IL	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	QL	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	QQ	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	bQ	166	LEU	CA-CB-CG	6.25	129.68	115.30
1	I1	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	Q3	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	X4	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	Y6	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	g7	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	C8	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	AE	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	SE	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	YG	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	CR	166	LEU	CA-CB-CG	6.25	129.67	115.30
1	C3	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	I4	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	f4	166	LEU	CA-CB-CG	6.24	129.66	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	g6	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	I8	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	Y8	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	KE	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	aE	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	IG	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	AJ	46	PHE	N-CA-C	6.24	127.86	111.00
1	IQ	166	LEU	CA-CB-CG	6.24	129.66	115.30
1	C1	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	I3	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	C4	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	Q4	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	C6	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	Y7	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	Q8	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	g8	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	QG	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	AP	46	PHE	N-CA-C	6.24	127.84	111.00
1	IR	166	LEU	CA-CB-CG	6.24	129.65	115.30
1	IS	46	PHE	N-CA-C	6.24	127.84	111.00
1	AK	46	PHE	N-CA-C	6.23	127.83	111.00
1	I6	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	Q6	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	I7	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	Q7	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	AD	46	PHE	N-CA-C	6.23	127.82	111.00
1	CL	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	YL	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	CQ	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	QR	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	YR	166	LEU	CA-CB-CG	6.23	129.63	115.30
1	gR	166	LEU	CA-CB-CG	6.23	129.63	115.30
3	AI	222	LEU	CA-CB-CG	6.22	129.61	115.30
3	A9	222	LEU	CA-CB-CG	6.21	129.57	115.30
3	AF	222	LEU	CA-CB-CG	6.21	129.58	115.30
3	AM	222	LEU	CA-CB-CG	6.20	129.57	115.30
3	A2	222	LEU	CA-CB-CG	6.20	129.55	115.30
3	AH	222	LEU	CA-CB-CG	6.20	129.55	115.30
3	AA	222	LEU	CA-CB-CG	6.19	129.55	115.30
3	AC	222	LEU	CA-CB-CG	6.19	129.53	115.30
3	AB	222	LEU	CA-CB-CG	6.18	129.52	115.30
3	A5	222	LEU	CA-CB-CG	6.18	129.52	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	AO	222	LEU	CA-CB-CG	6.18	129.51	115.30
3	AN	222	LEU	CA-CB-CG	6.18	129.51	115.30
1	AP	44	THR	N-CA-C	6.17	127.66	111.00
1	AJ	44	THR	N-CA-C	6.17	127.65	111.00
1	IS	44	THR	N-CA-C	6.17	127.64	111.00
1	AK	44	THR	N-CA-C	6.16	127.62	111.00
1	AD	44	THR	N-CA-C	6.15	127.59	111.00
1	AD	49	PHE	CA-C-N	-5.96	104.09	117.20
1	AK	49	PHE	CA-C-N	-5.96	104.09	117.20
1	AP	49	PHE	CA-C-N	-5.96	104.09	117.20
1	IS	49	PHE	CA-C-N	-5.95	104.10	117.20
1	AJ	49	PHE	CA-C-N	-5.95	104.11	117.20
1	B1	259	PHE	N-CA-C	-5.88	95.12	111.00
1	K3	259	PHE	N-CA-C	-5.88	95.12	111.00
1	B4	259	PHE	N-CA-C	-5.88	95.12	111.00
1	S4	259	PHE	N-CA-C	-5.88	95.12	111.00
1	B6	259	PHE	N-CA-C	-5.88	95.12	111.00
1	a7	259	PHE	N-CA-C	-5.88	95.12	111.00
1	S8	259	PHE	N-CA-C	-5.88	95.12	111.00
1	i8	259	PHE	N-CA-C	-5.88	95.12	111.00
1	SG	259	PHE	N-CA-C	-5.88	95.12	111.00
1	KR	259	PHE	N-CA-C	-5.88	95.12	111.00
1	B3	259	PHE	N-CA-C	-5.88	95.13	111.00
1	K4	259	PHE	N-CA-C	-5.88	95.13	111.00
1	h4	259	PHE	N-CA-C	-5.88	95.13	111.00
1	i6	259	PHE	N-CA-C	-5.88	95.13	111.00
1	K8	259	PHE	N-CA-C	-5.88	95.13	111.00
1	a8	259	PHE	N-CA-C	-5.88	95.13	111.00
1	ME	259	PHE	N-CA-C	-5.88	95.13	111.00
1	cE	259	PHE	N-CA-C	-5.88	95.13	111.00
1	KG	259	PHE	N-CA-C	-5.88	95.13	111.00
1	KQ	259	PHE	N-CA-C	-5.88	95.13	111.00
1	K1	259	PHE	N-CA-C	-5.87	95.14	111.00
1	S1	259	PHE	N-CA-C	-5.87	95.14	111.00
1	Z1	259	PHE	N-CA-C	-5.87	95.14	111.00
1	h1	259	PHE	N-CA-C	-5.87	95.14	111.00
1	S3	259	PHE	N-CA-C	-5.87	95.14	111.00
1	Z4	259	PHE	N-CA-C	-5.87	95.14	111.00
1	a6	259	PHE	N-CA-C	-5.87	95.14	111.00
1	B7	259	PHE	N-CA-C	-5.87	95.14	111.00
1	i7	259	PHE	N-CA-C	-5.87	95.14	111.00
1	B8	259	PHE	N-CA-C	-5.87	95.14	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CE	259	PHE	N-CA-C	-5.87	95.14	111.00
1	UE	259	PHE	N-CA-C	-5.87	95.14	111.00
1	BG	259	PHE	N-CA-C	-5.87	95.14	111.00
1	aG	259	PHE	N-CA-C	-5.87	95.14	111.00
1	iG	259	PHE	N-CA-C	-5.87	95.14	111.00
1	KL	259	PHE	N-CA-C	-5.87	95.14	111.00
1	SL	259	PHE	N-CA-C	-5.87	95.14	111.00
1	SQ	259	PHE	N-CA-C	-5.87	95.14	111.00
1	dQ	259	PHE	N-CA-C	-5.87	95.14	111.00
1	BR	259	PHE	N-CA-C	-5.87	95.14	111.00
1	K6	259	PHE	N-CA-C	-5.87	95.14	111.00
1	S6	259	PHE	N-CA-C	-5.87	95.14	111.00
1	K7	259	PHE	N-CA-C	-5.87	95.14	111.00
1	S7	259	PHE	N-CA-C	-5.87	95.14	111.00
1	BL	259	PHE	N-CA-C	-5.87	95.14	111.00
1	aL	259	PHE	N-CA-C	-5.87	95.14	111.00
1	BQ	259	PHE	N-CA-C	-5.87	95.14	111.00
1	SR	259	PHE	N-CA-C	-5.87	95.14	111.00
1	aR	259	PHE	N-CA-C	-5.87	95.14	111.00
1	iR	259	PHE	N-CA-C	-5.87	95.14	111.00
5	FF	116	LEU	CA-CB-CG	5.84	128.74	115.30
5	FC	116	LEU	CA-CB-CG	5.84	128.73	115.30
5	FM	116	LEU	CA-CB-CG	5.84	128.73	115.30
5	F5	116	LEU	CA-CB-CG	5.84	128.72	115.30
5	FI	116	LEU	CA-CB-CG	5.84	128.73	115.30
5	FN	116	LEU	CA-CB-CG	5.83	128.71	115.30
5	F2	116	LEU	CA-CB-CG	5.83	128.71	115.30
1	BS	344	ILE	CG1-CB-CG2	-5.83	98.58	111.40
5	F9	116	LEU	CA-CB-CG	5.82	128.69	115.30
5	FH	116	LEU	CA-CB-CG	5.82	128.69	115.30
1	CJ	344	ILE	CG1-CB-CG2	-5.82	98.60	111.40
5	FA	116	LEU	CA-CB-CG	5.82	128.68	115.30
5	FB	116	LEU	CA-CB-CG	5.82	128.67	115.30
1	CK	344	ILE	CG1-CB-CG2	-5.81	98.61	111.40
1	CP	344	ILE	CG1-CB-CG2	-5.81	98.62	111.40
1	CD	344	ILE	CG1-CB-CG2	-5.81	98.62	111.40
5	FO	116	LEU	CA-CB-CG	5.81	128.66	115.30
1	BK	235	LEU	CA-CB-CG	5.80	128.65	115.30
1	BJ	235	LEU	CA-CB-CG	5.79	128.62	115.30
1	BD	235	LEU	CA-CB-CG	5.79	128.61	115.30
1	AS	235	LEU	CA-CB-CG	5.78	128.59	115.30
1	BP	235	LEU	CA-CB-CG	5.78	128.59	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AK	251	LEU	CA-CB-CG	5.75	128.53	115.30
1	IS	251	LEU	CA-CB-CG	5.73	128.47	115.30
1	AP	251	LEU	CA-CB-CG	5.72	128.46	115.30
1	AD	251	LEU	CA-CB-CG	5.71	128.44	115.30
1	AJ	251	LEU	CA-CB-CG	5.71	128.44	115.30
1	KD	345	LEU	CA-CB-CG	5.60	128.18	115.30
1	KJ	345	LEU	CA-CB-CG	5.58	128.14	115.30
1	KK	345	LEU	CA-CB-CG	5.58	128.14	115.30
1	KP	345	LEU	CA-CB-CG	5.58	128.14	115.30
1	JS	345	LEU	CA-CB-CG	5.58	128.13	115.30
1	K1	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	S3	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	Z4	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	a6	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	i7	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	B8	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	CE	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	UE	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	aG	392	LEU	CA-CB-CG	5.55	128.06	115.30
1	BR	392	LEU	CA-CB-CG	5.55	128.06	115.30
3	A5	45	TYR	CA-CB-CG	5.54	123.93	113.40
1	K6	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	S6	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	K7	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	S7	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	BL	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	aL	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	BQ	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	SR	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	aR	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	iR	392	LEU	CA-CB-CG	5.54	128.03	115.30
1	B1	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	K3	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	B4	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	S4	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	B6	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	a7	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	S8	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	i8	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	SG	392	LEU	CA-CB-CG	5.53	128.01	115.30
1	KR	392	LEU	CA-CB-CG	5.53	128.01	115.30
3	AB	45	TYR	CA-CB-CG	5.52	123.90	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S1	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	Z1	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	h1	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	B7	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	BG	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	iG	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	KL	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	SL	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	SQ	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	dQ	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	B3	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	K4	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	h4	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	i6	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	K8	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	a8	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	ME	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	cE	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	KG	392	LEU	CA-CB-CG	5.52	128.00	115.30
1	KQ	392	LEU	CA-CB-CG	5.52	128.00	115.30
3	AN	45	TYR	CA-CB-CG	5.52	123.89	113.40
3	A9	45	TYR	CA-CB-CG	5.52	123.88	113.40
3	A2	45	TYR	CA-CB-CG	5.51	123.88	113.40
3	AA	45	TYR	CA-CB-CG	5.51	123.88	113.40
3	AC	45	TYR	CA-CB-CG	5.51	123.87	113.40
3	AM	45	TYR	CA-CB-CG	5.50	123.86	113.40
3	AH	45	TYR	CA-CB-CG	5.49	123.83	113.40
3	AI	45	TYR	CA-CB-CG	5.49	123.82	113.40
1	I6	317	PHE	N-CA-C	5.48	125.81	111.00
1	Q6	317	PHE	N-CA-C	5.48	125.81	111.00
1	I7	317	PHE	N-CA-C	5.48	125.81	111.00
1	Q7	317	PHE	N-CA-C	5.48	125.81	111.00
3	AF	45	TYR	CA-CB-CG	5.48	123.82	113.40
1	CL	317	PHE	N-CA-C	5.48	125.81	111.00
1	YL	317	PHE	N-CA-C	5.48	125.81	111.00
1	CQ	317	PHE	N-CA-C	5.48	125.81	111.00
1	QR	317	PHE	N-CA-C	5.48	125.81	111.00
1	YR	317	PHE	N-CA-C	5.48	125.81	111.00
1	gR	317	PHE	N-CA-C	5.48	125.81	111.00
3	AO	45	TYR	CA-CB-CG	5.48	123.81	113.40
1	I1	317	PHE	N-CA-C	5.48	125.79	111.00
1	C3	317	PHE	N-CA-C	5.48	125.79	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q3	317	PHE	N-CA-C	5.48	125.79	111.00
1	I4	317	PHE	N-CA-C	5.48	125.79	111.00
1	X4	317	PHE	N-CA-C	5.48	125.79	111.00
1	f4	317	PHE	N-CA-C	5.48	125.79	111.00
1	Y6	317	PHE	N-CA-C	5.48	125.79	111.00
1	g6	317	PHE	N-CA-C	5.48	125.79	111.00
1	g7	317	PHE	N-CA-C	5.48	125.79	111.00
1	C8	317	PHE	N-CA-C	5.48	125.79	111.00
1	I8	317	PHE	N-CA-C	5.48	125.79	111.00
1	Y8	317	PHE	N-CA-C	5.48	125.79	111.00
1	AE	317	PHE	N-CA-C	5.48	125.79	111.00
1	KE	317	PHE	N-CA-C	5.48	125.79	111.00
1	SE	317	PHE	N-CA-C	5.48	125.79	111.00
1	aE	317	PHE	N-CA-C	5.48	125.79	111.00
1	IG	317	PHE	N-CA-C	5.48	125.79	111.00
1	YG	317	PHE	N-CA-C	5.48	125.79	111.00
1	IQ	317	PHE	N-CA-C	5.48	125.79	111.00
1	CR	317	PHE	N-CA-C	5.48	125.79	111.00
1	Q1	317	PHE	N-CA-C	5.47	125.78	111.00
1	X1	317	PHE	N-CA-C	5.47	125.78	111.00
1	f1	317	PHE	N-CA-C	5.47	125.78	111.00
1	C7	317	PHE	N-CA-C	5.47	125.78	111.00
1	CG	317	PHE	N-CA-C	5.47	125.78	111.00
1	gG	317	PHE	N-CA-C	5.47	125.78	111.00
1	IL	317	PHE	N-CA-C	5.47	125.78	111.00
1	QL	317	PHE	N-CA-C	5.47	125.78	111.00
1	QQ	317	PHE	N-CA-C	5.47	125.78	111.00
1	bQ	317	PHE	N-CA-C	5.47	125.78	111.00
1	C1	317	PHE	N-CA-C	5.47	125.78	111.00
1	I3	317	PHE	N-CA-C	5.47	125.78	111.00
1	C4	317	PHE	N-CA-C	5.47	125.78	111.00
1	Q4	317	PHE	N-CA-C	5.47	125.78	111.00
1	C6	317	PHE	N-CA-C	5.47	125.78	111.00
1	Y7	317	PHE	N-CA-C	5.47	125.78	111.00
1	Q8	317	PHE	N-CA-C	5.47	125.78	111.00
1	g8	317	PHE	N-CA-C	5.47	125.78	111.00
1	QG	317	PHE	N-CA-C	5.47	125.78	111.00
1	IR	317	PHE	N-CA-C	5.47	125.78	111.00
3	AN	80	ILE	CG1-CB-CG2	-5.43	99.45	111.40
2	b1	45	ILE	N-CA-C	5.42	125.65	111.00
2	j1	45	ILE	N-CA-C	5.42	125.65	111.00
2	E7	45	ILE	N-CA-C	5.42	125.65	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	EG	45	ILE	N-CA-C	5.42	125.65	111.00
2	kG	45	ILE	N-CA-C	5.42	125.65	111.00
2	ML	45	ILE	N-CA-C	5.42	125.65	111.00
2	UL	45	ILE	N-CA-C	5.42	125.65	111.00
2	UQ	45	ILE	N-CA-C	5.42	125.65	111.00
2	ZQ	45	ILE	N-CA-C	5.42	125.65	111.00
2	fQ	45	ILE	N-CA-C	5.42	125.65	111.00
1	J1	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	R3	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	Y4	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	Z6	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	h7	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	A8	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	BE	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	TE	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	ZG	235	LEU	CA-CB-CG	5.42	127.76	115.30
1	AR	235	LEU	CA-CB-CG	5.42	127.76	115.30
2	E1	45	ILE	N-CA-C	5.41	125.62	111.00
2	M3	45	ILE	N-CA-C	5.41	125.62	111.00
2	E4	45	ILE	N-CA-C	5.41	125.62	111.00
2	E6	45	ILE	N-CA-C	5.41	125.62	111.00
2	c7	45	ILE	N-CA-C	5.41	125.62	111.00
2	U8	45	ILE	N-CA-C	5.41	125.62	111.00
2	k8	45	ILE	N-CA-C	5.41	125.62	111.00
2	EE	45	ILE	N-CA-C	5.41	125.62	111.00
2	UG	45	ILE	N-CA-C	5.41	125.62	111.00
2	MR	45	ILE	N-CA-C	5.41	125.62	111.00
3	AB	80	ILE	CG1-CB-CG2	-5.41	99.49	111.40
1	R1	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	Y1	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	g1	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	A7	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	AG	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	hG	235	LEU	CA-CB-CG	5.41	127.74	115.30
3	AI	80	ILE	CG1-CB-CG2	-5.41	99.50	111.40
1	JL	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	RL	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	RQ	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	cQ	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	J6	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	R6	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	J7	235	LEU	CA-CB-CG	5.41	127.74	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R7	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	AL	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	ZL	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	AQ	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	RR	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	ZR	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	hR	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	A1	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	E3	45	ILE	N-CA-C	5.41	125.60	111.00
1	J3	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	Z3	45	ILE	N-CA-C	5.41	125.60	111.00
1	A4	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	M4	45	ILE	N-CA-C	5.41	125.60	111.00
1	R4	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	A6	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	k6	45	ILE	N-CA-C	5.41	125.60	111.00
1	Z7	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	M8	45	ILE	N-CA-C	5.41	125.60	111.00
1	R8	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	c8	45	ILE	N-CA-C	5.41	125.60	111.00
1	h8	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	OE	45	ILE	N-CA-C	5.41	125.60	111.00
2	eE	45	ILE	N-CA-C	5.41	125.60	111.00
2	MG	45	ILE	N-CA-C	5.41	125.60	111.00
1	RG	235	LEU	CA-CB-CG	5.41	127.74	115.30
2	MQ	45	ILE	N-CA-C	5.41	125.60	111.00
1	JR	235	LEU	CA-CB-CG	5.41	127.74	115.30
1	A3	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	J4	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	g4	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	h6	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	J8	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	Z8	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	LE	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	bE	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	JG	235	LEU	CA-CB-CG	5.41	127.73	115.30
1	JQ	235	LEU	CA-CB-CG	5.41	127.73	115.30
2	M1	45	ILE	N-CA-C	5.40	125.58	111.00
2	U3	45	ILE	N-CA-C	5.40	125.58	111.00
2	c3	45	ILE	N-CA-C	5.40	125.58	111.00
2	b4	45	ILE	N-CA-C	5.40	125.58	111.00
2	M6	45	ILE	N-CA-C	5.40	125.58	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	U6	45	ILE	N-CA-C	5.40	125.58	111.00
2	c6	45	ILE	N-CA-C	5.40	125.58	111.00
2	M7	45	ILE	N-CA-C	5.40	125.58	111.00
2	U7	45	ILE	N-CA-C	5.40	125.58	111.00
2	k7	45	ILE	N-CA-C	5.40	125.58	111.00
2	E8	45	ILE	N-CA-C	5.40	125.58	111.00
2	WE	45	ILE	N-CA-C	5.40	125.58	111.00
2	cG	45	ILE	N-CA-C	5.40	125.58	111.00
2	EL	45	ILE	N-CA-C	5.40	125.58	111.00
2	cL	45	ILE	N-CA-C	5.40	125.58	111.00
2	hL	45	ILE	N-CA-C	5.40	125.58	111.00
2	EQ	45	ILE	N-CA-C	5.40	125.58	111.00
2	ER	45	ILE	N-CA-C	5.40	125.58	111.00
2	UR	45	ILE	N-CA-C	5.40	125.58	111.00
2	cR	45	ILE	N-CA-C	5.40	125.58	111.00
3	A5	80	ILE	CG1-CB-CG2	-5.40	99.53	111.40
3	AH	80	ILE	CG1-CB-CG2	-5.39	99.53	111.40
3	AA	80	ILE	CG1-CB-CG2	-5.39	99.54	111.40
3	AO	80	ILE	CG1-CB-CG2	-5.39	99.54	111.40
3	AF	80	ILE	CG1-CB-CG2	-5.39	99.55	111.40
3	A9	80	ILE	CG1-CB-CG2	-5.39	99.55	111.40
3	AC	80	ILE	CG1-CB-CG2	-5.38	99.55	111.40
3	A2	80	ILE	CG1-CB-CG2	-5.38	99.57	111.40
3	AM	80	ILE	CG1-CB-CG2	-5.37	99.58	111.40
1	AD	252	ASP	CB-CG-OD1	5.37	123.14	118.30
1	IS	252	ASP	CB-CG-OD1	5.34	123.11	118.30
1	AK	49	PHE	C-N-CA	-5.34	108.35	121.70
1	AD	49	PHE	C-N-CA	-5.34	108.35	121.70
1	D3	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	Y3	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	L4	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	i4	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	j6	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	L8	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	b8	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	NE	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	dE	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	LG	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	LQ	120	LEU	CA-CB-CG	5.33	127.57	115.30
1	D1	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	L3	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	D4	120	LEU	CA-CB-CG	5.33	127.56	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T4	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	D6	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	b7	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	T8	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	j8	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	DE	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	TG	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	AP	252	ASP	CB-CG-OD1	5.33	123.10	118.30
1	LR	120	LEU	CA-CB-CG	5.33	127.56	115.30
1	AP	49	PHE	C-N-CA	-5.33	108.38	121.70
1	L1	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	T3	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	b3	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	a4	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	b6	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	j7	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	D8	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	FE	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	VE	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	bG	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	AK	252	ASP	CB-CG-OD1	5.33	123.09	118.30
1	DR	120	LEU	CA-CB-CG	5.33	127.55	115.30
1	IS	49	PHE	C-N-CA	-5.33	108.39	121.70
1	L6	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	T6	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	L7	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	T7	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	DL	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	bL	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	gL	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	DQ	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	TR	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	bR	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	jR	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	T1	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	a1	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	i1	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	D7	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	DG	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	jG	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	AJ	49	PHE	C-N-CA	-5.32	108.40	121.70
1	LL	120	LEU	CA-CB-CG	5.32	127.54	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	TL	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	TQ	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	YQ	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	eQ	120	LEU	CA-CB-CG	5.32	127.54	115.30
1	AJ	252	ASP	CB-CG-OD1	5.29	123.06	118.30
1	CP	265	ASP	CB-CG-OD2	5.29	123.06	118.30
1	L1	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	T3	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	b3	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	a4	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	b6	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	j7	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	D8	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	FE	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	VE	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	bG	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	DR	166	LEU	CA-CB-CG	5.28	127.45	115.30
1	KK	265	ASP	CB-CG-OD2	5.28	123.05	118.30
1	D3	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	Y3	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	L4	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	i4	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	j6	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	L8	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	b8	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	NE	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	dE	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	LG	166	LEU	CA-CB-CG	5.28	127.44	115.30
3	AI	131	LEU	CA-CB-CG	5.28	127.44	115.30
1	LQ	166	LEU	CA-CB-CG	5.28	127.44	115.30
1	D1	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	T1	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	a1	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	i1	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	L3	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	D4	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	T4	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	D6	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	L6	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	T6	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	D7	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	L7	166	LEU	CA-CB-CG	5.28	127.43	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T7	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	b7	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	T8	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	j8	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	DE	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	DG	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	TG	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	jG	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	DL	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	LL	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	TL	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	bL	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	gL	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	DQ	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	TQ	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	YQ	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	eQ	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	LR	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	TR	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	bR	166	LEU	CA-CB-CG	5.28	127.43	115.30
1	jR	166	LEU	CA-CB-CG	5.28	127.43	115.30
3	AN	131	LEU	CA-CB-CG	5.27	127.43	115.30
1	LP	197	LEU	CA-CB-CG	5.27	127.41	115.30
1	KS	197	LEU	CA-CB-CG	5.26	127.41	115.30
3	AC	131	LEU	CA-CB-CG	5.26	127.40	115.30
1	LJ	197	LEU	CA-CB-CG	5.26	127.40	115.30
1	BS	265	ASP	CB-CG-OD2	5.26	123.03	118.30
3	AM	131	LEU	CA-CB-CG	5.26	127.39	115.30
3	AH	131	LEU	CA-CB-CG	5.25	127.39	115.30
1	CJ	265	ASP	CB-CG-OD2	5.25	123.03	118.30
1	LK	197	LEU	CA-CB-CG	5.25	127.39	115.30
3	AA	131	LEU	CA-CB-CG	5.25	127.38	115.30
3	A2	131	LEU	CA-CB-CG	5.25	127.38	115.30
3	A9	131	LEU	CA-CB-CG	5.25	127.38	115.30
3	AB	131	LEU	CA-CB-CG	5.25	127.38	115.30
3	A5	131	LEU	CA-CB-CG	5.25	127.37	115.30
1	CD	265	ASP	CB-CG-OD2	5.25	123.02	118.30
3	AF	131	LEU	CA-CB-CG	5.25	127.37	115.30
1	CD	235	LEU	CA-CB-CG	5.24	127.36	115.30
1	LD	197	LEU	CA-CB-CG	5.24	127.35	115.30
3	AO	131	LEU	CA-CB-CG	5.24	127.36	115.30
1	DK	265	ASP	CB-CG-OD2	5.24	123.02	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CJ	235	LEU	CA-CB-CG	5.24	127.34	115.30
1	AP	49	PHE	CA-C-O	5.24	131.09	120.10
2	N6	45	ILE	C-N-CA	5.23	134.78	121.70
2	V6	45	ILE	C-N-CA	5.23	134.78	121.70
2	N7	45	ILE	C-N-CA	5.23	134.78	121.70
2	V7	45	ILE	C-N-CA	5.23	134.78	121.70
1	DD	265	ASP	CB-CG-OD2	5.23	123.01	118.30
1	CK	235	LEU	CA-CB-CG	5.23	127.34	115.30
2	FL	45	ILE	C-N-CA	5.23	134.78	121.70
2	dL	45	ILE	C-N-CA	5.23	134.78	121.70
2	FQ	45	ILE	C-N-CA	5.23	134.78	121.70
2	VR	45	ILE	C-N-CA	5.23	134.78	121.70
2	dR	45	ILE	C-N-CA	5.23	134.78	121.70
2	kR	45	ILE	C-N-CA	5.23	134.78	121.70
1	C3	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	I4	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	f4	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	g6	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	I8	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	Y8	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	KE	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	aE	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	IG	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	CP	235	LEU	CA-CB-CG	5.23	127.33	115.30
1	DP	265	ASP	CB-CG-OD2	5.23	123.01	118.30
1	IQ	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	C1	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	I1	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	I3	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	Q3	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	C4	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	Q4	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	X4	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	C6	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	Y6	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	Y7	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	g7	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	C8	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	Q8	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	g8	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	LD	265	ASP	CB-CG-OD2	5.23	123.01	118.30
1	AE	120	LEU	CA-CB-CG	5.23	127.33	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	SE	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	QG	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	YG	120	LEU	CA-CB-CG	5.23	127.33	115.30
3	AN	153	ASP	CB-CG-OD2	5.23	123.01	118.30
1	CR	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	IR	120	LEU	CA-CB-CG	5.23	127.33	115.30
1	BS	235	LEU	CA-CB-CG	5.23	127.33	115.30
1	BK	265	ASP	CB-CG-OD2	5.23	123.01	118.30
2	U1	45	ILE	C-N-CA	5.23	134.76	121.70
2	c1	45	ILE	C-N-CA	5.23	134.76	121.70
2	k1	45	ILE	C-N-CA	5.23	134.76	121.70
2	F7	45	ILE	C-N-CA	5.23	134.76	121.70
2	FG	45	ILE	C-N-CA	5.23	134.76	121.70
2	lG	45	ILE	C-N-CA	5.23	134.76	121.70
1	AJ	49	PHE	CA-C-O	5.23	131.07	120.10
2	NL	45	ILE	C-N-CA	5.23	134.76	121.70
2	VL	45	ILE	C-N-CA	5.23	134.76	121.70
2	VQ	45	ILE	C-N-CA	5.23	134.76	121.70
2	gQ	45	ILE	C-N-CA	5.23	134.76	121.70
1	JS	265	ASP	CB-CG-OD2	5.23	123.00	118.30
1	Q1	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	X1	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	f1	120	LEU	CA-CB-CG	5.22	127.31	115.30
2	F3	45	ILE	C-N-CA	5.22	134.75	121.70
2	N4	45	ILE	C-N-CA	5.22	134.75	121.70
2	j4	45	ILE	C-N-CA	5.22	134.75	121.70
2	l6	45	ILE	C-N-CA	5.22	134.75	121.70
1	C7	120	LEU	CA-CB-CG	5.22	127.31	115.30
2	N8	45	ILE	C-N-CA	5.22	134.75	121.70
2	d8	45	ILE	C-N-CA	5.22	134.75	121.70
3	AA	153	ASP	CB-CG-OD2	5.22	123.00	118.30
2	PE	45	ILE	C-N-CA	5.22	134.75	121.70
2	fE	45	ILE	C-N-CA	5.22	134.75	121.70
1	CG	120	LEU	CA-CB-CG	5.22	127.31	115.30
2	NG	45	ILE	C-N-CA	5.22	134.75	121.70
1	gG	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	KJ	265	ASP	CB-CG-OD2	5.22	123.00	118.30
1	IL	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	QL	120	LEU	CA-CB-CG	5.22	127.31	115.30
2	NQ	45	ILE	C-N-CA	5.22	134.75	121.70
1	QQ	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	bQ	120	LEU	CA-CB-CG	5.22	127.31	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	IS	49	PHE	CA-C-O	5.22	131.06	120.10
1	I6	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	Q6	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	I7	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	Q7	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	CL	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	YL	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	CQ	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	QR	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	YR	120	LEU	CA-CB-CG	5.22	127.31	115.30
1	gR	120	LEU	CA-CB-CG	5.22	127.31	115.30
3	AB	153	ASP	CB-CG-OD2	5.21	122.99	118.30
2	N1	45	ILE	C-N-CA	5.21	134.73	121.70
2	V3	45	ILE	C-N-CA	5.21	134.73	121.70
2	c4	45	ILE	C-N-CA	5.21	134.73	121.70
2	d6	45	ILE	C-N-CA	5.21	134.73	121.70
2	l7	45	ILE	C-N-CA	5.21	134.73	121.70
2	F8	45	ILE	C-N-CA	5.21	134.73	121.70
2	HE	45	ILE	C-N-CA	5.21	134.73	121.70
2	XE	45	ILE	C-N-CA	5.21	134.73	121.70
2	dG	45	ILE	C-N-CA	5.21	134.73	121.70
2	FR	45	ILE	C-N-CA	5.21	134.73	121.70
1	LJ	265	ASP	CB-CG-OD2	5.21	122.99	118.30
2	F1	45	ILE	C-N-CA	5.21	134.72	121.70
2	N3	45	ILE	C-N-CA	5.21	134.72	121.70
2	F4	45	ILE	C-N-CA	5.21	134.72	121.70
2	U4	45	ILE	C-N-CA	5.21	134.72	121.70
3	A5	153	ASP	CB-CG-OD2	5.21	122.99	118.30
2	F6	45	ILE	C-N-CA	5.21	134.72	121.70
2	d7	45	ILE	C-N-CA	5.21	134.72	121.70
2	V8	45	ILE	C-N-CA	5.21	134.72	121.70
2	l8	45	ILE	C-N-CA	5.21	134.72	121.70
1	KD	265	ASP	CB-CG-OD2	5.21	122.99	118.30
2	VG	45	ILE	C-N-CA	5.21	134.72	121.70
1	DJ	265	ASP	CB-CG-OD2	5.21	122.99	118.30
2	NR	45	ILE	C-N-CA	5.21	134.72	121.70
1	AD	49	PHE	CA-C-O	5.21	131.03	120.10
1	AD	265	ASP	CB-CG-OD2	5.21	122.98	118.30
1	CK	265	ASP	CB-CG-OD2	5.21	122.98	118.30
1	AP	265	ASP	CB-CG-OD2	5.20	122.98	118.30
1	LK	265	ASP	CB-CG-OD2	5.20	122.98	118.30
1	AS	265	ASP	CB-CG-OD2	5.20	122.98	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	KS	265	ASP	CB-CG-OD2	5.20	122.98	118.30
2	E3	42	GLY	C-N-CA	5.19	134.68	121.70
2	Z3	42	GLY	C-N-CA	5.19	134.68	121.70
2	M4	42	GLY	C-N-CA	5.19	134.68	121.70
2	k6	42	GLY	C-N-CA	5.19	134.68	121.70
2	M8	42	GLY	C-N-CA	5.19	134.68	121.70
2	c8	42	GLY	C-N-CA	5.19	134.68	121.70
2	OE	42	GLY	C-N-CA	5.19	134.68	121.70
2	eE	42	GLY	C-N-CA	5.19	134.68	121.70
2	MG	42	GLY	C-N-CA	5.19	134.68	121.70
2	MQ	42	GLY	C-N-CA	5.19	134.68	121.70
1	CS	265	ASP	CB-CG-OD2	5.19	122.97	118.30
1	BJ	265	ASP	CB-CG-OD2	5.19	122.97	118.30
1	AK	49	PHE	CA-C-O	5.19	131.00	120.10
3	A9	153	ASP	CB-CG-OD2	5.19	122.97	118.30
1	AJ	265	ASP	CB-CG-OD2	5.19	122.97	118.30
1	KP	265	ASP	CB-CG-OD2	5.19	122.97	118.30
2	E1	42	GLY	C-N-CA	5.18	134.66	121.70
2	M3	42	GLY	C-N-CA	5.18	134.66	121.70
2	E4	42	GLY	C-N-CA	5.18	134.66	121.70
2	E6	42	GLY	C-N-CA	5.18	134.66	121.70
2	c7	42	GLY	C-N-CA	5.18	134.66	121.70
2	U8	42	GLY	C-N-CA	5.18	134.66	121.70
2	k8	42	GLY	C-N-CA	5.18	134.66	121.70
2	EE	42	GLY	C-N-CA	5.18	134.66	121.70
2	UG	42	GLY	C-N-CA	5.18	134.66	121.70
2	MR	42	GLY	C-N-CA	5.18	134.66	121.70
2	b1	42	GLY	C-N-CA	5.18	134.66	121.70
2	j1	42	GLY	C-N-CA	5.18	134.66	121.70
2	E7	42	GLY	C-N-CA	5.18	134.66	121.70
2	EG	42	GLY	C-N-CA	5.18	134.66	121.70
2	kG	42	GLY	C-N-CA	5.18	134.66	121.70
2	ML	42	GLY	C-N-CA	5.18	134.66	121.70
2	UL	42	GLY	C-N-CA	5.18	134.66	121.70
3	AO	153	ASP	CB-CG-OD2	5.18	122.96	118.30
2	UQ	42	GLY	C-N-CA	5.18	134.66	121.70
2	ZQ	42	GLY	C-N-CA	5.18	134.66	121.70
2	fQ	42	GLY	C-N-CA	5.18	134.66	121.70
3	AM	153	ASP	CB-CG-OD2	5.18	122.96	118.30
2	M6	42	GLY	C-N-CA	5.18	134.64	121.70
2	U6	42	GLY	C-N-CA	5.18	134.64	121.70
2	M7	42	GLY	C-N-CA	5.18	134.64	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	U7	42	GLY	C-N-CA	5.18	134.64	121.70
1	BD	175	LEU	CA-CB-CG	5.18	127.21	115.30
1	BD	265	ASP	CB-CG-OD2	5.18	122.96	118.30
2	EL	42	GLY	C-N-CA	5.18	134.64	121.70
2	cL	42	GLY	C-N-CA	5.18	134.64	121.70
2	hL	42	GLY	C-N-CA	5.18	134.64	121.70
2	EQ	42	GLY	C-N-CA	5.18	134.64	121.70
2	UR	42	GLY	C-N-CA	5.18	134.64	121.70
2	cR	42	GLY	C-N-CA	5.18	134.64	121.70
2	M1	42	GLY	C-N-CA	5.17	134.63	121.70
2	U3	42	GLY	C-N-CA	5.17	134.63	121.70
2	c3	42	GLY	C-N-CA	5.17	134.63	121.70
2	b4	42	GLY	C-N-CA	5.17	134.63	121.70
2	c6	42	GLY	C-N-CA	5.17	134.63	121.70
2	k7	42	GLY	C-N-CA	5.17	134.63	121.70
2	E8	42	GLY	C-N-CA	5.17	134.63	121.70
2	WE	42	GLY	C-N-CA	5.17	134.63	121.70
2	cG	42	GLY	C-N-CA	5.17	134.63	121.70
1	BJ	175	LEU	CA-CB-CG	5.17	127.20	115.30
2	ER	42	GLY	C-N-CA	5.17	134.63	121.70
3	A2	153	ASP	CB-CG-OD2	5.17	122.95	118.30
1	AS	175	LEU	CA-CB-CG	5.17	127.19	115.30
1	BP	175	LEU	CA-CB-CG	5.17	127.19	115.30
1	LP	265	ASP	CB-CG-OD2	5.17	122.95	118.30
1	BK	175	LEU	CA-CB-CG	5.16	127.17	115.30
3	AF	153	ASP	CB-CG-OD2	5.16	122.94	118.30
1	BP	265	ASP	CB-CG-OD2	5.16	122.94	118.30
1	J1	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	R3	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	Y4	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	Z6	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	h7	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	A8	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	BE	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	TE	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	ZG	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	AR	252	ASP	CB-CG-OD1	5.15	122.94	118.30
1	IS	265	ASP	CB-CG-OD2	5.15	122.94	118.30
3	AI	153	ASP	CB-CG-OD2	5.15	122.94	118.30
1	AK	265	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A3	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	J4	252	ASP	CB-CG-OD1	5.14	122.92	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	g4	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	h6	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	J8	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	Z8	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	LE	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	bE	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	JG	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	JQ	252	ASP	CB-CG-OD1	5.14	122.92	118.30
1	A1	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	J3	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	A4	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	R4	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	A6	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	Z7	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	R8	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	h8	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	RG	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	JR	183	LEU	CB-CG-CD1	5.13	119.73	111.00
1	R1	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	Y1	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	g1	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	A7	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	AG	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	hG	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	JL	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	RL	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	RQ	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	cQ	252	ASP	CB-CG-OD1	5.13	122.91	118.30
1	J6	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	R6	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	J7	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	R7	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	AL	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	ZL	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	AQ	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	RR	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	ZR	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	hR	252	ASP	CB-CG-OD1	5.12	122.91	118.30
1	R1	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	Y1	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	g1	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	A7	183	LEU	CB-CG-CD1	5.12	119.71	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AG	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	hG	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	JL	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	RL	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	RQ	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	cQ	183	LEU	CB-CG-CD1	5.12	119.71	111.00
1	J1	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	R3	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	Y4	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	Z6	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	h7	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	A8	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	BE	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	TE	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	ZG	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	AR	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	A3	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	J4	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	g4	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	J6	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	R6	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	h6	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	J7	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	R7	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	J8	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	Z8	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	LE	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	bE	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	JG	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	AL	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	ZL	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	AQ	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	JQ	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	RR	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	ZR	183	LEU	CB-CG-CD1	5.11	119.69	111.00
1	hR	183	LEU	CB-CG-CD1	5.11	119.69	111.00
3	AC	153	ASP	CB-CG-OD2	5.10	122.89	118.30
3	AH	153	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A1	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	J3	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	A4	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	R4	252	ASP	CB-CG-OD1	5.08	122.87	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A6	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	Z7	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	R8	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	h8	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	RG	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	JR	252	ASP	CB-CG-OD1	5.08	122.87	118.30
1	I1	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	Q3	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	X4	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	Y6	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	g7	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	C8	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	AE	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	SE	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	YG	326	GLU	N-CA-CB	-5.07	101.47	110.60
1	CR	326	GLU	N-CA-CB	-5.07	101.47	110.60
2	E1	40	SER	N-CA-C	5.06	124.66	111.00
2	M3	40	SER	N-CA-C	5.06	124.66	111.00
2	E4	40	SER	N-CA-C	5.06	124.66	111.00
2	E6	40	SER	N-CA-C	5.06	124.66	111.00
2	c7	40	SER	N-CA-C	5.06	124.66	111.00
2	U8	40	SER	N-CA-C	5.06	124.66	111.00
2	k8	40	SER	N-CA-C	5.06	124.66	111.00
2	EE	40	SER	N-CA-C	5.06	124.66	111.00
2	UG	40	SER	N-CA-C	5.06	124.66	111.00
2	MR	40	SER	N-CA-C	5.06	124.66	111.00
2	E3	40	SER	N-CA-C	5.06	124.65	111.00
2	Z3	40	SER	N-CA-C	5.06	124.65	111.00
2	M4	40	SER	N-CA-C	5.06	124.65	111.00
2	k6	40	SER	N-CA-C	5.06	124.65	111.00
2	M8	40	SER	N-CA-C	5.06	124.65	111.00
2	c8	40	SER	N-CA-C	5.06	124.65	111.00
2	OE	40	SER	N-CA-C	5.06	124.65	111.00
2	eE	40	SER	N-CA-C	5.06	124.65	111.00
2	MG	40	SER	N-CA-C	5.06	124.65	111.00
2	MQ	40	SER	N-CA-C	5.06	124.65	111.00
1	I6	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	Q6	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	I7	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	Q7	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	CL	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	YL	326	GLU	N-CA-CB	-5.05	101.50	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CQ	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	QR	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	YR	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	gR	326	GLU	N-CA-CB	-5.05	101.50	110.60
1	KK	109	LEU	CA-CB-CG	5.05	126.92	115.30
1	KP	109	LEU	CA-CB-CG	5.05	126.92	115.30
1	Q1	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	X1	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	f1	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	C3	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	I4	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	f4	326	GLU	N-CA-CB	-5.05	101.51	110.60
2	M6	40	SER	N-CA-C	5.05	124.63	111.00
2	U6	40	SER	N-CA-C	5.05	124.63	111.00
1	g6	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	C7	326	GLU	N-CA-CB	-5.05	101.51	110.60
2	M7	40	SER	N-CA-C	5.05	124.63	111.00
2	U7	40	SER	N-CA-C	5.05	124.63	111.00
1	I8	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	Y8	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	KE	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	aE	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	CG	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	IG	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	gG	326	GLU	N-CA-CB	-5.05	101.51	110.60
2	EL	40	SER	N-CA-C	5.05	124.63	111.00
1	IL	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	QL	326	GLU	N-CA-CB	-5.05	101.51	110.60
2	cL	40	SER	N-CA-C	5.05	124.63	111.00
2	hL	40	SER	N-CA-C	5.05	124.63	111.00
2	EQ	40	SER	N-CA-C	5.05	124.63	111.00
1	IQ	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	QQ	326	GLU	N-CA-CB	-5.05	101.51	110.60
1	bQ	326	GLU	N-CA-CB	-5.05	101.51	110.60
2	UR	40	SER	N-CA-C	5.05	124.63	111.00
2	cR	40	SER	N-CA-C	5.05	124.63	111.00
2	b1	40	SER	N-CA-C	5.05	124.63	111.00
2	j1	40	SER	N-CA-C	5.05	124.63	111.00
2	E7	40	SER	N-CA-C	5.05	124.63	111.00
2	EG	40	SER	N-CA-C	5.05	124.63	111.00
2	kG	40	SER	N-CA-C	5.05	124.63	111.00
2	ML	40	SER	N-CA-C	5.05	124.63	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	UL	40	SER	N-CA-C	5.05	124.63	111.00
2	UQ	40	SER	N-CA-C	5.05	124.63	111.00
2	ZQ	40	SER	N-CA-C	5.05	124.63	111.00
2	fQ	40	SER	N-CA-C	5.05	124.63	111.00
1	JS	109	LEU	CA-CB-CG	5.05	126.91	115.30
2	M1	40	SER	N-CA-C	5.04	124.62	111.00
2	U3	40	SER	N-CA-C	5.04	124.62	111.00
2	c3	40	SER	N-CA-C	5.04	124.62	111.00
2	b4	40	SER	N-CA-C	5.04	124.62	111.00
2	c6	40	SER	N-CA-C	5.04	124.62	111.00
2	k7	40	SER	N-CA-C	5.04	124.62	111.00
2	E8	40	SER	N-CA-C	5.04	124.62	111.00
2	WE	40	SER	N-CA-C	5.04	124.62	111.00
2	cG	40	SER	N-CA-C	5.04	124.62	111.00
2	ER	40	SER	N-CA-C	5.04	124.62	111.00
1	KJ	109	LEU	CA-CB-CG	5.04	126.88	115.30
1	C1	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	I3	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	C4	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	Q4	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	C6	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	Y7	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	Q8	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	g8	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	QG	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	IR	326	GLU	N-CA-CB	-5.03	101.54	110.60
1	KD	109	LEU	CA-CB-CG	5.03	126.86	115.30
3	AB	153	ASP	CB-CA-C	-5.03	100.35	110.40
3	AF	153	ASP	CB-CA-C	-5.02	100.35	110.40
3	AA	153	ASP	CB-CA-C	-5.02	100.36	110.40
1	LD	235	LEU	CA-CB-CG	5.02	126.84	115.30
3	AO	153	ASP	CB-CA-C	-5.02	100.37	110.40
3	A5	153	ASP	CB-CA-C	-5.01	100.39	110.40
1	KS	235	LEU	CA-CB-CG	5.01	126.82	115.30
1	LP	235	LEU	CA-CB-CG	5.00	126.81	115.30
3	A2	153	ASP	CB-CA-C	-5.00	100.39	110.40
3	A9	153	ASP	CB-CA-C	-5.00	100.39	110.40
1	LK	235	LEU	CA-CB-CG	5.00	126.81	115.30
1	LJ	235	LEU	CA-CB-CG	5.00	126.80	115.30

There are no chirality outliers.

All (732) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	204	ALA	Peptide
1	A1	61	THR	Mainchain
3	A2	13	SER	Peptide
3	A2	179	LYS	Peptide
3	A2	187	GLU	Peptide
3	A2	188	ILE	Peptide
3	A2	307	THR	Peptide
1	A3	204	ALA	Peptide
1	A3	61	THR	Mainchain
1	A4	204	ALA	Peptide
1	A4	61	THR	Mainchain
3	A5	13	SER	Peptide
3	A5	179	LYS	Peptide
3	A5	187	GLU	Peptide
3	A5	188	ILE	Peptide
3	A5	307	THR	Peptide
1	A6	204	ALA	Peptide
1	A6	61	THR	Mainchain
1	A7	204	ALA	Peptide
1	A7	61	THR	Mainchain
1	A8	204	ALA	Peptide
1	A8	61	THR	Mainchain
3	A9	13	SER	Peptide
3	A9	179	LYS	Peptide
3	A9	187	GLU	Peptide
3	A9	188	ILE	Peptide
3	A9	307	THR	Peptide
3	AA	13	SER	Peptide
3	AA	179	LYS	Peptide
3	AA	187	GLU	Peptide
3	AA	188	ILE	Peptide
3	AA	307	THR	Peptide
3	AB	13	SER	Peptide
3	AB	179	LYS	Peptide
3	AB	187	GLU	Peptide
3	AB	188	ILE	Peptide
3	AB	307	THR	Peptide
3	AC	13	SER	Peptide
3	AC	179	LYS	Peptide
3	AC	187	GLU	Peptide
3	AC	188	ILE	Peptide
3	AC	307	THR	Peptide
1	AD	70	ASN	Peptide

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Mol	Chain	Res	Type	Group
1	AE	347	ILE	Peptide
3	AF	13	SER	Peptide
3	AF	179	LYS	Peptide
3	AF	187	GLU	Peptide
3	AF	188	ILE	Peptide
3	AF	307	THR	Peptide
1	AG	204	ALA	Peptide
1	AG	61	THR	Mainchain
3	AH	13	SER	Peptide
3	AH	179	LYS	Peptide
3	AH	187	GLU	Peptide
3	AH	188	ILE	Peptide
3	AH	307	THR	Peptide
3	AI	13	SER	Peptide
3	AI	179	LYS	Peptide
3	AI	187	GLU	Peptide
3	AI	188	ILE	Peptide
3	AI	307	THR	Peptide
1	AJ	70	ASN	Peptide
1	AK	70	ASN	Peptide
1	AL	204	ALA	Peptide
1	AL	61	THR	Mainchain
3	AM	13	SER	Peptide
3	AM	179	LYS	Peptide
3	AM	187	GLU	Peptide
3	AM	188	ILE	Peptide
3	AM	307	THR	Peptide
3	AN	13	SER	Peptide
3	AN	179	LYS	Peptide
3	AN	187	GLU	Peptide
3	AN	188	ILE	Peptide
3	AN	307	THR	Peptide
3	AO	13	SER	Peptide
3	AO	179	LYS	Peptide
3	AO	187	GLU	Peptide
3	AO	188	ILE	Peptide
3	AO	307	THR	Peptide
1	AP	70	ASN	Peptide
1	AQ	204	ALA	Peptide
1	AQ	61	THR	Mainchain
1	AR	204	ALA	Peptide
1	AR	61	THR	Mainchain

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Mol	Chain	Res	Type	Group
1	AS	183	LEU	Peptide
1	AS	202	PHE	Peptide
1	B1	61	THR	Peptide
4	B2	113	TYR	Peptide
4	B2	114	SER	Peptide
1	B3	61	THR	Peptide
1	B4	61	THR	Peptide
4	B5	113	TYR	Peptide
4	B5	114	SER	Peptide
1	B6	61	THR	Peptide
1	B7	61	THR	Peptide
1	B8	61	THR	Peptide
4	B9	113	TYR	Peptide
4	B9	114	SER	Peptide
4	BA	113	TYR	Peptide
4	BA	114	SER	Peptide
4	BB	113	TYR	Peptide
4	BB	114	SER	Peptide
4	BC	113	TYR	Peptide
4	BC	114	SER	Peptide
1	BD	183	LEU	Peptide
1	BD	202	PHE	Peptide
1	BE	204	ALA	Peptide
1	BE	61	THR	Mainchain
4	BF	113	TYR	Peptide
4	BF	114	SER	Peptide
1	BG	61	THR	Peptide
4	BH	113	TYR	Peptide
4	BH	114	SER	Peptide
4	BI	113	TYR	Peptide
4	BI	114	SER	Peptide
1	BJ	183	LEU	Peptide
1	BJ	202	PHE	Peptide
1	BK	183	LEU	Peptide
1	BK	202	PHE	Peptide
1	BL	61	THR	Peptide
4	BM	113	TYR	Peptide
4	BM	114	SER	Peptide
4	BN	113	TYR	Peptide
4	BN	114	SER	Peptide
4	BO	113	TYR	Peptide
4	BO	114	SER	Peptide

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Mol	Chain	Res	Type	Group
1	BP	183	LEU	Peptide
1	BP	202	PHE	Peptide
1	BQ	61	THR	Peptide
1	BR	61	THR	Peptide
1	C1	347	ILE	Peptide
1	C3	347	ILE	Peptide
1	C4	347	ILE	Peptide
1	C6	347	ILE	Peptide
1	C7	347	ILE	Peptide
1	C8	347	ILE	Peptide
1	CE	61	THR	Peptide
1	CG	347	ILE	Peptide
1	CL	347	ILE	Peptide
1	CQ	347	ILE	Peptide
1	CR	347	ILE	Peptide
1	CS	206	LEU	Peptide
1	CS	347	ILE	Peptide
1	DD	206	LEU	Peptide
1	DD	347	ILE	Peptide
1	DJ	206	LEU	Peptide
1	DJ	347	ILE	Peptide
1	DK	206	LEU	Peptide
1	DK	347	ILE	Peptide
1	DP	206	LEU	Peptide
1	DP	347	ILE	Peptide
2	DS	24	THR	Peptide
2	DS	25	GLU	Peptide
2	DS	45	ILE	Peptide
2	E1	9	SER	Peptide
2	E3	9	SER	Peptide
2	E4	9	SER	Peptide
2	E6	9	SER	Peptide
2	E7	9	SER	Peptide
2	E8	9	SER	Peptide
2	ED	24	THR	Peptide
2	ED	25	GLU	Peptide
2	ED	45	ILE	Peptide
2	EE	9	SER	Peptide
2	EG	9	SER	Peptide
2	EJ	24	THR	Peptide
2	EJ	25	GLU	Peptide
2	EJ	45	ILE	Peptide

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Mol	Chain	Res	Type	Group
2	EK	24	THR	Peptide
2	EK	25	GLU	Peptide
2	EK	45	ILE	Peptide
2	EL	9	SER	Peptide
2	EP	24	THR	Peptide
2	EP	25	GLU	Peptide
2	EP	45	ILE	Peptide
2	EQ	9	SER	Peptide
2	ER	9	SER	Peptide
2	ES	11	MET	Peptide
2	ES	44	GLN	Peptide
2	F1	24	THR	Peptide
2	F1	43	VAL	Peptide
5	F2	110	LYS	Peptide
2	F3	24	THR	Peptide
2	F3	43	VAL	Peptide
2	F4	24	THR	Peptide
2	F4	43	VAL	Peptide
5	F5	110	LYS	Peptide
2	F6	24	THR	Peptide
2	F6	43	VAL	Peptide
2	F7	24	THR	Peptide
2	F7	43	VAL	Peptide
2	F8	24	THR	Peptide
2	F8	43	VAL	Peptide
5	F9	110	LYS	Peptide
5	FA	110	LYS	Peptide
5	FB	110	LYS	Peptide
5	FC	110	LYS	Peptide
2	FD	11	MET	Peptide
2	FD	44	GLN	Peptide
5	FF	110	LYS	Peptide
2	FG	24	THR	Peptide
2	FG	43	VAL	Peptide
5	FH	110	LYS	Peptide
5	FI	110	LYS	Peptide
2	FJ	11	MET	Peptide
2	FJ	44	GLN	Peptide
2	FK	11	MET	Peptide
2	FK	44	GLN	Peptide
2	FL	24	THR	Peptide
2	FL	43	VAL	Peptide

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Mol	Chain	Res	Type	Group
5	FM	110	LYS	Peptide
5	FN	110	LYS	Peptide
5	FO	110	LYS	Peptide
2	FP	11	MET	Peptide
2	FP	44	GLN	Peptide
2	FQ	24	THR	Peptide
2	FQ	43	VAL	Peptide
2	FR	24	THR	Peptide
2	FR	43	VAL	Peptide
2	G1	16	GLU	Peptide
2	G1	24	THR	Peptide
2	G1	9	SER	Peptide
2	G3	16	GLU	Peptide
2	G3	24	THR	Peptide
2	G3	9	SER	Peptide
2	G4	16	GLU	Peptide
2	G4	24	THR	Peptide
2	G4	9	SER	Peptide
2	G6	16	GLU	Peptide
2	G6	24	THR	Peptide
2	G6	9	SER	Peptide
2	G7	16	GLU	Peptide
2	G7	24	THR	Peptide
2	G7	9	SER	Peptide
2	G8	16	GLU	Peptide
2	G8	24	THR	Peptide
2	G8	9	SER	Peptide
2	GE	16	GLU	Peptide
2	GE	24	THR	Peptide
2	GE	9	SER	Peptide
2	GG	16	GLU	Peptide
2	GG	24	THR	Peptide
2	GG	9	SER	Peptide
2	GL	16	GLU	Peptide
2	GL	24	THR	Peptide
2	GL	9	SER	Peptide
2	GQ	16	GLU	Peptide
2	GQ	24	THR	Peptide
2	GQ	9	SER	Peptide
2	GR	16	GLU	Peptide
2	GR	24	THR	Peptide
2	GR	9	SER	Peptide

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Mol	Chain	Res	Type	Group
2	H1	44	GLN	Peptide
2	H3	44	GLN	Peptide
2	H4	44	GLN	Peptide
2	H6	44	GLN	Peptide
2	H7	44	GLN	Peptide
2	H8	44	GLN	Peptide
2	HE	24	THR	Peptide
2	HE	43	VAL	Peptide
2	HG	44	GLN	Peptide
2	HL	44	GLN	Peptide
2	HQ	44	GLN	Peptide
2	HR	44	GLN	Peptide
1	I1	347	ILE	Peptide
1	I3	347	ILE	Peptide
1	I4	347	ILE	Peptide
1	I6	347	ILE	Peptide
1	I7	347	ILE	Peptide
1	I8	347	ILE	Peptide
2	IE	16	GLU	Peptide
2	IE	24	THR	Peptide
2	IE	9	SER	Peptide
1	IG	347	ILE	Peptide
1	IL	347	ILE	Peptide
1	IQ	347	ILE	Peptide
1	IR	347	ILE	Peptide
1	IS	70	ASN	Peptide
1	J1	204	ALA	Peptide
1	J1	61	THR	Mainchain
1	J3	204	ALA	Peptide
1	J3	61	THR	Mainchain
1	J4	204	ALA	Peptide
1	J4	61	THR	Mainchain
1	J6	204	ALA	Peptide
1	J6	61	THR	Mainchain
1	J7	204	ALA	Peptide
1	J7	61	THR	Mainchain
1	J8	204	ALA	Peptide
1	J8	61	THR	Mainchain
2	JE	44	GLN	Peptide
1	JG	204	ALA	Peptide
1	JG	61	THR	Mainchain
1	JL	204	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	JL	61	THR	Mainchain
1	JQ	204	ALA	Peptide
1	JQ	61	THR	Mainchain
1	JR	204	ALA	Peptide
1	JR	61	THR	Mainchain
1	JS	345	LEU	Peptide
1	K1	61	THR	Peptide
1	K3	61	THR	Peptide
1	K4	61	THR	Peptide
1	K6	61	THR	Peptide
1	K7	61	THR	Peptide
1	K8	61	THR	Peptide
1	KD	345	LEU	Peptide
1	KE	347	ILE	Peptide
1	KG	61	THR	Peptide
1	KJ	159	LYS	Peptide
1	KJ	345	LEU	Peptide
1	KK	345	LEU	Peptide
1	KL	61	THR	Peptide
1	KP	345	LEU	Peptide
1	KQ	61	THR	Peptide
1	KR	61	THR	Peptide
1	KS	206	LEU	Peptide
1	LD	206	LEU	Peptide
1	LE	204	ALA	Peptide
1	LE	61	THR	Mainchain
1	LJ	206	LEU	Peptide
1	LK	206	LEU	Peptide
1	LP	206	LEU	Peptide
2	LS	45	ILE	Peptide
2	M1	9	SER	Peptide
2	M3	9	SER	Peptide
2	M4	9	SER	Peptide
2	M6	9	SER	Peptide
2	M7	9	SER	Peptide
2	M8	9	SER	Peptide
2	MD	45	ILE	Peptide
1	ME	61	THR	Peptide
2	MG	9	SER	Peptide
2	MJ	45	ILE	Peptide
2	MK	45	ILE	Peptide
2	ML	9	SER	Peptide

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Mol	Chain	Res	Type	Group
2	MP	45	ILE	Peptide
2	MQ	9	SER	Peptide
2	MR	9	SER	Peptide
2	MS	44	GLN	Peptide
2	N1	24	THR	Peptide
2	N1	43	VAL	Peptide
2	N3	24	THR	Peptide
2	N3	43	VAL	Peptide
2	N4	24	THR	Peptide
2	N4	43	VAL	Peptide
2	N6	24	THR	Peptide
2	N6	43	VAL	Peptide
2	N7	24	THR	Peptide
2	N7	43	VAL	Peptide
2	N8	24	THR	Peptide
2	N8	43	VAL	Peptide
2	ND	44	GLN	Peptide
2	NG	24	THR	Peptide
2	NG	43	VAL	Peptide
2	NJ	44	GLN	Peptide
2	NK	44	GLN	Peptide
2	NL	24	THR	Peptide
2	NL	43	VAL	Peptide
2	NP	44	GLN	Peptide
2	NQ	24	THR	Peptide
2	NQ	43	VAL	Peptide
2	NR	24	THR	Peptide
2	NR	43	VAL	Peptide
2	O1	16	GLU	Peptide
2	O1	24	THR	Peptide
2	O1	9	SER	Peptide
2	O3	16	GLU	Peptide
2	O3	24	THR	Peptide
2	O3	9	SER	Peptide
2	O4	16	GLU	Peptide
2	O4	24	THR	Peptide
2	O4	9	SER	Peptide
2	O6	16	GLU	Peptide
2	O6	24	THR	Peptide
2	O6	9	SER	Peptide
2	O7	16	GLU	Peptide
2	O7	24	THR	Peptide

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Mol	Chain	Res	Type	Group
2	O7	9	SER	Peptide
2	O8	16	GLU	Peptide
2	O8	24	THR	Peptide
2	O8	9	SER	Peptide
2	OE	9	SER	Peptide
2	OG	16	GLU	Peptide
2	OG	24	THR	Peptide
2	OG	9	SER	Peptide
2	OL	16	GLU	Peptide
2	OL	24	THR	Peptide
2	OL	9	SER	Peptide
2	OQ	16	GLU	Peptide
2	OQ	24	THR	Peptide
2	OQ	9	SER	Peptide
2	OR	16	GLU	Peptide
2	OR	24	THR	Peptide
2	OR	9	SER	Peptide
2	P1	44	GLN	Peptide
2	P3	44	GLN	Peptide
2	P4	44	GLN	Peptide
2	P6	44	GLN	Peptide
2	P7	44	GLN	Peptide
2	P8	44	GLN	Peptide
2	PE	24	THR	Peptide
2	PE	43	VAL	Peptide
2	PG	44	GLN	Peptide
2	PL	44	GLN	Peptide
2	PQ	44	GLN	Peptide
2	PR	44	GLN	Peptide
1	Q1	347	ILE	Peptide
1	Q3	347	ILE	Peptide
1	Q4	347	ILE	Peptide
1	Q6	347	ILE	Peptide
1	Q7	347	ILE	Peptide
1	Q8	347	ILE	Peptide
2	QE	16	GLU	Peptide
2	QE	24	THR	Peptide
2	QE	9	SER	Peptide
1	QG	347	ILE	Peptide
1	QL	347	ILE	Peptide
1	QQ	347	ILE	Peptide
1	QR	347	ILE	Peptide

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Mol	Chain	Res	Type	Group
1	R1	204	ALA	Peptide
1	R1	61	THR	Mainchain
1	R3	204	ALA	Peptide
1	R3	61	THR	Mainchain
1	R4	204	ALA	Peptide
1	R4	61	THR	Mainchain
1	R6	204	ALA	Peptide
1	R6	61	THR	Mainchain
1	R7	204	ALA	Peptide
1	R7	61	THR	Mainchain
1	R8	204	ALA	Peptide
1	R8	61	THR	Mainchain
2	RE	44	GLN	Peptide
1	RG	204	ALA	Peptide
1	RG	61	THR	Mainchain
1	RL	204	ALA	Peptide
1	RL	61	THR	Mainchain
1	RQ	204	ALA	Peptide
1	RQ	61	THR	Mainchain
1	RR	204	ALA	Peptide
1	RR	61	THR	Mainchain
1	S1	61	THR	Peptide
1	S3	61	THR	Peptide
1	S4	61	THR	Peptide
1	S6	61	THR	Peptide
1	S7	61	THR	Peptide
1	S8	61	THR	Peptide
1	SE	347	ILE	Peptide
1	SG	61	THR	Peptide
1	SL	61	THR	Peptide
1	SQ	61	THR	Peptide
1	SR	61	THR	Peptide
1	TE	204	ALA	Peptide
1	TE	61	THR	Mainchain
2	U1	24	THR	Peptide
2	U1	43	VAL	Peptide
2	U3	9	SER	Peptide
2	U4	24	THR	Peptide
2	U4	43	VAL	Peptide
2	U6	9	SER	Peptide
2	U7	9	SER	Peptide
2	U8	9	SER	Peptide

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Mol	Chain	Res	Type	Group
1	UE	61	THR	Peptide
2	UG	9	SER	Peptide
2	UL	9	SER	Peptide
2	UQ	9	SER	Peptide
2	UR	9	SER	Peptide
2	V1	16	GLU	Peptide
2	V1	24	THR	Peptide
2	V1	9	SER	Peptide
2	V3	24	THR	Peptide
2	V3	43	VAL	Peptide
2	V4	16	GLU	Peptide
2	V4	24	THR	Peptide
2	V4	9	SER	Peptide
2	V6	24	THR	Peptide
2	V6	43	VAL	Peptide
2	V7	24	THR	Peptide
2	V7	43	VAL	Peptide
2	V8	24	THR	Peptide
2	V8	43	VAL	Peptide
2	VG	24	THR	Peptide
2	VG	43	VAL	Peptide
2	VL	24	THR	Peptide
2	VL	43	VAL	Peptide
2	VQ	24	THR	Peptide
2	VQ	43	VAL	Peptide
2	VR	24	THR	Peptide
2	VR	43	VAL	Peptide
2	W1	44	GLN	Peptide
2	W3	16	GLU	Peptide
2	W3	24	THR	Peptide
2	W3	9	SER	Peptide
2	W4	44	GLN	Peptide
2	W6	16	GLU	Peptide
2	W6	24	THR	Peptide
2	W6	9	SER	Peptide
2	W7	16	GLU	Peptide
2	W7	24	THR	Peptide
2	W7	9	SER	Peptide
2	W8	16	GLU	Peptide
2	W8	24	THR	Peptide
2	W8	9	SER	Peptide
2	WE	9	SER	Peptide

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Mol	Chain	Res	Type	Group
2	WG	16	GLU	Peptide
2	WG	24	THR	Peptide
2	WG	9	SER	Peptide
2	WL	16	GLU	Peptide
2	WL	24	THR	Peptide
2	WL	9	SER	Peptide
2	WQ	16	GLU	Peptide
2	WQ	24	THR	Peptide
2	WQ	9	SER	Peptide
2	WR	16	GLU	Peptide
2	WR	24	THR	Peptide
2	WR	9	SER	Peptide
1	X1	347	ILE	Peptide
2	X3	44	GLN	Peptide
1	X4	347	ILE	Peptide
2	X6	44	GLN	Peptide
2	X7	44	GLN	Peptide
2	X8	44	GLN	Peptide
2	XE	24	THR	Peptide
2	XE	43	VAL	Peptide
2	XG	44	GLN	Peptide
2	XL	44	GLN	Peptide
2	XQ	44	GLN	Peptide
2	XR	44	GLN	Peptide
1	Y1	204	ALA	Peptide
1	Y1	61	THR	Mainchain
1	Y4	204	ALA	Peptide
1	Y4	61	THR	Mainchain
1	Y6	347	ILE	Peptide
1	Y7	347	ILE	Peptide
1	Y8	347	ILE	Peptide
2	YE	16	GLU	Peptide
2	YE	24	THR	Peptide
2	YE	9	SER	Peptide
1	YG	347	ILE	Peptide
1	YL	347	ILE	Peptide
1	YR	347	ILE	Peptide
1	Z1	61	THR	Peptide
2	Z3	9	SER	Peptide
1	Z4	61	THR	Peptide
1	Z6	204	ALA	Peptide
1	Z6	61	THR	Mainchain

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Mol	Chain	Res	Type	Group
1	Z7	204	ALA	Peptide
1	Z7	61	THR	Mainchain
1	Z8	204	ALA	Peptide
1	Z8	61	THR	Mainchain
2	ZE	44	GLN	Peptide
1	ZG	204	ALA	Peptide
1	ZG	61	THR	Mainchain
1	ZL	204	ALA	Peptide
1	ZL	61	THR	Mainchain
2	ZQ	9	SER	Peptide
1	ZR	204	ALA	Peptide
1	ZR	61	THR	Mainchain
2	a3	16	GLU	Peptide
2	a3	24	THR	Peptide
2	a3	9	SER	Peptide
1	a6	61	THR	Peptide
1	a7	61	THR	Peptide
1	a8	61	THR	Peptide
1	aE	347	ILE	Peptide
1	aG	61	THR	Peptide
1	aL	61	THR	Peptide
2	aQ	16	GLU	Peptide
2	aQ	24	THR	Peptide
2	aQ	9	SER	Peptide
1	aR	61	THR	Peptide
2	b1	9	SER	Peptide
2	b4	9	SER	Peptide
1	bE	204	ALA	Peptide
1	bE	61	THR	Mainchain
1	bQ	347	ILE	Peptide
2	c1	24	THR	Peptide
2	c1	43	VAL	Peptide
2	c3	9	SER	Peptide
2	c4	24	THR	Peptide
2	c4	43	VAL	Peptide
2	c6	9	SER	Peptide
2	c7	9	SER	Peptide
2	c8	9	SER	Peptide
1	cE	61	THR	Peptide
2	cG	9	SER	Peptide
2	cL	9	SER	Peptide
1	cQ	204	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	cQ	61	THR	Mainchain
2	cR	9	SER	Peptide
2	d1	16	GLU	Peptide
2	d1	24	THR	Peptide
2	d1	9	SER	Peptide
2	d3	16	GLU	Peptide
2	d3	24	THR	Peptide
2	d3	9	SER	Peptide
2	d4	16	GLU	Peptide
2	d4	24	THR	Peptide
2	d4	9	SER	Peptide
2	d6	24	THR	Peptide
2	d6	43	VAL	Peptide
2	d7	24	THR	Peptide
2	d7	43	VAL	Peptide
2	d8	24	THR	Peptide
2	d8	43	VAL	Peptide
2	dG	24	THR	Peptide
2	dG	43	VAL	Peptide
2	dL	24	THR	Peptide
2	dL	43	VAL	Peptide
1	dQ	61	THR	Peptide
2	dR	24	THR	Peptide
2	dR	43	VAL	Peptide
2	e1	44	GLN	Peptide
2	e4	44	GLN	Peptide
2	e6	16	GLU	Peptide
2	e6	24	THR	Peptide
2	e6	9	SER	Peptide
2	e7	16	GLU	Peptide
2	e7	24	THR	Peptide
2	e7	9	SER	Peptide
2	e8	16	GLU	Peptide
2	e8	24	THR	Peptide
2	e8	9	SER	Peptide
2	eE	9	SER	Peptide
2	eG	16	GLU	Peptide
2	eG	24	THR	Peptide
2	eG	9	SER	Peptide
2	eL	16	GLU	Peptide
2	eL	24	THR	Peptide
2	eL	9	SER	Peptide

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Mol	Chain	Res	Type	Group
2	eR	16	GLU	Peptide
2	eR	24	THR	Peptide
2	eR	9	SER	Peptide
1	f1	347	ILE	Peptide
1	f4	347	ILE	Peptide
2	f6	44	GLN	Peptide
2	f7	44	GLN	Peptide
2	f8	44	GLN	Peptide
2	fE	24	THR	Peptide
2	fE	43	VAL	Peptide
2	fG	44	GLN	Peptide
2	fL	44	GLN	Peptide
2	fQ	9	SER	Peptide
2	fR	44	GLN	Peptide
1	g1	204	ALA	Peptide
1	g1	61	THR	Mainchain
1	g4	204	ALA	Peptide
1	g4	61	THR	Mainchain
1	g6	347	ILE	Peptide
1	g7	347	ILE	Peptide
1	g8	347	ILE	Peptide
2	gE	16	GLU	Peptide
2	gE	24	THR	Peptide
2	gE	9	SER	Peptide
1	gG	347	ILE	Peptide
2	gQ	24	THR	Peptide
2	gQ	43	VAL	Peptide
1	gR	347	ILE	Peptide
1	h1	61	THR	Peptide
1	h4	61	THR	Peptide
1	h6	204	ALA	Peptide
1	h6	61	THR	Mainchain
1	h7	204	ALA	Peptide
1	h7	61	THR	Mainchain
1	h8	204	ALA	Peptide
1	h8	61	THR	Mainchain
2	hE	44	GLN	Peptide
1	hG	204	ALA	Peptide
1	hG	61	THR	Mainchain
2	hL	9	SER	Peptide
2	hQ	16	GLU	Peptide
2	hQ	24	THR	Peptide

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Mol	Chain	Res	Type	Group
2	hQ	9	SER	Peptide
1	hR	204	ALA	Peptide
1	hR	61	THR	Mainchain
1	i6	61	THR	Peptide
1	i7	61	THR	Peptide
1	i8	61	THR	Peptide
1	iG	61	THR	Peptide
2	iL	16	GLU	Peptide
2	iL	24	THR	Peptide
2	iL	9	SER	Peptide
2	iQ	44	GLN	Peptide
1	iR	61	THR	Peptide
2	j1	9	SER	Peptide
2	j4	24	THR	Peptide
2	j4	43	VAL	Peptide
2	k1	24	THR	Peptide
2	k1	43	VAL	Peptide
2	k4	16	GLU	Peptide
2	k4	24	THR	Peptide
2	k4	9	SER	Peptide
2	k6	9	SER	Peptide
2	k7	9	SER	Peptide
2	k8	9	SER	Peptide
2	kG	9	SER	Peptide
2	kR	24	THR	Peptide
2	kR	43	VAL	Peptide
2	l1	16	GLU	Peptide
2	l1	24	THR	Peptide
2	l1	9	SER	Peptide
2	l4	44	GLN	Peptide
2	l6	24	THR	Peptide
2	l6	43	VAL	Peptide
2	l7	24	THR	Peptide
2	l7	43	VAL	Peptide
2	l8	24	THR	Peptide
2	l8	43	VAL	Peptide
2	lG	24	THR	Peptide
2	lG	43	VAL	Peptide
2	lR	16	GLU	Peptide
2	lR	24	THR	Peptide
2	lR	9	SER	Peptide
2	m1	44	GLN	Peptide

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Mol	Chain	Res	Type	Group
2	m6	16	GLU	Peptide
2	m6	24	THR	Peptide
2	m6	9	SER	Peptide
2	m7	16	GLU	Peptide
2	m7	24	THR	Peptide
2	m7	9	SER	Peptide
2	m8	16	GLU	Peptide
2	m8	24	THR	Peptide
2	m8	9	SER	Peptide
2	mG	16	GLU	Peptide
2	mG	24	THR	Peptide
2	mG	9	SER	Peptide
2	mR	44	GLN	Peptide
2	n6	44	GLN	Peptide
2	n7	44	GLN	Peptide
2	n8	44	GLN	Peptide
2	nG	44	GLN	Peptide

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 (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	A1	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	A3	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	A4	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	A6	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	A7	388/408 (95%)	360 (93%)	28 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A8	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	AD	352/408 (86%)	310 (88%)	40 (11%)	2 (1%)	25	62
1	AE	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	AG	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	AJ	352/408 (86%)	309 (88%)	41 (12%)	2 (1%)	25	62
1	AK	352/408 (86%)	310 (88%)	40 (11%)	2 (1%)	25	62
1	AL	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	AP	352/408 (86%)	310 (88%)	40 (11%)	2 (1%)	25	62
1	AQ	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	AR	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	AS	391/408 (96%)	352 (90%)	39 (10%)	0	100	100
1	B1	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	B3	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	B4	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	B6	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	B7	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	B8	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	BD	391/408 (96%)	352 (90%)	39 (10%)	0	100	100
1	BE	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	BG	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	BJ	391/408 (96%)	352 (90%)	39 (10%)	0	100	100
1	BK	391/408 (96%)	352 (90%)	39 (10%)	0	100	100
1	BL	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	BP	391/408 (96%)	352 (90%)	39 (10%)	0	100	100
1	BQ	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	BR	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	BS	384/408 (94%)	345 (90%)	39 (10%)	0	100	100
1	C1	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	C3	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	C4	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	C6	383/408 (94%)	357 (93%)	26 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C7	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	C8	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	CD	384/408 (94%)	345 (90%)	39 (10%)	0	100	100
1	CE	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	CG	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	CJ	384/408 (94%)	344 (90%)	40 (10%)	0	100	100
1	CK	384/408 (94%)	345 (90%)	39 (10%)	0	100	100
1	CL	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	CP	384/408 (94%)	344 (90%)	40 (10%)	0	100	100
1	CQ	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	CR	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	CS	384/408 (94%)	344 (90%)	39 (10%)	1 (0%)	41	74
1	D1	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	D3	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	D4	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	D6	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	D7	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	D8	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	DD	384/408 (94%)	345 (90%)	38 (10%)	1 (0%)	41	74
1	DE	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	DG	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	DJ	384/408 (94%)	344 (90%)	39 (10%)	1 (0%)	41	74
1	DK	384/408 (94%)	344 (90%)	39 (10%)	1 (0%)	41	74
1	DL	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	DP	384/408 (94%)	344 (90%)	39 (10%)	1 (0%)	41	74
1	DQ	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	DR	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	FE	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	I1	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	I3	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	I4	383/408 (94%)	357 (93%)	26 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I6	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	I7	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	I8	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	IG	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	IL	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	IQ	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	IR	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	IS	352/408 (86%)	309 (88%)	41 (12%)	2 (1%)	25	62
1	J1	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	J3	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	J4	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	J6	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	J7	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	J8	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	JG	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	JL	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	JQ	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	JR	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	JS	378/408 (93%)	338 (89%)	40 (11%)	0	100	100
1	K1	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	K3	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	K4	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	K6	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	K7	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	K8	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	KD	378/408 (93%)	337 (89%)	41 (11%)	0	100	100
1	KE	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	KG	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	KJ	378/408 (93%)	337 (89%)	41 (11%)	0	100	100
1	KK	378/408 (93%)	337 (89%)	41 (11%)	0	100	100
1	KL	383/408 (94%)	350 (91%)	33 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	KP	378/408 (93%)	337 (89%)	41 (11%)	0	100	100
1	KQ	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	KR	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	KS	384/408 (94%)	347 (90%)	36 (9%)	1 (0%)	41	74
1	L1	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	L3	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	L4	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	L6	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	L7	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	L8	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	LD	384/408 (94%)	347 (90%)	36 (9%)	1 (0%)	41	74
1	LE	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	LG	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	LJ	384/408 (94%)	347 (90%)	36 (9%)	1 (0%)	41	74
1	LK	384/408 (94%)	348 (91%)	35 (9%)	1 (0%)	41	74
1	LL	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	LP	384/408 (94%)	348 (91%)	35 (9%)	1 (0%)	41	74
1	LQ	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	LR	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	ME	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	NE	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	Q1	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Q3	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Q4	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Q6	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Q7	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Q8	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	QG	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	QL	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	QQ	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	QR	383/408 (94%)	357 (93%)	26 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R1	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	R3	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	R4	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	R6	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	R7	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	R8	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	RG	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	RL	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	RQ	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	RR	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	S1	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	S3	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	S4	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	S6	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	S7	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	S8	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	SE	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	SG	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	SL	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	SQ	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	SR	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	T1	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	T3	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	T4	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	T6	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	T7	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	T8	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	TE	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	TG	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	TL	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	TQ	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	TR	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	UE	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	VE	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	X1	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	X4	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Y1	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	Y3	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	Y4	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	Y6	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Y7	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Y8	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	YG	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	YL	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	YQ	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	YR	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	Z1	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	Z4	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	Z6	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	Z7	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	Z8	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	ZG	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	ZL	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	ZR	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	a1	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	a4	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	a6	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	a7	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	a8	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	aE	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	aG	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	aL	383/408 (94%)	350 (91%)	33 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	aR	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	b3	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	b6	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	b7	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	b8	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	bE	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	bG	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	bL	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	bQ	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	bR	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	cE	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	cQ	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	dE	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	dQ	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	eQ	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	f1	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	f4	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	g1	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	g4	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	g6	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	g7	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	g8	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	gG	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	gL	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	gR	383/408 (94%)	357 (93%)	26 (7%)	0	100	100
1	h1	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	h4	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	h6	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	h7	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	h8	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	hG	388/408 (95%)	360 (93%)	28 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	hR	388/408 (95%)	360 (93%)	28 (7%)	0	100	100
1	i1	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	i4	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	i6	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	i7	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	i8	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	iG	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	iR	383/408 (94%)	350 (91%)	33 (9%)	0	100	100
1	j6	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	j7	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	j8	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	jG	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
1	jR	391/408 (96%)	368 (94%)	22 (6%)	1 (0%)	41	74
2	DS	53/60 (88%)	42 (79%)	11 (21%)	0	100	100
2	E1	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	E3	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	E4	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	E6	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	E7	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	E8	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	ED	53/60 (88%)	42 (79%)	11 (21%)	0	100	100
2	EE	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	EG	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	EJ	53/60 (88%)	42 (79%)	11 (21%)	0	100	100
2	EK	53/60 (88%)	42 (79%)	11 (21%)	0	100	100
2	EL	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	EP	53/60 (88%)	42 (79%)	11 (21%)	0	100	100
2	EQ	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	ER	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	ES	53/60 (88%)	40 (76%)	12 (23%)	1 (2%)	8	42
2	F1	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F3	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	F4	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	F6	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	F7	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	F8	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	FD	53/60 (88%)	40 (76%)	12 (23%)	1 (2%)	8	42
2	FG	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	FJ	53/60 (88%)	39 (74%)	13 (24%)	1 (2%)	8	42
2	FK	53/60 (88%)	40 (76%)	12 (23%)	1 (2%)	8	42
2	FL	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	FP	53/60 (88%)	40 (76%)	12 (23%)	1 (2%)	8	42
2	FQ	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	FR	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	FS	28/60 (47%)	18 (64%)	10 (36%)	0	100	100
2	G1	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	G3	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	G4	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	G6	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	G7	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	G8	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	GD	28/60 (47%)	18 (64%)	10 (36%)	0	100	100
2	GE	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	GG	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	GJ	28/60 (47%)	18 (64%)	10 (36%)	0	100	100
2	GK	28/60 (47%)	18 (64%)	10 (36%)	0	100	100
2	GL	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	GP	28/60 (47%)	18 (64%)	10 (36%)	0	100	100
2	GQ	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	GR	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	GS	52/60 (87%)	38 (73%)	14 (27%)	0	100	100
2	H1	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H3	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	H4	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	H6	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	H7	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	H8	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	HD	52/60 (87%)	38 (73%)	14 (27%)	0	100	100
2	HE	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	HG	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	HJ	52/60 (87%)	38 (73%)	14 (27%)	0	100	100
2	HK	52/60 (87%)	38 (73%)	14 (27%)	0	100	100
2	HL	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	HP	52/60 (87%)	38 (73%)	14 (27%)	0	100	100
2	HQ	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	HR	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	IE	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	JE	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	LS	53/60 (88%)	40 (76%)	13 (24%)	0	100	100
2	M1	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	M3	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	M4	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	M6	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	M7	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	M8	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	MD	53/60 (88%)	40 (76%)	13 (24%)	0	100	100
2	MG	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	MJ	53/60 (88%)	40 (76%)	13 (24%)	0	100	100
2	MK	53/60 (88%)	40 (76%)	13 (24%)	0	100	100
2	ML	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	MP	53/60 (88%)	40 (76%)	13 (24%)	0	100	100
2	MQ	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	MR	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	MS	53/60 (88%)	41 (77%)	10 (19%)	2 (4%)	3	29
2	N1	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	N3	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	N4	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	N6	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	N7	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	N8	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	ND	53/60 (88%)	40 (76%)	11 (21%)	2 (4%)	3	29
2	NG	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	NJ	53/60 (88%)	41 (77%)	10 (19%)	2 (4%)	3	29
2	NK	53/60 (88%)	41 (77%)	10 (19%)	2 (4%)	3	29
2	NL	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	NP	53/60 (88%)	41 (77%)	10 (19%)	2 (4%)	3	29
2	NQ	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	NR	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	O1	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	O3	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	O4	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	O6	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	O7	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	O8	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	OE	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	OG	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	OL	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	OQ	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	OR	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	P1	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	P3	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	P4	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	P6	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	P7	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P8	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	PE	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	PG	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	PL	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	PQ	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	PR	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	QE	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	RE	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	U1	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	U3	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	U4	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	U6	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	U7	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	U8	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	UG	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	UL	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	UQ	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	UR	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	V1	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	V3	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	V4	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	V6	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	V7	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	V8	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	VG	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	VL	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	VQ	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	VR	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	W1	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	W3	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	W4	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	W6	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	W7	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	W8	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	WE	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	WG	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	WL	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	WQ	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	WR	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	X3	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	X6	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	X7	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	X8	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	XE	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	XG	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	XL	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	XQ	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	XR	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	YE	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	Z3	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	ZE	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	ZQ	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	a3	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	aQ	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	b1	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	b4	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	c1	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	c3	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	c4	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	c6	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	c7	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	c8	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	cG	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	cL	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	cR	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	d1	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	d3	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	d4	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	d6	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	d7	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	d8	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	dG	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	dL	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	dR	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	e1	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	e4	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	e6	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	e7	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	e8	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	eE	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	eG	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	eL	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	eR	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	f6	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	f7	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	f8	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	fE	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	fG	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	fL	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	fQ	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	fR	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	gE	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	gQ	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	hE	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	hL	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	hQ	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	iL	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	iQ	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	j1	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	j4	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	k1	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	k4	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	k6	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	k7	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	k8	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	kG	52/60 (87%)	40 (77%)	11 (21%)	1 (2%)	8	42
2	kR	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	l1	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	l4	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	l6	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	l7	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	l8	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	lG	53/60 (88%)	35 (66%)	15 (28%)	3 (6%)	1	21
2	lR	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	m1	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	m6	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	m7	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	m8	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	mG	25/60 (42%)	20 (80%)	5 (20%)	0	100	100
2	mR	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	n6	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	n7	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	n8	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42
2	nG	53/60 (88%)	37 (70%)	15 (28%)	1 (2%)	8	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A2	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	A5	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	A9	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	AA	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	AB	295/327 (90%)	245 (83%)	50 (17%)	0	100	100
3	AC	295/327 (90%)	245 (83%)	49 (17%)	1 (0%)	41	74
3	AF	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	AH	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	AI	295/327 (90%)	245 (83%)	50 (17%)	0	100	100
3	AM	295/327 (90%)	245 (83%)	49 (17%)	1 (0%)	41	74
3	AN	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
3	AO	295/327 (90%)	244 (83%)	51 (17%)	0	100	100
4	B2	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	B5	216/251 (86%)	179 (83%)	37 (17%)	0	100	100
4	B9	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	BA	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	BB	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	BC	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	BF	216/251 (86%)	179 (83%)	37 (17%)	0	100	100
4	BH	216/251 (86%)	179 (83%)	37 (17%)	0	100	100
4	BI	216/251 (86%)	179 (83%)	37 (17%)	0	100	100
4	BM	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	BN	216/251 (86%)	180 (83%)	36 (17%)	0	100	100
4	BO	216/251 (86%)	179 (83%)	37 (17%)	0	100	100
5	C2	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	C5	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	C9	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CA	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CB	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CC	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CF	497/647 (77%)	483 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CH	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CI	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CM	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CN	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	CO	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	D2	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	D5	130/647 (20%)	119 (92%)	10 (8%)	1 (1%)	19	57
5	D9	130/647 (20%)	119 (92%)	10 (8%)	1 (1%)	19	57
5	DA	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	DB	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	DC	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	DF	130/647 (20%)	119 (92%)	10 (8%)	1 (1%)	19	57
5	DH	130/647 (20%)	119 (92%)	10 (8%)	1 (1%)	19	57
5	DI	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	DM	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	DN	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	DO	130/647 (20%)	120 (92%)	9 (7%)	1 (1%)	19	57
5	E2	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	E5	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	E9	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	EA	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	EB	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	EC	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	EF	134/647 (21%)	121 (90%)	12 (9%)	1 (1%)	22	60
5	EH	134/647 (21%)	120 (90%)	13 (10%)	1 (1%)	22	60
5	EI	134/647 (21%)	120 (90%)	13 (10%)	1 (1%)	22	60
5	EM	134/647 (21%)	120 (90%)	13 (10%)	1 (1%)	22	60
5	EN	134/647 (21%)	120 (90%)	13 (10%)	1 (1%)	22	60
5	EO	134/647 (21%)	120 (90%)	13 (10%)	1 (1%)	22	60
5	F2	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	F5	108/647 (17%)	98 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	F9	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FA	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FB	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FC	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FF	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FH	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FI	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FM	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FN	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	FO	108/647 (17%)	98 (91%)	10 (9%)	0	100	100
5	N2	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	N5	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	N9	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NA	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NB	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NC	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NF	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NH	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NI	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NM	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NN	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	NO	497/647 (77%)	483 (97%)	14 (3%)	0	100	100
5	O2	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	O5	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	O9	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OA	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OB	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OC	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OF	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OH	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OI	496/647 (77%)	481 (97%)	15 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	OM	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	ON	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
5	OO	496/647 (77%)	482 (97%)	14 (3%)	0	100	100
6	G2	16/133 (12%)	16 (100%)	0	0	100	100
6	G5	16/133 (12%)	16 (100%)	0	0	100	100
6	G9	16/133 (12%)	16 (100%)	0	0	100	100
6	GA	16/133 (12%)	16 (100%)	0	0	100	100
6	GB	16/133 (12%)	16 (100%)	0	0	100	100
6	GC	16/133 (12%)	16 (100%)	0	0	100	100
6	GF	16/133 (12%)	16 (100%)	0	0	100	100
6	GH	16/133 (12%)	16 (100%)	0	0	100	100
6	GI	16/133 (12%)	16 (100%)	0	0	100	100
6	GM	16/133 (12%)	16 (100%)	0	0	100	100
6	GN	16/133 (12%)	16 (100%)	0	0	100	100
6	GO	16/133 (12%)	16 (100%)	0	0	100	100
6	H2	16/133 (12%)	16 (100%)	0	0	100	100
6	H5	16/133 (12%)	16 (100%)	0	0	100	100
6	H9	16/133 (12%)	16 (100%)	0	0	100	100
6	HA	16/133 (12%)	16 (100%)	0	0	100	100
6	HB	16/133 (12%)	16 (100%)	0	0	100	100
6	HC	16/133 (12%)	16 (100%)	0	0	100	100
6	HF	16/133 (12%)	16 (100%)	0	0	100	100
6	HH	16/133 (12%)	16 (100%)	0	0	100	100
6	HI	16/133 (12%)	16 (100%)	0	0	100	100
6	HM	16/133 (12%)	16 (100%)	0	0	100	100
6	HN	16/133 (12%)	16 (100%)	0	0	100	100
6	HO	16/133 (12%)	16 (100%)	0	0	100	100
6	I2	22/133 (16%)	22 (100%)	0	0	100	100
6	I5	22/133 (16%)	22 (100%)	0	0	100	100
6	I9	22/133 (16%)	22 (100%)	0	0	100	100
6	IA	22/133 (16%)	22 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	IB	22/133 (16%)	22 (100%)	0	0	100	100
6	IC	22/133 (16%)	22 (100%)	0	0	100	100
6	IF	22/133 (16%)	22 (100%)	0	0	100	100
6	IH	22/133 (16%)	22 (100%)	0	0	100	100
6	II	22/133 (16%)	22 (100%)	0	0	100	100
6	IM	22/133 (16%)	22 (100%)	0	0	100	100
6	IN	22/133 (16%)	22 (100%)	0	0	100	100
6	IO	22/133 (16%)	22 (100%)	0	0	100	100
6	J2	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	J5	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	J9	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JA	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JB	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JC	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JF	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JH	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JI	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JM	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JN	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	JO	22/133 (16%)	21 (96%)	1 (4%)	0	100	100
6	K2	20/133 (15%)	20 (100%)	0	0	100	100
6	K5	20/133 (15%)	20 (100%)	0	0	100	100
6	K9	20/133 (15%)	20 (100%)	0	0	100	100
6	KA	20/133 (15%)	20 (100%)	0	0	100	100
6	KB	20/133 (15%)	20 (100%)	0	0	100	100
6	KC	20/133 (15%)	20 (100%)	0	0	100	100
6	KF	20/133 (15%)	20 (100%)	0	0	100	100
6	KH	20/133 (15%)	20 (100%)	0	0	100	100
6	KI	20/133 (15%)	20 (100%)	0	0	100	100
6	KM	20/133 (15%)	20 (100%)	0	0	100	100
6	KN	20/133 (15%)	20 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	KO	20/133 (15%)	20 (100%)	0	0	100	100
6	L2	22/133 (16%)	22 (100%)	0	0	100	100
6	L5	22/133 (16%)	22 (100%)	0	0	100	100
6	L9	22/133 (16%)	22 (100%)	0	0	100	100
6	LA	22/133 (16%)	22 (100%)	0	0	100	100
6	LB	22/133 (16%)	22 (100%)	0	0	100	100
6	LC	22/133 (16%)	22 (100%)	0	0	100	100
6	LF	22/133 (16%)	22 (100%)	0	0	100	100
6	LH	22/133 (16%)	22 (100%)	0	0	100	100
6	LI	22/133 (16%)	22 (100%)	0	0	100	100
6	LM	22/133 (16%)	22 (100%)	0	0	100	100
6	LN	22/133 (16%)	22 (100%)	0	0	100	100
6	LO	22/133 (16%)	22 (100%)	0	0	100	100
7	HS	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	ID	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	IJ	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	IK	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	IP	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	NS	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	OD	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	OJ	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	OK	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	OP	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	SD	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	SJ	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	SK	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	SP	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
7	SS	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
8	PD	15/17 (88%)	14 (93%)	1 (7%)	0	100	100
8	PJ	15/17 (88%)	14 (93%)	1 (7%)	0	100	100
8	PK	15/17 (88%)	14 (93%)	1 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	PP	15/17 (88%)	14 (93%)	1 (7%)	0	100	100
8	PS	15/17 (88%)	14 (93%)	1 (7%)	0	100	100
8	QD	14/17 (82%)	14 (100%)	0	0	100	100
8	QJ	14/17 (82%)	14 (100%)	0	0	100	100
8	QK	14/17 (82%)	14 (100%)	0	0	100	100
8	QP	14/17 (82%)	14 (100%)	0	0	100	100
8	QS	14/17 (82%)	14 (100%)	0	0	100	100
8	RD	10/17 (59%)	9 (90%)	1 (10%)	0	100	100
8	RJ	10/17 (59%)	9 (90%)	1 (10%)	0	100	100
8	RK	10/17 (59%)	9 (90%)	1 (10%)	0	100	100
8	RP	10/17 (59%)	9 (90%)	1 (10%)	0	100	100
8	RS	10/17 (59%)	9 (90%)	1 (10%)	0	100	100
All	All	132187/174156 (76%)	120358 (91%)	11463 (9%)	366 (0%)	44	74

All (366) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F1	44	GLN
2	N1	44	GLN
2	U1	44	GLN
2	c1	44	GLN
2	k1	44	GLN
2	F3	44	GLN
2	N3	44	GLN
2	V3	44	GLN
2	F4	44	GLN
2	N4	44	GLN
2	U4	44	GLN
2	c4	44	GLN
2	j4	44	GLN
2	F6	44	GLN
2	N6	44	GLN
2	V6	44	GLN
2	d6	44	GLN
2	l6	44	GLN
2	F7	44	GLN
2	N7	44	GLN
2	V7	44	GLN

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Mol	Chain	Res	Type
2	d7	44	GLN
2	l7	44	GLN
2	F8	44	GLN
2	N8	44	GLN
2	V8	44	GLN
2	d8	44	GLN
2	l8	44	GLN
1	AD	46	PHE
2	HE	44	GLN
2	PE	44	GLN
2	XE	44	GLN
2	fE	44	GLN
2	FG	44	GLN
2	NG	44	GLN
2	VG	44	GLN
2	dG	44	GLN
2	lG	44	GLN
1	AJ	46	PHE
1	AK	46	PHE
2	FL	44	GLN
2	NL	44	GLN
2	VL	44	GLN
2	dL	44	GLN
1	AP	46	PHE
2	FQ	44	GLN
2	NQ	44	GLN
2	VQ	44	GLN
2	gQ	44	GLN
2	FR	44	GLN
2	NR	44	GLN
2	VR	44	GLN
2	dR	44	GLN
2	kR	44	GLN
1	IS	46	PHE
2	H1	45	ILE
2	P1	45	ILE
2	W1	45	ILE
2	e1	45	ILE
2	m1	45	ILE
2	H3	45	ILE
2	P3	45	ILE
2	X3	45	ILE

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Mol	Chain	Res	Type
2	H4	45	ILE
2	P4	45	ILE
2	W4	45	ILE
2	e4	45	ILE
2	l4	45	ILE
2	H6	45	ILE
2	P6	45	ILE
2	X6	45	ILE
2	f6	45	ILE
2	n6	45	ILE
2	H7	45	ILE
2	P7	45	ILE
2	X7	45	ILE
2	f7	45	ILE
2	n7	45	ILE
2	H8	45	ILE
2	P8	45	ILE
2	X8	45	ILE
2	f8	45	ILE
2	n8	45	ILE
2	FD	45	ILE
2	ND	45	ILE
2	JE	45	ILE
2	RE	45	ILE
2	ZE	45	ILE
2	hE	45	ILE
2	HG	45	ILE
2	PG	45	ILE
2	XG	45	ILE
2	fG	45	ILE
2	nG	45	ILE
2	FJ	45	ILE
2	NJ	45	ILE
2	FK	45	ILE
2	NK	45	ILE
2	HL	45	ILE
2	PL	45	ILE
2	XL	45	ILE
2	fL	45	ILE
2	FP	45	ILE
2	NP	45	ILE
2	HQ	45	ILE

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Mol	Chain	Res	Type
2	PQ	45	ILE
2	XQ	45	ILE
2	iQ	45	ILE
2	HR	45	ILE
2	PR	45	ILE
2	XR	45	ILE
2	fR	45	ILE
2	mR	45	ILE
2	ES	45	ILE
2	MS	45	ILE
2	E1	44	GLN
2	M1	44	GLN
2	b1	44	GLN
2	j1	44	GLN
5	D2	39	ASN
5	E2	108	GLU
2	E3	44	GLN
2	M3	44	GLN
2	U3	44	GLN
2	Z3	44	GLN
2	c3	44	GLN
2	E4	44	GLN
2	M4	44	GLN
2	b4	44	GLN
5	D5	39	ASN
5	E5	108	GLU
2	E6	44	GLN
2	M6	44	GLN
2	U6	44	GLN
2	c6	44	GLN
2	k6	44	GLN
2	E7	44	GLN
2	M7	44	GLN
2	U7	44	GLN
2	c7	44	GLN
2	k7	44	GLN
2	E8	44	GLN
2	M8	44	GLN
2	U8	44	GLN
2	c8	44	GLN
2	k8	44	GLN
5	D9	39	ASN

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Mol	Chain	Res	Type
5	E9	108	GLU
5	DA	39	ASN
5	EA	108	GLU
5	DB	39	ASN
5	EB	108	GLU
5	DC	39	ASN
5	EC	108	GLU
1	DD	181	ASN
2	EE	44	GLN
2	OE	44	GLN
2	WE	44	GLN
2	eE	44	GLN
5	DF	39	ASN
5	EF	108	GLU
2	EG	44	GLN
2	MG	44	GLN
2	UG	44	GLN
2	cG	44	GLN
2	kG	44	GLN
5	DH	39	ASN
5	EH	108	GLU
5	DI	39	ASN
5	EI	108	GLU
1	DJ	181	ASN
1	DK	181	ASN
2	EL	44	GLN
2	ML	44	GLN
2	UL	44	GLN
2	cL	44	GLN
2	hL	44	GLN
5	DM	39	ASN
5	EM	108	GLU
5	DN	39	ASN
5	EN	108	GLU
5	DO	39	ASN
5	EO	108	GLU
1	DP	181	ASN
2	EQ	44	GLN
2	MQ	44	GLN
2	UQ	44	GLN
2	ZQ	44	GLN
2	fQ	44	GLN

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Mol	Chain	Res	Type
2	ER	44	GLN
2	MR	44	GLN
2	UR	44	GLN
2	cR	44	GLN
1	CS	181	ASN
1	D1	339	ASP
2	F1	46	HIS
1	L1	339	ASP
2	N1	46	HIS
1	T1	339	ASP
2	U1	46	HIS
1	a1	339	ASP
2	c1	46	HIS
1	i1	339	ASP
2	k1	46	HIS
1	D3	339	ASP
2	F3	46	HIS
1	L3	339	ASP
2	N3	46	HIS
1	T3	339	ASP
2	V3	46	HIS
1	Y3	339	ASP
1	b3	339	ASP
1	D4	339	ASP
2	F4	46	HIS
1	L4	339	ASP
2	N4	46	HIS
1	T4	339	ASP
2	U4	46	HIS
1	a4	339	ASP
2	c4	46	HIS
1	i4	339	ASP
2	j4	46	HIS
1	D6	339	ASP
2	F6	46	HIS
1	L6	339	ASP
2	N6	46	HIS
1	T6	339	ASP
2	V6	46	HIS
1	b6	339	ASP
2	d6	46	HIS
1	j6	339	ASP

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Mol	Chain	Res	Type
2	l6	46	HIS
1	D7	339	ASP
2	F7	46	HIS
1	L7	339	ASP
2	N7	46	HIS
1	T7	339	ASP
2	V7	46	HIS
1	b7	339	ASP
2	d7	46	HIS
1	j7	339	ASP
2	l7	46	HIS
1	D8	339	ASP
2	F8	46	HIS
1	L8	339	ASP
2	N8	46	HIS
1	T8	339	ASP
2	V8	46	HIS
1	b8	339	ASP
2	d8	46	HIS
1	j8	339	ASP
2	l8	46	HIS
1	AD	59	ASN
2	ND	13	THR
1	DE	339	ASP
1	FE	339	ASP
2	HE	46	HIS
1	NE	339	ASP
2	PE	46	HIS
1	VE	339	ASP
2	XE	46	HIS
1	dE	339	ASP
2	fE	46	HIS
1	DG	339	ASP
2	FG	46	HIS
1	LG	339	ASP
2	NG	46	HIS
1	TG	339	ASP
2	VG	46	HIS
1	bG	339	ASP
2	dG	46	HIS
1	jG	339	ASP
2	lG	46	HIS

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Mol	Chain	Res	Type
1	AJ	59	ASN
2	NJ	13	THR
1	AK	59	ASN
2	NK	13	THR
1	DL	339	ASP
2	FL	46	HIS
1	LL	339	ASP
2	NL	46	HIS
1	TL	339	ASP
2	VL	46	HIS
1	bL	339	ASP
2	dL	46	HIS
1	gL	339	ASP
1	AP	59	ASN
2	NP	13	THR
1	DQ	339	ASP
2	FQ	46	HIS
1	LQ	339	ASP
2	NQ	46	HIS
1	TQ	339	ASP
2	VQ	46	HIS
1	YQ	339	ASP
1	eQ	339	ASP
2	gQ	46	HIS
1	DR	339	ASP
2	FR	46	HIS
1	LR	339	ASP
2	NR	46	HIS
1	TR	339	ASP
2	VR	46	HIS
1	bR	339	ASP
2	dR	46	HIS
1	jR	339	ASP
2	kR	46	HIS
1	IS	59	ASN
2	MS	13	THR
3	AC	45	TYR
1	LD	235	LEU
1	LJ	235	LEU
1	LK	235	LEU
3	AM	45	TYR
1	LP	235	LEU

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Mol	Chain	Res	Type
1	KS	235	LEU
2	F1	45	ILE
2	N1	45	ILE
2	U1	45	ILE
2	c1	45	ILE
2	k1	45	ILE
2	F3	45	ILE
2	N3	45	ILE
2	V3	45	ILE
2	F4	45	ILE
2	N4	45	ILE
2	U4	45	ILE
2	c4	45	ILE
2	j4	45	ILE
2	F6	45	ILE
2	N6	45	ILE
2	V6	45	ILE
2	d6	45	ILE
2	l6	45	ILE
2	F7	45	ILE
2	N7	45	ILE
2	V7	45	ILE
2	d7	45	ILE
2	l7	45	ILE
2	F8	45	ILE
2	N8	45	ILE
2	V8	45	ILE
2	d8	45	ILE
2	l8	45	ILE
2	HE	45	ILE
2	PE	45	ILE
2	XE	45	ILE
2	fE	45	ILE
2	FG	45	ILE
2	NG	45	ILE
2	VG	45	ILE
2	dG	45	ILE
2	lG	45	ILE
2	FL	45	ILE
2	NL	45	ILE
2	VL	45	ILE
2	dL	45	ILE

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Mol	Chain	Res	Type
2	FQ	45	ILE
2	NQ	45	ILE
2	VQ	45	ILE
2	gQ	45	ILE
2	FR	45	ILE
2	NR	45	ILE
2	VR	45	ILE
2	dR	45	ILE
2	kR	45	ILE

5.3.2 Protein sidechains (i)

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	A1	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	A3	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	A4	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	A6	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	A7	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	A8	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	AD	304/367 (83%)	294 (97%)	10 (3%)	38	65
1	AE	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	AG	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	AJ	304/367 (83%)	294 (97%)	10 (3%)	38	65
1	AK	304/367 (83%)	294 (97%)	10 (3%)	38	65
1	AL	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	AP	304/367 (83%)	294 (97%)	10 (3%)	38	65
1	AQ	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	AR	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	AS	353/367 (96%)	344 (98%)	9 (2%)	47	70
1	B1	344/367 (94%)	338 (98%)	6 (2%)	60	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B3	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	B4	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	B6	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	B7	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	B8	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	BD	353/367 (96%)	344 (98%)	9 (2%)	47	70
1	BE	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	BG	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	BJ	353/367 (96%)	344 (98%)	9 (2%)	47	70
1	BK	353/367 (96%)	344 (98%)	9 (2%)	47	70
1	BL	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	BP	353/367 (96%)	344 (98%)	9 (2%)	47	70
1	BQ	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	BR	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	BS	346/367 (94%)	339 (98%)	7 (2%)	55	75
1	C1	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	C3	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	C4	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	C6	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	C7	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	C8	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	CD	346/367 (94%)	339 (98%)	7 (2%)	55	75
1	CE	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	CG	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	CJ	346/367 (94%)	339 (98%)	7 (2%)	55	75
1	CK	346/367 (94%)	339 (98%)	7 (2%)	55	75
1	CL	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	CP	346/367 (94%)	339 (98%)	7 (2%)	55	75
1	CQ	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	CR	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	CS	345/367 (94%)	336 (97%)	9 (3%)	46	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D1	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	D3	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	D4	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	D6	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	D7	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	D8	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	DD	345/367 (94%)	336 (97%)	9 (3%)	46	69
1	DE	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	DG	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	DJ	345/367 (94%)	336 (97%)	9 (3%)	46	69
1	DK	345/367 (94%)	336 (97%)	9 (3%)	46	69
1	DL	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	DP	345/367 (94%)	336 (97%)	9 (3%)	46	69
1	DQ	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	DR	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	FE	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	I1	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	I3	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	I4	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	I6	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	I7	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	I8	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	IG	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	IL	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	IQ	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	IR	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	IS	304/367 (83%)	294 (97%)	10 (3%)	38	65
1	J1	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	J3	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	J4	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	J6	351/367 (96%)	344 (98%)	7 (2%)	55	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J7	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	J8	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	JG	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	JL	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	JQ	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	JR	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	JS	343/367 (94%)	336 (98%)	7 (2%)	55	75
1	K1	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	K3	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	K4	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	K6	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	K7	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	K8	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	KD	343/367 (94%)	336 (98%)	7 (2%)	55	75
1	KE	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	KG	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	KJ	343/367 (94%)	336 (98%)	7 (2%)	55	75
1	KK	343/367 (94%)	336 (98%)	7 (2%)	55	75
1	KL	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	KP	343/367 (94%)	336 (98%)	7 (2%)	55	75
1	KQ	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	KR	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	KS	346/367 (94%)	340 (98%)	6 (2%)	60	78
1	L1	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	L3	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	L4	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	L6	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	L7	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	L8	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	LD	346/367 (94%)	340 (98%)	6 (2%)	60	78
1	LE	351/367 (96%)	344 (98%)	7 (2%)	55	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LG	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	LJ	346/367 (94%)	340 (98%)	6 (2%)	60	78
1	LK	346/367 (94%)	340 (98%)	6 (2%)	60	78
1	LL	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	LP	346/367 (94%)	340 (98%)	6 (2%)	60	78
1	LQ	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	LR	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	ME	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	NE	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	Q1	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Q3	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Q4	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Q6	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Q7	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Q8	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	QG	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	QL	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	QQ	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	QR	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	R1	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	R3	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	R4	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	R6	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	R7	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	R8	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	RG	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	RL	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	RQ	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	RR	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	S1	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	S3	344/367 (94%)	338 (98%)	6 (2%)	60	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S4	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	S6	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	S7	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	S8	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	SE	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	SG	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	SL	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	SQ	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	SR	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	T1	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	T3	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	T4	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	T6	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	T7	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	T8	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	TE	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	TG	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	TL	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	TQ	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	TR	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	UE	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	VE	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	X1	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	X4	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Y1	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	Y3	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	Y4	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	Y6	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Y7	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Y8	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	YG	344/367 (94%)	340 (99%)	4 (1%)	71	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	YL	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	YQ	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	YR	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	Z1	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	Z4	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	Z6	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	Z7	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	Z8	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	ZG	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	ZL	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	ZR	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	a1	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	a4	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	a6	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	a7	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	a8	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	aE	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	aG	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	aL	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	aR	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	b3	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	b6	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	b7	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	b8	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	bE	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	bG	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	bL	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	bQ	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	bR	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	cE	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	cQ	351/367 (96%)	344 (98%)	7 (2%)	55	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	dE	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	dQ	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	eQ	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	f1	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	f4	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	g1	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	g4	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	g6	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	g7	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	g8	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	gG	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	gL	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	gR	344/367 (94%)	340 (99%)	4 (1%)	71	84
1	h1	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	h4	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	h6	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	h7	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	h8	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	hG	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	hR	351/367 (96%)	344 (98%)	7 (2%)	55	75
1	i1	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	i4	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	i6	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	i7	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	i8	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	iG	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	iR	344/367 (94%)	338 (98%)	6 (2%)	60	78
1	j6	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	j7	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	j8	353/367 (96%)	351 (99%)	2 (1%)	86	92
1	jG	353/367 (96%)	351 (99%)	2 (1%)	86	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	jR	353/367 (96%)	351 (99%)	2 (1%)	86	92
2	DS	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	E1	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	E3	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	E4	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	E6	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	E7	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	E8	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	ED	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	EE	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	EG	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	EJ	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	EK	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	EL	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	EP	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	EQ	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	ER	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	ES	51/56 (91%)	48 (94%)	3 (6%)	19	51
2	F1	50/56 (89%)	50 (100%)	0	100	100
2	F3	50/56 (89%)	50 (100%)	0	100	100
2	F4	50/56 (89%)	50 (100%)	0	100	100
2	F6	50/56 (89%)	50 (100%)	0	100	100
2	F7	50/56 (89%)	50 (100%)	0	100	100
2	F8	50/56 (89%)	50 (100%)	0	100	100
2	FD	51/56 (91%)	48 (94%)	3 (6%)	19	51
2	FG	50/56 (89%)	50 (100%)	0	100	100
2	FJ	51/56 (91%)	48 (94%)	3 (6%)	19	51
2	FK	51/56 (91%)	48 (94%)	3 (6%)	19	51
2	FL	50/56 (89%)	50 (100%)	0	100	100
2	FP	51/56 (91%)	48 (94%)	3 (6%)	19	51
2	FQ	50/56 (89%)	50 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	FR	50/56 (89%)	50 (100%)	0	100	100
2	FS	29/56 (52%)	26 (90%)	3 (10%)	7	31
2	G1	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	G3	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	G4	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	G6	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	G7	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	G8	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	GD	29/56 (52%)	26 (90%)	3 (10%)	7	31
2	GE	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	GG	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	GJ	29/56 (52%)	26 (90%)	3 (10%)	7	31
2	GK	29/56 (52%)	26 (90%)	3 (10%)	7	31
2	GL	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	GP	29/56 (52%)	26 (90%)	3 (10%)	7	31
2	GQ	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	GR	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	GS	51/56 (91%)	51 (100%)	0	100	100
2	H1	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	H3	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	H4	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	H6	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	H7	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	H8	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	HD	51/56 (91%)	51 (100%)	0	100	100
2	HE	50/56 (89%)	50 (100%)	0	100	100
2	HG	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	HJ	51/56 (91%)	51 (100%)	0	100	100
2	HK	51/56 (91%)	51 (100%)	0	100	100
2	HL	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	HP	51/56 (91%)	51 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	HQ	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	HR	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	IE	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	JE	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	LS	51/56 (91%)	47 (92%)	4 (8%)	12	42
2	M1	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	M3	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	M4	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	M6	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	M7	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	M8	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	MD	51/56 (91%)	47 (92%)	4 (8%)	12	42
2	MG	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	MJ	51/56 (91%)	47 (92%)	4 (8%)	12	42
2	MK	51/56 (91%)	47 (92%)	4 (8%)	12	42
2	ML	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	MP	51/56 (91%)	47 (92%)	4 (8%)	12	42
2	MQ	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	MR	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	MS	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	N1	50/56 (89%)	50 (100%)	0	100	100
2	N3	50/56 (89%)	50 (100%)	0	100	100
2	N4	50/56 (89%)	50 (100%)	0	100	100
2	N6	50/56 (89%)	50 (100%)	0	100	100
2	N7	50/56 (89%)	50 (100%)	0	100	100
2	N8	50/56 (89%)	50 (100%)	0	100	100
2	ND	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	NG	50/56 (89%)	50 (100%)	0	100	100
2	NJ	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	NK	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	NL	50/56 (89%)	50 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	NP	51/56 (91%)	50 (98%)	1 (2%)	55	75
2	NQ	50/56 (89%)	50 (100%)	0	100	100
2	NR	50/56 (89%)	50 (100%)	0	100	100
2	O1	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	O3	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	O4	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	O6	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	O7	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	O8	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	OE	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	OG	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	OL	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	OQ	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	OR	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	P1	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	P3	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	P4	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	P6	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	P7	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	P8	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	PE	50/56 (89%)	50 (100%)	0	100	100
2	PG	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	PL	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	PQ	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	PR	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	QE	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	RE	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	U1	50/56 (89%)	50 (100%)	0	100	100
2	U3	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	U4	50/56 (89%)	50 (100%)	0	100	100
2	U6	50/56 (89%)	47 (94%)	3 (6%)	19	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U7	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	U8	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	UG	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	UL	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	UQ	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	UR	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	V1	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	V3	50/56 (89%)	50 (100%)	0	100	100
2	V4	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	V6	50/56 (89%)	50 (100%)	0	100	100
2	V7	50/56 (89%)	50 (100%)	0	100	100
2	V8	50/56 (89%)	50 (100%)	0	100	100
2	VG	50/56 (89%)	50 (100%)	0	100	100
2	VL	50/56 (89%)	50 (100%)	0	100	100
2	VQ	50/56 (89%)	50 (100%)	0	100	100
2	VR	50/56 (89%)	50 (100%)	0	100	100
2	W1	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	W3	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	W4	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	W6	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	W7	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	W8	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	WE	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	WG	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	WL	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	WQ	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	WR	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	X3	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	X6	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	X7	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	X8	49/56 (88%)	48 (98%)	1 (2%)	55	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	XE	50/56 (89%)	50 (100%)	0	100	100
2	XG	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	XL	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	XQ	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	XR	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	YE	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	Z3	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	ZE	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	ZQ	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	a3	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	aQ	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	b1	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	b4	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	c1	50/56 (89%)	50 (100%)	0	100	100
2	c3	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	c4	50/56 (89%)	50 (100%)	0	100	100
2	c6	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	c7	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	c8	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	cG	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	cL	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	cR	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	d1	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	d3	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	d4	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	d6	50/56 (89%)	50 (100%)	0	100	100
2	d7	50/56 (89%)	50 (100%)	0	100	100
2	d8	50/56 (89%)	50 (100%)	0	100	100
2	dG	50/56 (89%)	50 (100%)	0	100	100
2	dL	50/56 (89%)	50 (100%)	0	100	100
2	dR	50/56 (89%)	50 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	e1	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	e4	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	e6	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	e7	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	e8	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	eE	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	eG	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	eL	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	eR	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	f6	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	f7	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	f8	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	fE	50/56 (89%)	50 (100%)	0	100	100
2	fG	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	fL	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	fQ	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	fR	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	gE	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	gQ	50/56 (89%)	50 (100%)	0	100	100
2	hE	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	hL	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	hQ	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	iL	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	iQ	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	j1	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	j4	50/56 (89%)	50 (100%)	0	100	100
2	k1	50/56 (89%)	50 (100%)	0	100	100
2	k4	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	k6	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	k7	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	k8	50/56 (89%)	47 (94%)	3 (6%)	19	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	kG	50/56 (89%)	47 (94%)	3 (6%)	19	50
2	kR	50/56 (89%)	50 (100%)	0	100	100
2	l1	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	l4	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	l6	50/56 (89%)	50 (100%)	0	100	100
2	l7	50/56 (89%)	50 (100%)	0	100	100
2	l8	50/56 (89%)	50 (100%)	0	100	100
2	lG	50/56 (89%)	50 (100%)	0	100	100
2	lR	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	m1	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	m6	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	m7	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	m8	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	mG	25/56 (45%)	23 (92%)	2 (8%)	12	42
2	mR	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	n6	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	n7	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	n8	49/56 (88%)	48 (98%)	1 (2%)	55	75
2	nG	49/56 (88%)	48 (98%)	1 (2%)	55	75
3	A2	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	A5	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	A9	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AA	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AB	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AC	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AF	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AH	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AI	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AM	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AN	258/304 (85%)	256 (99%)	2 (1%)	81	89
3	AO	258/304 (85%)	256 (99%)	2 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B2	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	B5	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	B9	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BA	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BB	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BC	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BF	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BH	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BI	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BM	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BN	193/233 (83%)	192 (100%)	1 (0%)	88	94
4	BO	193/233 (83%)	192 (100%)	1 (0%)	88	94
5	C2	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	C5	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	C9	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CA	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CB	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CC	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CF	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CH	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CI	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CM	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CN	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	CO	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	D2	115/567 (20%)	115 (100%)	0	100	100
5	D5	115/567 (20%)	115 (100%)	0	100	100
5	D9	115/567 (20%)	115 (100%)	0	100	100
5	DA	115/567 (20%)	115 (100%)	0	100	100
5	DB	115/567 (20%)	115 (100%)	0	100	100
5	DC	115/567 (20%)	115 (100%)	0	100	100
5	DF	115/567 (20%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	DH	115/567 (20%)	115 (100%)	0	100	100
5	DI	115/567 (20%)	115 (100%)	0	100	100
5	DM	115/567 (20%)	115 (100%)	0	100	100
5	DN	115/567 (20%)	115 (100%)	0	100	100
5	DO	115/567 (20%)	115 (100%)	0	100	100
5	E2	126/567 (22%)	126 (100%)	0	100	100
5	E5	126/567 (22%)	126 (100%)	0	100	100
5	E9	126/567 (22%)	126 (100%)	0	100	100
5	EA	126/567 (22%)	126 (100%)	0	100	100
5	EB	126/567 (22%)	126 (100%)	0	100	100
5	EC	126/567 (22%)	126 (100%)	0	100	100
5	EF	126/567 (22%)	126 (100%)	0	100	100
5	EH	126/567 (22%)	126 (100%)	0	100	100
5	EI	126/567 (22%)	126 (100%)	0	100	100
5	EM	126/567 (22%)	126 (100%)	0	100	100
5	EN	126/567 (22%)	126 (100%)	0	100	100
5	EO	126/567 (22%)	126 (100%)	0	100	100
5	F2	97/567 (17%)	97 (100%)	0	100	100
5	F5	97/567 (17%)	97 (100%)	0	100	100
5	F9	97/567 (17%)	97 (100%)	0	100	100
5	FA	97/567 (17%)	97 (100%)	0	100	100
5	FB	97/567 (17%)	97 (100%)	0	100	100
5	FC	97/567 (17%)	97 (100%)	0	100	100
5	FF	97/567 (17%)	97 (100%)	0	100	100
5	FH	97/567 (17%)	97 (100%)	0	100	100
5	FI	97/567 (17%)	97 (100%)	0	100	100
5	FM	97/567 (17%)	97 (100%)	0	100	100
5	FN	97/567 (17%)	97 (100%)	0	100	100
5	FO	97/567 (17%)	97 (100%)	0	100	100
5	N2	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	N5	432/567 (76%)	431 (100%)	1 (0%)	93	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	N9	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NA	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NB	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NC	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NF	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NH	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NI	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NM	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NN	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	NO	432/567 (76%)	431 (100%)	1 (0%)	93	97
5	O2	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	O5	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	O9	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OA	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OB	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OC	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OF	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OH	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OI	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OM	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	ON	431/567 (76%)	430 (100%)	1 (0%)	93	97
5	OO	431/567 (76%)	430 (100%)	1 (0%)	93	97
6	K2	1/132 (1%)	1 (100%)	0	100	100
6	K5	1/132 (1%)	1 (100%)	0	100	100
6	K9	1/132 (1%)	1 (100%)	0	100	100
6	KA	1/132 (1%)	1 (100%)	0	100	100
6	KB	1/132 (1%)	1 (100%)	0	100	100
6	KC	1/132 (1%)	1 (100%)	0	100	100
6	KF	1/132 (1%)	1 (100%)	0	100	100
6	KH	1/132 (1%)	1 (100%)	0	100	100
6	KI	1/132 (1%)	1 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	KM	1/132 (1%)	1 (100%)	0	100	100
6	KN	1/132 (1%)	1 (100%)	0	100	100
6	KO	1/132 (1%)	1 (100%)	0	100	100
All	All	116815/148257 (79%)	115173 (99%)	1642 (1%)	68	81

All (1642) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C1	98	ASN
1	C1	206	LEU
1	C1	207	ASN
1	C1	319	TYR
1	A1	31	LYS
1	A1	62	LEU
1	A1	65	ASP
1	A1	74	TRP
1	A1	183	LEU
1	A1	259	PHE
1	A1	348	ASN
1	B1	73	ASN
1	B1	94	THR
1	B1	98	ASN
1	B1	109	LEU
1	B1	259	PHE
1	B1	261	ILE
1	D1	98	ASN
1	D1	235	LEU
2	E1	38	GLU
2	E1	41	TYR
2	E1	45	ILE
2	G1	8	ARG
2	G1	21	ASN
2	H1	22	LYS
1	I1	98	ASN
1	I1	206	LEU
1	I1	207	ASN
1	I1	319	TYR
1	J1	31	LYS
1	J1	62	LEU
1	J1	65	ASP
1	J1	74	TRP

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Mol	Chain	Res	Type
1	J1	183	LEU
1	J1	259	PHE
1	J1	348	ASN
1	K1	73	ASN
1	K1	94	THR
1	K1	98	ASN
1	K1	109	LEU
1	K1	259	PHE
1	K1	261	ILE
1	L1	98	ASN
1	L1	235	LEU
2	M1	38	GLU
2	M1	41	TYR
2	M1	45	ILE
2	O1	8	ARG
2	O1	21	ASN
2	P1	22	LYS
1	Q1	98	ASN
1	Q1	206	LEU
1	Q1	207	ASN
1	Q1	319	TYR
1	R1	31	LYS
1	R1	62	LEU
1	R1	65	ASP
1	R1	74	TRP
1	R1	183	LEU
1	R1	259	PHE
1	R1	348	ASN
1	S1	73	ASN
1	S1	94	THR
1	S1	98	ASN
1	S1	109	LEU
1	S1	259	PHE
1	S1	261	ILE
1	T1	98	ASN
1	T1	235	LEU
2	V1	8	ARG
2	V1	21	ASN
2	W1	22	LYS
1	X1	98	ASN
1	X1	206	LEU
1	X1	207	ASN

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Mol	Chain	Res	Type
1	X1	319	TYR
1	Y1	31	LYS
1	Y1	62	LEU
1	Y1	65	ASP
1	Y1	74	TRP
1	Y1	183	LEU
1	Y1	259	PHE
1	Y1	348	ASN
1	Z1	73	ASN
1	Z1	94	THR
1	Z1	98	ASN
1	Z1	109	LEU
1	Z1	259	PHE
1	Z1	261	ILE
1	a1	98	ASN
1	a1	235	LEU
2	b1	38	GLU
2	b1	41	TYR
2	b1	45	ILE
2	d1	8	ARG
2	d1	21	ASN
2	e1	22	LYS
1	f1	98	ASN
1	f1	206	LEU
1	f1	207	ASN
1	f1	319	TYR
1	g1	31	LYS
1	g1	62	LEU
1	g1	65	ASP
1	g1	74	TRP
1	g1	183	LEU
1	g1	259	PHE
1	g1	348	ASN
1	h1	73	ASN
1	h1	94	THR
1	h1	98	ASN
1	h1	109	LEU
1	h1	259	PHE
1	h1	261	ILE
1	i1	98	ASN
1	i1	235	LEU
2	j1	38	GLU

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Mol	Chain	Res	Type
2	j1	41	TYR
2	j1	45	ILE
2	l1	8	ARG
2	l1	21	ASN
2	m1	22	LYS
3	A2	6	ARG
3	A2	41	LEU
4	B2	220	THR
5	C2	388	LYS
5	N2	388	LYS
5	O2	388	LYS
1	C3	98	ASN
1	C3	206	LEU
1	C3	207	ASN
1	C3	319	TYR
1	A3	31	LYS
1	A3	62	LEU
1	A3	65	ASP
1	A3	74	TRP
1	A3	183	LEU
1	A3	259	PHE
1	A3	348	ASN
1	B3	73	ASN
1	B3	94	THR
1	B3	98	ASN
1	B3	109	LEU
1	B3	259	PHE
1	B3	261	ILE
1	D3	98	ASN
1	D3	235	LEU
2	E3	38	GLU
2	E3	41	TYR
2	E3	45	ILE
2	G3	8	ARG
2	G3	21	ASN
2	H3	22	LYS
1	I3	98	ASN
1	I3	206	LEU
1	I3	207	ASN
1	I3	319	TYR
1	J3	31	LYS
1	J3	62	LEU

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Mol	Chain	Res	Type
1	J3	65	ASP
1	J3	74	TRP
1	J3	183	LEU
1	J3	259	PHE
1	J3	348	ASN
1	K3	73	ASN
1	K3	94	THR
1	K3	98	ASN
1	K3	109	LEU
1	K3	259	PHE
1	K3	261	ILE
1	L3	98	ASN
1	L3	235	LEU
2	M3	38	GLU
2	M3	41	TYR
2	M3	45	ILE
2	O3	8	ARG
2	O3	21	ASN
2	P3	22	LYS
1	Q3	98	ASN
1	Q3	206	LEU
1	Q3	207	ASN
1	Q3	319	TYR
1	R3	31	LYS
1	R3	62	LEU
1	R3	65	ASP
1	R3	74	TRP
1	R3	183	LEU
1	R3	259	PHE
1	R3	348	ASN
1	S3	73	ASN
1	S3	94	THR
1	S3	98	ASN
1	S3	109	LEU
1	S3	259	PHE
1	S3	261	ILE
1	T3	98	ASN
1	T3	235	LEU
2	U3	38	GLU
2	U3	41	TYR
2	U3	45	ILE
2	W3	8	ARG

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Mol	Chain	Res	Type
2	W3	21	ASN
2	X3	22	LYS
1	Y3	98	ASN
1	Y3	235	LEU
2	Z3	38	GLU
2	Z3	41	TYR
2	Z3	45	ILE
2	a3	8	ARG
2	a3	21	ASN
1	b3	98	ASN
1	b3	235	LEU
2	c3	38	GLU
2	c3	41	TYR
2	c3	45	ILE
2	d3	8	ARG
2	d3	21	ASN
1	C4	98	ASN
1	C4	206	LEU
1	C4	207	ASN
1	C4	319	TYR
1	A4	31	LYS
1	A4	62	LEU
1	A4	65	ASP
1	A4	74	TRP
1	A4	183	LEU
1	A4	259	PHE
1	A4	348	ASN
1	B4	73	ASN
1	B4	94	THR
1	B4	98	ASN
1	B4	109	LEU
1	B4	259	PHE
1	B4	261	ILE
1	D4	98	ASN
1	D4	235	LEU
2	E4	38	GLU
2	E4	41	TYR
2	E4	45	ILE
2	G4	8	ARG
2	G4	21	ASN
2	H4	22	LYS
1	I4	98	ASN

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Mol	Chain	Res	Type
1	I4	206	LEU
1	I4	207	ASN
1	I4	319	TYR
1	J4	31	LYS
1	J4	62	LEU
1	J4	65	ASP
1	J4	74	TRP
1	J4	183	LEU
1	J4	259	PHE
1	J4	348	ASN
1	K4	73	ASN
1	K4	94	THR
1	K4	98	ASN
1	K4	109	LEU
1	K4	259	PHE
1	K4	261	ILE
1	L4	98	ASN
1	L4	235	LEU
2	M4	38	GLU
2	M4	41	TYR
2	M4	45	ILE
2	O4	8	ARG
2	O4	21	ASN
2	P4	22	LYS
1	Q4	98	ASN
1	Q4	206	LEU
1	Q4	207	ASN
1	Q4	319	TYR
1	R4	31	LYS
1	R4	62	LEU
1	R4	65	ASP
1	R4	74	TRP
1	R4	183	LEU
1	R4	259	PHE
1	R4	348	ASN
1	S4	73	ASN
1	S4	94	THR
1	S4	98	ASN
1	S4	109	LEU
1	S4	259	PHE
1	S4	261	ILE
1	T4	98	ASN

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Mol	Chain	Res	Type
1	T4	235	LEU
2	V4	8	ARG
2	V4	21	ASN
2	W4	22	LYS
1	X4	98	ASN
1	X4	206	LEU
1	X4	207	ASN
1	X4	319	TYR
1	Y4	31	LYS
1	Y4	62	LEU
1	Y4	65	ASP
1	Y4	74	TRP
1	Y4	183	LEU
1	Y4	259	PHE
1	Y4	348	ASN
1	Z4	73	ASN
1	Z4	94	THR
1	Z4	98	ASN
1	Z4	109	LEU
1	Z4	259	PHE
1	Z4	261	ILE
1	a4	98	ASN
1	a4	235	LEU
2	b4	38	GLU
2	b4	41	TYR
2	b4	45	ILE
2	d4	8	ARG
2	d4	21	ASN
2	e4	22	LYS
1	f4	98	ASN
1	f4	206	LEU
1	f4	207	ASN
1	f4	319	TYR
1	g4	31	LYS
1	g4	62	LEU
1	g4	65	ASP
1	g4	74	TRP
1	g4	183	LEU
1	g4	259	PHE
1	g4	348	ASN
1	h4	73	ASN
1	h4	94	THR

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Mol	Chain	Res	Type
1	h4	98	ASN
1	h4	109	LEU
1	h4	259	PHE
1	h4	261	ILE
1	i4	98	ASN
1	i4	235	LEU
2	k4	8	ARG
2	k4	21	ASN
2	l4	22	LYS
3	A5	6	ARG
3	A5	41	LEU
4	B5	220	THR
5	C5	388	LYS
5	N5	388	LYS
5	O5	388	LYS
1	C6	98	ASN
1	C6	206	LEU
1	C6	207	ASN
1	C6	319	TYR
1	A6	31	LYS
1	A6	62	LEU
1	A6	65	ASP
1	A6	74	TRP
1	A6	183	LEU
1	A6	259	PHE
1	A6	348	ASN
1	B6	73	ASN
1	B6	94	THR
1	B6	98	ASN
1	B6	109	LEU
1	B6	259	PHE
1	B6	261	ILE
1	D6	98	ASN
1	D6	235	LEU
2	E6	38	GLU
2	E6	41	TYR
2	E6	45	ILE
2	G6	8	ARG
2	G6	21	ASN
2	H6	22	LYS
1	I6	98	ASN
1	I6	206	LEU

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Mol	Chain	Res	Type
1	I6	207	ASN
1	I6	319	TYR
1	J6	31	LYS
1	J6	62	LEU
1	J6	65	ASP
1	J6	74	TRP
1	J6	183	LEU
1	J6	259	PHE
1	J6	348	ASN
1	K6	73	ASN
1	K6	94	THR
1	K6	98	ASN
1	K6	109	LEU
1	K6	259	PHE
1	K6	261	ILE
1	L6	98	ASN
1	L6	235	LEU
2	M6	38	GLU
2	M6	41	TYR
2	M6	45	ILE
2	O6	8	ARG
2	O6	21	ASN
2	P6	22	LYS
1	Q6	98	ASN
1	Q6	206	LEU
1	Q6	207	ASN
1	Q6	319	TYR
1	R6	31	LYS
1	R6	62	LEU
1	R6	65	ASP
1	R6	74	TRP
1	R6	183	LEU
1	R6	259	PHE
1	R6	348	ASN
1	S6	73	ASN
1	S6	94	THR
1	S6	98	ASN
1	S6	109	LEU
1	S6	259	PHE
1	S6	261	ILE
1	T6	98	ASN
1	T6	235	LEU

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Mol	Chain	Res	Type
2	U6	38	GLU
2	U6	41	TYR
2	U6	45	ILE
2	W6	8	ARG
2	W6	21	ASN
2	X6	22	LYS
1	Y6	98	ASN
1	Y6	206	LEU
1	Y6	207	ASN
1	Y6	319	TYR
1	Z6	31	LYS
1	Z6	62	LEU
1	Z6	65	ASP
1	Z6	74	TRP
1	Z6	183	LEU
1	Z6	259	PHE
1	Z6	348	ASN
1	a6	73	ASN
1	a6	94	THR
1	a6	98	ASN
1	a6	109	LEU
1	a6	259	PHE
1	a6	261	ILE
1	b6	98	ASN
1	b6	235	LEU
2	c6	38	GLU
2	c6	41	TYR
2	c6	45	ILE
2	e6	8	ARG
2	e6	21	ASN
2	f6	22	LYS
1	g6	98	ASN
1	g6	206	LEU
1	g6	207	ASN
1	g6	319	TYR
1	h6	31	LYS
1	h6	62	LEU
1	h6	65	ASP
1	h6	74	TRP
1	h6	183	LEU
1	h6	259	PHE
1	h6	348	ASN

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Mol	Chain	Res	Type
1	i6	73	ASN
1	i6	94	THR
1	i6	98	ASN
1	i6	109	LEU
1	i6	259	PHE
1	i6	261	ILE
1	j6	98	ASN
1	j6	235	LEU
2	k6	38	GLU
2	k6	41	TYR
2	k6	45	ILE
2	m6	8	ARG
2	m6	21	ASN
2	n6	22	LYS
1	C7	98	ASN
1	C7	206	LEU
1	C7	207	ASN
1	C7	319	TYR
1	A7	31	LYS
1	A7	62	LEU
1	A7	65	ASP
1	A7	74	TRP
1	A7	183	LEU
1	A7	259	PHE
1	A7	348	ASN
1	B7	73	ASN
1	B7	94	THR
1	B7	98	ASN
1	B7	109	LEU
1	B7	259	PHE
1	B7	261	ILE
1	D7	98	ASN
1	D7	235	LEU
2	E7	38	GLU
2	E7	41	TYR
2	E7	45	ILE
2	G7	8	ARG
2	G7	21	ASN
2	H7	22	LYS
1	I7	98	ASN
1	I7	206	LEU
1	I7	207	ASN

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Mol	Chain	Res	Type
1	I7	319	TYR
1	J7	31	LYS
1	J7	62	LEU
1	J7	65	ASP
1	J7	74	TRP
1	J7	183	LEU
1	J7	259	PHE
1	J7	348	ASN
1	K7	73	ASN
1	K7	94	THR
1	K7	98	ASN
1	K7	109	LEU
1	K7	259	PHE
1	K7	261	ILE
1	L7	98	ASN
1	L7	235	LEU
2	M7	38	GLU
2	M7	41	TYR
2	M7	45	ILE
2	O7	8	ARG
2	O7	21	ASN
2	P7	22	LYS
1	Q7	98	ASN
1	Q7	206	LEU
1	Q7	207	ASN
1	Q7	319	TYR
1	R7	31	LYS
1	R7	62	LEU
1	R7	65	ASP
1	R7	74	TRP
1	R7	183	LEU
1	R7	259	PHE
1	R7	348	ASN
1	S7	73	ASN
1	S7	94	THR
1	S7	98	ASN
1	S7	109	LEU
1	S7	259	PHE
1	S7	261	ILE
1	T7	98	ASN
1	T7	235	LEU
2	U7	38	GLU

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Mol	Chain	Res	Type
2	U7	41	TYR
2	U7	45	ILE
2	W7	8	ARG
2	W7	21	ASN
2	X7	22	LYS
1	Y7	98	ASN
1	Y7	206	LEU
1	Y7	207	ASN
1	Y7	319	TYR
1	Z7	31	LYS
1	Z7	62	LEU
1	Z7	65	ASP
1	Z7	74	TRP
1	Z7	183	LEU
1	Z7	259	PHE
1	Z7	348	ASN
1	a7	73	ASN
1	a7	94	THR
1	a7	98	ASN
1	a7	109	LEU
1	a7	259	PHE
1	a7	261	ILE
1	b7	98	ASN
1	b7	235	LEU
2	c7	38	GLU
2	c7	41	TYR
2	c7	45	ILE
2	e7	8	ARG
2	e7	21	ASN
2	f7	22	LYS
1	g7	98	ASN
1	g7	206	LEU
1	g7	207	ASN
1	g7	319	TYR
1	h7	31	LYS
1	h7	62	LEU
1	h7	65	ASP
1	h7	74	TRP
1	h7	183	LEU
1	h7	259	PHE
1	h7	348	ASN
1	i7	73	ASN

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Mol	Chain	Res	Type
1	i7	94	THR
1	i7	98	ASN
1	i7	109	LEU
1	i7	259	PHE
1	i7	261	ILE
1	j7	98	ASN
1	j7	235	LEU
2	k7	38	GLU
2	k7	41	TYR
2	k7	45	ILE
2	m7	8	ARG
2	m7	21	ASN
2	n7	22	LYS
1	C8	98	ASN
1	C8	206	LEU
1	C8	207	ASN
1	C8	319	TYR
1	A8	31	LYS
1	A8	62	LEU
1	A8	65	ASP
1	A8	74	TRP
1	A8	183	LEU
1	A8	259	PHE
1	A8	348	ASN
1	B8	73	ASN
1	B8	94	THR
1	B8	98	ASN
1	B8	109	LEU
1	B8	259	PHE
1	B8	261	ILE
1	D8	98	ASN
1	D8	235	LEU
2	E8	38	GLU
2	E8	41	TYR
2	E8	45	ILE
2	G8	8	ARG
2	G8	21	ASN
2	H8	22	LYS
1	I8	98	ASN
1	I8	206	LEU
1	I8	207	ASN
1	I8	319	TYR

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Mol	Chain	Res	Type
1	J8	31	LYS
1	J8	62	LEU
1	J8	65	ASP
1	J8	74	TRP
1	J8	183	LEU
1	J8	259	PHE
1	J8	348	ASN
1	K8	73	ASN
1	K8	94	THR
1	K8	98	ASN
1	K8	109	LEU
1	K8	259	PHE
1	K8	261	ILE
1	L8	98	ASN
1	L8	235	LEU
2	M8	38	GLU
2	M8	41	TYR
2	M8	45	ILE
2	O8	8	ARG
2	O8	21	ASN
2	P8	22	LYS
1	Q8	98	ASN
1	Q8	206	LEU
1	Q8	207	ASN
1	Q8	319	TYR
1	R8	31	LYS
1	R8	62	LEU
1	R8	65	ASP
1	R8	74	TRP
1	R8	183	LEU
1	R8	259	PHE
1	R8	348	ASN
1	S8	73	ASN
1	S8	94	THR
1	S8	98	ASN
1	S8	109	LEU
1	S8	259	PHE
1	S8	261	ILE
1	T8	98	ASN
1	T8	235	LEU
2	U8	38	GLU
2	U8	41	TYR

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Mol	Chain	Res	Type
2	U8	45	ILE
2	W8	8	ARG
2	W8	21	ASN
2	X8	22	LYS
1	Y8	98	ASN
1	Y8	206	LEU
1	Y8	207	ASN
1	Y8	319	TYR
1	Z8	31	LYS
1	Z8	62	LEU
1	Z8	65	ASP
1	Z8	74	TRP
1	Z8	183	LEU
1	Z8	259	PHE
1	Z8	348	ASN
1	a8	73	ASN
1	a8	94	THR
1	a8	98	ASN
1	a8	109	LEU
1	a8	259	PHE
1	a8	261	ILE
1	b8	98	ASN
1	b8	235	LEU
2	c8	38	GLU
2	c8	41	TYR
2	c8	45	ILE
2	e8	8	ARG
2	e8	21	ASN
2	f8	22	LYS
1	g8	98	ASN
1	g8	206	LEU
1	g8	207	ASN
1	g8	319	TYR
1	h8	31	LYS
1	h8	62	LEU
1	h8	65	ASP
1	h8	74	TRP
1	h8	183	LEU
1	h8	259	PHE
1	h8	348	ASN
1	i8	73	ASN
1	i8	94	THR

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Mol	Chain	Res	Type
1	i8	98	ASN
1	i8	109	LEU
1	i8	259	PHE
1	i8	261	ILE
1	j8	98	ASN
1	j8	235	LEU
2	k8	38	GLU
2	k8	41	TYR
2	k8	45	ILE
2	m8	8	ARG
2	m8	21	ASN
2	n8	22	LYS
3	A9	6	ARG
3	A9	41	LEU
4	B9	220	THR
5	C9	388	LYS
5	N9	388	LYS
5	O9	388	LYS
3	AA	6	ARG
3	AA	41	LEU
4	BA	220	THR
5	CA	388	LYS
5	NA	388	LYS
5	OA	388	LYS
3	AB	6	ARG
3	AB	41	LEU
4	BB	220	THR
5	CB	388	LYS
5	NB	388	LYS
5	OB	388	LYS
3	AC	6	ARG
3	AC	41	LEU
4	BC	220	THR
5	CC	388	LYS
5	NC	388	LYS
5	OC	388	LYS
1	AD	58	ILE
1	AD	59	ASN
1	AD	60	GLU
1	AD	62	LEU
1	AD	63	LEU
1	AD	79	GLN

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Mol	Chain	Res	Type
1	AD	111	ARG
1	AD	115	ARG
1	AD	172	ARG
1	AD	251	LEU
1	BD	4	GLN
1	BD	31	LYS
1	BD	45	MET
1	BD	70	ASN
1	BD	111	ARG
1	BD	167	GLU
1	BD	172	ARG
1	BD	236	LYS
1	BD	240	ILE
1	CD	19	LYS
1	CD	70	ASN
1	CD	73	ASN
1	CD	94	THR
1	CD	172	ARG
1	CD	337	LYS
1	CD	382	LYS
1	DD	16	LYS
1	DD	45	MET
1	DD	70	ASN
1	DD	94	THR
1	DD	103	LYS
1	DD	115	ARG
1	DD	166	LEU
1	DD	175	LEU
1	DD	382	LYS
2	ED	8	ARG
2	FD	13	THR
2	FD	19	ARG
2	FD	22	LYS
2	GD	30	MET
2	GD	34	THR
2	GD	36	LYS
1	KD	19	LYS
1	KD	73	ASN
1	KD	77	LYS
1	KD	172	ARG
1	KD	250	LEU
1	KD	337	LYS

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Mol	Chain	Res	Type
1	KD	351	LYS
1	LD	45	MET
1	LD	92	MET
1	LD	94	THR
1	LD	175	LEU
1	LD	235	LEU
1	LD	382	LYS
2	MD	8	ARG
2	MD	22	LYS
2	MD	23	ARG
2	MD	30	MET
2	ND	30	MET
1	DE	98	ASN
1	DE	235	LEU
2	EE	38	GLU
2	EE	41	TYR
2	EE	45	ILE
2	GE	8	ARG
2	GE	21	ASN
1	AE	98	ASN
1	AE	206	LEU
1	AE	207	ASN
1	AE	319	TYR
1	BE	31	LYS
1	BE	62	LEU
1	BE	65	ASP
1	BE	74	TRP
1	BE	183	LEU
1	BE	259	PHE
1	BE	348	ASN
1	CE	73	ASN
1	CE	94	THR
1	CE	98	ASN
1	CE	109	LEU
1	CE	259	PHE
1	CE	261	ILE
1	FE	98	ASN
1	FE	235	LEU
2	IE	8	ARG
2	IE	21	ASN
2	JE	22	LYS
1	KE	98	ASN

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Mol	Chain	Res	Type
1	KE	206	LEU
1	KE	207	ASN
1	KE	319	TYR
1	LE	31	LYS
1	LE	62	LEU
1	LE	65	ASP
1	LE	74	TRP
1	LE	183	LEU
1	LE	259	PHE
1	LE	348	ASN
1	ME	73	ASN
1	ME	94	THR
1	ME	98	ASN
1	ME	109	LEU
1	ME	259	PHE
1	ME	261	ILE
1	NE	98	ASN
1	NE	235	LEU
2	OE	38	GLU
2	OE	41	TYR
2	OE	45	ILE
2	QE	8	ARG
2	QE	21	ASN
2	RE	22	LYS
1	SE	98	ASN
1	SE	206	LEU
1	SE	207	ASN
1	SE	319	TYR
1	TE	31	LYS
1	TE	62	LEU
1	TE	65	ASP
1	TE	74	TRP
1	TE	183	LEU
1	TE	259	PHE
1	TE	348	ASN
1	UE	73	ASN
1	UE	94	THR
1	UE	98	ASN
1	UE	109	LEU
1	UE	259	PHE
1	UE	261	ILE
1	VE	98	ASN

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Mol	Chain	Res	Type
1	VE	235	LEU
2	WE	38	GLU
2	WE	41	TYR
2	WE	45	ILE
2	YE	8	ARG
2	YE	21	ASN
2	ZE	22	LYS
1	aE	98	ASN
1	aE	206	LEU
1	aE	207	ASN
1	aE	319	TYR
1	bE	31	LYS
1	bE	62	LEU
1	bE	65	ASP
1	bE	74	TRP
1	bE	183	LEU
1	bE	259	PHE
1	bE	348	ASN
1	cE	73	ASN
1	cE	94	THR
1	cE	98	ASN
1	cE	109	LEU
1	cE	259	PHE
1	cE	261	ILE
1	dE	98	ASN
1	dE	235	LEU
2	eE	38	GLU
2	eE	41	TYR
2	eE	45	ILE
2	gE	8	ARG
2	gE	21	ASN
2	hE	22	LYS
3	AF	6	ARG
3	AF	41	LEU
4	BF	220	THR
5	CF	388	LYS
5	NF	388	LYS
5	OF	388	LYS
1	CG	98	ASN
1	CG	206	LEU
1	CG	207	ASN
1	CG	319	TYR

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Mol	Chain	Res	Type
1	AG	31	LYS
1	AG	62	LEU
1	AG	65	ASP
1	AG	74	TRP
1	AG	183	LEU
1	AG	259	PHE
1	AG	348	ASN
1	BG	73	ASN
1	BG	94	THR
1	BG	98	ASN
1	BG	109	LEU
1	BG	259	PHE
1	BG	261	ILE
1	DG	98	ASN
1	DG	235	LEU
2	EG	38	GLU
2	EG	41	TYR
2	EG	45	ILE
2	GG	8	ARG
2	GG	21	ASN
2	HG	22	LYS
1	IG	98	ASN
1	IG	206	LEU
1	IG	207	ASN
1	IG	319	TYR
1	JG	31	LYS
1	JG	62	LEU
1	JG	65	ASP
1	JG	74	TRP
1	JG	183	LEU
1	JG	259	PHE
1	JG	348	ASN
1	KG	73	ASN
1	KG	94	THR
1	KG	98	ASN
1	KG	109	LEU
1	KG	259	PHE
1	KG	261	ILE
1	LG	98	ASN
1	LG	235	LEU
2	MG	38	GLU
2	MG	41	TYR

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Mol	Chain	Res	Type
2	MG	45	ILE
2	OG	8	ARG
2	OG	21	ASN
2	PG	22	LYS
1	QG	98	ASN
1	QG	206	LEU
1	QG	207	ASN
1	QG	319	TYR
1	RG	31	LYS
1	RG	62	LEU
1	RG	65	ASP
1	RG	74	TRP
1	RG	183	LEU
1	RG	259	PHE
1	RG	348	ASN
1	SG	73	ASN
1	SG	94	THR
1	SG	98	ASN
1	SG	109	LEU
1	SG	259	PHE
1	SG	261	ILE
1	TG	98	ASN
1	TG	235	LEU
2	UG	38	GLU
2	UG	41	TYR
2	UG	45	ILE
2	WG	8	ARG
2	WG	21	ASN
2	XG	22	LYS
1	YG	98	ASN
1	YG	206	LEU
1	YG	207	ASN
1	YG	319	TYR
1	ZG	31	LYS
1	ZG	62	LEU
1	ZG	65	ASP
1	ZG	74	TRP
1	ZG	183	LEU
1	ZG	259	PHE
1	ZG	348	ASN
1	aG	73	ASN
1	aG	94	THR

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Mol	Chain	Res	Type
1	aG	98	ASN
1	aG	109	LEU
1	aG	259	PHE
1	aG	261	ILE
1	bG	98	ASN
1	bG	235	LEU
2	cG	38	GLU
2	cG	41	TYR
2	cG	45	ILE
2	eG	8	ARG
2	eG	21	ASN
2	fG	22	LYS
1	gG	98	ASN
1	gG	206	LEU
1	gG	207	ASN
1	gG	319	TYR
1	hG	31	LYS
1	hG	62	LEU
1	hG	65	ASP
1	hG	74	TRP
1	hG	183	LEU
1	hG	259	PHE
1	hG	348	ASN
1	iG	73	ASN
1	iG	94	THR
1	iG	98	ASN
1	iG	109	LEU
1	iG	259	PHE
1	iG	261	ILE
1	jG	98	ASN
1	jG	235	LEU
2	kG	38	GLU
2	kG	41	TYR
2	kG	45	ILE
2	mG	8	ARG
2	mG	21	ASN
2	nG	22	LYS
3	AH	6	ARG
3	AH	41	LEU
4	BH	220	THR
5	CH	388	LYS
5	NH	388	LYS

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Mol	Chain	Res	Type
5	OH	388	LYS
3	AI	6	ARG
3	AI	41	LEU
4	BI	220	THR
5	CI	388	LYS
5	NI	388	LYS
5	OI	388	LYS
1	AJ	58	ILE
1	AJ	59	ASN
1	AJ	60	GLU
1	AJ	62	LEU
1	AJ	63	LEU
1	AJ	79	GLN
1	AJ	111	ARG
1	AJ	115	ARG
1	AJ	172	ARG
1	AJ	251	LEU
1	BJ	4	GLN
1	BJ	31	LYS
1	BJ	45	MET
1	BJ	70	ASN
1	BJ	111	ARG
1	BJ	167	GLU
1	BJ	172	ARG
1	BJ	236	LYS
1	BJ	240	ILE
1	CJ	19	LYS
1	CJ	70	ASN
1	CJ	73	ASN
1	CJ	94	THR
1	CJ	172	ARG
1	CJ	337	LYS
1	CJ	382	LYS
1	DJ	16	LYS
1	DJ	45	MET
1	DJ	70	ASN
1	DJ	94	THR
1	DJ	103	LYS
1	DJ	115	ARG
1	DJ	166	LEU
1	DJ	175	LEU
1	DJ	382	LYS

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Mol	Chain	Res	Type
2	EJ	8	ARG
2	FJ	13	THR
2	FJ	19	ARG
2	FJ	22	LYS
2	GJ	30	MET
2	GJ	34	THR
2	GJ	36	LYS
1	KJ	19	LYS
1	KJ	73	ASN
1	KJ	77	LYS
1	KJ	172	ARG
1	KJ	250	LEU
1	KJ	337	LYS
1	KJ	351	LYS
1	LJ	45	MET
1	LJ	92	MET
1	LJ	94	THR
1	LJ	175	LEU
1	LJ	235	LEU
1	LJ	382	LYS
2	MJ	8	ARG
2	MJ	22	LYS
2	MJ	23	ARG
2	MJ	30	MET
2	NJ	30	MET
1	AK	58	ILE
1	AK	59	ASN
1	AK	60	GLU
1	AK	62	LEU
1	AK	63	LEU
1	AK	79	GLN
1	AK	111	ARG
1	AK	115	ARG
1	AK	172	ARG
1	AK	251	LEU
1	BK	4	GLN
1	BK	31	LYS
1	BK	45	MET
1	BK	70	ASN
1	BK	111	ARG
1	BK	167	GLU
1	BK	172	ARG

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Mol	Chain	Res	Type
1	BK	236	LYS
1	BK	240	ILE
1	CK	19	LYS
1	CK	70	ASN
1	CK	73	ASN
1	CK	94	THR
1	CK	172	ARG
1	CK	337	LYS
1	CK	382	LYS
1	DK	16	LYS
1	DK	45	MET
1	DK	70	ASN
1	DK	94	THR
1	DK	103	LYS
1	DK	115	ARG
1	DK	166	LEU
1	DK	175	LEU
1	DK	382	LYS
2	EK	8	ARG
2	FK	13	THR
2	FK	19	ARG
2	FK	22	LYS
2	GK	30	MET
2	GK	34	THR
2	GK	36	LYS
1	KK	19	LYS
1	KK	73	ASN
1	KK	77	LYS
1	KK	172	ARG
1	KK	250	LEU
1	KK	337	LYS
1	KK	351	LYS
1	LK	45	MET
1	LK	92	MET
1	LK	94	THR
1	LK	175	LEU
1	LK	235	LEU
1	LK	382	LYS
2	MK	8	ARG
2	MK	22	LYS
2	MK	23	ARG
2	MK	30	MET

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Mol	Chain	Res	Type
2	NK	30	MET
1	CL	98	ASN
1	CL	206	LEU
1	CL	207	ASN
1	CL	319	TYR
1	AL	31	LYS
1	AL	62	LEU
1	AL	65	ASP
1	AL	74	TRP
1	AL	183	LEU
1	AL	259	PHE
1	AL	348	ASN
1	BL	73	ASN
1	BL	94	THR
1	BL	98	ASN
1	BL	109	LEU
1	BL	259	PHE
1	BL	261	ILE
1	DL	98	ASN
1	DL	235	LEU
2	EL	38	GLU
2	EL	41	TYR
2	EL	45	ILE
2	GL	8	ARG
2	GL	21	ASN
2	HL	22	LYS
1	IL	98	ASN
1	IL	206	LEU
1	IL	207	ASN
1	IL	319	TYR
1	JL	31	LYS
1	JL	62	LEU
1	JL	65	ASP
1	JL	74	TRP
1	JL	183	LEU
1	JL	259	PHE
1	JL	348	ASN
1	KL	73	ASN
1	KL	94	THR
1	KL	98	ASN
1	KL	109	LEU
1	KL	259	PHE

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Mol	Chain	Res	Type
1	KL	261	ILE
1	LL	98	ASN
1	LL	235	LEU
2	ML	38	GLU
2	ML	41	TYR
2	ML	45	ILE
2	OL	8	ARG
2	OL	21	ASN
2	PL	22	LYS
1	QL	98	ASN
1	QL	206	LEU
1	QL	207	ASN
1	QL	319	TYR
1	RL	31	LYS
1	RL	62	LEU
1	RL	65	ASP
1	RL	74	TRP
1	RL	183	LEU
1	RL	259	PHE
1	RL	348	ASN
1	SL	73	ASN
1	SL	94	THR
1	SL	98	ASN
1	SL	109	LEU
1	SL	259	PHE
1	SL	261	ILE
1	TL	98	ASN
1	TL	235	LEU
2	UL	38	GLU
2	UL	41	TYR
2	UL	45	ILE
2	WL	8	ARG
2	WL	21	ASN
2	XL	22	LYS
1	YL	98	ASN
1	YL	206	LEU
1	YL	207	ASN
1	YL	319	TYR
1	ZL	31	LYS
1	ZL	62	LEU
1	ZL	65	ASP
1	ZL	74	TRP

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Mol	Chain	Res	Type
1	ZL	183	LEU
1	ZL	259	PHE
1	ZL	348	ASN
1	aL	73	ASN
1	aL	94	THR
1	aL	98	ASN
1	aL	109	LEU
1	aL	259	PHE
1	aL	261	ILE
1	bL	98	ASN
1	bL	235	LEU
2	cL	38	GLU
2	cL	41	TYR
2	cL	45	ILE
2	eL	8	ARG
2	eL	21	ASN
2	fL	22	LYS
1	gL	98	ASN
1	gL	235	LEU
2	hL	38	GLU
2	hL	41	TYR
2	hL	45	ILE
2	iL	8	ARG
2	iL	21	ASN
3	AM	6	ARG
3	AM	41	LEU
4	BM	220	THR
5	CM	388	LYS
5	NM	388	LYS
5	OM	388	LYS
3	AN	6	ARG
3	AN	41	LEU
4	BN	220	THR
5	CN	388	LYS
5	NN	388	LYS
5	ON	388	LYS
3	AO	6	ARG
3	AO	41	LEU
4	BO	220	THR
5	CO	388	LYS
5	NO	388	LYS
5	OO	388	LYS

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Mol	Chain	Res	Type
1	AP	58	ILE
1	AP	59	ASN
1	AP	60	GLU
1	AP	62	LEU
1	AP	63	LEU
1	AP	79	GLN
1	AP	111	ARG
1	AP	115	ARG
1	AP	172	ARG
1	AP	251	LEU
1	BP	4	GLN
1	BP	31	LYS
1	BP	45	MET
1	BP	70	ASN
1	BP	111	ARG
1	BP	167	GLU
1	BP	172	ARG
1	BP	236	LYS
1	BP	240	ILE
1	CP	19	LYS
1	CP	70	ASN
1	CP	73	ASN
1	CP	94	THR
1	CP	172	ARG
1	CP	337	LYS
1	CP	382	LYS
1	DP	16	LYS
1	DP	45	MET
1	DP	70	ASN
1	DP	94	THR
1	DP	103	LYS
1	DP	115	ARG
1	DP	166	LEU
1	DP	175	LEU
1	DP	382	LYS
2	EP	8	ARG
2	FP	13	THR
2	FP	19	ARG
2	FP	22	LYS
2	GP	30	MET
2	GP	34	THR
2	GP	36	LYS

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Mol	Chain	Res	Type
1	KP	19	LYS
1	KP	73	ASN
1	KP	77	LYS
1	KP	172	ARG
1	KP	250	LEU
1	KP	337	LYS
1	KP	351	LYS
1	LP	45	MET
1	LP	92	MET
1	LP	94	THR
1	LP	175	LEU
1	LP	235	LEU
1	LP	382	LYS
2	MP	8	ARG
2	MP	22	LYS
2	MP	23	ARG
2	MP	30	MET
2	NP	30	MET
1	CQ	98	ASN
1	CQ	206	LEU
1	CQ	207	ASN
1	CQ	319	TYR
1	AQ	31	LYS
1	AQ	62	LEU
1	AQ	65	ASP
1	AQ	74	TRP
1	AQ	183	LEU
1	AQ	259	PHE
1	AQ	348	ASN
1	BQ	73	ASN
1	BQ	94	THR
1	BQ	98	ASN
1	BQ	109	LEU
1	BQ	259	PHE
1	BQ	261	ILE
1	DQ	98	ASN
1	DQ	235	LEU
2	EQ	38	GLU
2	EQ	41	TYR
2	EQ	45	ILE
2	GQ	8	ARG
2	GQ	21	ASN

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Mol	Chain	Res	Type
2	HQ	22	LYS
1	IQ	98	ASN
1	IQ	206	LEU
1	IQ	207	ASN
1	IQ	319	TYR
1	JQ	31	LYS
1	JQ	62	LEU
1	JQ	65	ASP
1	JQ	74	TRP
1	JQ	183	LEU
1	JQ	259	PHE
1	JQ	348	ASN
1	KQ	73	ASN
1	KQ	94	THR
1	KQ	98	ASN
1	KQ	109	LEU
1	KQ	259	PHE
1	KQ	261	ILE
1	LQ	98	ASN
1	LQ	235	LEU
2	MQ	38	GLU
2	MQ	41	TYR
2	MQ	45	ILE
2	OQ	8	ARG
2	OQ	21	ASN
2	PQ	22	LYS
1	QQ	98	ASN
1	QQ	206	LEU
1	QQ	207	ASN
1	QQ	319	TYR
1	RQ	31	LYS
1	RQ	62	LEU
1	RQ	65	ASP
1	RQ	74	TRP
1	RQ	183	LEU
1	RQ	259	PHE
1	RQ	348	ASN
1	SQ	73	ASN
1	SQ	94	THR
1	SQ	98	ASN
1	SQ	109	LEU
1	SQ	259	PHE

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Mol	Chain	Res	Type
1	SQ	261	ILE
1	TQ	98	ASN
1	TQ	235	LEU
2	UQ	38	GLU
2	UQ	41	TYR
2	UQ	45	ILE
2	WQ	8	ARG
2	WQ	21	ASN
2	XQ	22	LYS
1	YQ	98	ASN
1	YQ	235	LEU
2	ZQ	38	GLU
2	ZQ	41	TYR
2	ZQ	45	ILE
2	aQ	8	ARG
2	aQ	21	ASN
1	bQ	98	ASN
1	bQ	206	LEU
1	bQ	207	ASN
1	bQ	319	TYR
1	cQ	31	LYS
1	cQ	62	LEU
1	cQ	65	ASP
1	cQ	74	TRP
1	cQ	183	LEU
1	cQ	259	PHE
1	cQ	348	ASN
1	dQ	73	ASN
1	dQ	94	THR
1	dQ	98	ASN
1	dQ	109	LEU
1	dQ	259	PHE
1	dQ	261	ILE
1	eQ	98	ASN
1	eQ	235	LEU
2	fQ	38	GLU
2	fQ	41	TYR
2	fQ	45	ILE
2	hQ	8	ARG
2	hQ	21	ASN
2	iQ	22	LYS
1	CR	98	ASN

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Mol	Chain	Res	Type
1	CR	206	LEU
1	CR	207	ASN
1	CR	319	TYR
1	AR	31	LYS
1	AR	62	LEU
1	AR	65	ASP
1	AR	74	TRP
1	AR	183	LEU
1	AR	259	PHE
1	AR	348	ASN
1	BR	73	ASN
1	BR	94	THR
1	BR	98	ASN
1	BR	109	LEU
1	BR	259	PHE
1	BR	261	ILE
1	DR	98	ASN
1	DR	235	LEU
2	ER	38	GLU
2	ER	41	TYR
2	ER	45	ILE
2	GR	8	ARG
2	GR	21	ASN
2	HR	22	LYS
1	IR	98	ASN
1	IR	206	LEU
1	IR	207	ASN
1	IR	319	TYR
1	JR	31	LYS
1	JR	62	LEU
1	JR	65	ASP
1	JR	74	TRP
1	JR	183	LEU
1	JR	259	PHE
1	JR	348	ASN
1	KR	73	ASN
1	KR	94	THR
1	KR	98	ASN
1	KR	109	LEU
1	KR	259	PHE
1	KR	261	ILE
1	LR	98	ASN

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Mol	Chain	Res	Type
1	LR	235	LEU
2	MR	38	GLU
2	MR	41	TYR
2	MR	45	ILE
2	OR	8	ARG
2	OR	21	ASN
2	PR	22	LYS
1	QR	98	ASN
1	QR	206	LEU
1	QR	207	ASN
1	QR	319	TYR
1	RR	31	LYS
1	RR	62	LEU
1	RR	65	ASP
1	RR	74	TRP
1	RR	183	LEU
1	RR	259	PHE
1	RR	348	ASN
1	SR	73	ASN
1	SR	94	THR
1	SR	98	ASN
1	SR	109	LEU
1	SR	259	PHE
1	SR	261	ILE
1	TR	98	ASN
1	TR	235	LEU
2	UR	38	GLU
2	UR	41	TYR
2	UR	45	ILE
2	WR	8	ARG
2	WR	21	ASN
2	XR	22	LYS
1	YR	98	ASN
1	YR	206	LEU
1	YR	207	ASN
1	YR	319	TYR
1	ZR	31	LYS
1	ZR	62	LEU
1	ZR	65	ASP
1	ZR	74	TRP
1	ZR	183	LEU
1	ZR	259	PHE

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Mol	Chain	Res	Type
1	ZR	348	ASN
1	aR	73	ASN
1	aR	94	THR
1	aR	98	ASN
1	aR	109	LEU
1	aR	259	PHE
1	aR	261	ILE
1	bR	98	ASN
1	bR	235	LEU
2	cR	38	GLU
2	cR	41	TYR
2	cR	45	ILE
2	eR	8	ARG
2	eR	21	ASN
2	fR	22	LYS
1	gR	98	ASN
1	gR	206	LEU
1	gR	207	ASN
1	gR	319	TYR
1	hR	31	LYS
1	hR	62	LEU
1	hR	65	ASP
1	hR	74	TRP
1	hR	183	LEU
1	hR	259	PHE
1	hR	348	ASN
1	iR	73	ASN
1	iR	94	THR
1	iR	98	ASN
1	iR	109	LEU
1	iR	259	PHE
1	iR	261	ILE
1	jR	98	ASN
1	jR	235	LEU
2	lR	8	ARG
2	lR	21	ASN
2	mR	22	LYS
1	AS	4	GLN
1	AS	31	LYS
1	AS	45	MET
1	AS	70	ASN
1	AS	111	ARG

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Mol	Chain	Res	Type
1	AS	167	GLU
1	AS	172	ARG
1	AS	236	LYS
1	AS	240	ILE
1	BS	19	LYS
1	BS	70	ASN
1	BS	73	ASN
1	BS	94	THR
1	BS	172	ARG
1	BS	337	LYS
1	BS	382	LYS
1	CS	16	LYS
1	CS	45	MET
1	CS	70	ASN
1	CS	94	THR
1	CS	103	LYS
1	CS	115	ARG
1	CS	166	LEU
1	CS	175	LEU
1	CS	382	LYS
2	DS	8	ARG
2	ES	13	THR
2	ES	19	ARG
2	ES	22	LYS
2	FS	30	MET
2	FS	34	THR
2	FS	36	LYS
1	IS	58	ILE
1	IS	59	ASN
1	IS	60	GLU
1	IS	62	LEU
1	IS	63	LEU
1	IS	79	GLN
1	IS	111	ARG
1	IS	115	ARG
1	IS	172	ARG
1	IS	251	LEU
1	JS	19	LYS
1	JS	73	ASN
1	JS	77	LYS
1	JS	172	ARG
1	JS	250	LEU

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Mol	Chain	Res	Type
1	JS	337	LYS
1	JS	351	LYS
1	KS	45	MET
1	KS	92	MET
1	KS	94	THR
1	KS	175	LEU
1	KS	235	LEU
1	KS	382	LYS
2	LS	8	ARG
2	LS	22	LYS
2	LS	23	ARG
2	LS	30	MET
2	MS	30	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (765) such sidechains are listed below:

Mol	Chain	Res	Type
1	C1	23	GLN
1	C1	27	HIS
1	C1	365	HIS
1	C1	377	HIS
1	A1	207	ASN
1	A1	210	ASN
1	A1	348	ASN
1	B1	150	ASN
1	B1	365	HIS
1	B1	377	HIS
1	I1	23	GLN
1	I1	27	HIS
1	I1	377	HIS
1	J1	207	ASN
1	J1	210	ASN
1	J1	348	ASN
1	K1	150	ASN
1	K1	365	HIS
1	K1	377	HIS
1	Q1	23	GLN
1	Q1	27	HIS
1	Q1	365	HIS
1	Q1	377	HIS
1	R1	98	ASN
1	R1	123	ASN

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Mol	Chain	Res	Type
1	R1	207	ASN
1	R1	210	ASN
1	R1	348	ASN
1	S1	98	ASN
1	S1	150	ASN
1	S1	365	HIS
1	S1	377	HIS
1	T1	26	ASN
1	T1	51	ASN
1	T1	150	ASN
1	T1	374	HIS
1	X1	23	GLN
1	X1	27	HIS
1	X1	365	HIS
1	X1	377	HIS
1	Y1	207	ASN
1	Y1	210	ASN
1	Y1	348	ASN
1	Z1	150	ASN
1	Z1	365	HIS
1	Z1	377	HIS
1	f1	23	GLN
1	f1	27	HIS
1	f1	377	HIS
1	g1	207	ASN
1	g1	210	ASN
1	g1	348	ASN
1	h1	150	ASN
1	h1	365	HIS
1	h1	377	HIS
3	A2	23	HIS
3	A2	33	ASN
3	A2	134	ASN
3	A2	202	ASN
3	A2	270	ASN
4	B2	38	GLN
4	B2	144	GLN
5	C2	275	ASN
5	C2	433	HIS
5	N2	433	HIS
5	O2	433	HIS
1	C3	23	GLN

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Mol	Chain	Res	Type
1	C3	27	HIS
1	C3	365	HIS
1	C3	377	HIS
1	A3	207	ASN
1	A3	210	ASN
1	A3	348	ASN
1	B3	150	ASN
1	B3	365	HIS
1	B3	377	HIS
1	I3	23	GLN
1	I3	27	HIS
1	I3	365	HIS
1	I3	377	HIS
1	J3	207	ASN
1	J3	210	ASN
1	J3	348	ASN
1	K3	150	ASN
1	K3	365	HIS
1	K3	377	HIS
1	L3	98	ASN
1	Q3	23	GLN
1	Q3	27	HIS
1	Q3	365	HIS
1	Q3	377	HIS
1	R3	207	ASN
1	R3	210	ASN
1	R3	348	ASN
1	S3	150	ASN
1	S3	365	HIS
1	S3	377	HIS
1	C4	23	GLN
1	C4	27	HIS
1	C4	365	HIS
1	C4	377	HIS
1	A4	207	ASN
1	A4	210	ASN
1	A4	348	ASN
1	B4	150	ASN
1	B4	365	HIS
1	B4	377	HIS
1	D4	98	ASN
1	I4	23	GLN

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Mol	Chain	Res	Type
1	I4	27	HIS
1	I4	377	HIS
1	J4	207	ASN
1	J4	210	ASN
1	J4	348	ASN
1	K4	150	ASN
1	K4	365	HIS
1	K4	377	HIS
1	Q4	23	GLN
1	Q4	27	HIS
1	Q4	365	HIS
1	Q4	377	HIS
1	R4	98	ASN
1	R4	123	ASN
1	R4	207	ASN
1	R4	210	ASN
1	R4	348	ASN
1	S4	98	ASN
1	S4	150	ASN
1	S4	365	HIS
1	S4	377	HIS
1	T4	26	ASN
1	T4	51	ASN
1	T4	150	ASN
1	T4	374	HIS
1	X4	23	GLN
1	X4	27	HIS
1	X4	377	HIS
1	Y4	207	ASN
1	Y4	210	ASN
1	Y4	348	ASN
1	Z4	150	ASN
1	Z4	365	HIS
1	Z4	377	HIS
1	f4	23	GLN
1	f4	27	HIS
1	f4	365	HIS
1	f4	377	HIS
1	g4	98	ASN
1	g4	123	ASN
1	g4	207	ASN
1	g4	210	ASN

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Mol	Chain	Res	Type
1	g4	348	ASN
1	h4	98	ASN
1	h4	150	ASN
1	h4	365	HIS
1	h4	377	HIS
1	i4	26	ASN
1	i4	51	ASN
1	i4	98	ASN
1	i4	150	ASN
1	i4	374	HIS
3	A5	23	HIS
3	A5	134	ASN
3	A5	194	ASN
3	A5	202	ASN
3	A5	270	ASN
4	B5	38	GLN
4	B5	144	GLN
5	C5	275	ASN
5	C5	433	HIS
5	N5	433	HIS
5	O5	433	HIS
1	C6	23	GLN
1	C6	27	HIS
1	C6	365	HIS
1	C6	377	HIS
1	A6	207	ASN
1	A6	210	ASN
1	A6	348	ASN
1	B6	150	ASN
1	B6	365	HIS
1	B6	377	HIS
1	I6	23	GLN
1	I6	27	HIS
1	I6	365	HIS
1	I6	377	HIS
1	J6	207	ASN
1	J6	210	ASN
1	J6	348	ASN
1	K6	150	ASN
1	K6	365	HIS
1	Q6	365	HIS
1	Q6	377	HIS

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Mol	Chain	Res	Type
1	R6	207	ASN
1	R6	210	ASN
1	R6	348	ASN
1	S6	365	HIS
1	S6	377	HIS
1	T6	98	ASN
1	Y6	23	GLN
1	Y6	27	HIS
1	Y6	365	HIS
1	Y6	377	HIS
1	Z6	207	ASN
1	Z6	210	ASN
1	Z6	348	ASN
1	a6	150	ASN
1	a6	365	HIS
1	a6	377	HIS
1	g6	365	HIS
1	g6	377	HIS
1	h6	207	ASN
1	h6	210	ASN
1	h6	348	ASN
1	i6	365	HIS
1	i6	377	HIS
1	j6	98	ASN
1	C7	365	HIS
1	C7	377	HIS
1	A7	207	ASN
1	A7	210	ASN
1	A7	348	ASN
1	B7	365	HIS
1	B7	377	HIS
1	D7	98	ASN
1	I7	23	GLN
1	I7	27	HIS
1	I7	377	HIS
1	J7	207	ASN
1	J7	210	ASN
1	J7	348	ASN
1	K7	150	ASN
1	K7	365	HIS
1	K7	377	HIS
1	Q7	23	GLN

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Mol	Chain	Res	Type
1	Q7	27	HIS
1	Q7	377	HIS
1	R7	207	ASN
1	R7	210	ASN
1	R7	348	ASN
1	S7	150	ASN
1	S7	365	HIS
1	S7	377	HIS
1	Y7	23	GLN
1	Y7	27	HIS
1	Y7	377	HIS
1	Z7	207	ASN
1	Z7	210	ASN
1	Z7	348	ASN
1	a7	150	ASN
1	a7	365	HIS
1	a7	377	HIS
1	g7	23	GLN
1	g7	27	HIS
1	g7	365	HIS
1	g7	377	HIS
1	h7	207	ASN
1	h7	210	ASN
1	h7	348	ASN
1	i7	150	ASN
1	i7	365	HIS
1	i7	377	HIS
1	C8	23	GLN
1	C8	27	HIS
1	C8	365	HIS
1	C8	377	HIS
1	A8	207	ASN
1	A8	210	ASN
1	A8	348	ASN
1	B8	150	ASN
1	B8	365	HIS
1	B8	377	HIS
1	I8	23	GLN
1	I8	27	HIS
1	I8	365	HIS
1	I8	377	HIS
1	J8	207	ASN

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Mol	Chain	Res	Type
1	J8	210	ASN
1	J8	348	ASN
1	K8	150	ASN
1	K8	365	HIS
1	K8	377	HIS
1	Q8	23	GLN
1	Q8	27	HIS
1	Q8	365	HIS
1	Q8	377	HIS
1	R8	207	ASN
1	R8	210	ASN
1	R8	348	ASN
1	S8	150	ASN
1	S8	365	HIS
1	S8	377	HIS
1	T8	98	ASN
1	Y8	23	GLN
1	Y8	27	HIS
1	Y8	365	HIS
1	Y8	377	HIS
1	Z8	207	ASN
1	Z8	210	ASN
1	Z8	348	ASN
1	a8	150	ASN
1	a8	365	HIS
1	a8	377	HIS
1	b8	98	ASN
1	g8	365	HIS
1	g8	377	HIS
1	h8	207	ASN
1	h8	210	ASN
1	h8	348	ASN
1	i8	365	HIS
1	i8	377	HIS
1	j8	98	ASN
3	A9	23	HIS
3	A9	67	ASN
3	A9	134	ASN
3	A9	149	GLN
3	A9	194	ASN
3	A9	202	ASN
3	A9	270	ASN

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Mol	Chain	Res	Type
4	B9	38	GLN
4	B9	144	GLN
5	C9	275	ASN
5	C9	433	HIS
5	N9	433	HIS
5	O9	433	HIS
3	AA	23	HIS
3	AA	33	ASN
3	AA	134	ASN
3	AA	202	ASN
3	AA	270	ASN
4	BA	38	GLN
4	BA	144	GLN
5	CA	275	ASN
5	CA	433	HIS
5	NA	433	HIS
5	OA	433	HIS
3	AB	23	HIS
3	AB	134	ASN
3	AB	194	ASN
3	AB	202	ASN
3	AB	270	ASN
4	BB	38	GLN
4	BB	144	GLN
5	CB	275	ASN
5	CB	433	HIS
5	NB	433	HIS
5	OB	433	HIS
3	AC	23	HIS
3	AC	25	ASN
3	AC	134	ASN
3	AC	194	ASN
3	AC	202	ASN
3	AC	270	ASN
4	BC	38	GLN
4	BC	144	GLN
5	CC	275	ASN
5	CC	433	HIS
5	NC	433	HIS
5	OC	433	HIS
1	AD	304	GLN
1	BD	51	ASN

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Mol	Chain	Res	Type
1	BD	136	ASN
1	BD	211	ASN
1	BD	290	ASN
1	BD	374	HIS
1	CD	98	ASN
1	CD	143	GLN
1	CD	377	HIS
1	DD	27	HIS
1	DD	104	ASN
1	DD	123	ASN
1	DD	129	GLN
1	DD	143	GLN
1	DD	304	GLN
1	KD	51	ASN
1	KD	79	GLN
1	KD	98	ASN
1	LD	98	ASN
1	LD	150	ASN
1	LD	365	HIS
1	LD	377	HIS
1	AE	23	GLN
1	AE	27	HIS
1	AE	365	HIS
1	AE	377	HIS
1	BE	98	ASN
1	BE	123	ASN
1	BE	207	ASN
1	BE	210	ASN
1	BE	348	ASN
1	CE	98	ASN
1	CE	150	ASN
1	CE	365	HIS
1	CE	377	HIS
1	FE	26	ASN
1	FE	51	ASN
1	FE	374	HIS
1	KE	23	GLN
1	KE	27	HIS
1	KE	377	HIS
1	LE	207	ASN
1	LE	210	ASN
1	LE	348	ASN

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Mol	Chain	Res	Type
1	ME	150	ASN
1	ME	365	HIS
1	ME	377	HIS
1	SE	23	GLN
1	SE	27	HIS
1	SE	365	HIS
1	SE	377	HIS
1	TE	207	ASN
1	TE	210	ASN
1	TE	348	ASN
1	UE	150	ASN
1	UE	365	HIS
1	UE	377	HIS
1	aE	23	GLN
1	aE	27	HIS
1	aE	365	HIS
1	aE	377	HIS
1	bE	207	ASN
1	bE	210	ASN
1	bE	348	ASN
1	cE	150	ASN
1	cE	365	HIS
1	cE	377	HIS
3	AF	23	HIS
3	AF	134	ASN
3	AF	202	ASN
3	AF	270	ASN
4	BF	38	GLN
4	BF	144	GLN
5	CF	275	ASN
5	CF	433	HIS
5	NF	433	HIS
5	OF	433	HIS
1	CG	23	GLN
1	CG	27	HIS
1	CG	365	HIS
1	CG	377	HIS
1	AG	207	ASN
1	AG	210	ASN
1	AG	348	ASN
1	BG	150	ASN
1	BG	365	HIS

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Mol	Chain	Res	Type
1	BG	377	HIS
1	DG	98	ASN
1	IG	23	GLN
1	IG	27	HIS
1	IG	377	HIS
1	JG	207	ASN
1	JG	210	ASN
1	JG	348	ASN
1	KG	150	ASN
1	KG	365	HIS
1	KG	377	HIS
1	QG	23	GLN
1	QG	27	HIS
1	QG	365	HIS
1	QG	377	HIS
1	RG	207	ASN
1	RG	210	ASN
1	RG	348	ASN
1	SG	150	ASN
1	SG	365	HIS
1	SG	377	HIS
1	TG	98	ASN
1	YG	365	HIS
1	YG	377	HIS
1	ZG	207	ASN
1	ZG	210	ASN
1	ZG	348	ASN
1	aG	365	HIS
1	aG	377	HIS
1	bG	98	ASN
1	gG	23	GLN
1	gG	27	HIS
1	gG	377	HIS
1	hG	207	ASN
1	hG	210	ASN
1	hG	348	ASN
1	iG	150	ASN
1	iG	365	HIS
1	iG	377	HIS
3	AH	23	HIS
3	AH	134	ASN
3	AH	194	ASN

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Mol	Chain	Res	Type
3	AH	202	ASN
3	AH	270	ASN
4	BH	38	GLN
4	BH	144	GLN
5	CH	275	ASN
5	CH	433	HIS
5	NH	433	HIS
5	OH	433	HIS
3	AI	23	HIS
3	AI	104	GLN
3	AI	134	ASN
3	AI	194	ASN
3	AI	202	ASN
3	AI	270	ASN
4	BI	38	GLN
4	BI	144	GLN
5	CI	275	ASN
5	CI	433	HIS
5	NI	433	HIS
5	OI	433	HIS
1	AJ	123	ASN
1	AJ	304	GLN
1	BJ	51	ASN
1	BJ	136	ASN
1	BJ	211	ASN
1	BJ	290	ASN
1	BJ	374	HIS
1	CJ	98	ASN
1	CJ	143	GLN
1	CJ	377	HIS
1	DJ	27	HIS
1	DJ	123	ASN
1	DJ	129	GLN
1	DJ	143	GLN
1	DJ	260	GLN
1	DJ	304	GLN
1	KJ	51	ASN
1	KJ	79	GLN
1	KJ	98	ASN
1	LJ	98	ASN
1	LJ	150	ASN
1	LJ	365	HIS

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Mol	Chain	Res	Type
1	LJ	377	HIS
2	MJ	27	ASN
1	AK	150	ASN
1	AK	304	GLN
1	BK	51	ASN
1	BK	136	ASN
1	BK	290	ASN
1	BK	374	HIS
1	CK	98	ASN
1	CK	143	GLN
1	CK	150	ASN
1	CK	377	HIS
1	DK	27	HIS
1	DK	123	ASN
1	DK	129	GLN
1	DK	143	GLN
1	DK	304	GLN
1	KK	51	ASN
1	KK	79	GLN
1	KK	98	ASN
1	LK	98	ASN
1	LK	150	ASN
1	LK	365	HIS
1	LK	377	HIS
1	CL	23	GLN
1	CL	27	HIS
1	CL	377	HIS
1	AL	207	ASN
1	AL	210	ASN
1	AL	348	ASN
1	BL	150	ASN
1	BL	365	HIS
1	BL	377	HIS
1	IL	23	GLN
1	IL	27	HIS
1	IL	377	HIS
1	JL	207	ASN
1	JL	210	ASN
1	JL	348	ASN
1	KL	150	ASN
1	KL	365	HIS
1	KL	377	HIS

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Mol	Chain	Res	Type
1	QL	23	GLN
1	QL	27	HIS
1	QL	365	HIS
1	QL	377	HIS
1	RL	207	ASN
1	RL	210	ASN
1	RL	348	ASN
1	SL	150	ASN
1	SL	365	HIS
1	SL	377	HIS
1	YL	23	GLN
1	YL	27	HIS
1	YL	377	HIS
1	ZL	207	ASN
1	ZL	210	ASN
1	ZL	348	ASN
1	aL	150	ASN
1	aL	365	HIS
1	aL	377	HIS
3	AM	23	HIS
3	AM	134	ASN
3	AM	194	ASN
3	AM	202	ASN
3	AM	270	ASN
4	BM	38	GLN
4	BM	144	GLN
5	CM	275	ASN
5	CM	433	HIS
5	NM	433	HIS
5	OM	433	HIS
3	AN	23	HIS
3	AN	134	ASN
3	AN	202	ASN
3	AN	270	ASN
4	BN	38	GLN
4	BN	144	GLN
5	CN	275	ASN
5	CN	433	HIS
5	NN	433	HIS
5	ON	433	HIS
3	AO	23	HIS
3	AO	134	ASN

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Mol	Chain	Res	Type
3	AO	202	ASN
3	AO	270	ASN
4	BO	38	GLN
4	BO	144	GLN
5	CO	275	ASN
5	CO	433	HIS
5	NO	433	HIS
5	OO	433	HIS
1	AP	304	GLN
1	AP	365	HIS
1	BP	51	ASN
1	BP	136	ASN
1	BP	290	ASN
1	BP	304	GLN
1	BP	374	HIS
1	CP	98	ASN
1	CP	143	GLN
1	CP	377	HIS
1	DP	27	HIS
1	DP	123	ASN
1	DP	129	GLN
1	DP	143	GLN
1	DP	260	GLN
1	DP	304	GLN
1	KP	51	ASN
1	KP	98	ASN
1	LP	98	ASN
1	LP	150	ASN
1	LP	365	HIS
1	LP	377	HIS
2	MP	51	GLN
1	CQ	23	GLN
1	CQ	27	HIS
1	CQ	365	HIS
1	CQ	377	HIS
1	AQ	207	ASN
1	AQ	210	ASN
1	AQ	348	ASN
1	BQ	150	ASN
1	BQ	365	HIS
1	BQ	377	HIS
1	IQ	23	GLN

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Mol	Chain	Res	Type
1	IQ	27	HIS
1	IQ	365	HIS
1	IQ	377	HIS
1	JQ	207	ASN
1	JQ	210	ASN
1	JQ	348	ASN
1	KQ	150	ASN
1	KQ	365	HIS
1	KQ	377	HIS
1	QQ	23	GLN
1	QQ	27	HIS
1	QQ	365	HIS
1	QQ	377	HIS
1	RQ	207	ASN
1	RQ	210	ASN
1	RQ	348	ASN
1	SQ	150	ASN
1	SQ	365	HIS
1	SQ	377	HIS
1	YQ	98	ASN
1	bQ	23	GLN
1	bQ	27	HIS
1	bQ	377	HIS
1	cQ	207	ASN
1	cQ	210	ASN
1	cQ	348	ASN
1	dQ	150	ASN
1	dQ	365	HIS
1	dQ	377	HIS
1	CR	23	GLN
1	CR	27	HIS
1	CR	365	HIS
1	CR	377	HIS
1	AR	207	ASN
1	AR	210	ASN
1	AR	348	ASN
1	BR	150	ASN
1	BR	365	HIS
1	BR	377	HIS
1	IR	23	GLN
1	IR	27	HIS
1	IR	365	HIS

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Mol	Chain	Res	Type
1	IR	377	HIS
1	JR	207	ASN
1	JR	210	ASN
1	JR	348	ASN
1	KR	150	ASN
1	KR	365	HIS
1	QR	23	GLN
1	QR	27	HIS
1	QR	365	HIS
1	QR	377	HIS
1	RR	207	ASN
1	RR	210	ASN
1	RR	348	ASN
1	SR	150	ASN
1	SR	365	HIS
1	SR	377	HIS
1	YR	23	GLN
1	YR	27	HIS
1	YR	365	HIS
1	YR	377	HIS
1	ZR	207	ASN
1	ZR	210	ASN
1	ZR	348	ASN
1	aR	150	ASN
1	aR	365	HIS
1	aR	377	HIS
1	bR	98	ASN
1	gR	23	GLN
1	gR	27	HIS
1	gR	365	HIS
1	gR	377	HIS
1	hR	98	ASN
1	hR	123	ASN
1	hR	207	ASN
1	hR	210	ASN
1	hR	348	ASN
1	iR	98	ASN
1	iR	150	ASN
1	iR	365	HIS
1	jR	26	ASN
1	jR	51	ASN
1	jR	150	ASN

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Mol	Chain	Res	Type
1	jR	374	HIS
1	AS	51	ASN
1	AS	136	ASN
1	AS	211	ASN
1	AS	290	ASN
1	AS	374	HIS
1	BS	98	ASN
1	BS	143	GLN
1	BS	377	HIS
1	CS	27	HIS
1	CS	123	ASN
1	CS	129	GLN
1	CS	143	GLN
1	CS	260	GLN
1	CS	304	GLN
1	IS	150	ASN
1	IS	304	GLN
1	IS	365	HIS
1	JS	51	ASN
1	JS	79	GLN
1	JS	98	ASN
1	KS	98	ASN
1	KS	150	ASN
1	KS	365	HIS
1	KS	377	HIS
2	LS	51	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R1	1
1	Y1	1
1	g1	1
1	J6	1
1	R6	1
1	A7	1
1	J7	1
1	R7	1
1	AG	1
1	hG	1
1	AL	1
1	JL	1
1	RL	1
1	ZL	1
1	AQ	1
1	RQ	1
1	cQ	1
1	RR	1
1	ZR	1
1	hR	1
1	A1	1
1	J1	1
1	A3	1
1	J3	1
1	R3	1
1	A4	1
1	J4	1
1	R4	1
1	Y4	1
1	g4	1

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Mol	Chain	Number of breaks
1	A6	1
1	Z6	1
1	h6	1
1	Z7	1
1	h7	1
1	A8	1
1	J8	1
1	R8	1
1	Z8	1
1	h8	1
1	BE	1
1	LE	1
1	TE	1
1	bE	1
1	JG	1
1	RG	1
1	ZG	1
1	JQ	1
1	AR	1
1	JR	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R1	20:SER	C	21:ALA	N	3.93
1	Y1	20:SER	C	21:ALA	N	3.93
1	g1	20:SER	C	21:ALA	N	3.93
1	J6	20:SER	C	21:ALA	N	3.93
1	R6	20:SER	C	21:ALA	N	3.93
1	A7	20:SER	C	21:ALA	N	3.93
1	J7	20:SER	C	21:ALA	N	3.93
1	R7	20:SER	C	21:ALA	N	3.93
1	AG	20:SER	C	21:ALA	N	3.93
1	hG	20:SER	C	21:ALA	N	3.93
1	AL	20:SER	C	21:ALA	N	3.93
1	JL	20:SER	C	21:ALA	N	3.93
1	RL	20:SER	C	21:ALA	N	3.93
1	ZL	20:SER	C	21:ALA	N	3.93
1	AQ	20:SER	C	21:ALA	N	3.93
1	RQ	20:SER	C	21:ALA	N	3.93
1	cQ	20:SER	C	21:ALA	N	3.93
1	RR	20:SER	C	21:ALA	N	3.93
1	ZR	20:SER	C	21:ALA	N	3.93

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	hR	20:SER	C	21:ALA	N	3.93
1	A1	20:SER	C	21:ALA	N	3.92
1	J1	20:SER	C	21:ALA	N	3.92
1	A3	20:SER	C	21:ALA	N	3.92
1	J3	20:SER	C	21:ALA	N	3.92
1	R3	20:SER	C	21:ALA	N	3.92
1	A4	20:SER	C	21:ALA	N	3.92
1	J4	20:SER	C	21:ALA	N	3.92
1	R4	20:SER	C	21:ALA	N	3.92
1	Y4	20:SER	C	21:ALA	N	3.92
1	g4	20:SER	C	21:ALA	N	3.92
1	A6	20:SER	C	21:ALA	N	3.92
1	Z6	20:SER	C	21:ALA	N	3.92
1	h6	20:SER	C	21:ALA	N	3.92
1	Z7	20:SER	C	21:ALA	N	3.92
1	h7	20:SER	C	21:ALA	N	3.92
1	A8	20:SER	C	21:ALA	N	3.92
1	J8	20:SER	C	21:ALA	N	3.92
1	R8	20:SER	C	21:ALA	N	3.92
1	Z8	20:SER	C	21:ALA	N	3.92
1	h8	20:SER	C	21:ALA	N	3.92
1	BE	20:SER	C	21:ALA	N	3.92
1	LE	20:SER	C	21:ALA	N	3.92
1	TE	20:SER	C	21:ALA	N	3.92
1	bE	20:SER	C	21:ALA	N	3.92
1	JG	20:SER	C	21:ALA	N	3.92
1	RG	20:SER	C	21:ALA	N	3.92
1	ZG	20:SER	C	21:ALA	N	3.92
1	JQ	20:SER	C	21:ALA	N	3.92
1	AR	20:SER	C	21:ALA	N	3.92
1	JR	20:SER	C	21:ALA	N	3.92

6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4459. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

This section was not generated.

6.2 Central slices (i)

This section was not generated.

6.3 Largest variance slices (i)

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color) (i)

This section was not generated.

6.5 Orthogonal surface views (i)

This section was not generated.

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)

This section was not generated.

7.2 Volume estimate versus contour level (i)

This section was not generated.

7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation (i)

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

9 Map-model fit (i)

This section was not generated.