



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:45 AM UTC

PDB ID : 7VS5 / pdb_00007vs5
EMDB ID : EMD-32109
Title : The expanded head structure of phage T4
Authors : Fang, Q.; Tang, W.; Fokine, A.; Mahalingam, M.; Shao, Q.; Rossmann, M.G.;
Rao, V.B.
Deposited on : 2021-10-25
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

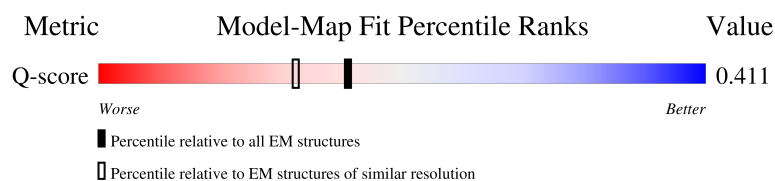
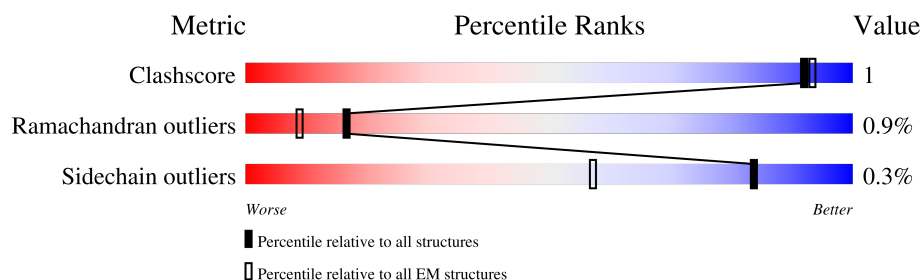
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

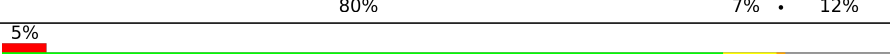
The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



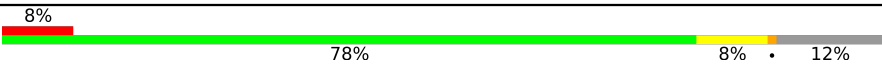
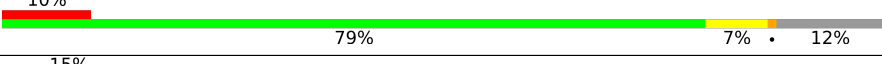
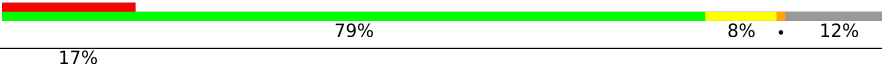
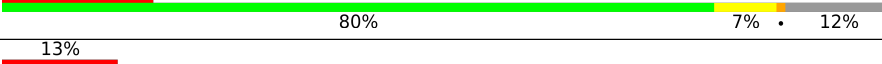
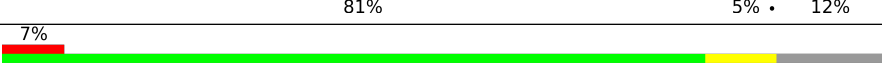
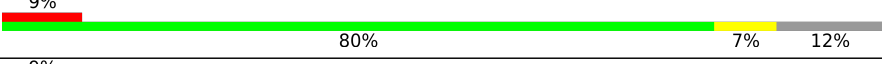
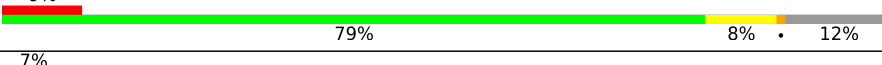
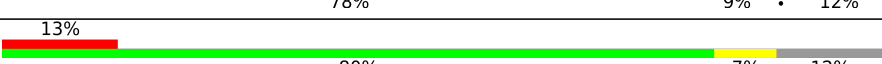
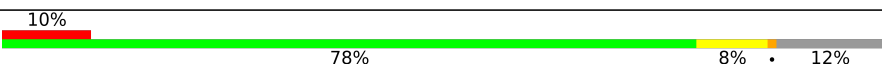
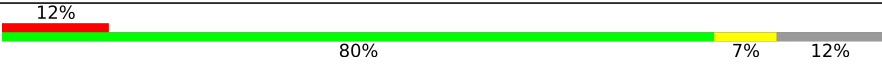
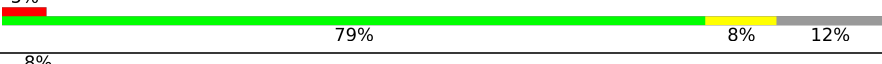
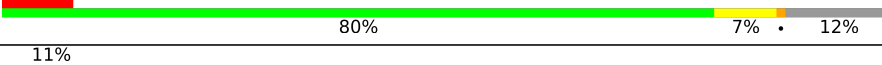
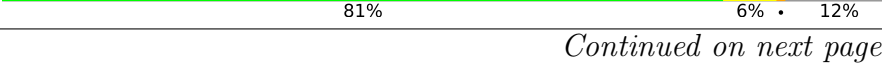
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	aa	521	
1	ab	521	
1	ac	521	
1	ad	521	

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Mol	Chain	Length	Quality of chain
1	ae	521	
1	af	521	
1	ag	521	
1	ah	521	
1	ai	521	
1	aj	521	
1	ak	521	
1	al	521	
1	am	521	
1	an	521	
1	ao	521	
1	ap	521	
1	aq	521	
1	ar	521	
1	as	521	
1	at	521	
1	au	521	
1	av	521	
1	aw	521	
1	ax	521	
1	ay	521	
1	az	521	
1	ba	521	
1	bb	521	
1	bc	521	

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Mol	Chain	Length	Quality of chain
1	bd	521	
1	be	521	
1	bf	521	
1	bg	521	
1	bh	521	
1	bi	521	
1	bj	521	
1	bk	521	
1	bl	521	
1	bm	521	
1	bn	521	
1	bo	521	
1	bp	521	
1	bq	521	
1	br	521	
1	bs	521	
1	bt	521	
1	bu	521	
1	bv	521	
1	bw	521	
1	bx	521	
1	by	521	
1	bz	521	
1	ca	521	
1	cb	521	

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Mol	Chain	Length	Quality of chain
1	cc	521	
1	cd	521	
1	ce	521	
1	cf	521	
1	cg	521	
1	ch	521	
1	ci	521	
1	cj	521	
1	ck	521	
1	cl	521	
1	cm	521	
1	cn	521	
1	co	521	
1	cp	521	
1	cq	521	
1	cr	521	
1	cs	521	
1	ct	521	
1	cu	521	
1	cv	521	
1	cw	521	
1	cx	521	
1	cy	521	
1	cz	521	
1	da	521	

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Mol	Chain	Length	Quality of chain
1	db	521	
1	dc	521	
1	dd	521	
1	de	521	
1	df	521	
1	dg	521	
1	dh	521	
1	di	521	
1	dj	521	
1	dk	521	
1	dl	521	
1	dm	521	
1	dn	521	
1	do	521	
1	dp	521	
1	dq	521	
1	dr	521	
1	ds	521	
1	dt	521	
1	du	521	
1	dv	521	
1	dw	521	
1	dx	521	
1	dy	521	
1	dz	521	

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Mol	Chain	Length	Quality of chain
1	ea	521	
1	eb	521	
1	ec	521	
1	ed	521	
1	ee	521	
1	ef	521	
1	eg	521	
1	eh	521	
1	ei	521	
1	ej	521	
1	ek	521	
1	el	521	
1	em	521	
1	en	521	
1	eo	521	
1	ep	521	
1	eq	521	
1	er	521	
1	es	521	
1	et	521	
1	eu	521	
1	ev	521	
1	ew	521	
1	ex	521	
1	ey	521	

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Mol	Chain	Length	Quality of chain
1	ez	521	
1	fa	521	
1	fb	521	
1	fc	521	
1	fd	521	
1	fe	521	
1	ff	521	
1	fg	521	
1	fh	521	
1	fi	521	
1	fj	521	
1	fk	521	
1	fl	521	
1	fm	521	
1	fn	521	
1	fo	521	
1	fp	521	
1	fq	521	
1	fr	521	
1	fs	521	
1	ft	521	
1	fu	521	
1	fv	521	
1	fw	521	
1	fx	521	

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Mol	Chain	Length	Quality of chain
1	fy	521	
1	fz	521	
1	ga	521	
1	gb	521	
1	gc	521	
1	gd	521	
1	ge	521	
1	gf	521	
1	gg	521	
1	gh	521	
1	gi	521	
1	gj	521	
1	gk	521	
1	gl	521	
1	gm	521	
1	gn	521	
1	go	521	
1	gp	521	
1	gq	521	
1	gr	521	
1	gs	521	
1	gt	521	
1	gu	521	
1	gv	521	
1	gw	521	

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Mol	Chain	Length	Quality of chain
1	gx	521	
1	gy	521	
1	gz	521	
1	ha	521	
1	hb	521	
1	hc	521	
1	hd	521	
2	he	427	
2	hf	427	
2	hg	427	
2	hh	427	
2	hi	427	
2	hj	427	
2	hk	427	
2	hl	427	
2	hm	427	
2	hn	427	
2	ho	427	
3	hp	80	
3	hq	80	
3	hr	80	
3	hs	80	
3	ht	80	
3	hu	80	
3	hv	80	

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Mol	Chain	Length	Quality of chain
3	hw	80	95% 86% 12% .
3	hx	80	89% 90% 9% .
3	hy	80	99% 89% 10% .
3	hz	80	75% 81% 16% ..
3	ia	80	91% 86% 12% .
3	ib	80	89% 88% 11% .
3	ic	80	74% 88% 10% ..
3	id	80	99% 89% 10% .
3	ie	80	96% 86% 12% .
3	if	80	95% 90% 9% .
3	ig	80	91% 86% 12% .
3	ih	80	68% 84% 15% .
3	ii	80	88% 86% 12% .
3	ij	80	61% 81% 18% .
3	ik	80	81% 79% 19% ..
3	il	80	99% 86% 11% ..
3	im	80	95% 84% 15% .
3	in	80	98% 85% 14% .
3	io	80	99% 85% 14% .
3	ip	80	91% 86% 12% .
3	iq	80	99% 81% 18% .
3	ir	80	98% 85% 12% ..
3	is	80	98% 88% 11% .
3	it	80	95% 88% 11% .
3	iu	80	92% 79% 19% ..

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Mol	Chain	Length	Quality of chain
3	iv	80	98% 85%14%
3	iw	80	98% 80%19%
3	ix	80	99% 86%12%
3	iy	80	99% 84%15%
3	iz	80	82% 82%16%
3	ja	80	59% 85%14%
3	jb	80	99% 84%15%
3	jc	80	99% 79%20%
3	jd	80	95% 89%10%
3	je	80	91% 82%16%
3	jf	80	94% 81%18%
3	jg	80	82% 78%20%
3	jh	80	98% 82%16%
3	ji	80	96% 81%16%
3	jj	80	98% 92%6%
3	jk	80	95% 91%8%
3	jl	80	86% 84%14%
3	jm	80	96% 89%10%
3	jn	80	94% 84%15%
3	jo	80	99% 85%14%
3	jp	80	99% 91%6%
3	jq	80	99% 88%11%
3	jr	80	92% 84%14%
3	js	80	84% 89%10%
3	jt	80	98% 85%14%

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Mol	Chain	Length	Quality of chain
3	ju	80	95% 84% 15% .
3	jv	80	99% 92% 6% .
3	jw	80	99% 82% 16% .
3	jx	80	91% 88% 11% .
3	jy	80	95% 86% 12% .
3	jz	80	99% 81% 16% ..
3	ka	80	99% 81% 16% ..
3	kb	80	98% 82% 16% .
3	kc	80	99% 88% 10% ..
3	kd	80	99% 89% 9% ..
3	ke	80	98% 82% 16% .
3	kf	80	99% 90% 9% .
3	kg	80	92% 81% 18% .
3	kh	80	88% 90% 9% .
3	ki	80	96% 90% 9% .
3	kj	80	99% 91% 8% .
3	kk	80	98% 82% 16% .
3	kl	80	99% 84% 15% .
3	km	80	99% 88% 11% .
3	kn	80	98% 84% 15% .
3	ko	80	99% 82% 16% .
3	kp	80	99% 78% 21% .
3	kq	80	99% 81% 16% ..
3	kr	80	98% 85% 14% .
3	ks	80	95% 86% 12% .

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Mol	Chain	Length	Quality of chain
3	kt	80	96% 84% 15%
3	ku	80	95% 85% 12%
3	kv	80	99% 81% 18%
3	kw	80	99% 89% 10%
3	kx	80	99% 86% 11%
3	ky	80	99% 80% 19%
3	kz	80	99% 89% 10%
3	la	80	74% 81% 16%
3	lb	80	98% 84% 15%
3	lc	80	95% 86% 12%
3	ld	80	95% 89% 10%
3	le	80	92% 85% 12%
3	lf	80	71% 85% 14%
3	lg	80	99% 79% 20%
3	lh	80	85% 89% 10%
3	li	80	90% 84% 15%
3	lj	80	86% 80% 19%
3	lk	80	88% 85% 14%
3	ll	80	89% 91% 6%
3	lm	80	85% 82% 16%
3	ln	80	88% 89% 10%
3	lo	80	96% 86% 12%
3	lp	80	81% 79% 20%
3	lq	80	69% 85% 14%
3	lr	80	85% 94% 5%

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Mol	Chain	Length	Quality of chain
3	ls	80	91% 89% 9% ..
3	lt	80	48% 78% 21% .
3	lu	80	64% 81% 18% .
3	lv	80	98% 82% 16% .
3	lw	80	90% 85% 14% .
3	lx	80	99% 88% 11% .
3	ly	80	95% 86% 12% .
3	lz	80	90% 82% 15% ..
3	ma	80	94% 88% 11% .
3	mb	80	99% 88% 11% .
3	mc	80	96% 92% 6% .
3	md	80	91% 91% 8% .
3	me	80	79% 84% 15% .
3	mf	80	79% 82% 16% .
3	mg	80	80% 89% 10% .
3	mh	80	95% 85% 12% ..
3	mi	80	86% 85% 14% .
3	mj	80	76% 80% 19% .
3	mk	80	60% 85% 14% .
3	ml	80	98% 90% 9% .
3	mm	80	99% 84% 15% .
3	mn	80	80% 84% 15% .
3	mo	80	75% 81% 18% .
3	mp	80	80% 86% 12% .
3	mq	80	54% 84% 15% .

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Mol	Chain	Length	Quality of chain
3	ms	80	99% 80% 19% .
3	mt	80	99% 81% 18% .
3	mu	80	96% 88% 11% .
3	mv	80	99% 86% 12% .
3	mw	80	95% 94% 5% .
3	mx	80	96% 84% 14% ..
3	my	80	99% 81% 16% ..
3	mz	80	99% 80% 19% .
3	na	80	99% 88% 11% .
3	nb	80	99% 85% 14% .
3	nc	80	92% 89% 10% .
3	nd	80	95% 86% 11% ..
3	ne	80	99% 89% 10% .
3	nf	80	95% 85% 14% .
3	ng	80	88% 88% 11% .
3	nh	80	98% 82% 15% ..
3	ni	80	99% 88% 11% .
3	nj	80	99% 85% 12% ..
3	nk	80	96% 80% 19% .
3	nl	80	99% 88% 11% .
3	nm	80	98% 90% 9% .
3	nn	80	96% 79% 20% .
3	no	80	96% 86% 12% .
3	np	80	96% 85% 14% .
3	nq	80	92% 82% 15% ..

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Mol	Chain	Length	Quality of chain
3	ns	80	92% 86% 12% .
3	nt	80	99% 85% 12% ..
3	nu	80	99% 78% 20% ..
3	nv	80	92% 85% 12% ..
3	nw	80	88% 82% 15% ..
3	nx	80	98% 90% 9% .
3	ny	80	98% 82% 15% ..
3	nz	80	99% 91% 8% .
3	oa	80	99% 89% 10% .
3	ob	80	99% 82% 16% .
3	oc	80	98% 90% 9% .
3	od	80	96% 89% 10% .
3	oe	80	99% 80% 19% .
3	of	80	99% 86% 12% .
3	og	80	98% 90% 9% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 781038 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 capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	aa	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ab	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ac	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ad	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ae	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	af	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ag	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ah	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ai	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	aj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ak	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	al	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	am	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	an	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ao	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ap	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	aq	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ar	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	as	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	at	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	au	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	av	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	aw	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ax	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ay	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	az	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ba	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bb	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bc	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bd	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	be	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bf	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bg	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bh	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bi	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bk	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bl	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	bm	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bn	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bo	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bp	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bq	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	br	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bs	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bt	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bu	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bv	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bw	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bx	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	by	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	bz	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ca	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cb	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cc	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cd	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ce	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cf	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cg	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ch	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ci	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ck	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cl	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cm	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cn	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	co	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cp	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cq	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cr	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cs	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ct	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cu	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cv	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cw	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cx	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cy	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	cz	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	da	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	db	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	dc	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dd	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	de	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	df	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dg	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dh	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	di	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dk	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dl	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dm	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dn	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	do	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dp	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dq	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dr	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ds	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dt	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	du	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dv	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	dw	430	Total	C	N	O	S	0	0
			3249	2062	552	620	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	dx	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	dy	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	dz	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ea	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	eb	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ec	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ed	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ee	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ef	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	eg	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	eh	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ei	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ej	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ek	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	el	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	em	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	en	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	eo	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	ep	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	eq	456	Total 3425	C 2167	N 584	O 659	S 15	0	0
1	er	456	Total 3425	C 2167	N 584	O 659	S 15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	es	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	et	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	eu	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ev	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ew	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ex	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ey	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ez	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fa	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fb	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fc	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fd	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fe	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ff	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fg	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fh	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fi	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fk	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fl	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fm	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	fn	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fo	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fp	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fq	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fr	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fs	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ft	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fu	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fv	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fw	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fx	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fy	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	fz	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ga	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gb	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gc	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gd	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ge	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gf	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gg	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gh	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	gi	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gk	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gl	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gm	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gn	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	go	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gp	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gq	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gr	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gs	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gt	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gu	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gv	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gw	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gx	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gy	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	gz	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	ha	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	hb	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
1	hc	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	hd	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

- Molecule 2 is a protein called Capsid vertex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	he	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hf	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hg	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hh	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hi	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hj	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hk	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hl	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hm	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	hn	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		
2	ho	415	Total	C	N	O	S	0	0
			3208	2039	521	640	8		

- Molecule 3 is a protein called Small outer capsid protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	hp	79	Total	C	N	O	0	0
			633	403	106	124		
3	hq	79	Total	C	N	O	0	0
			633	403	106	124		
3	hr	79	Total	C	N	O	0	0
			633	403	106	124		
3	hs	79	Total	C	N	O	0	0
			633	403	106	124		
3	ht	79	Total	C	N	O	0	0
			633	403	106	124		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	hu	79	Total 633	C 403	N 106	O 124	0	0
3	hv	79	Total 633	C 403	N 106	O 124	0	0
3	hw	79	Total 633	C 403	N 106	O 124	0	0
3	hx	79	Total 633	C 403	N 106	O 124	0	0
3	hy	79	Total 633	C 403	N 106	O 124	0	0
3	hz	79	Total 633	C 403	N 106	O 124	0	0
3	ia	79	Total 633	C 403	N 106	O 124	0	0
3	ib	79	Total 633	C 403	N 106	O 124	0	0
3	ic	79	Total 633	C 403	N 106	O 124	0	0
3	id	79	Total 633	C 403	N 106	O 124	0	0
3	ie	79	Total 633	C 403	N 106	O 124	0	0
3	if	79	Total 633	C 403	N 106	O 124	0	0
3	ig	79	Total 633	C 403	N 106	O 124	0	0
3	ih	79	Total 633	C 403	N 106	O 124	0	0
3	ii	79	Total 633	C 403	N 106	O 124	0	0
3	ij	79	Total 633	C 403	N 106	O 124	0	0
3	ik	79	Total 633	C 403	N 106	O 124	0	0
3	il	79	Total 633	C 403	N 106	O 124	0	0
3	im	79	Total 633	C 403	N 106	O 124	0	0
3	in	79	Total 633	C 403	N 106	O 124	0	0
3	io	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	ip	79	Total 633	C 403	N 106	O 124	0	0
3	iq	79	Total 633	C 403	N 106	O 124	0	0
3	ir	79	Total 633	C 403	N 106	O 124	0	0
3	is	79	Total 633	C 403	N 106	O 124	0	0
3	it	79	Total 633	C 403	N 106	O 124	0	0
3	iu	79	Total 633	C 403	N 106	O 124	0	0
3	iv	79	Total 633	C 403	N 106	O 124	0	0
3	iw	79	Total 633	C 403	N 106	O 124	0	0
3	ix	79	Total 633	C 403	N 106	O 124	0	0
3	iy	79	Total 633	C 403	N 106	O 124	0	0
3	iz	79	Total 633	C 403	N 106	O 124	0	0
3	ja	79	Total 633	C 403	N 106	O 124	0	0
3	jb	79	Total 633	C 403	N 106	O 124	0	0
3	jc	79	Total 633	C 403	N 106	O 124	0	0
3	jd	79	Total 633	C 403	N 106	O 124	0	0
3	je	79	Total 633	C 403	N 106	O 124	0	0
3	jf	79	Total 633	C 403	N 106	O 124	0	0
3	jg	79	Total 633	C 403	N 106	O 124	0	0
3	jh	79	Total 633	C 403	N 106	O 124	0	0
3	ji	79	Total 633	C 403	N 106	O 124	0	0
3	jj	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	jk	79	Total 633	C 403	N 106	O 124	0	0
3	jl	79	Total 633	C 403	N 106	O 124	0	0
3	jm	79	Total 633	C 403	N 106	O 124	0	0
3	jn	79	Total 633	C 403	N 106	O 124	0	0
3	jo	79	Total 633	C 403	N 106	O 124	0	0
3	jp	79	Total 633	C 403	N 106	O 124	0	0
3	jq	79	Total 633	C 403	N 106	O 124	0	0
3	jr	79	Total 633	C 403	N 106	O 124	0	0
3	js	79	Total 633	C 403	N 106	O 124	0	0
3	jt	79	Total 633	C 403	N 106	O 124	0	0
3	ju	79	Total 633	C 403	N 106	O 124	0	0
3	jv	79	Total 633	C 403	N 106	O 124	0	0
3	jw	79	Total 633	C 403	N 106	O 124	0	0
3	jx	79	Total 633	C 403	N 106	O 124	0	0
3	jy	79	Total 633	C 403	N 106	O 124	0	0
3	jz	79	Total 633	C 403	N 106	O 124	0	0
3	ka	79	Total 633	C 403	N 106	O 124	0	0
3	kb	79	Total 633	C 403	N 106	O 124	0	0
3	kc	79	Total 633	C 403	N 106	O 124	0	0
3	kd	79	Total 633	C 403	N 106	O 124	0	0
3	ke	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	kf	79	Total 633	C 403	N 106	O 124	0	0
3	kg	79	Total 633	C 403	N 106	O 124	0	0
3	kh	79	Total 633	C 403	N 106	O 124	0	0
3	ki	79	Total 633	C 403	N 106	O 124	0	0
3	kj	79	Total 633	C 403	N 106	O 124	0	0
3	kk	79	Total 633	C 403	N 106	O 124	0	0
3	kl	79	Total 633	C 403	N 106	O 124	0	0
3	km	79	Total 633	C 403	N 106	O 124	0	0
3	kn	79	Total 633	C 403	N 106	O 124	0	0
3	ko	79	Total 633	C 403	N 106	O 124	0	0
3	kp	79	Total 633	C 403	N 106	O 124	0	0
3	kq	79	Total 633	C 403	N 106	O 124	0	0
3	kr	79	Total 633	C 403	N 106	O 124	0	0
3	ks	79	Total 633	C 403	N 106	O 124	0	0
3	kt	79	Total 633	C 403	N 106	O 124	0	0
3	ku	79	Total 633	C 403	N 106	O 124	0	0
3	kv	79	Total 633	C 403	N 106	O 124	0	0
3	kw	79	Total 633	C 403	N 106	O 124	0	0
3	kx	79	Total 633	C 403	N 106	O 124	0	0
3	ky	79	Total 633	C 403	N 106	O 124	0	0
3	kz	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	la	79	Total 633	C 403	N 106	O 124	0	0
3	lb	79	Total 633	C 403	N 106	O 124	0	0
3	lc	79	Total 633	C 403	N 106	O 124	0	0
3	ld	79	Total 633	C 403	N 106	O 124	0	0
3	le	79	Total 633	C 403	N 106	O 124	0	0
3	lf	79	Total 633	C 403	N 106	O 124	0	0
3	lg	79	Total 633	C 403	N 106	O 124	0	0
3	lh	79	Total 633	C 403	N 106	O 124	0	0
3	li	79	Total 633	C 403	N 106	O 124	0	0
3	lj	79	Total 633	C 403	N 106	O 124	0	0
3	lk	79	Total 633	C 403	N 106	O 124	0	0
3	ll	79	Total 633	C 403	N 106	O 124	0	0
3	lm	79	Total 633	C 403	N 106	O 124	0	0
3	ln	79	Total 633	C 403	N 106	O 124	0	0
3	lo	79	Total 633	C 403	N 106	O 124	0	0
3	lp	79	Total 633	C 403	N 106	O 124	0	0
3	lq	79	Total 633	C 403	N 106	O 124	0	0
3	lr	79	Total 633	C 403	N 106	O 124	0	0
3	ls	79	Total 633	C 403	N 106	O 124	0	0
3	lt	79	Total 633	C 403	N 106	O 124	0	0
3	lu	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	lv	79	Total 633	C 403	N 106	O 124	0	0
3	lw	79	Total 633	C 403	N 106	O 124	0	0
3	lx	79	Total 633	C 403	N 106	O 124	0	0
3	ly	79	Total 633	C 403	N 106	O 124	0	0
3	lz	79	Total 633	C 403	N 106	O 124	0	0
3	ma	79	Total 633	C 403	N 106	O 124	0	0
3	mb	79	Total 633	C 403	N 106	O 124	0	0
3	mc	79	Total 633	C 403	N 106	O 124	0	0
3	md	79	Total 633	C 403	N 106	O 124	0	0
3	me	79	Total 633	C 403	N 106	O 124	0	0
3	mf	79	Total 633	C 403	N 106	O 124	0	0
3	mg	79	Total 633	C 403	N 106	O 124	0	0
3	mh	79	Total 633	C 403	N 106	O 124	0	0
3	mi	79	Total 633	C 403	N 106	O 124	0	0
3	mj	79	Total 633	C 403	N 106	O 124	0	0
3	mk	79	Total 633	C 403	N 106	O 124	0	0
3	ml	79	Total 633	C 403	N 106	O 124	0	0
3	mm	79	Total 633	C 403	N 106	O 124	0	0
3	mn	79	Total 633	C 403	N 106	O 124	0	0
3	mo	79	Total 633	C 403	N 106	O 124	0	0
3	mp	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	mq	79	Total 633	C 403	N 106	O 124	0	0
3	ms	79	Total 633	C 403	N 106	O 124	0	0
3	mt	79	Total 633	C 403	N 106	O 124	0	0
3	mu	79	Total 633	C 403	N 106	O 124	0	0
3	mv	79	Total 633	C 403	N 106	O 124	0	0
3	mw	79	Total 633	C 403	N 106	O 124	0	0
3	mx	79	Total 633	C 403	N 106	O 124	0	0
3	my	79	Total 633	C 403	N 106	O 124	0	0
3	mz	79	Total 633	C 403	N 106	O 124	0	0
3	na	79	Total 633	C 403	N 106	O 124	0	0
3	nb	79	Total 633	C 403	N 106	O 124	0	0
3	nc	79	Total 633	C 403	N 106	O 124	0	0
3	nd	79	Total 633	C 403	N 106	O 124	0	0
3	ne	79	Total 633	C 403	N 106	O 124	0	0
3	nf	79	Total 633	C 403	N 106	O 124	0	0
3	ng	79	Total 633	C 403	N 106	O 124	0	0
3	nh	79	Total 633	C 403	N 106	O 124	0	0
3	ni	79	Total 633	C 403	N 106	O 124	0	0
3	nj	79	Total 633	C 403	N 106	O 124	0	0
3	nk	79	Total 633	C 403	N 106	O 124	0	0
3	nl	79	Total 633	C 403	N 106	O 124	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	nm	79	Total 633	C 403	N 106	O 124	0	0
3	nn	79	Total 633	C 403	N 106	O 124	0	0
3	no	79	Total 633	C 403	N 106	O 124	0	0
3	np	79	Total 633	C 403	N 106	O 124	0	0
3	nq	79	Total 633	C 403	N 106	O 124	0	0
3	ns	79	Total 633	C 403	N 106	O 124	0	0
3	nt	79	Total 633	C 403	N 106	O 124	0	0
3	nu	79	Total 633	C 403	N 106	O 124	0	0
3	nv	79	Total 633	C 403	N 106	O 124	0	0
3	nw	79	Total 633	C 403	N 106	O 124	0	0
3	nx	79	Total 633	C 403	N 106	O 124	0	0
3	ny	79	Total 633	C 403	N 106	O 124	0	0
3	nz	79	Total 633	C 403	N 106	O 124	0	0
3	oa	79	Total 633	C 403	N 106	O 124	0	0
3	ob	79	Total 633	C 403	N 106	O 124	0	0
3	oc	79	Total 633	C 403	N 106	O 124	0	0
3	od	79	Total 633	C 403	N 106	O 124	0	0
3	oe	79	Total 633	C 403	N 106	O 124	0	0
3	of	79	Total 633	C 403	N 106	O 124	0	0
3	og	79	Total 633	C 403	N 106	O 124	0	0

There are 344 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
hp	4	ALA	THR	conflict	UNP P03715
hp	28	VAL	ILE	conflict	UNP P03715
hq	4	ALA	THR	conflict	UNP P03715
hq	28	VAL	ILE	conflict	UNP P03715
hr	4	ALA	THR	conflict	UNP P03715
hr	28	VAL	ILE	conflict	UNP P03715
hs	4	ALA	THR	conflict	UNP P03715
hs	28	VAL	ILE	conflict	UNP P03715
ht	4	ALA	THR	conflict	UNP P03715
ht	28	VAL	ILE	conflict	UNP P03715
hu	4	ALA	THR	conflict	UNP P03715
hu	28	VAL	ILE	conflict	UNP P03715
hv	4	ALA	THR	conflict	UNP P03715
hv	28	VAL	ILE	conflict	UNP P03715
hw	4	ALA	THR	conflict	UNP P03715
hw	28	VAL	ILE	conflict	UNP P03715
hx	4	ALA	THR	conflict	UNP P03715
hx	28	VAL	ILE	conflict	UNP P03715
hy	4	ALA	THR	conflict	UNP P03715
hy	28	VAL	ILE	conflict	UNP P03715
hz	4	ALA	THR	conflict	UNP P03715
hz	28	VAL	ILE	conflict	UNP P03715
ia	4	ALA	THR	conflict	UNP P03715
ia	28	VAL	ILE	conflict	UNP P03715
ib	4	ALA	THR	conflict	UNP P03715
ib	28	VAL	ILE	conflict	UNP P03715
ic	4	ALA	THR	conflict	UNP P03715
ic	28	VAL	ILE	conflict	UNP P03715
id	4	ALA	THR	conflict	UNP P03715
id	28	VAL	ILE	conflict	UNP P03715
ie	4	ALA	THR	conflict	UNP P03715
ie	28	VAL	ILE	conflict	UNP P03715
if	4	ALA	THR	conflict	UNP P03715
if	28	VAL	ILE	conflict	UNP P03715
ig	4	ALA	THR	conflict	UNP P03715
ig	28	VAL	ILE	conflict	UNP P03715
ih	4	ALA	THR	conflict	UNP P03715
ih	28	VAL	ILE	conflict	UNP P03715
ii	4	ALA	THR	conflict	UNP P03715
ii	28	VAL	ILE	conflict	UNP P03715
ij	4	ALA	THR	conflict	UNP P03715
ij	28	VAL	ILE	conflict	UNP P03715
ik	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
ik	28	VAL	ILE	conflict	UNP P03715
il	4	ALA	THR	conflict	UNP P03715
il	28	VAL	ILE	conflict	UNP P03715
im	4	ALA	THR	conflict	UNP P03715
im	28	VAL	ILE	conflict	UNP P03715
in	4	ALA	THR	conflict	UNP P03715
in	28	VAL	ILE	conflict	UNP P03715
io	4	ALA	THR	conflict	UNP P03715
io	28	VAL	ILE	conflict	UNP P03715
ip	4	ALA	THR	conflict	UNP P03715
ip	28	VAL	ILE	conflict	UNP P03715
iq	4	ALA	THR	conflict	UNP P03715
iq	28	VAL	ILE	conflict	UNP P03715
ir	4	ALA	THR	conflict	UNP P03715
ir	28	VAL	ILE	conflict	UNP P03715
is	4	ALA	THR	conflict	UNP P03715
is	28	VAL	ILE	conflict	UNP P03715
it	4	ALA	THR	conflict	UNP P03715
it	28	VAL	ILE	conflict	UNP P03715
iu	4	ALA	THR	conflict	UNP P03715
iu	28	VAL	ILE	conflict	UNP P03715
iv	4	ALA	THR	conflict	UNP P03715
iv	28	VAL	ILE	conflict	UNP P03715
iw	4	ALA	THR	conflict	UNP P03715
iw	28	VAL	ILE	conflict	UNP P03715
ix	4	ALA	THR	conflict	UNP P03715
ix	28	VAL	ILE	conflict	UNP P03715
iy	4	ALA	THR	conflict	UNP P03715
iy	28	VAL	ILE	conflict	UNP P03715
iz	4	ALA	THR	conflict	UNP P03715
iz	28	VAL	ILE	conflict	UNP P03715
ja	4	ALA	THR	conflict	UNP P03715
ja	28	VAL	ILE	conflict	UNP P03715
jb	4	ALA	THR	conflict	UNP P03715
jb	28	VAL	ILE	conflict	UNP P03715
jc	4	ALA	THR	conflict	UNP P03715
jc	28	VAL	ILE	conflict	UNP P03715
jd	4	ALA	THR	conflict	UNP P03715
jd	28	VAL	ILE	conflict	UNP P03715
je	4	ALA	THR	conflict	UNP P03715
je	28	VAL	ILE	conflict	UNP P03715
jf	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
jf	28	VAL	ILE	conflict	UNP P03715
yg	4	ALA	THR	conflict	UNP P03715
yg	28	VAL	ILE	conflict	UNP P03715
yh	4	ALA	THR	conflict	UNP P03715
yh	28	VAL	ILE	conflict	UNP P03715
ji	4	ALA	THR	conflict	UNP P03715
ji	28	VAL	ILE	conflict	UNP P03715
jj	4	ALA	THR	conflict	UNP P03715
jj	28	VAL	ILE	conflict	UNP P03715
jk	4	ALA	THR	conflict	UNP P03715
jk	28	VAL	ILE	conflict	UNP P03715
jl	4	ALA	THR	conflict	UNP P03715
jl	28	VAL	ILE	conflict	UNP P03715
jm	4	ALA	THR	conflict	UNP P03715
jm	28	VAL	ILE	conflict	UNP P03715
jn	4	ALA	THR	conflict	UNP P03715
jn	28	VAL	ILE	conflict	UNP P03715
jo	4	ALA	THR	conflict	UNP P03715
jo	28	VAL	ILE	conflict	UNP P03715
jp	4	ALA	THR	conflict	UNP P03715
jp	28	VAL	ILE	conflict	UNP P03715
jq	4	ALA	THR	conflict	UNP P03715
jq	28	VAL	ILE	conflict	UNP P03715
jr	4	ALA	THR	conflict	UNP P03715
jr	28	VAL	ILE	conflict	UNP P03715
js	4	ALA	THR	conflict	UNP P03715
js	28	VAL	ILE	conflict	UNP P03715
jt	4	ALA	THR	conflict	UNP P03715
jt	28	VAL	ILE	conflict	UNP P03715
ju	4	ALA	THR	conflict	UNP P03715
ju	28	VAL	ILE	conflict	UNP P03715
jv	4	ALA	THR	conflict	UNP P03715
jv	28	VAL	ILE	conflict	UNP P03715
jw	4	ALA	THR	conflict	UNP P03715
jw	28	VAL	ILE	conflict	UNP P03715
jx	4	ALA	THR	conflict	UNP P03715
jx	28	VAL	ILE	conflict	UNP P03715
jy	4	ALA	THR	conflict	UNP P03715
jy	28	VAL	ILE	conflict	UNP P03715
jz	4	ALA	THR	conflict	UNP P03715
jz	28	VAL	ILE	conflict	UNP P03715
ka	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
ka	28	VAL	ILE	conflict	UNP P03715
kb	4	ALA	THR	conflict	UNP P03715
kb	28	VAL	ILE	conflict	UNP P03715
kc	4	ALA	THR	conflict	UNP P03715
kc	28	VAL	ILE	conflict	UNP P03715
kd	4	ALA	THR	conflict	UNP P03715
kd	28	VAL	ILE	conflict	UNP P03715
ke	4	ALA	THR	conflict	UNP P03715
ke	28	VAL	ILE	conflict	UNP P03715
kf	4	ALA	THR	conflict	UNP P03715
kf	28	VAL	ILE	conflict	UNP P03715
kg	4	ALA	THR	conflict	UNP P03715
kg	28	VAL	ILE	conflict	UNP P03715
kh	4	ALA	THR	conflict	UNP P03715
kh	28	VAL	ILE	conflict	UNP P03715
ki	4	ALA	THR	conflict	UNP P03715
ki	28	VAL	ILE	conflict	UNP P03715
kj	4	ALA	THR	conflict	UNP P03715
kj	28	VAL	ILE	conflict	UNP P03715
kk	4	ALA	THR	conflict	UNP P03715
kk	28	VAL	ILE	conflict	UNP P03715
kl	4	ALA	THR	conflict	UNP P03715
kl	28	VAL	ILE	conflict	UNP P03715
km	4	ALA	THR	conflict	UNP P03715
km	28	VAL	ILE	conflict	UNP P03715
kn	4	ALA	THR	conflict	UNP P03715
kn	28	VAL	ILE	conflict	UNP P03715
ko	4	ALA	THR	conflict	UNP P03715
ko	28	VAL	ILE	conflict	UNP P03715
kp	4	ALA	THR	conflict	UNP P03715
kp	28	VAL	ILE	conflict	UNP P03715
kq	4	ALA	THR	conflict	UNP P03715
kq	28	VAL	ILE	conflict	UNP P03715
kr	4	ALA	THR	conflict	UNP P03715
kr	28	VAL	ILE	conflict	UNP P03715
ks	4	ALA	THR	conflict	UNP P03715
ks	28	VAL	ILE	conflict	UNP P03715
kt	4	ALA	THR	conflict	UNP P03715
kt	28	VAL	ILE	conflict	UNP P03715
ku	4	ALA	THR	conflict	UNP P03715
ku	28	VAL	ILE	conflict	UNP P03715
kv	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
kv	28	VAL	ILE	conflict	UNP P03715
kw	4	ALA	THR	conflict	UNP P03715
kw	28	VAL	ILE	conflict	UNP P03715
kx	4	ALA	THR	conflict	UNP P03715
kx	28	VAL	ILE	conflict	UNP P03715
ky	4	ALA	THR	conflict	UNP P03715
ky	28	VAL	ILE	conflict	UNP P03715
kz	4	ALA	THR	conflict	UNP P03715
kz	28	VAL	ILE	conflict	UNP P03715
la	4	ALA	THR	conflict	UNP P03715
la	28	VAL	ILE	conflict	UNP P03715
lb	4	ALA	THR	conflict	UNP P03715
lb	28	VAL	ILE	conflict	UNP P03715
lc	4	ALA	THR	conflict	UNP P03715
lc	28	VAL	ILE	conflict	UNP P03715
ld	4	ALA	THR	conflict	UNP P03715
ld	28	VAL	ILE	conflict	UNP P03715
le	4	ALA	THR	conflict	UNP P03715
le	28	VAL	ILE	conflict	UNP P03715
lf	4	ALA	THR	conflict	UNP P03715
lf	28	VAL	ILE	conflict	UNP P03715
lg	4	ALA	THR	conflict	UNP P03715
lg	28	VAL	ILE	conflict	UNP P03715
lh	4	ALA	THR	conflict	UNP P03715
lh	28	VAL	ILE	conflict	UNP P03715
li	4	ALA	THR	conflict	UNP P03715
li	28	VAL	ILE	conflict	UNP P03715
lj	4	ALA	THR	conflict	UNP P03715
lj	28	VAL	ILE	conflict	UNP P03715
lk	4	ALA	THR	conflict	UNP P03715
lk	28	VAL	ILE	conflict	UNP P03715
ll	4	ALA	THR	conflict	UNP P03715
ll	28	VAL	ILE	conflict	UNP P03715
lm	4	ALA	THR	conflict	UNP P03715
lm	28	VAL	ILE	conflict	UNP P03715
ln	4	ALA	THR	conflict	UNP P03715
ln	28	VAL	ILE	conflict	UNP P03715
lo	4	ALA	THR	conflict	UNP P03715
lo	28	VAL	ILE	conflict	UNP P03715
lp	4	ALA	THR	conflict	UNP P03715
lp	28	VAL	ILE	conflict	UNP P03715
lq	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
lq	28	VAL	ILE	conflict	UNP P03715
lr	4	ALA	THR	conflict	UNP P03715
lr	28	VAL	ILE	conflict	UNP P03715
ls	4	ALA	THR	conflict	UNP P03715
ls	28	VAL	ILE	conflict	UNP P03715
lt	4	ALA	THR	conflict	UNP P03715
lt	28	VAL	ILE	conflict	UNP P03715
lu	4	ALA	THR	conflict	UNP P03715
lu	28	VAL	ILE	conflict	UNP P03715
lv	4	ALA	THR	conflict	UNP P03715
lv	28	VAL	ILE	conflict	UNP P03715
lw	4	ALA	THR	conflict	UNP P03715
lw	28	VAL	ILE	conflict	UNP P03715
lx	4	ALA	THR	conflict	UNP P03715
lx	28	VAL	ILE	conflict	UNP P03715
ly	4	ALA	THR	conflict	UNP P03715
ly	28	VAL	ILE	conflict	UNP P03715
lz	4	ALA	THR	conflict	UNP P03715
lz	28	VAL	ILE	conflict	UNP P03715
ma	4	ALA	THR	conflict	UNP P03715
ma	28	VAL	ILE	conflict	UNP P03715
mb	4	ALA	THR	conflict	UNP P03715
mb	28	VAL	ILE	conflict	UNP P03715
mc	4	ALA	THR	conflict	UNP P03715
mc	28	VAL	ILE	conflict	UNP P03715
md	4	ALA	THR	conflict	UNP P03715
md	28	VAL	ILE	conflict	UNP P03715
me	4	ALA	THR	conflict	UNP P03715
me	28	VAL	ILE	conflict	UNP P03715
mf	4	ALA	THR	conflict	UNP P03715
mf	28	VAL	ILE	conflict	UNP P03715
mg	4	ALA	THR	conflict	UNP P03715
mg	28	VAL	ILE	conflict	UNP P03715
mh	4	ALA	THR	conflict	UNP P03715
mh	28	VAL	ILE	conflict	UNP P03715
mi	4	ALA	THR	conflict	UNP P03715
mi	28	VAL	ILE	conflict	UNP P03715
mj	4	ALA	THR	conflict	UNP P03715
mj	28	VAL	ILE	conflict	UNP P03715
mk	4	ALA	THR	conflict	UNP P03715
mk	28	VAL	ILE	conflict	UNP P03715
ml	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
ml	28	VAL	ILE	conflict	UNP P03715
mm	4	ALA	THR	conflict	UNP P03715
mm	28	VAL	ILE	conflict	UNP P03715
mn	4	ALA	THR	conflict	UNP P03715
mn	28	VAL	ILE	conflict	UNP P03715
mo	4	ALA	THR	conflict	UNP P03715
mo	28	VAL	ILE	conflict	UNP P03715
mp	4	ALA	THR	conflict	UNP P03715
mp	28	VAL	ILE	conflict	UNP P03715
mq	4	ALA	THR	conflict	UNP P03715
mq	28	VAL	ILE	conflict	UNP P03715
ms	4	ALA	THR	conflict	UNP P03715
ms	28	VAL	ILE	conflict	UNP P03715
mt	4	ALA	THR	conflict	UNP P03715
mt	28	VAL	ILE	conflict	UNP P03715
mu	4	ALA	THR	conflict	UNP P03715
mu	28	VAL	ILE	conflict	UNP P03715
mv	4	ALA	THR	conflict	UNP P03715
mv	28	VAL	ILE	conflict	UNP P03715
mw	4	ALA	THR	conflict	UNP P03715
mw	28	VAL	ILE	conflict	UNP P03715
mx	4	ALA	THR	conflict	UNP P03715
mx	28	VAL	ILE	conflict	UNP P03715
my	4	ALA	THR	conflict	UNP P03715
my	28	VAL	ILE	conflict	UNP P03715
mz	4	ALA	THR	conflict	UNP P03715
mz	28	VAL	ILE	conflict	UNP P03715
na	4	ALA	THR	conflict	UNP P03715
na	28	VAL	ILE	conflict	UNP P03715
nb	4	ALA	THR	conflict	UNP P03715
nb	28	VAL	ILE	conflict	UNP P03715
nc	4	ALA	THR	conflict	UNP P03715
nc	28	VAL	ILE	conflict	UNP P03715
nd	4	ALA	THR	conflict	UNP P03715
nd	28	VAL	ILE	conflict	UNP P03715
ne	4	ALA	THR	conflict	UNP P03715
ne	28	VAL	ILE	conflict	UNP P03715
nf	4	ALA	THR	conflict	UNP P03715
nf	28	VAL	ILE	conflict	UNP P03715
ng	4	ALA	THR	conflict	UNP P03715
ng	28	VAL	ILE	conflict	UNP P03715
nh	4	ALA	THR	conflict	UNP P03715

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Chain	Residue	Modelled	Actual	Comment	Reference
nh	28	VAL	ILE	conflict	UNP P03715
ni	4	ALA	THR	conflict	UNP P03715
ni	28	VAL	ILE	conflict	UNP P03715
nj	4	ALA	THR	conflict	UNP P03715
nj	28	VAL	ILE	conflict	UNP P03715
nk	4	ALA	THR	conflict	UNP P03715
nk	28	VAL	ILE	conflict	UNP P03715
nl	4	ALA	THR	conflict	UNP P03715
nl	28	VAL	ILE	conflict	UNP P03715
nm	4	ALA	THR	conflict	UNP P03715
nm	28	VAL	ILE	conflict	UNP P03715
nn	4	ALA	THR	conflict	UNP P03715
nn	28	VAL	ILE	conflict	UNP P03715
no	4	ALA	THR	conflict	UNP P03715
no	28	VAL	ILE	conflict	UNP P03715
np	4	ALA	THR	conflict	UNP P03715
np	28	VAL	ILE	conflict	UNP P03715
nq	4	ALA	THR	conflict	UNP P03715
nq	28	VAL	ILE	conflict	UNP P03715
ns	4	ALA	THR	conflict	UNP P03715
ns	28	VAL	ILE	conflict	UNP P03715
nt	4	ALA	THR	conflict	UNP P03715
nt	28	VAL	ILE	conflict	UNP P03715
nu	4	ALA	THR	conflict	UNP P03715
nu	28	VAL	ILE	conflict	UNP P03715
nv	4	ALA	THR	conflict	UNP P03715
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nw	4	ALA	THR	conflict	UNP P03715
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nx	4	ALA	THR	conflict	UNP P03715
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ny	4	ALA	THR	conflict	UNP P03715
ny	28	VAL	ILE	conflict	UNP P03715
nz	4	ALA	THR	conflict	UNP P03715
nz	28	VAL	ILE	conflict	UNP P03715
oa	4	ALA	THR	conflict	UNP P03715
oa	28	VAL	ILE	conflict	UNP P03715
ob	4	ALA	THR	conflict	UNP P03715
ob	28	VAL	ILE	conflict	UNP P03715
oc	4	ALA	THR	conflict	UNP P03715
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od	4	ALA	THR	conflict	UNP P03715

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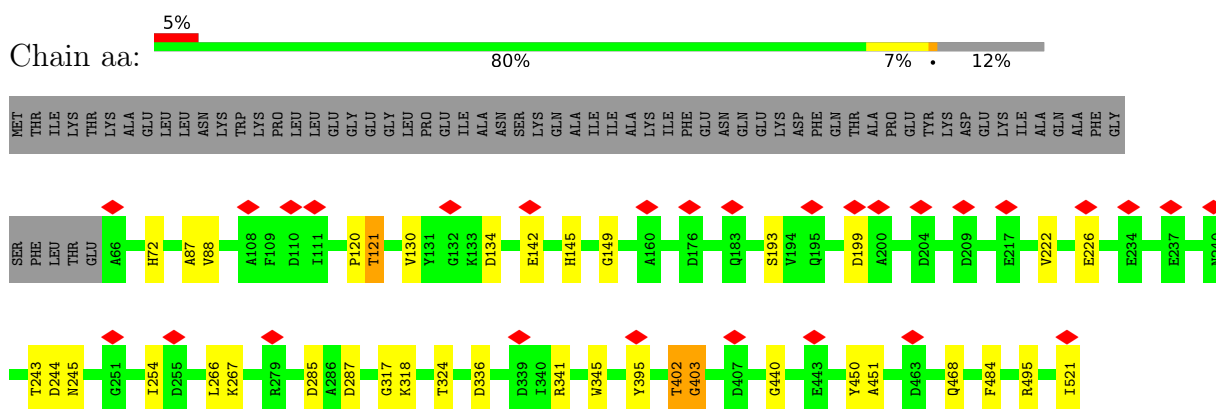
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Chain	Residue	Modelled	Actual	Comment	Reference
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oe	28	VAL	ILE	conflict	UNP P03715
of	4	ALA	THR	conflict	UNP P03715
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og	28	VAL	ILE	conflict	UNP P03715

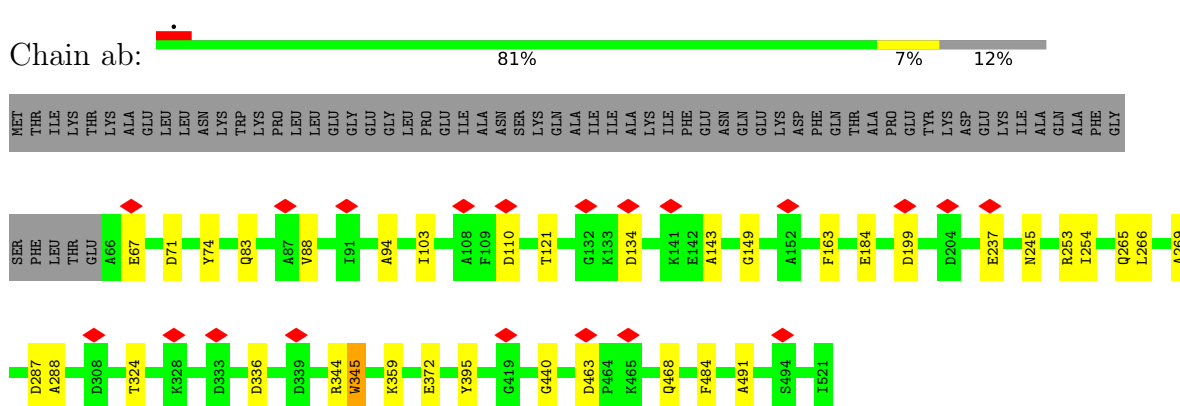
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

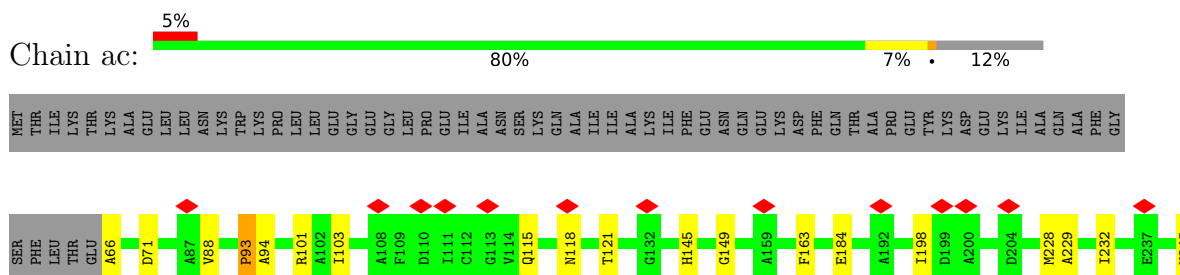
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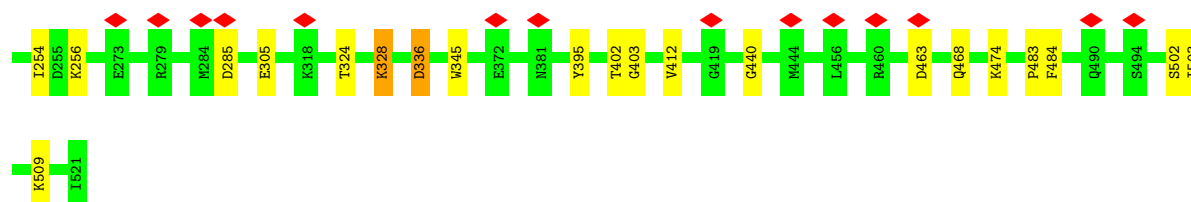


- Molecule 1: Major capsid protein

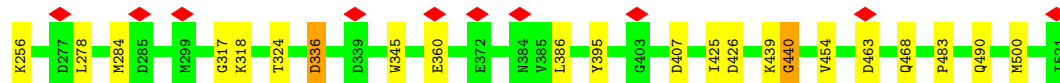
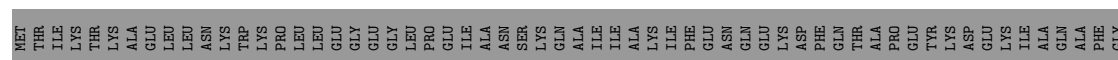
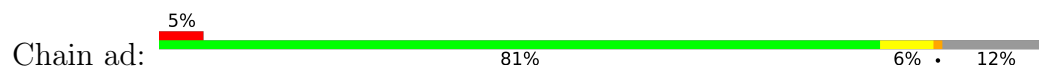


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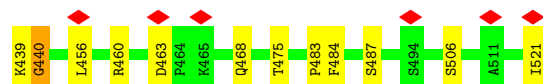
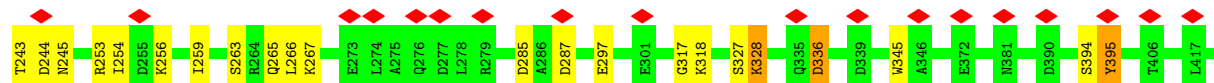
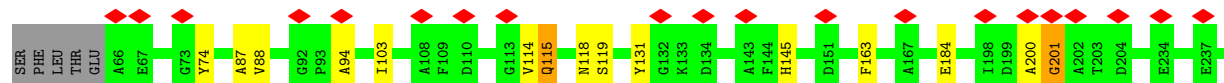
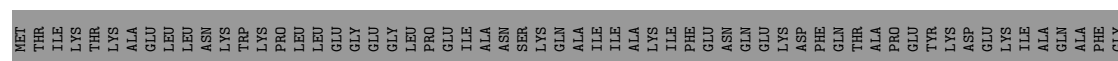
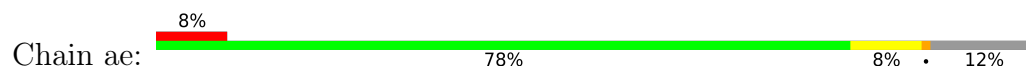




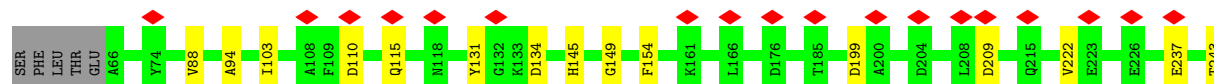
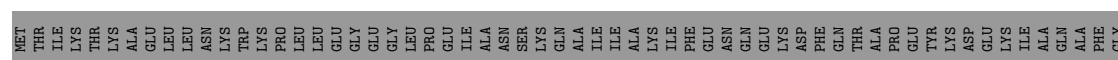
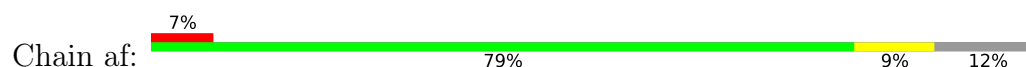
• Molecule 1: Major capsid protein

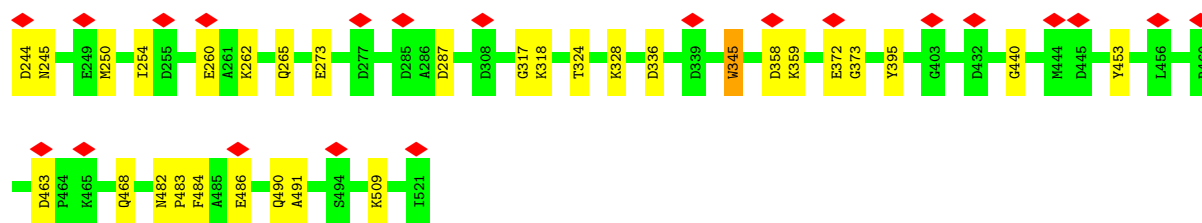


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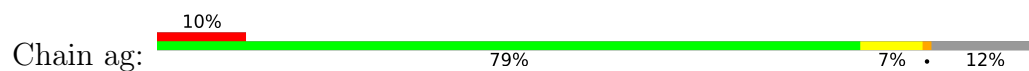


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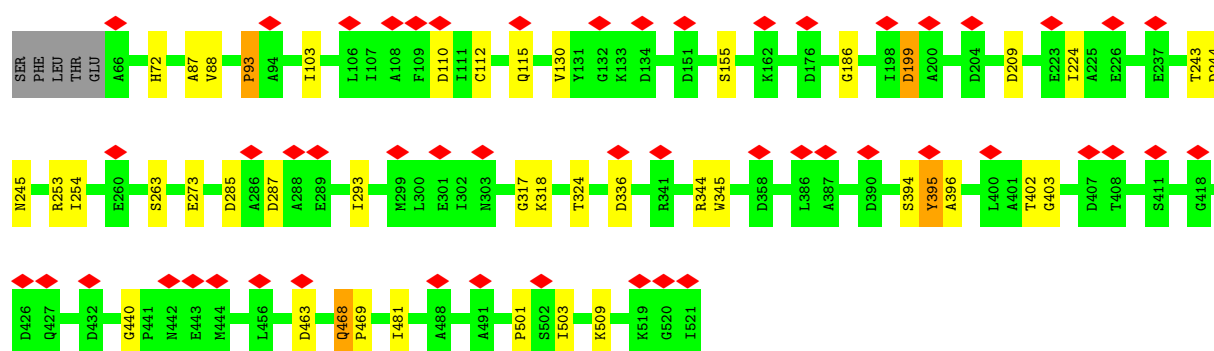




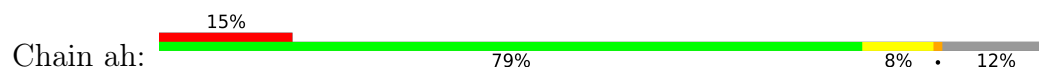
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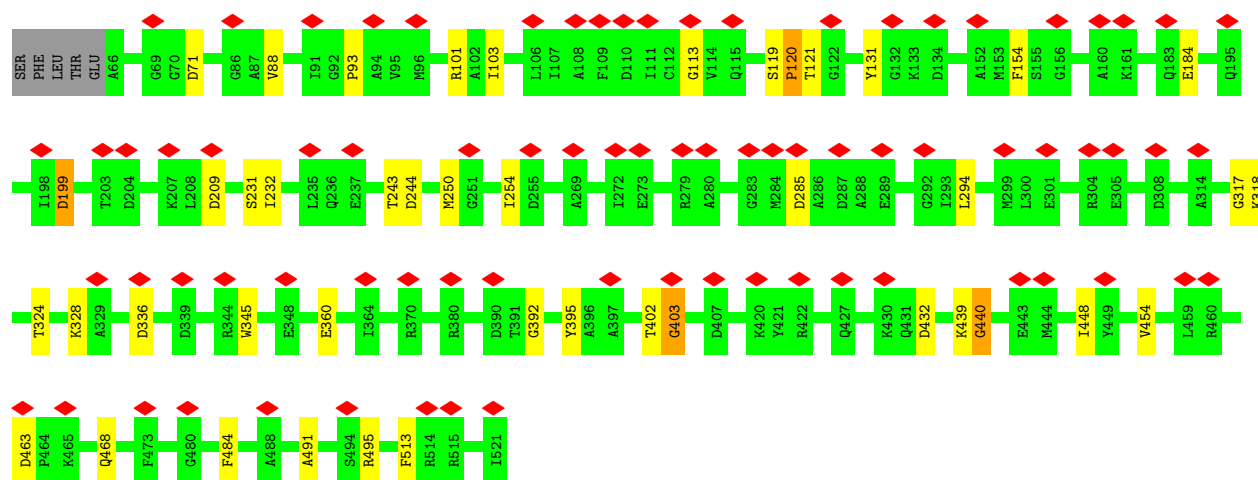
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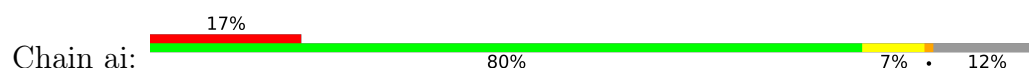
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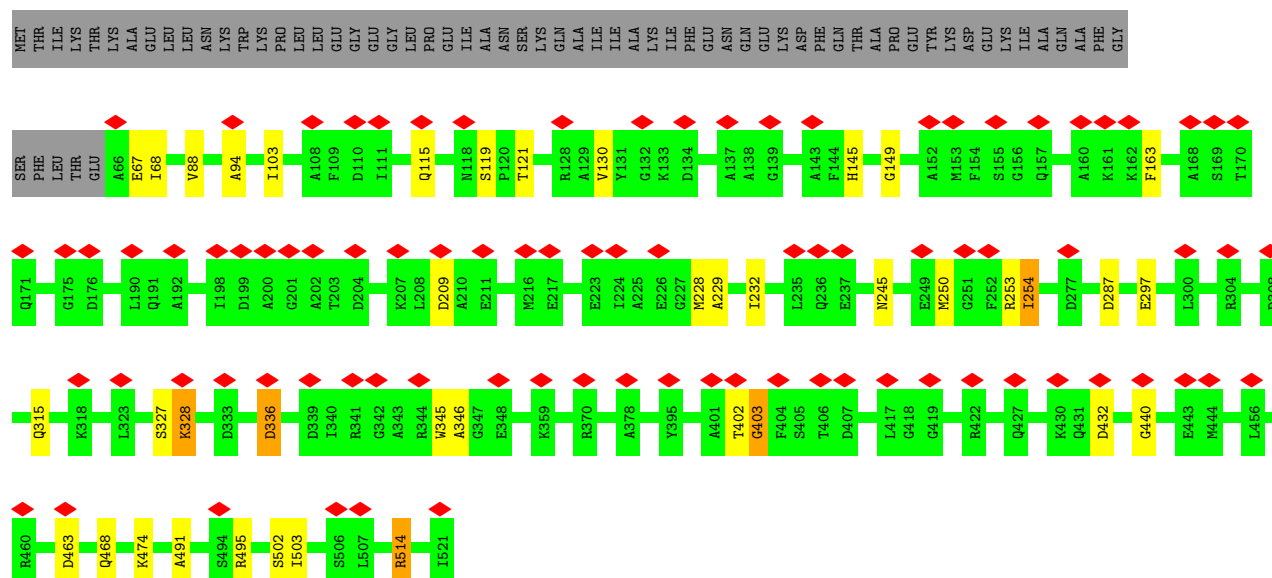


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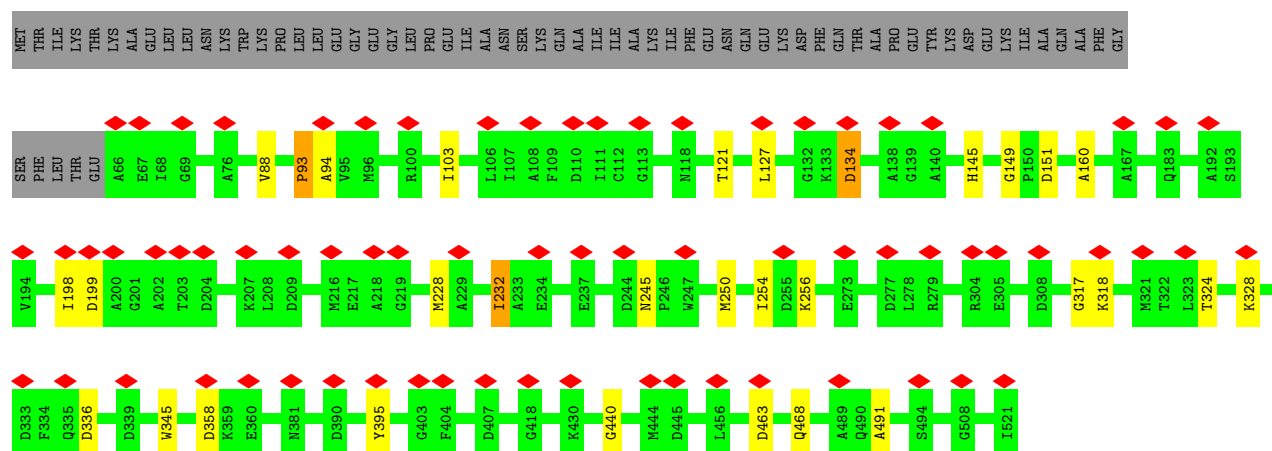
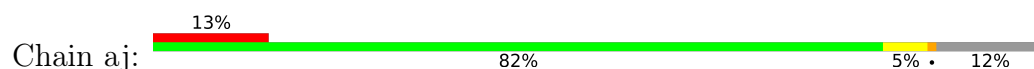


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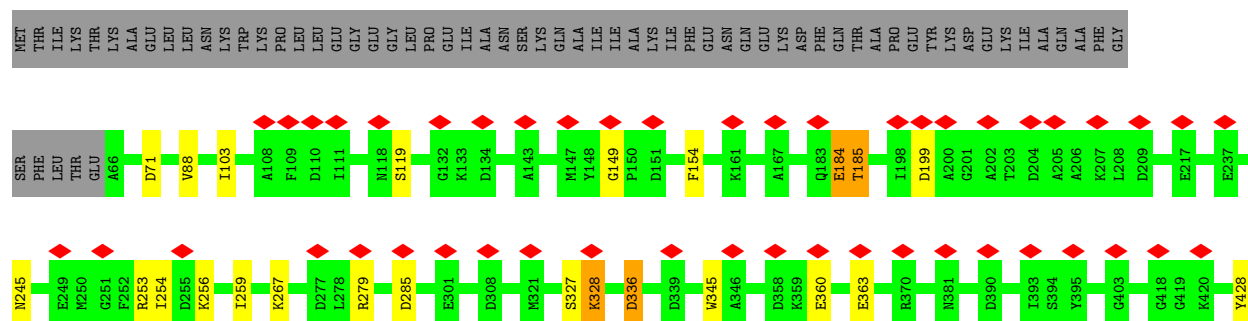
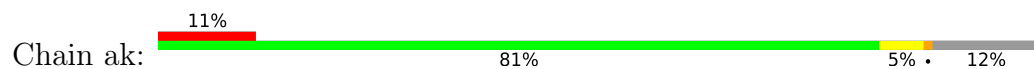




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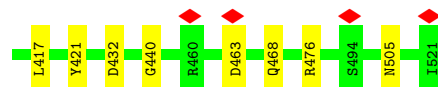
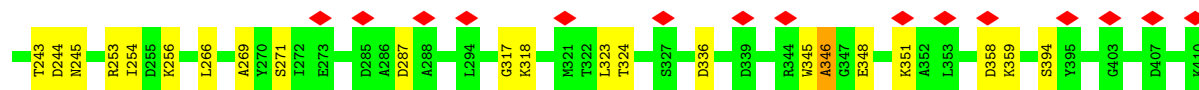
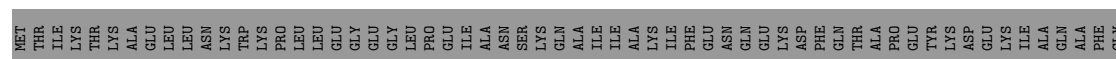
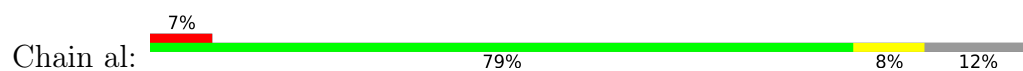


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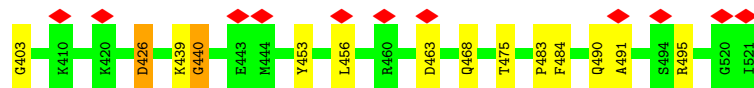
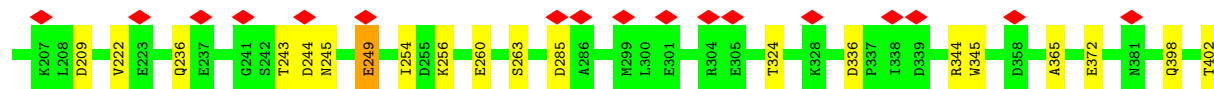
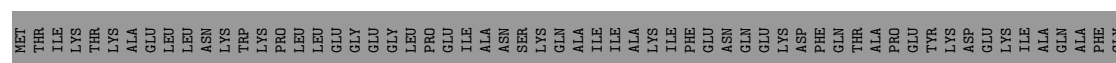
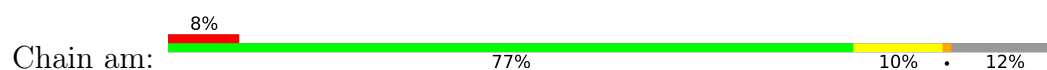




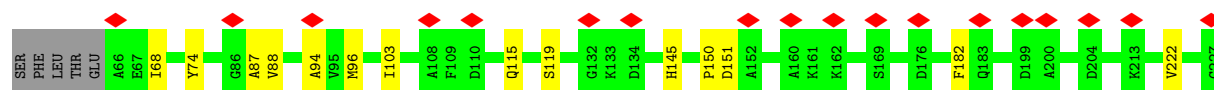
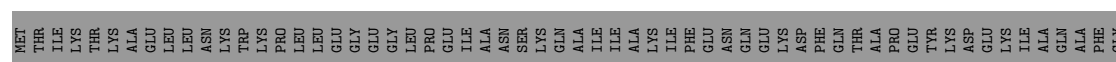
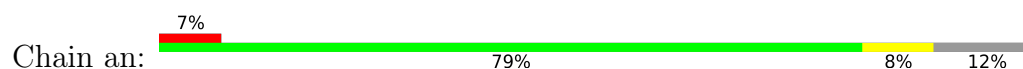
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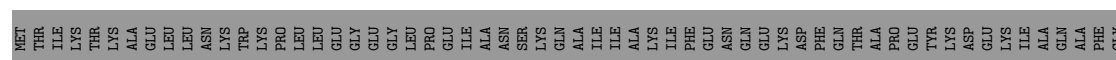


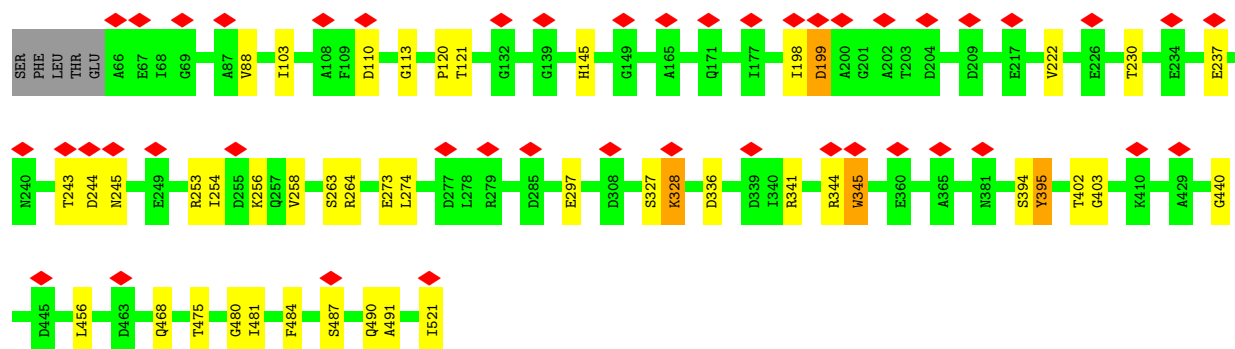
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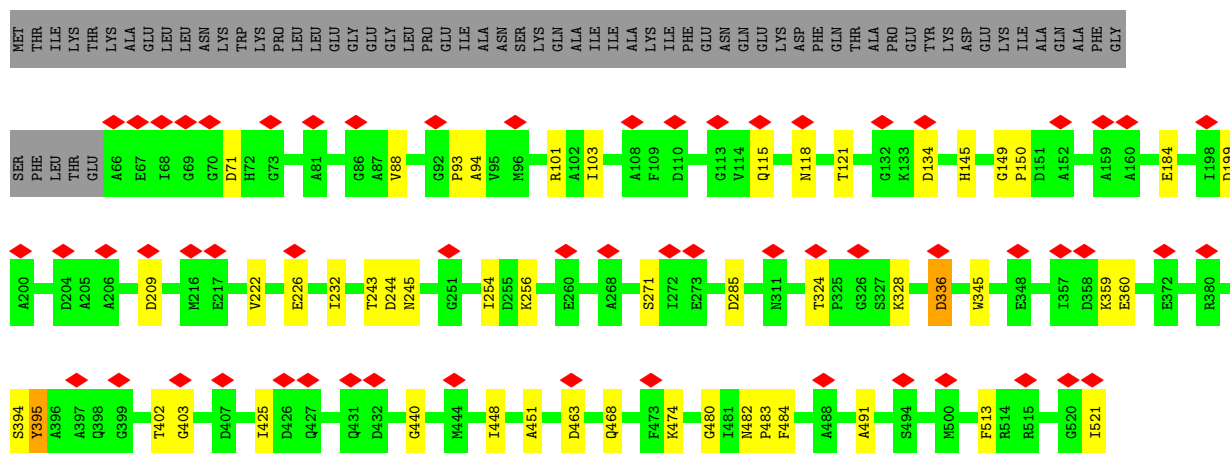


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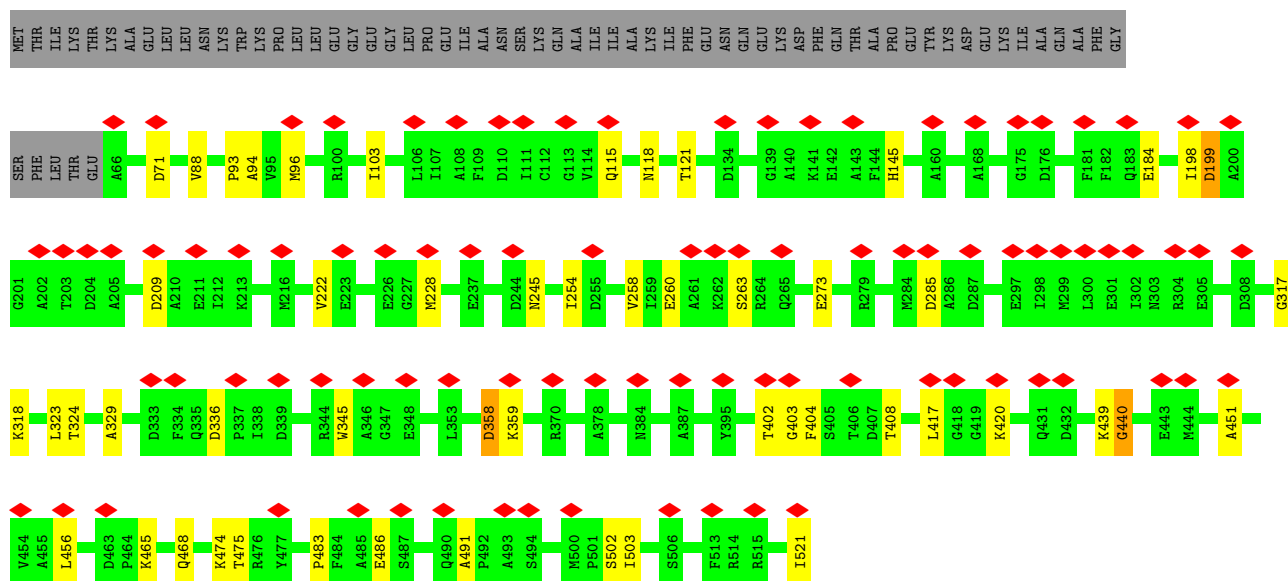
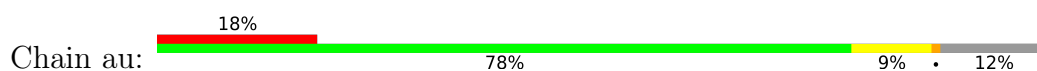




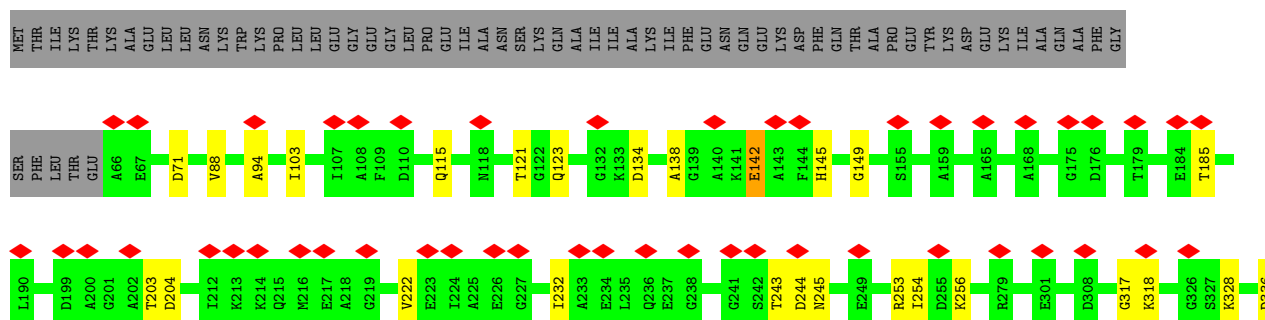
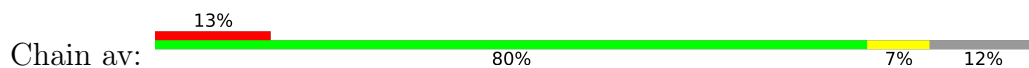




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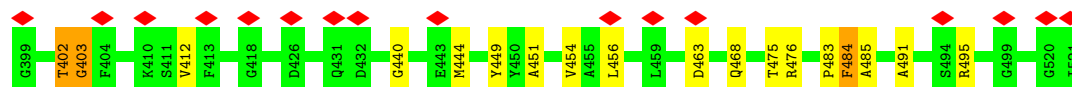
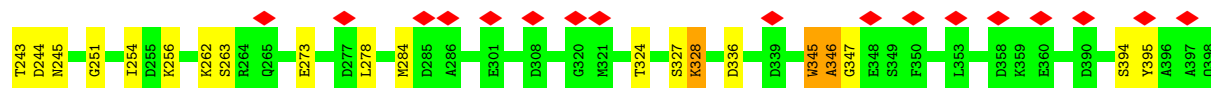
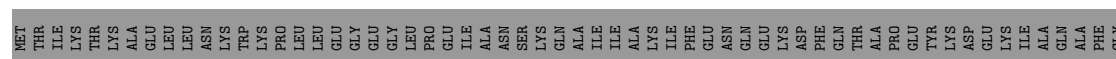
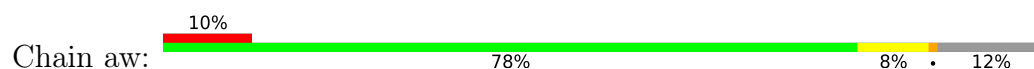


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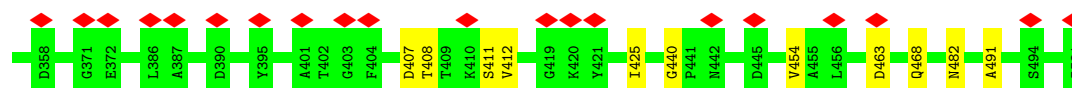
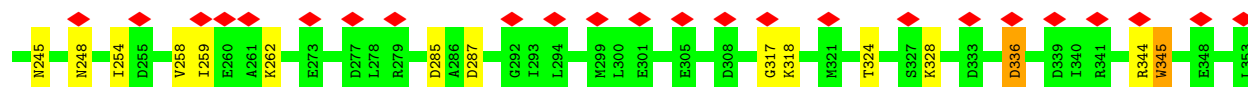
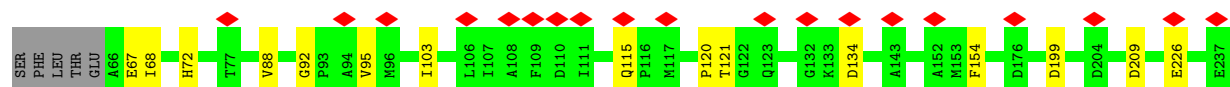
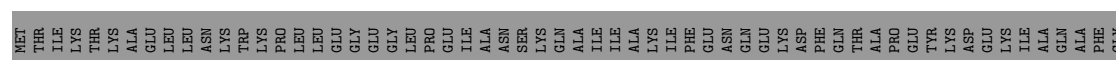
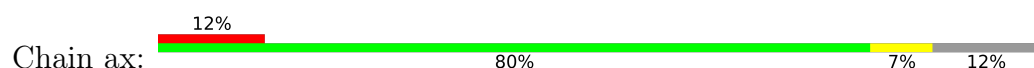




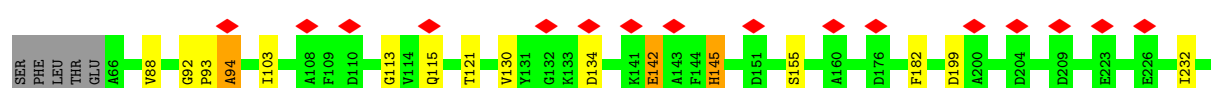
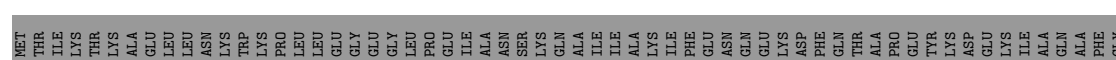
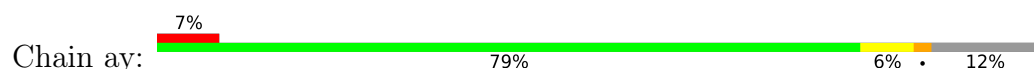
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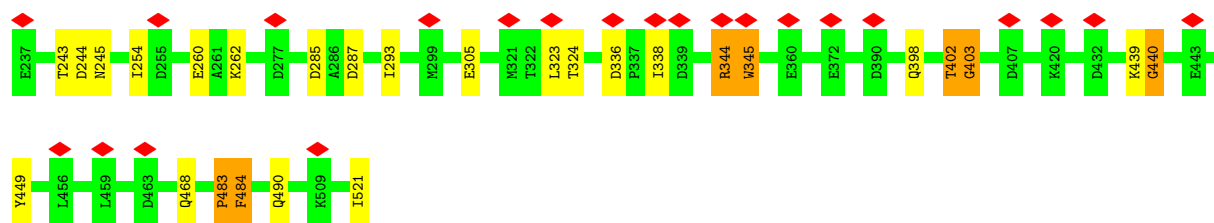


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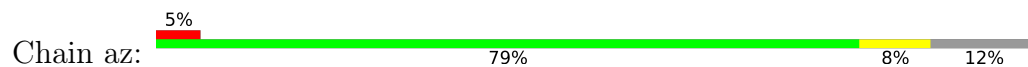


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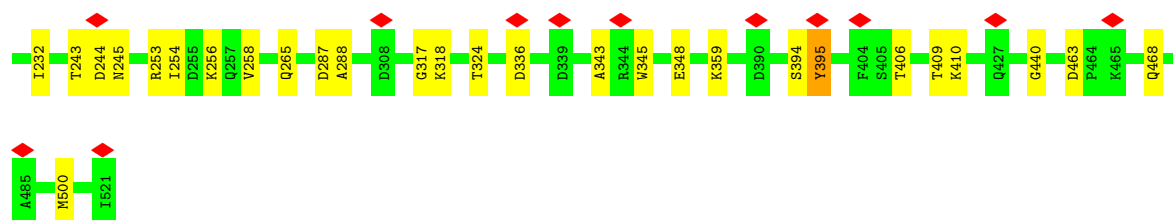
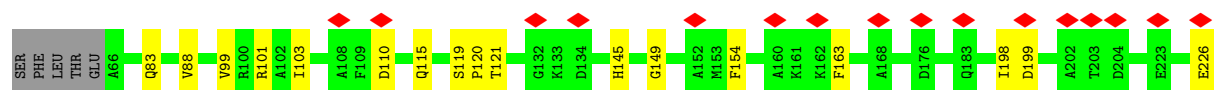




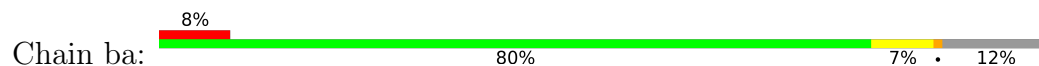
- Molecule 1: Major capsid protein



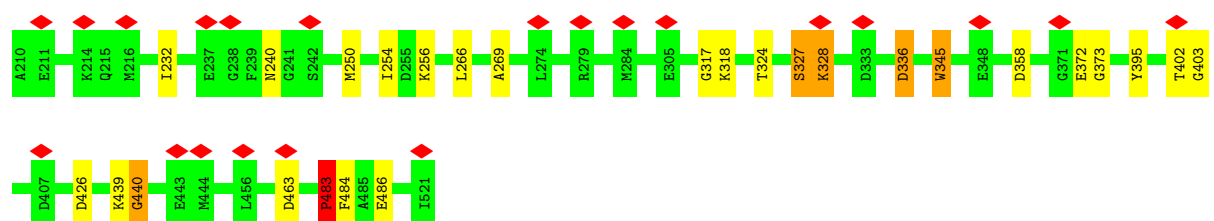
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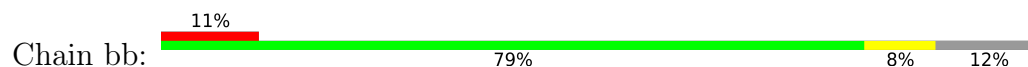
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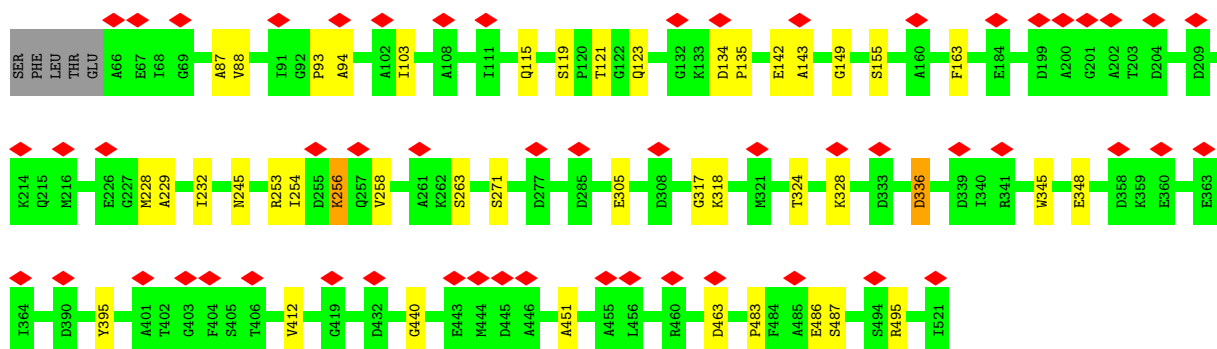
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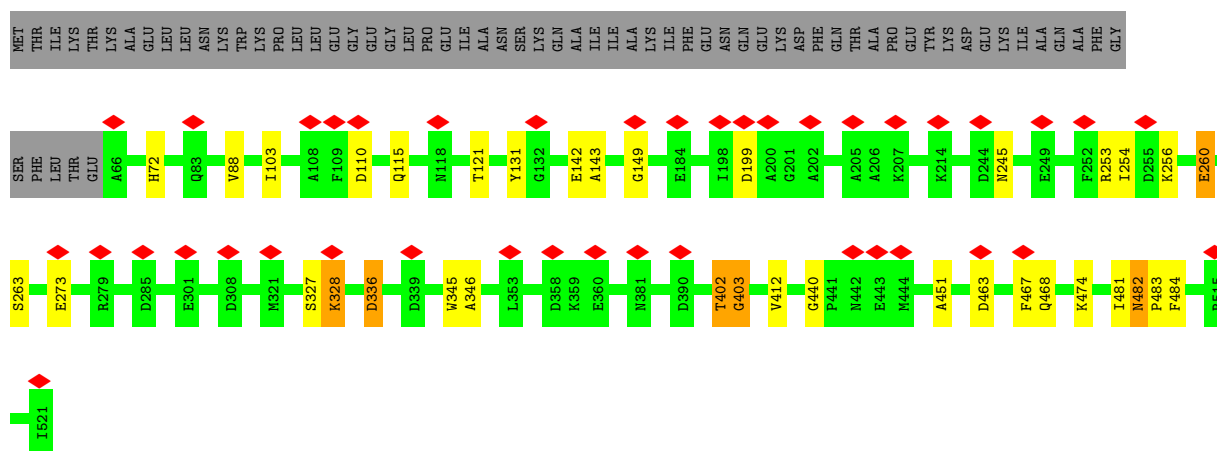
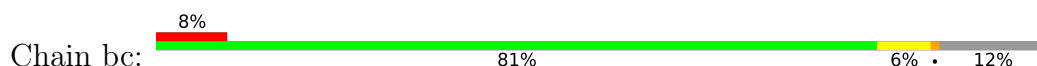
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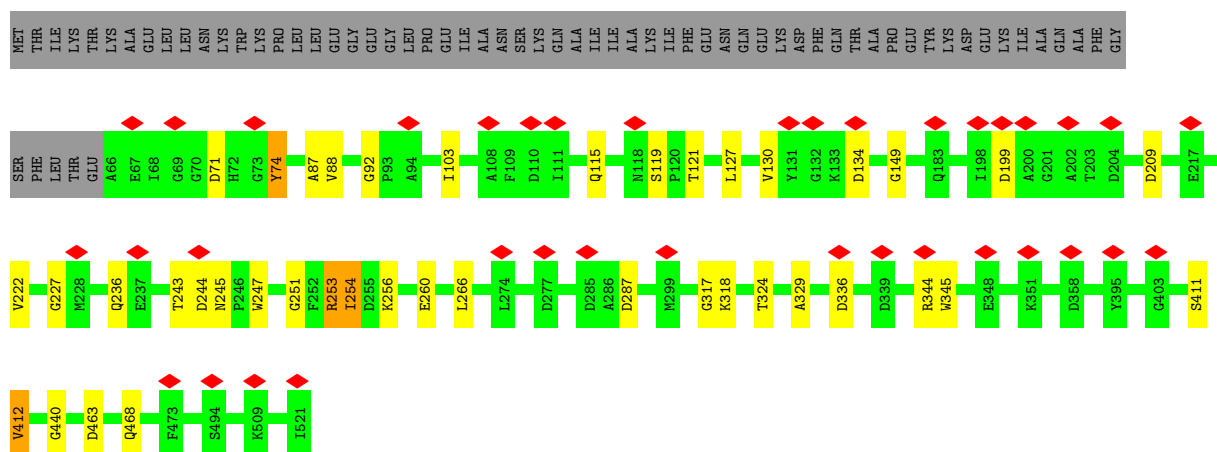
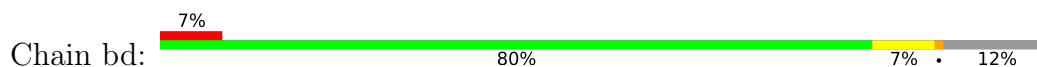
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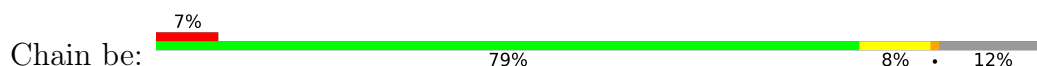
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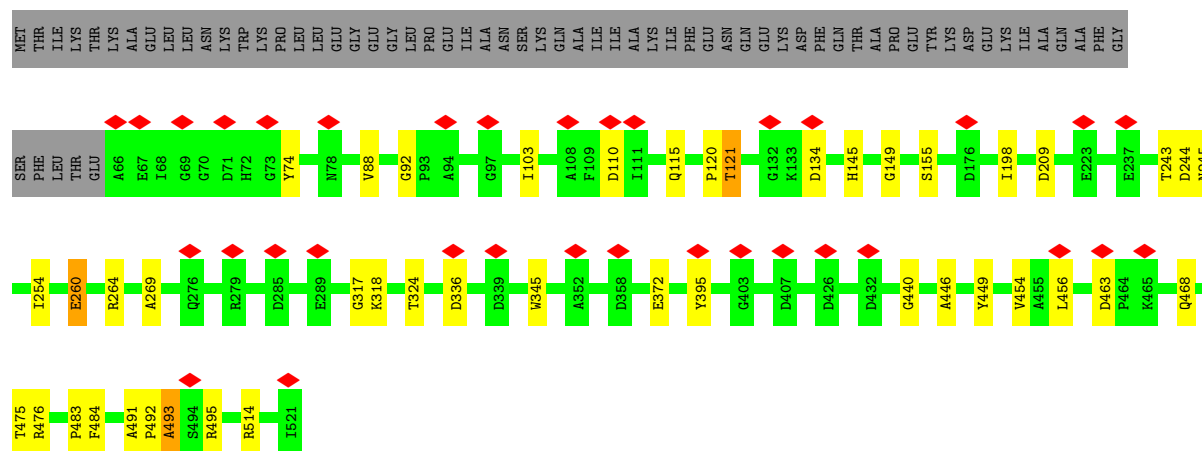


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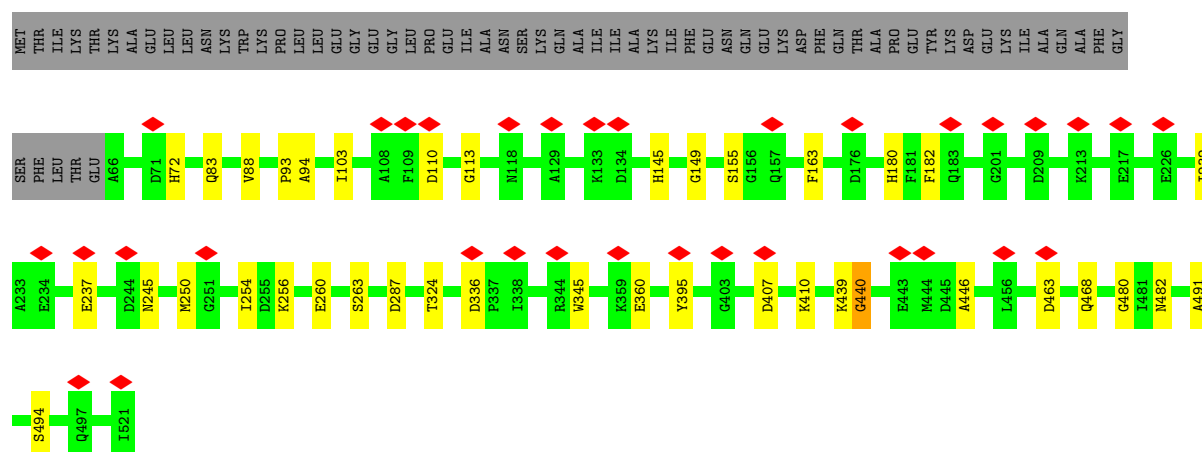
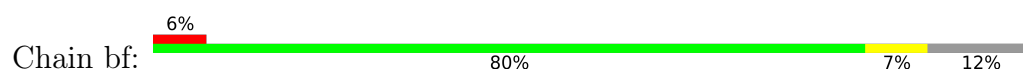


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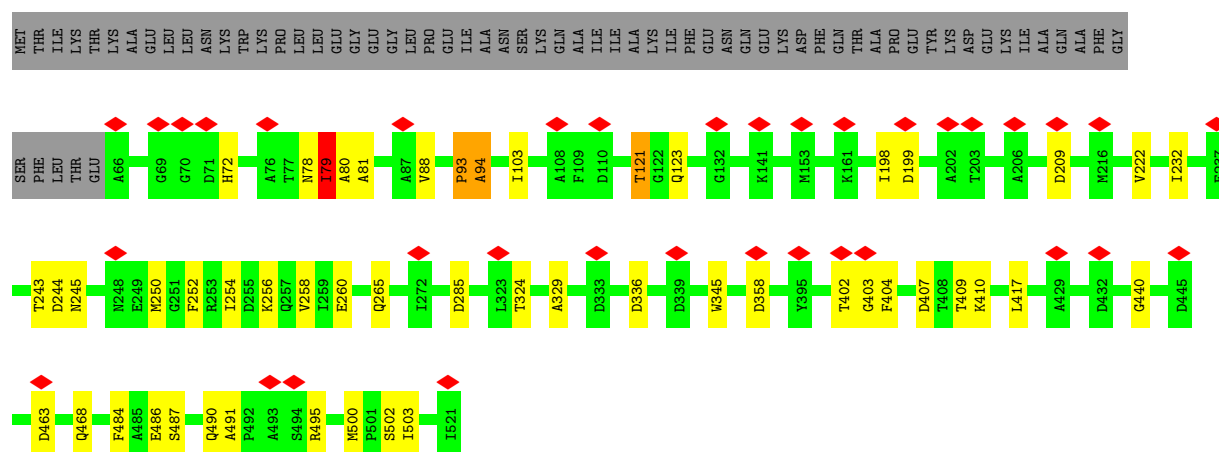
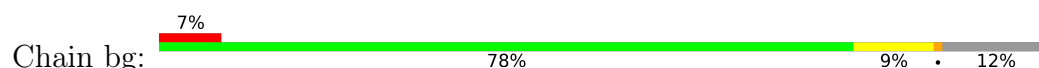




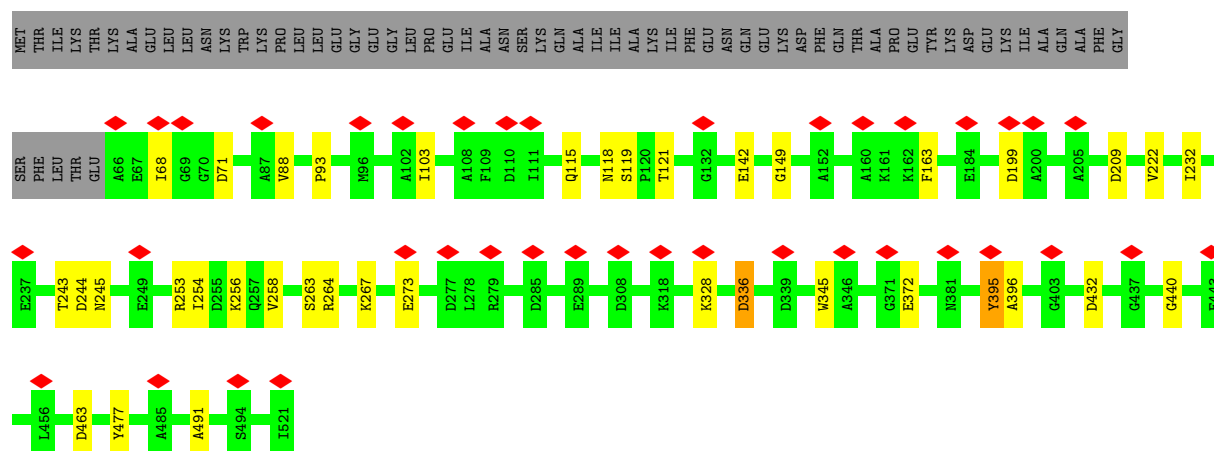
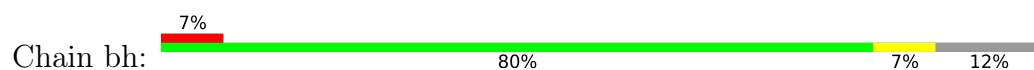
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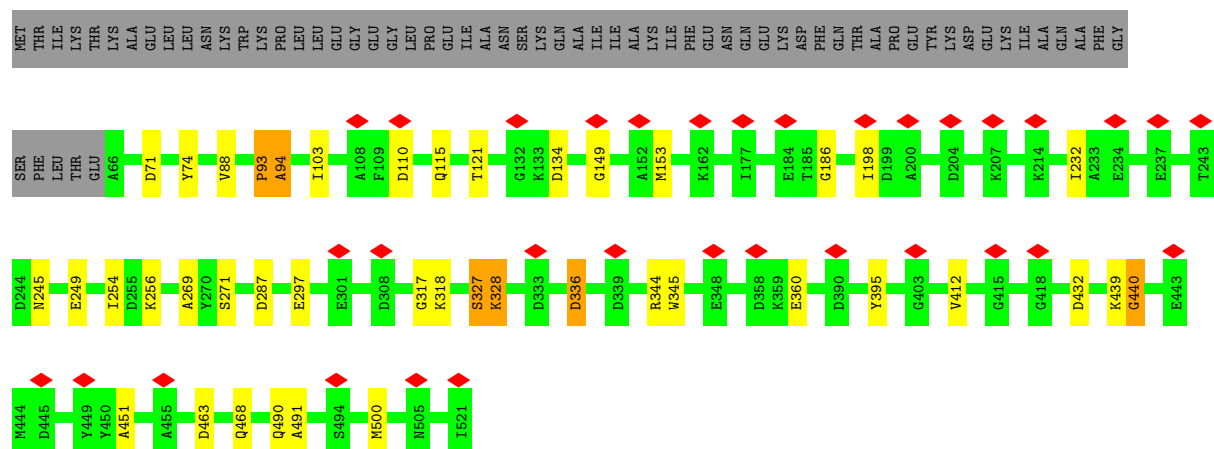
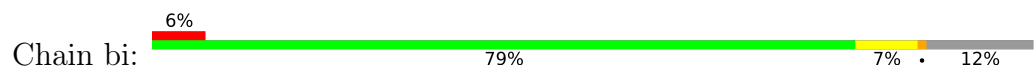
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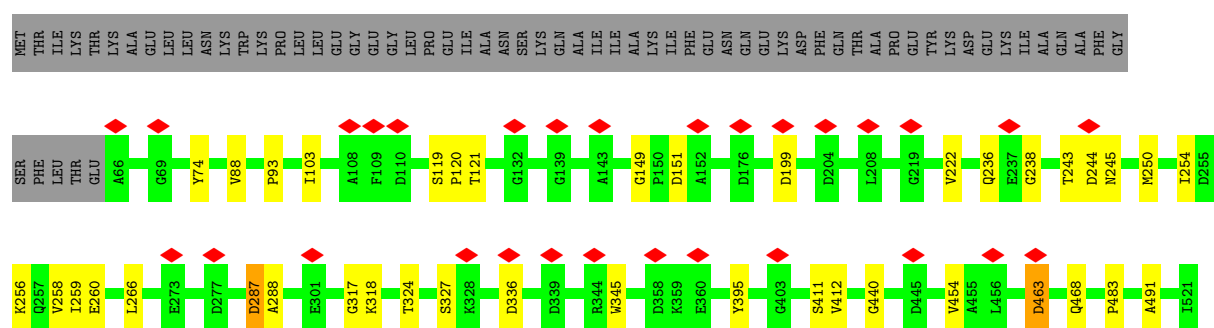
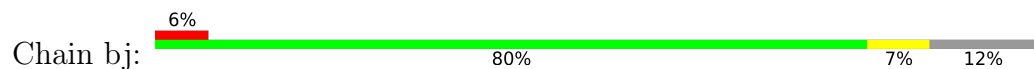
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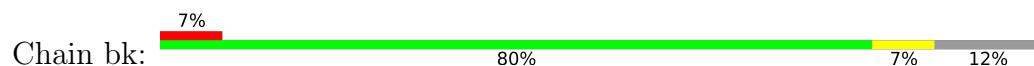
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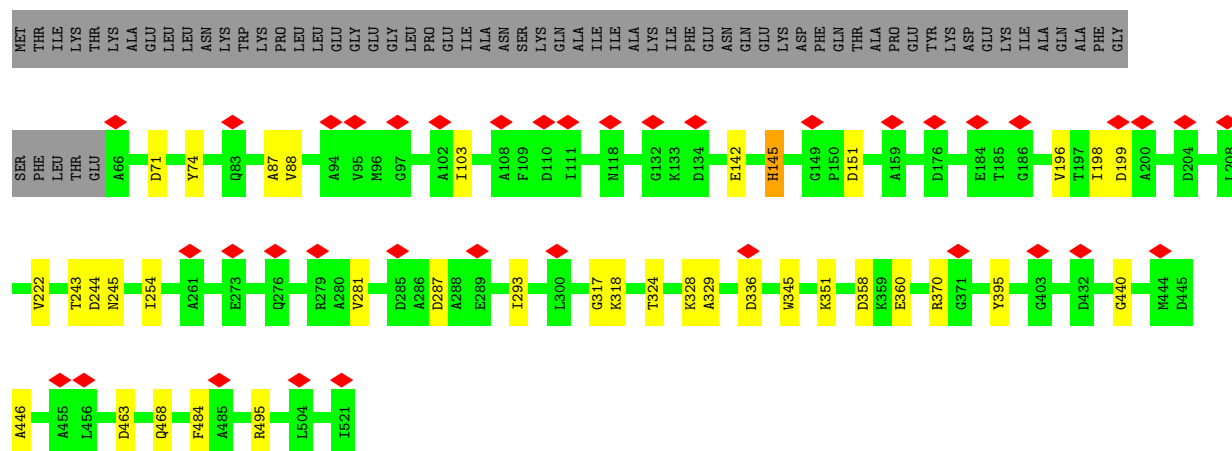


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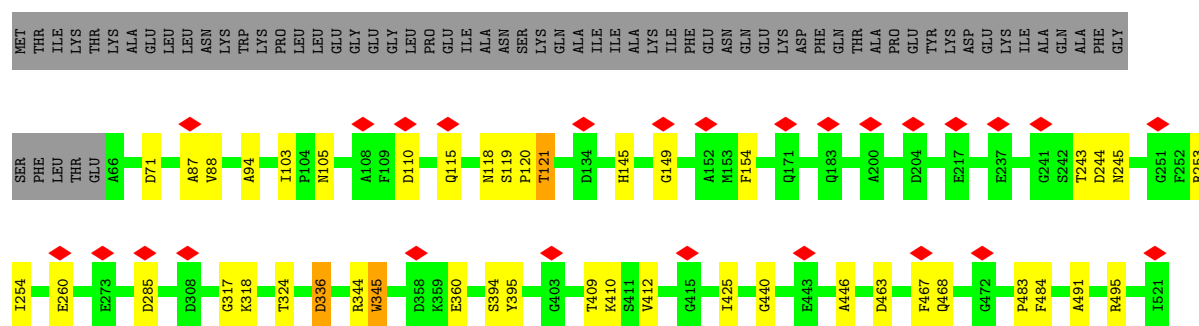
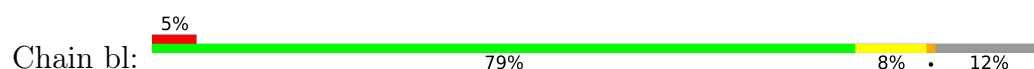


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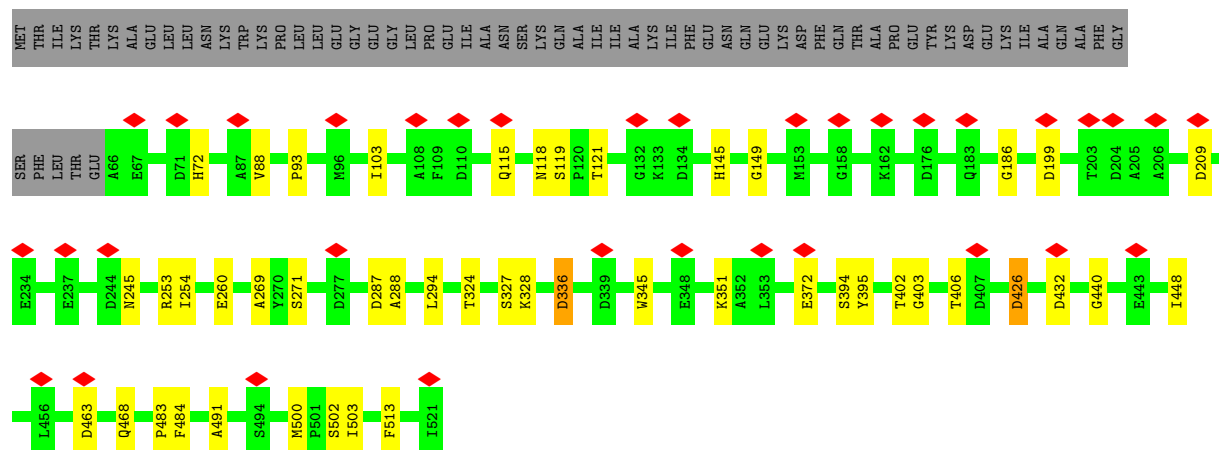
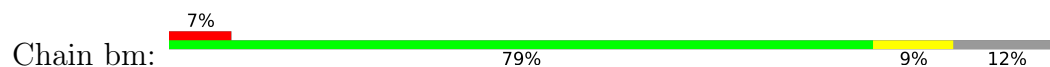




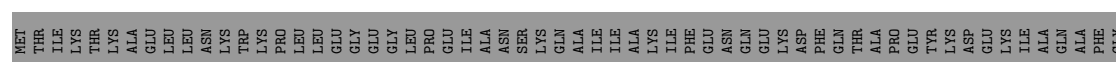
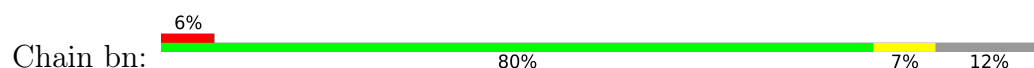
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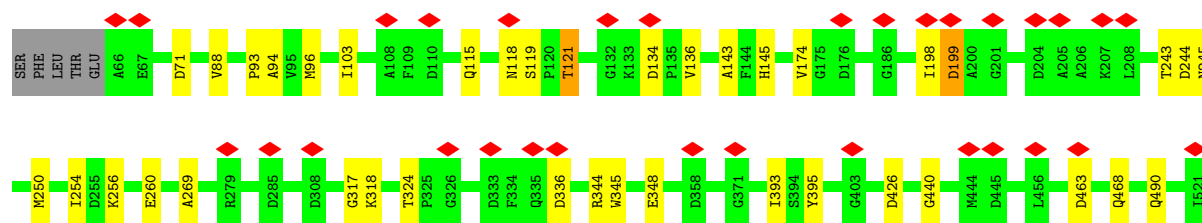


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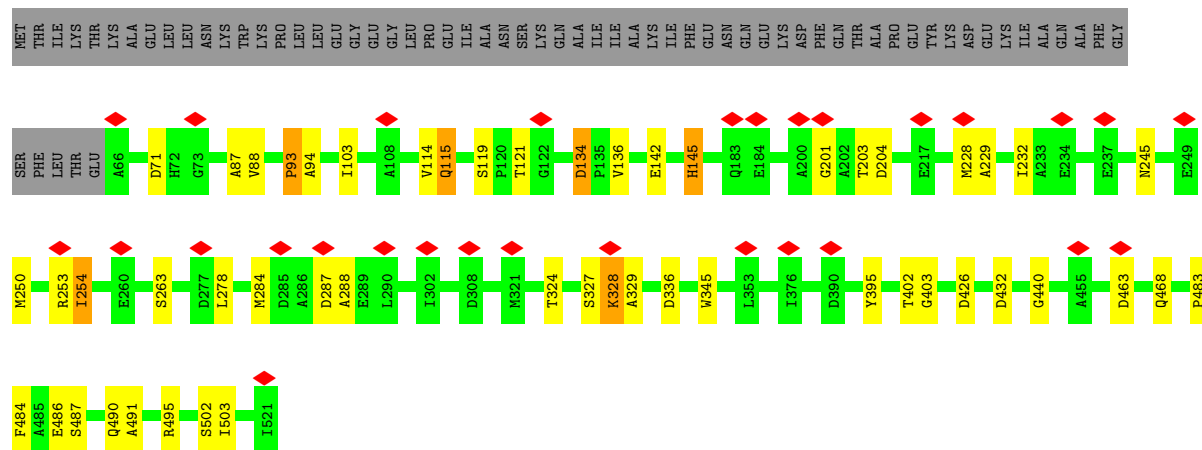
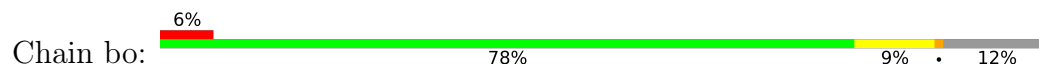


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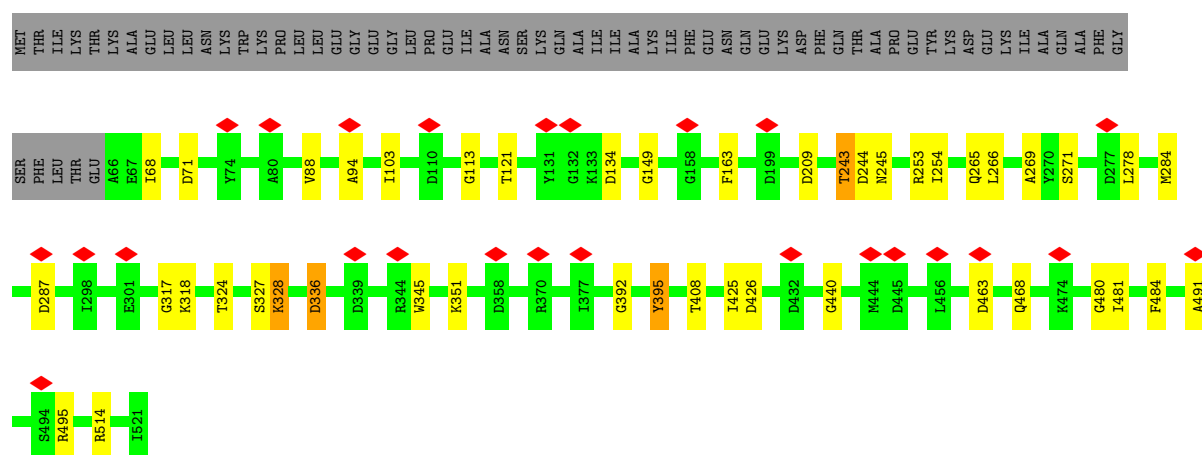
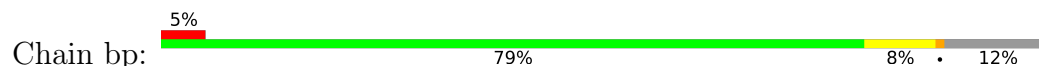




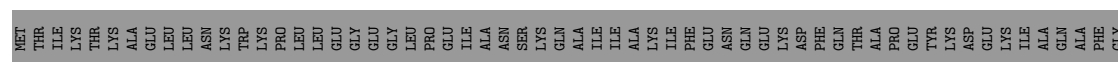
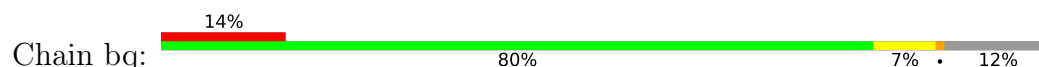
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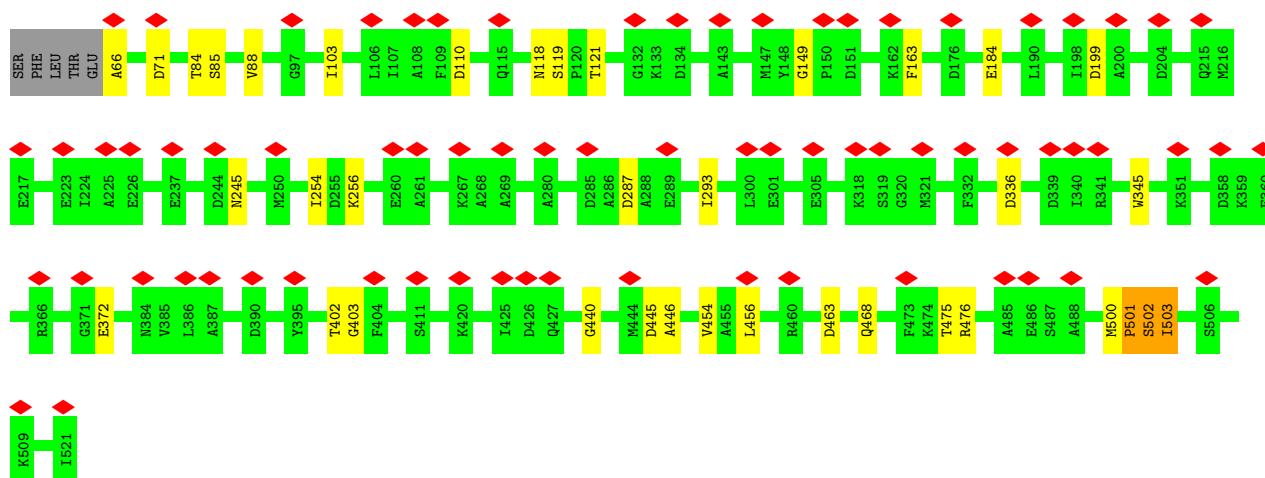


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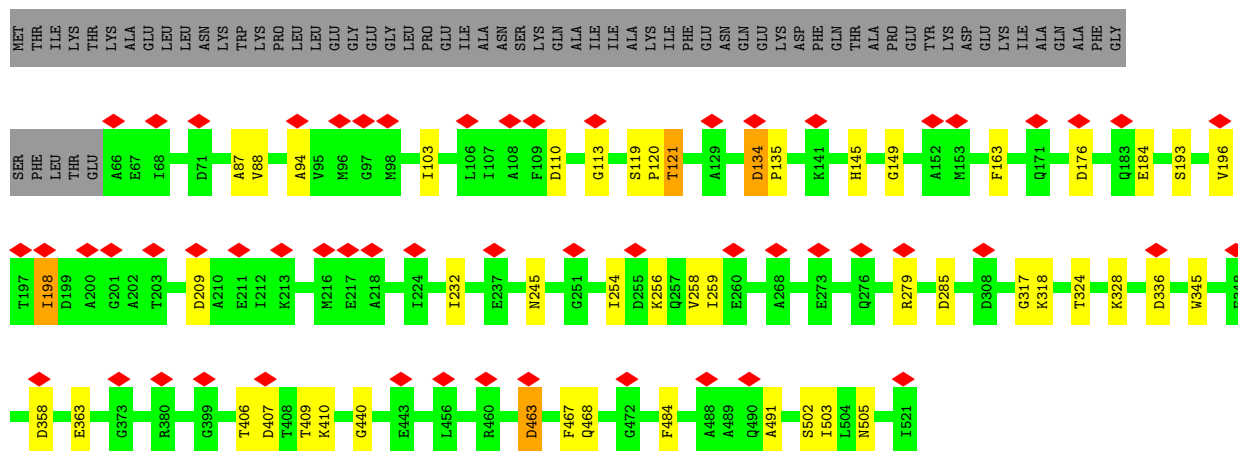
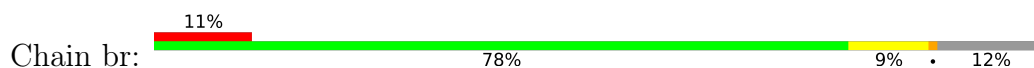


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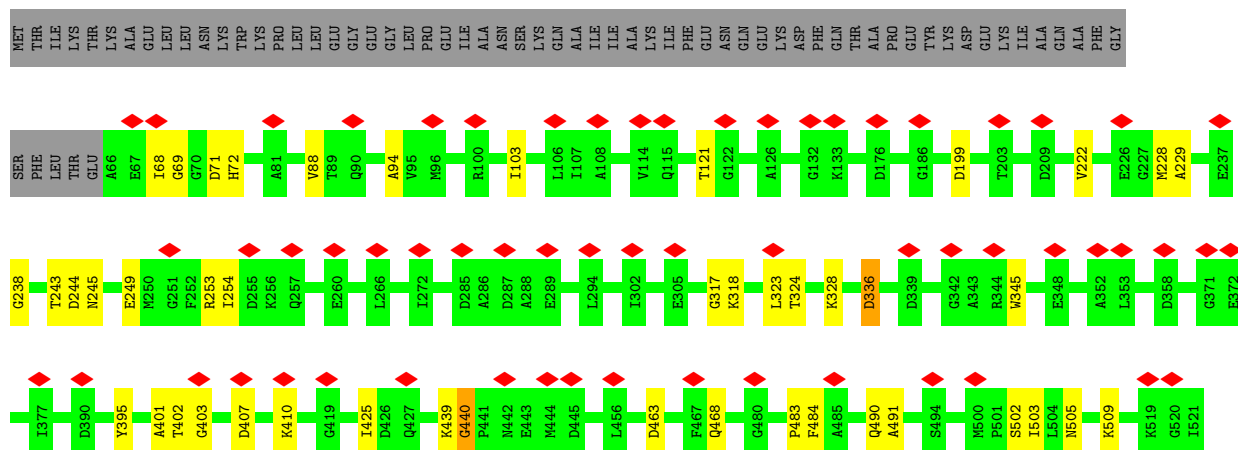
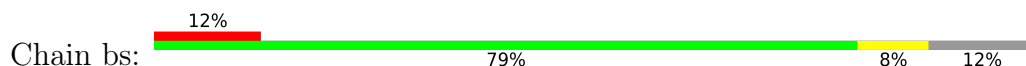




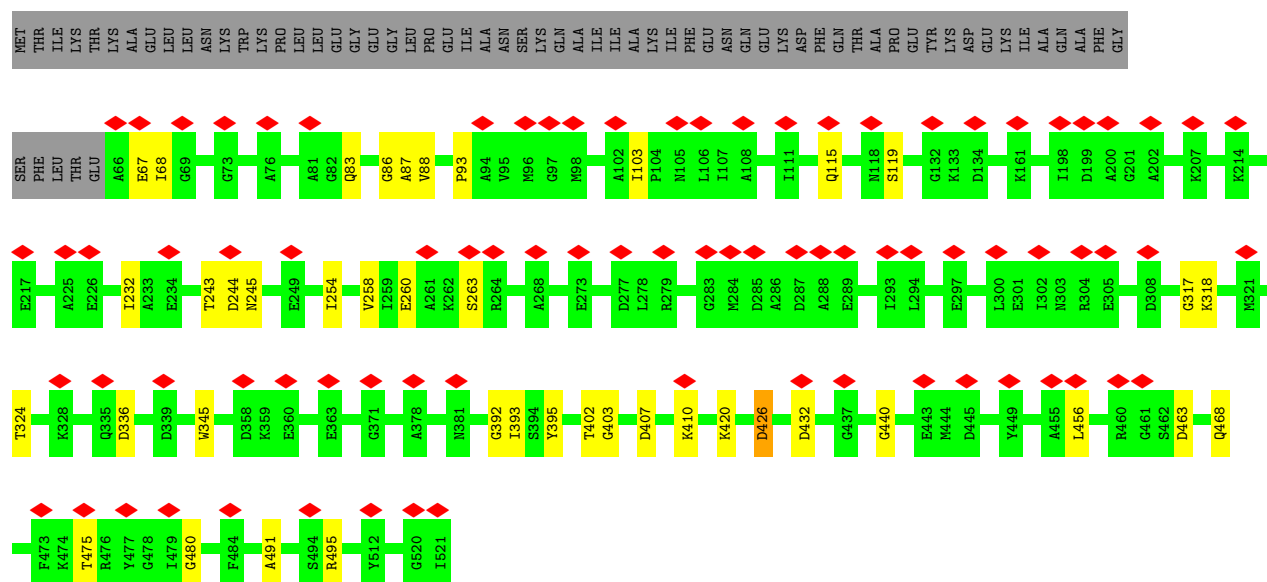
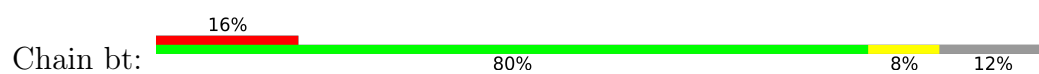
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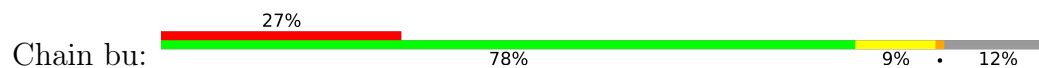
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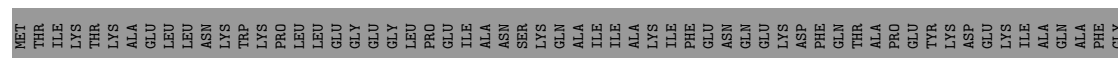
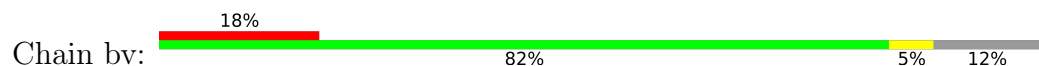
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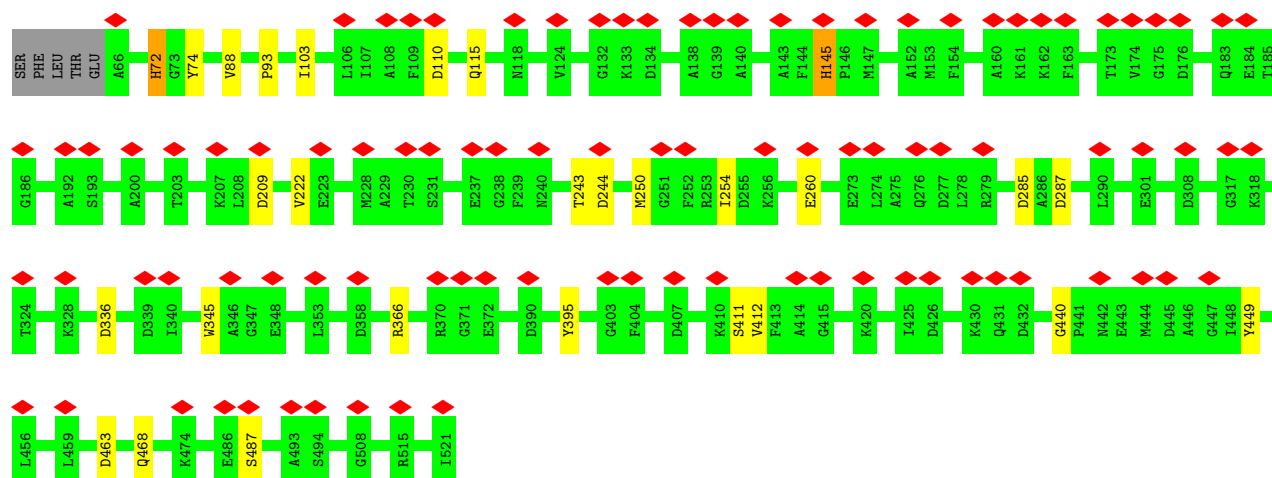


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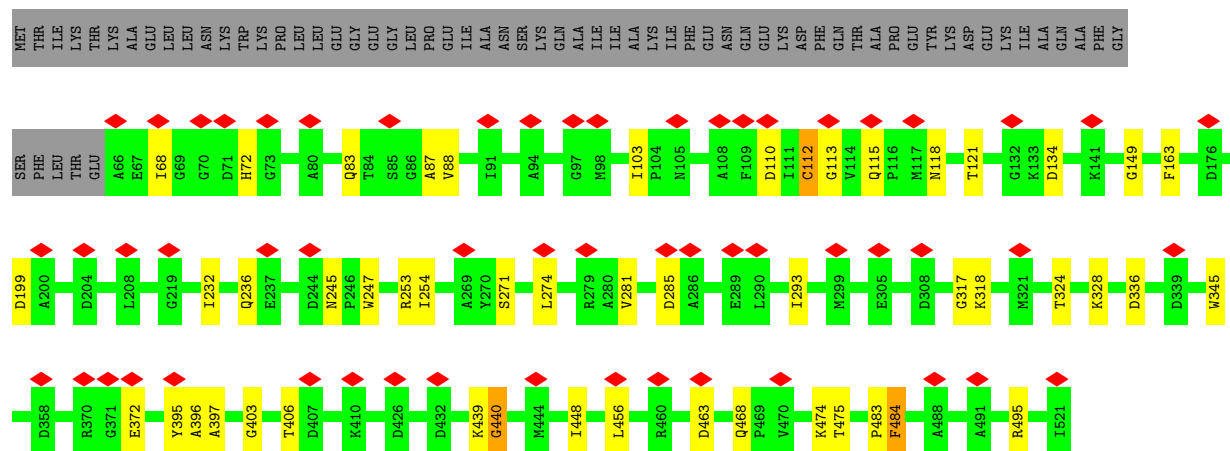
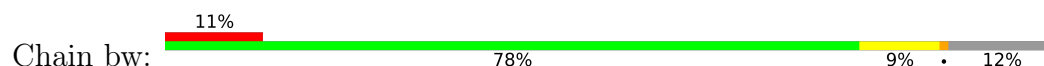


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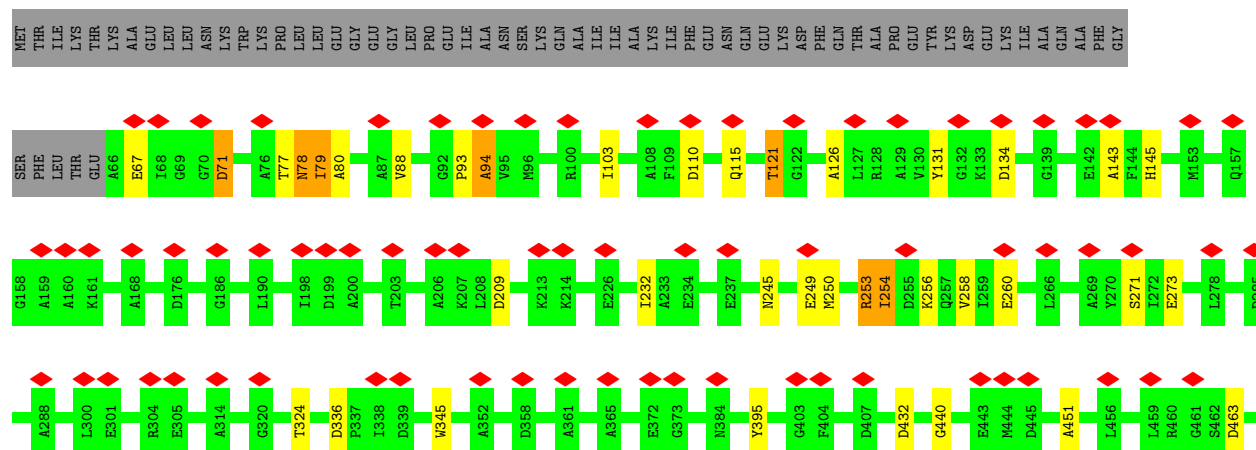
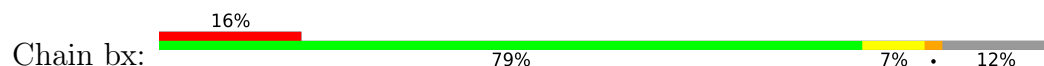


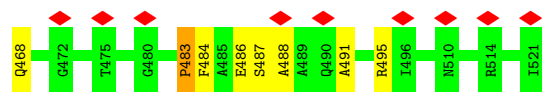


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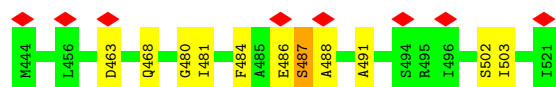
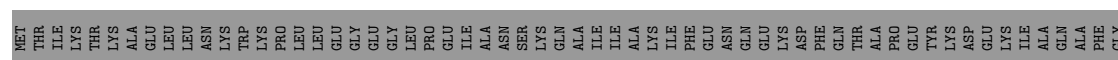
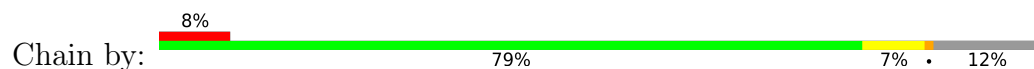


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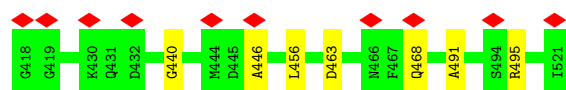
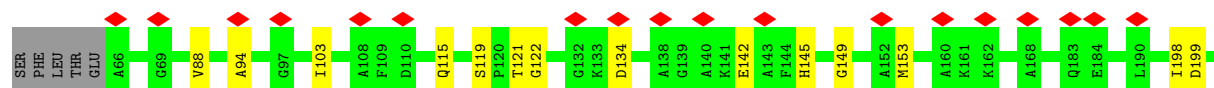
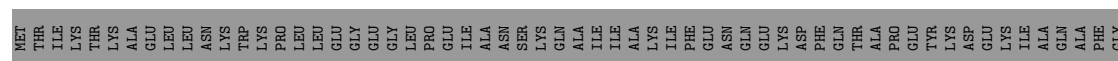
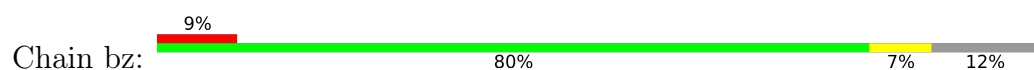




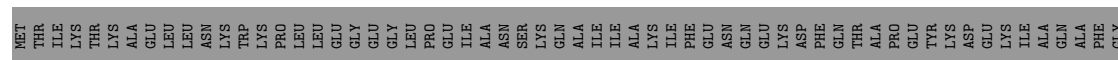
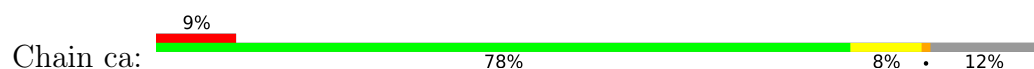
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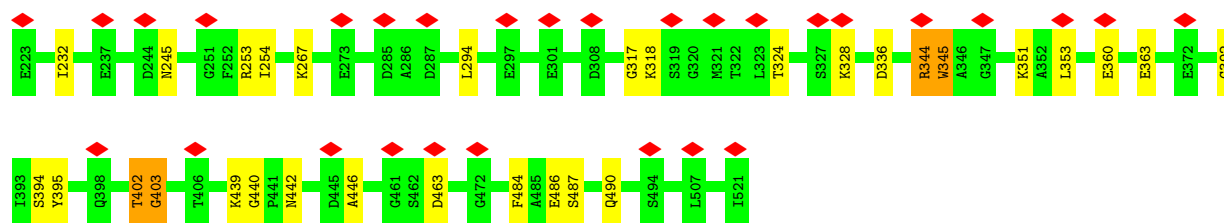


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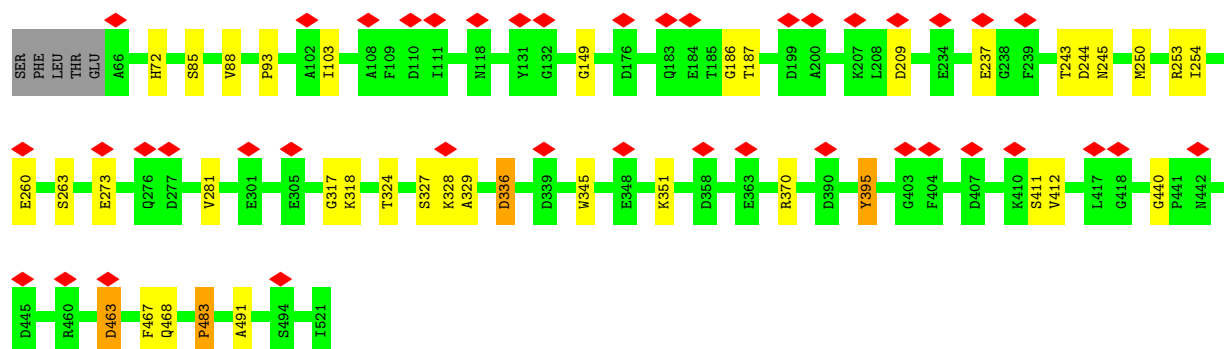
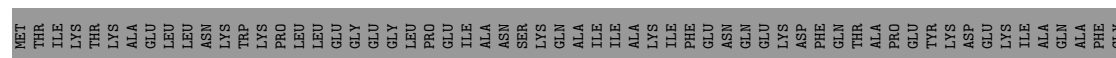
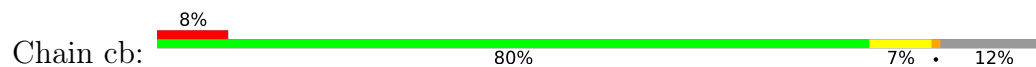


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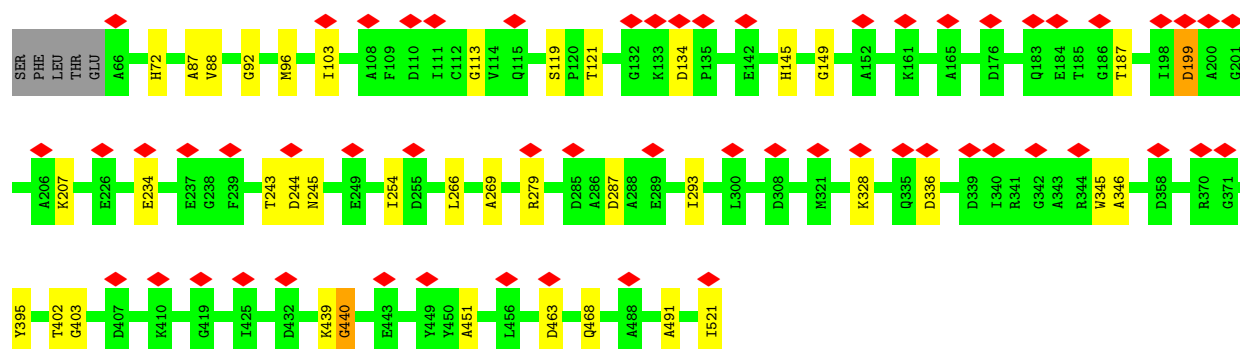
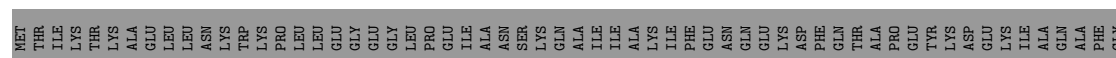
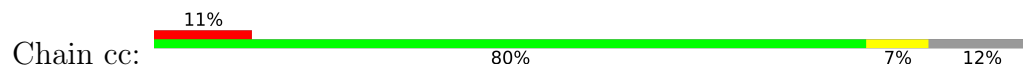




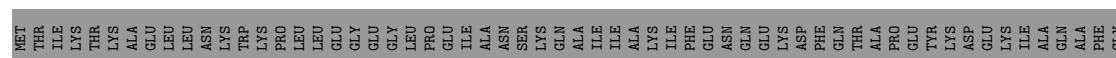
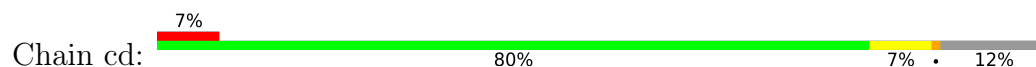
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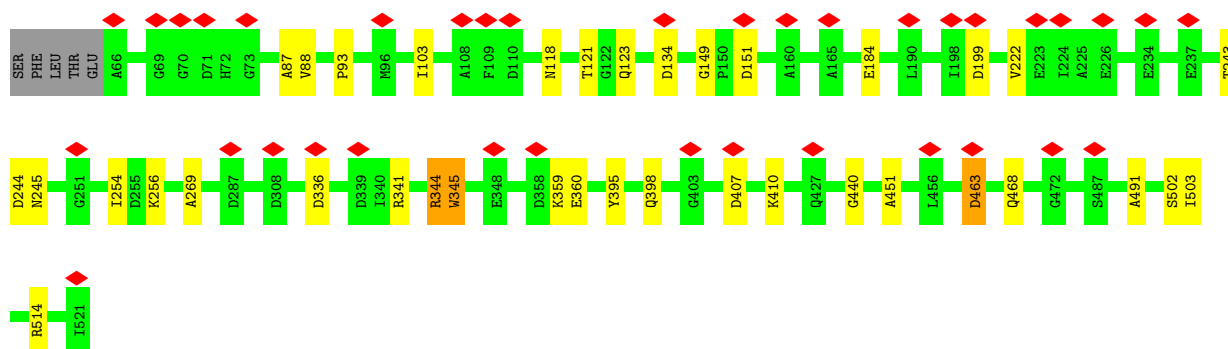


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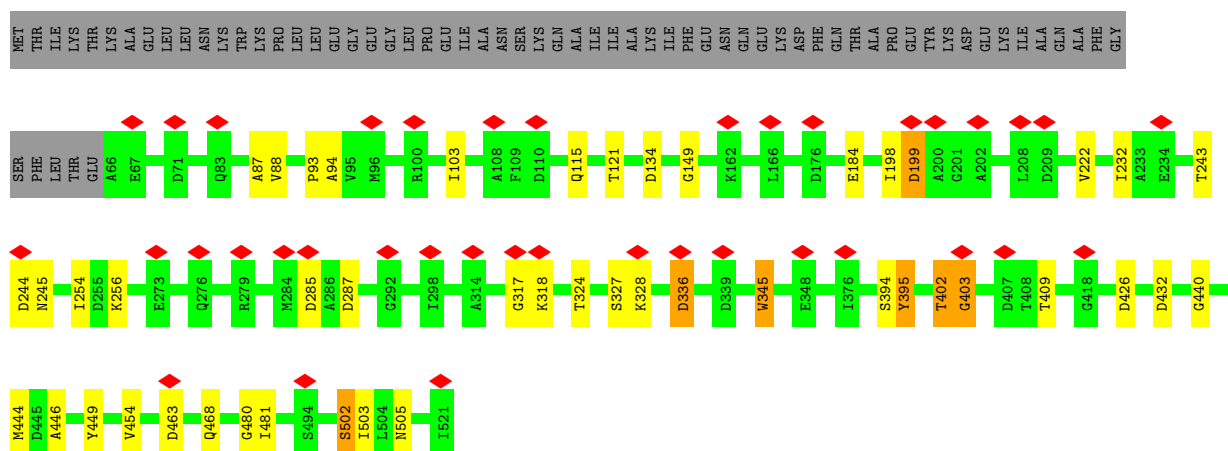
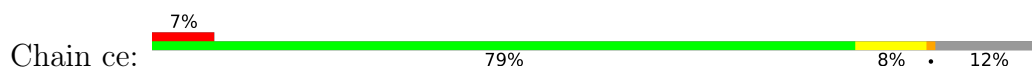


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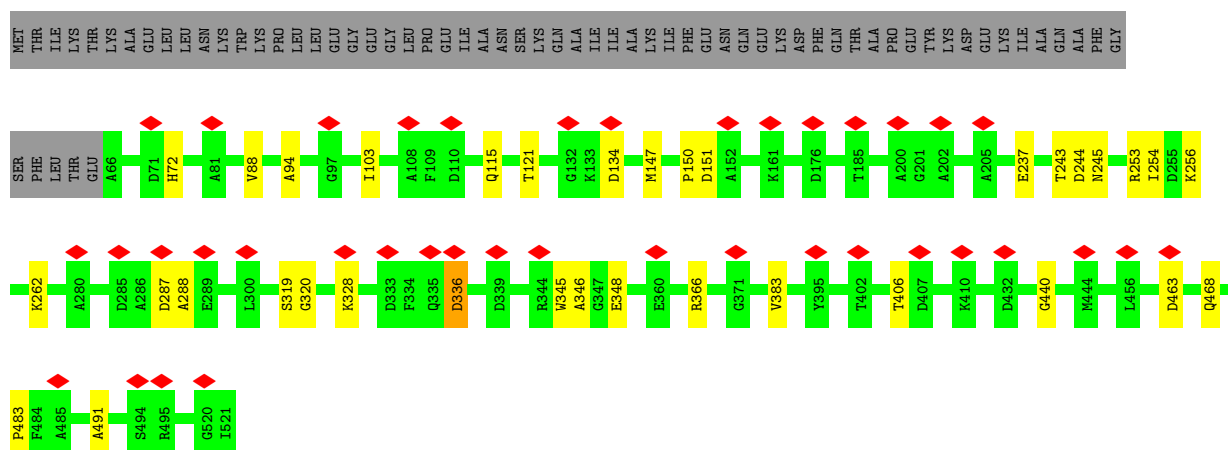
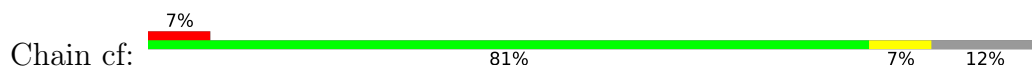




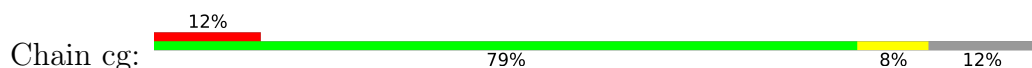
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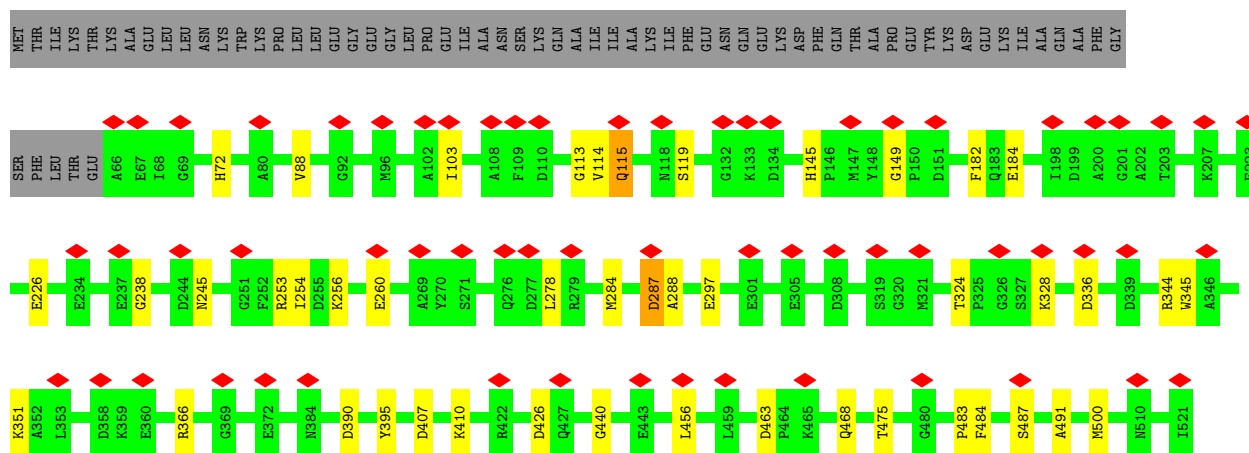


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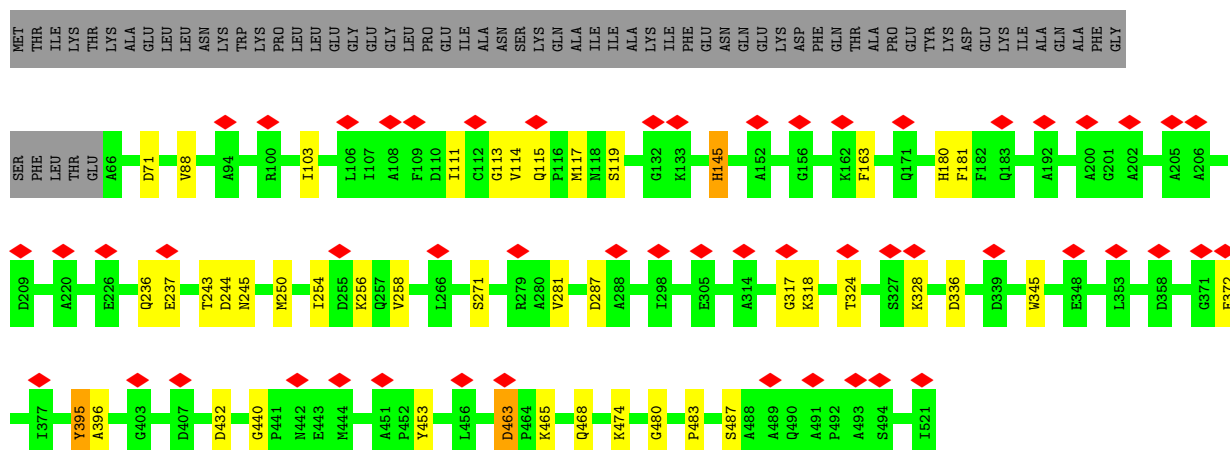
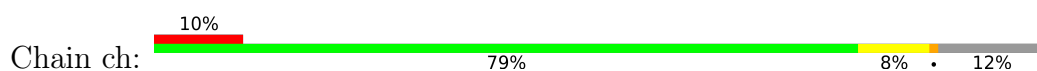


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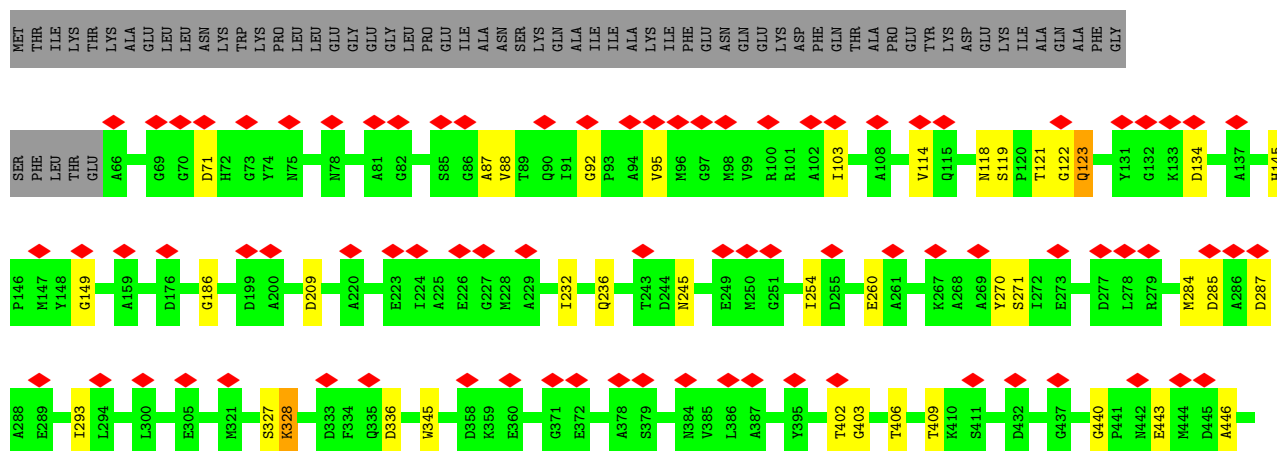
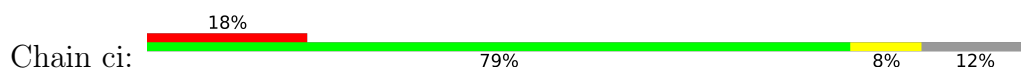


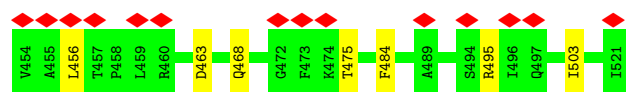


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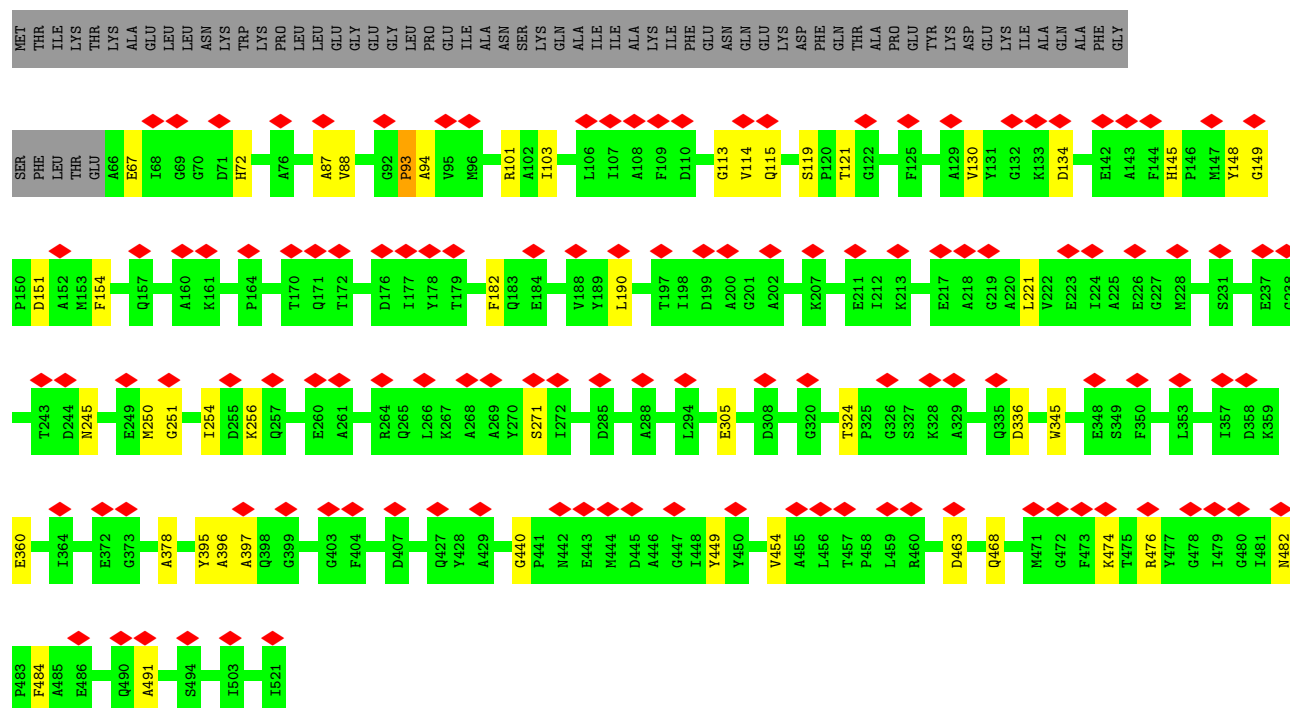
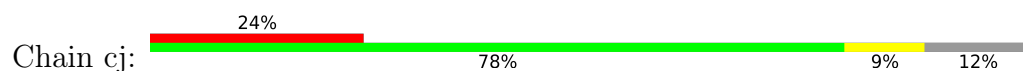


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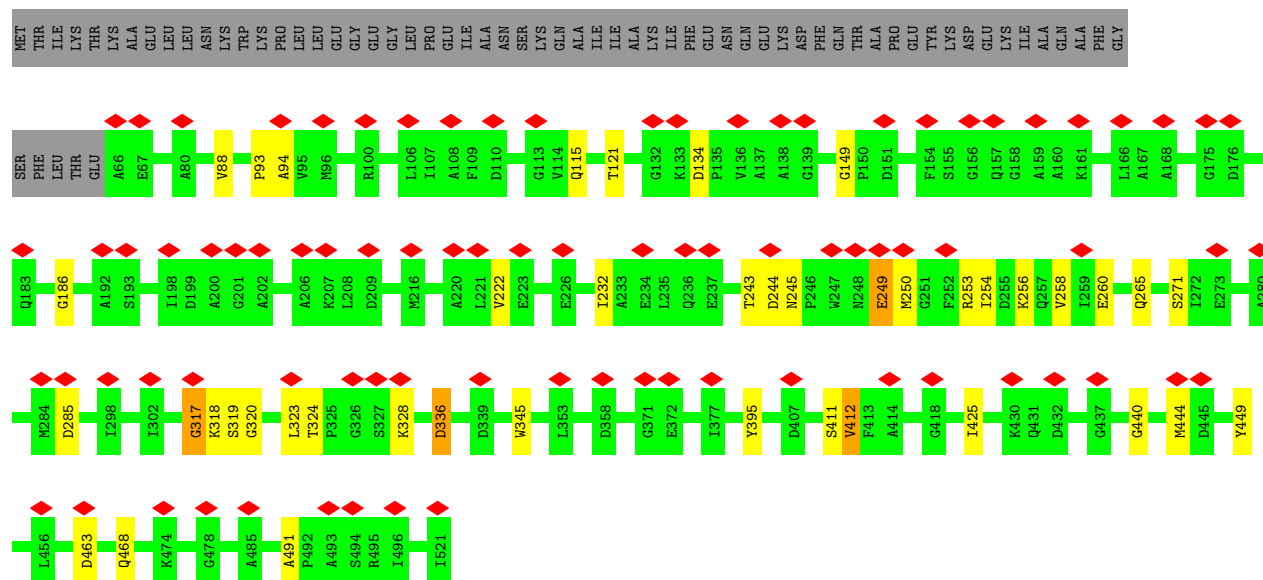
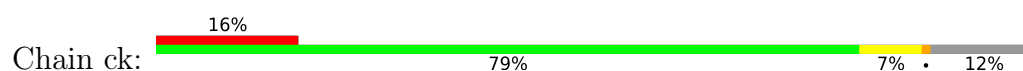




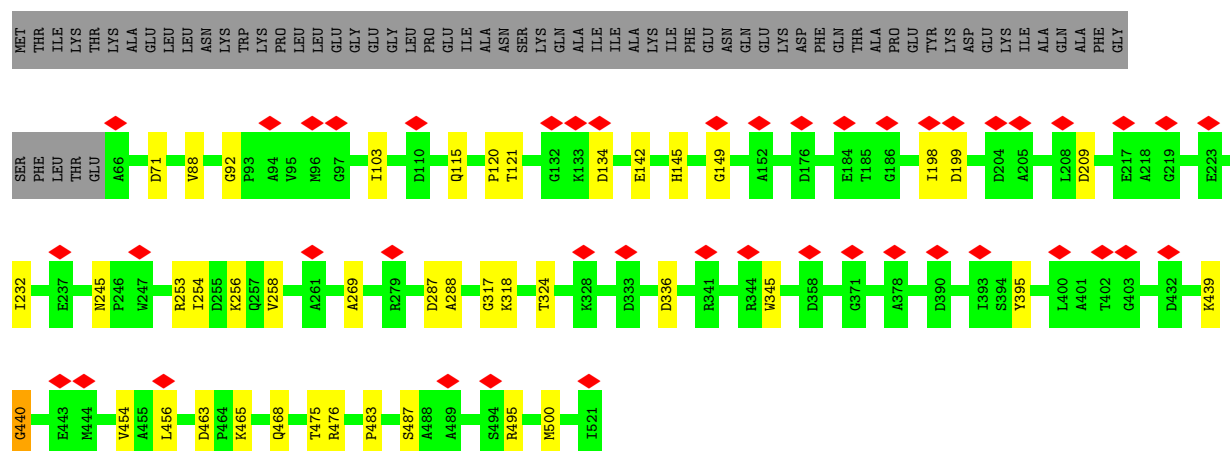
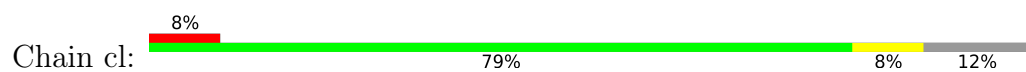
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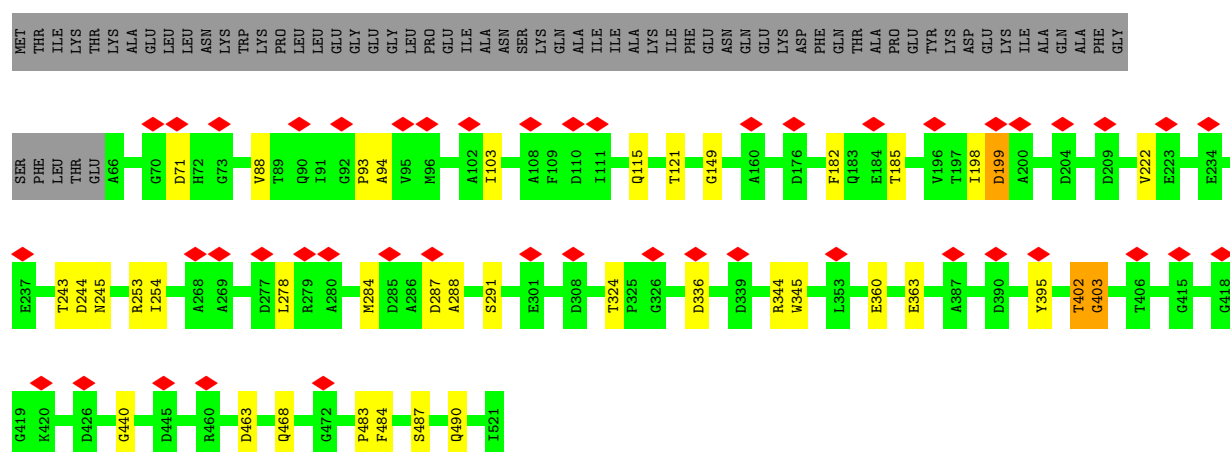
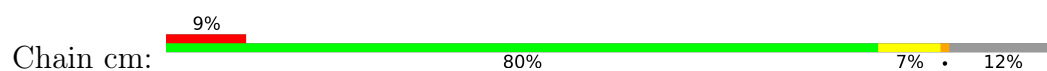
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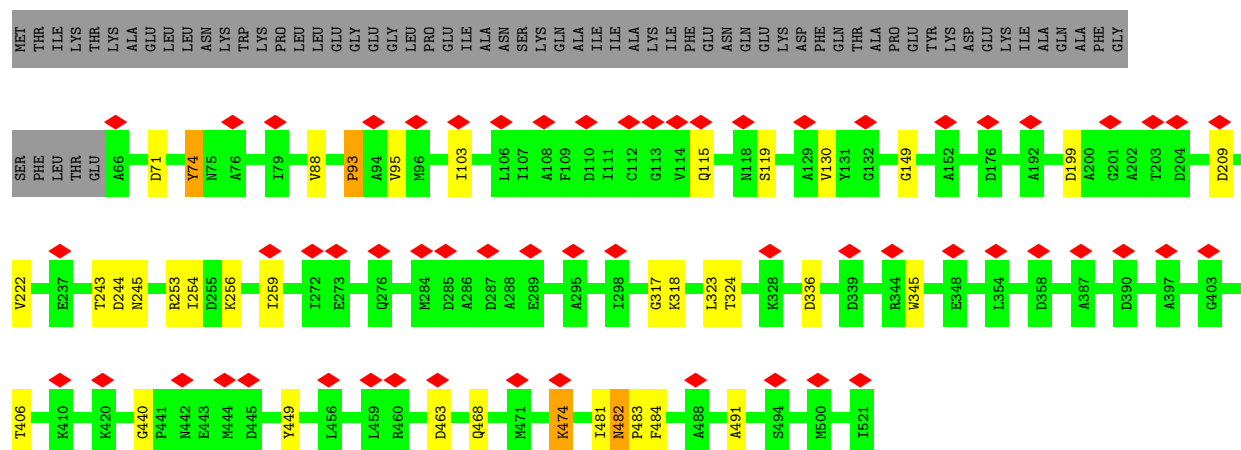
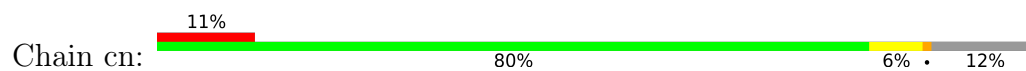
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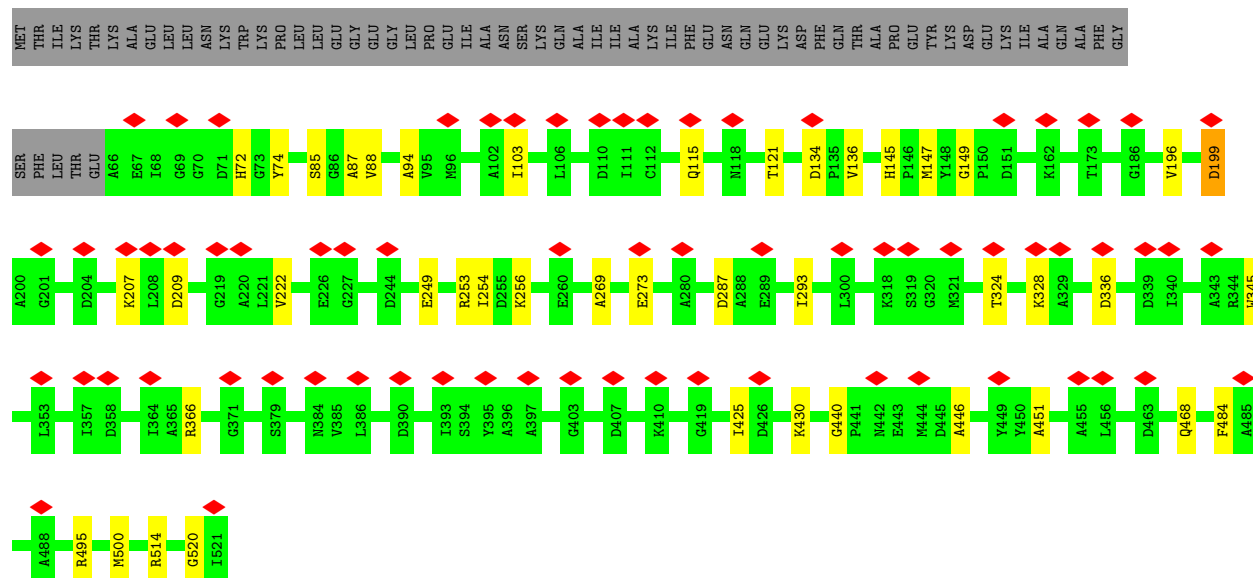


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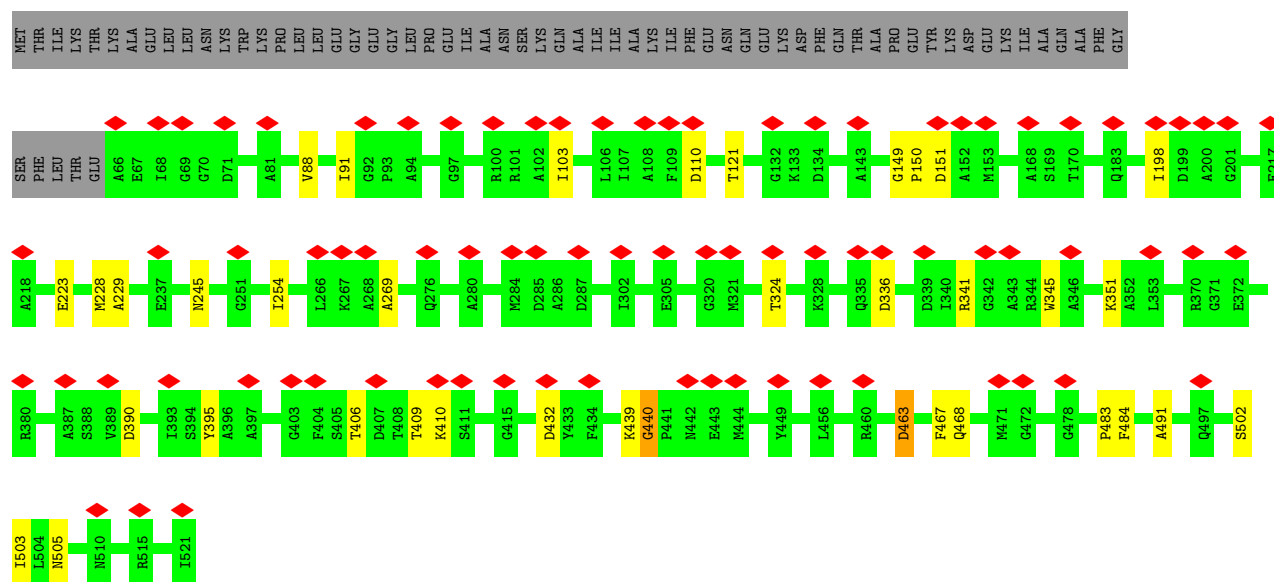
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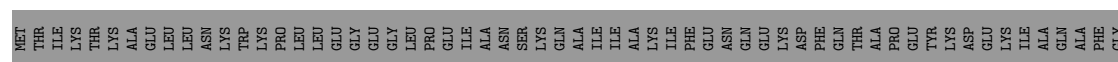
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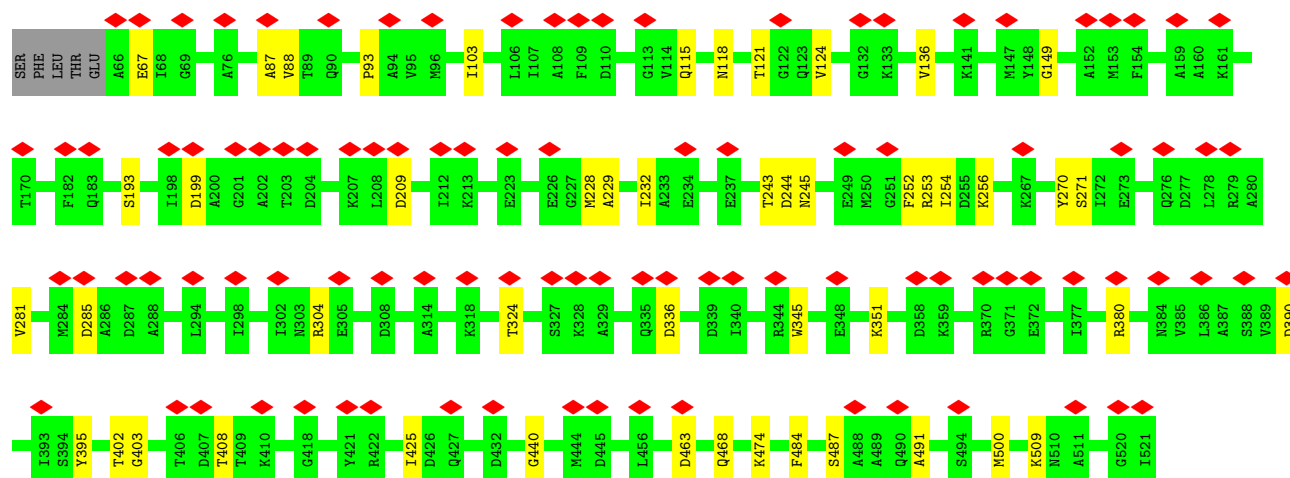
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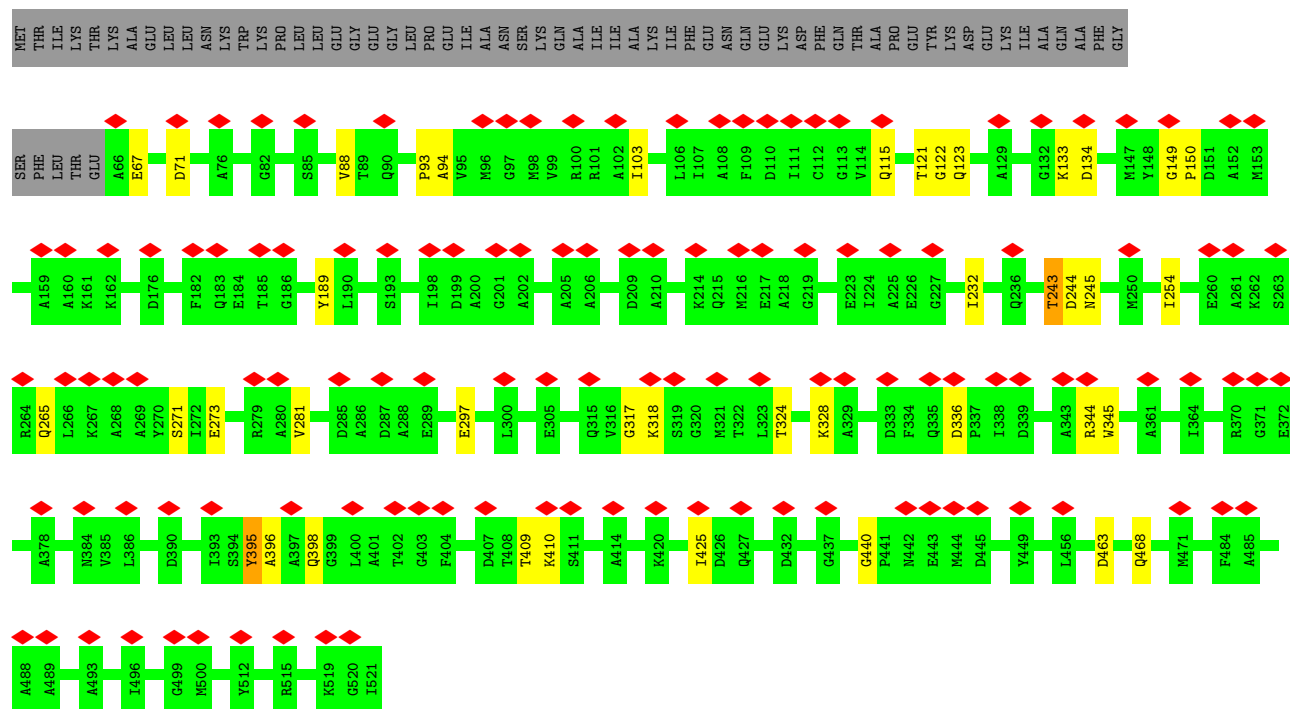
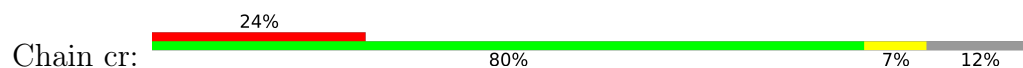
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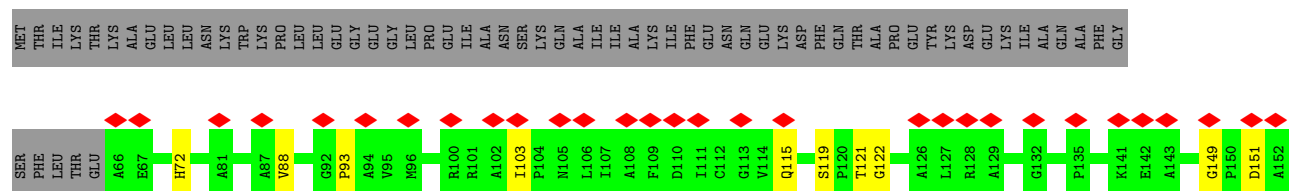
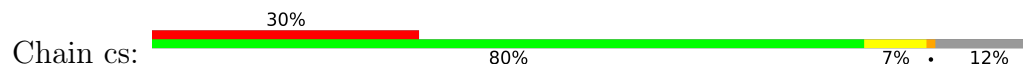


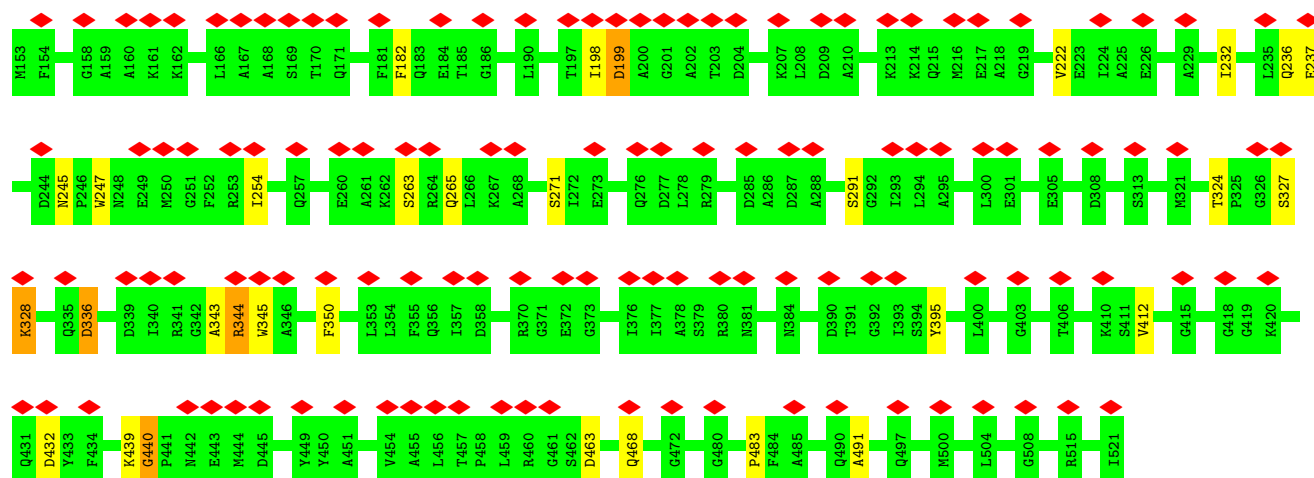


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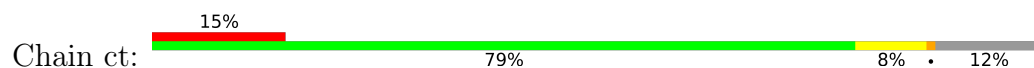


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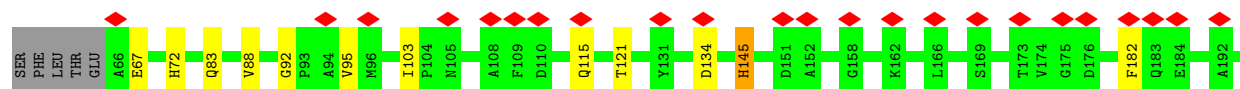




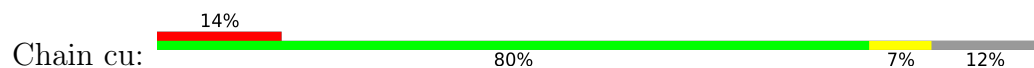
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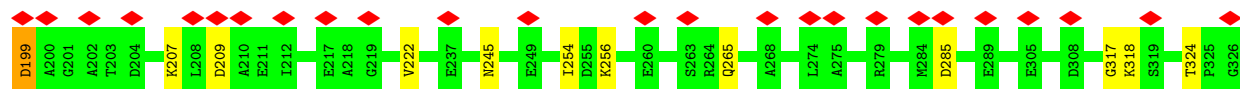
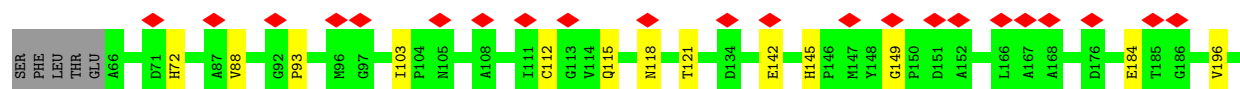
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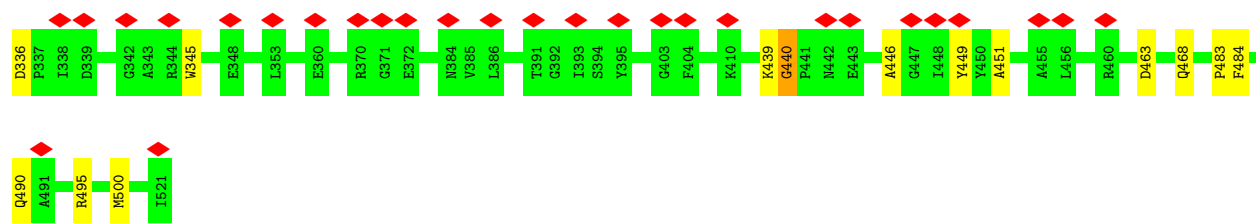


• Molecule 1: Major capsid protein

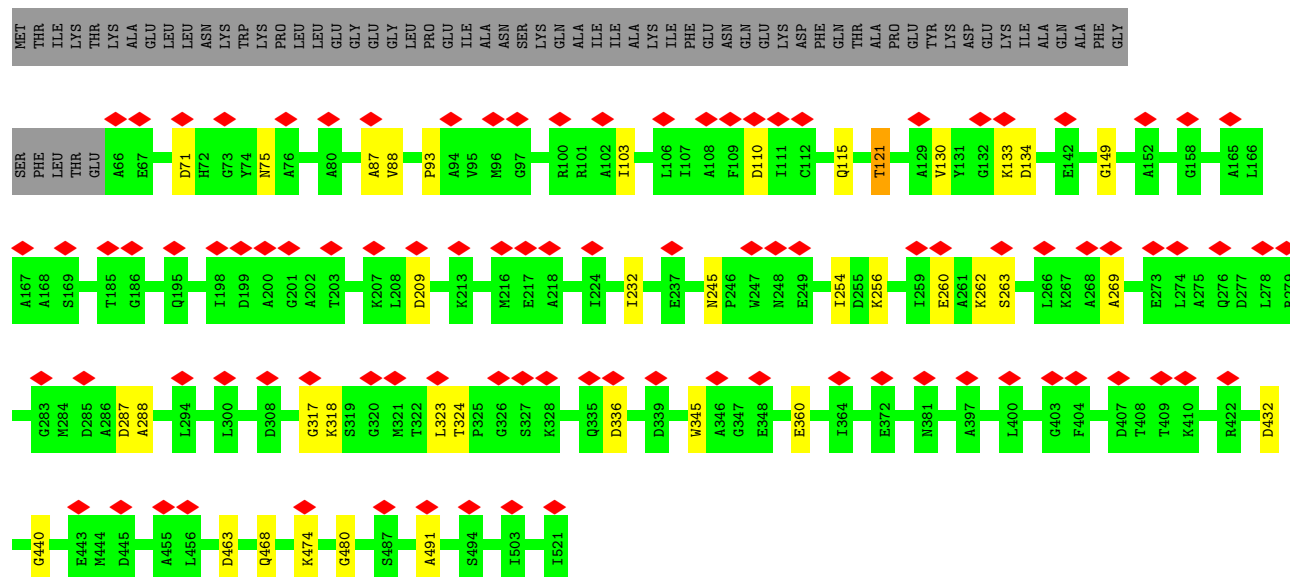
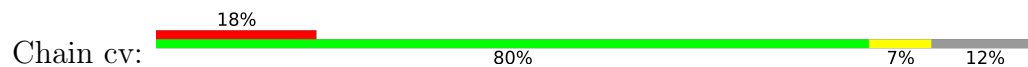


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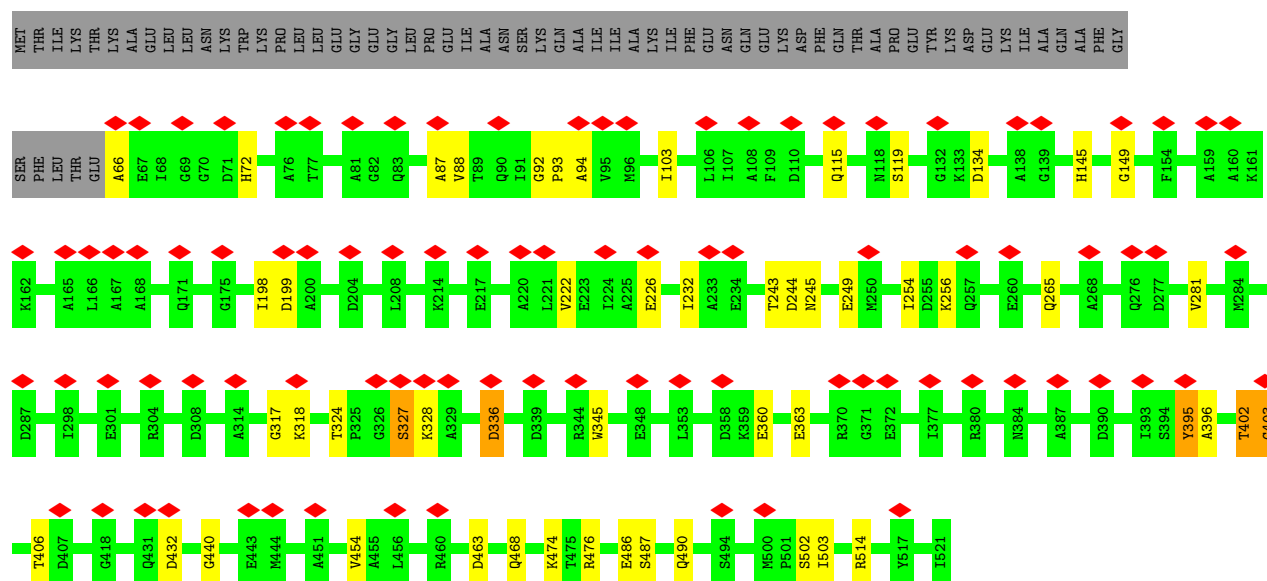
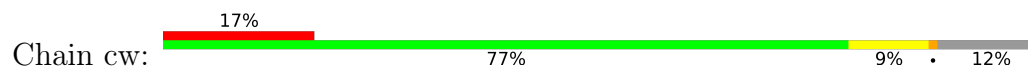




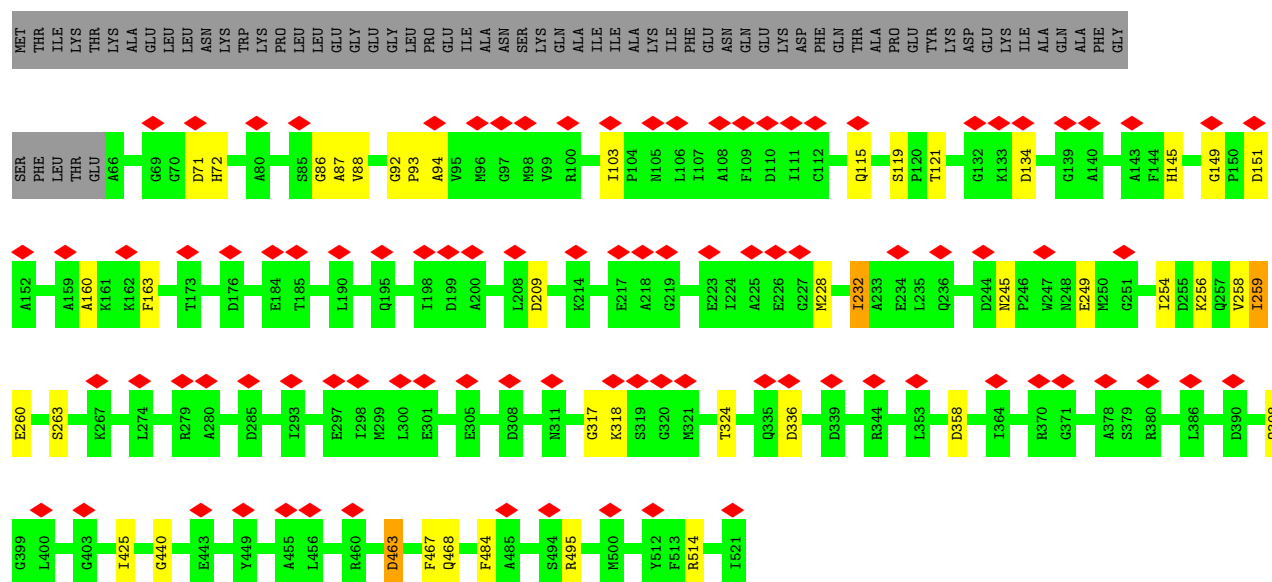
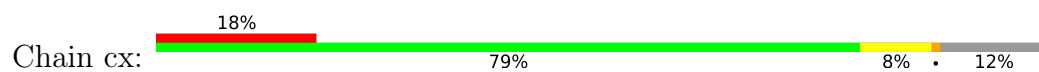
• Molecule 1: Major capsid protein



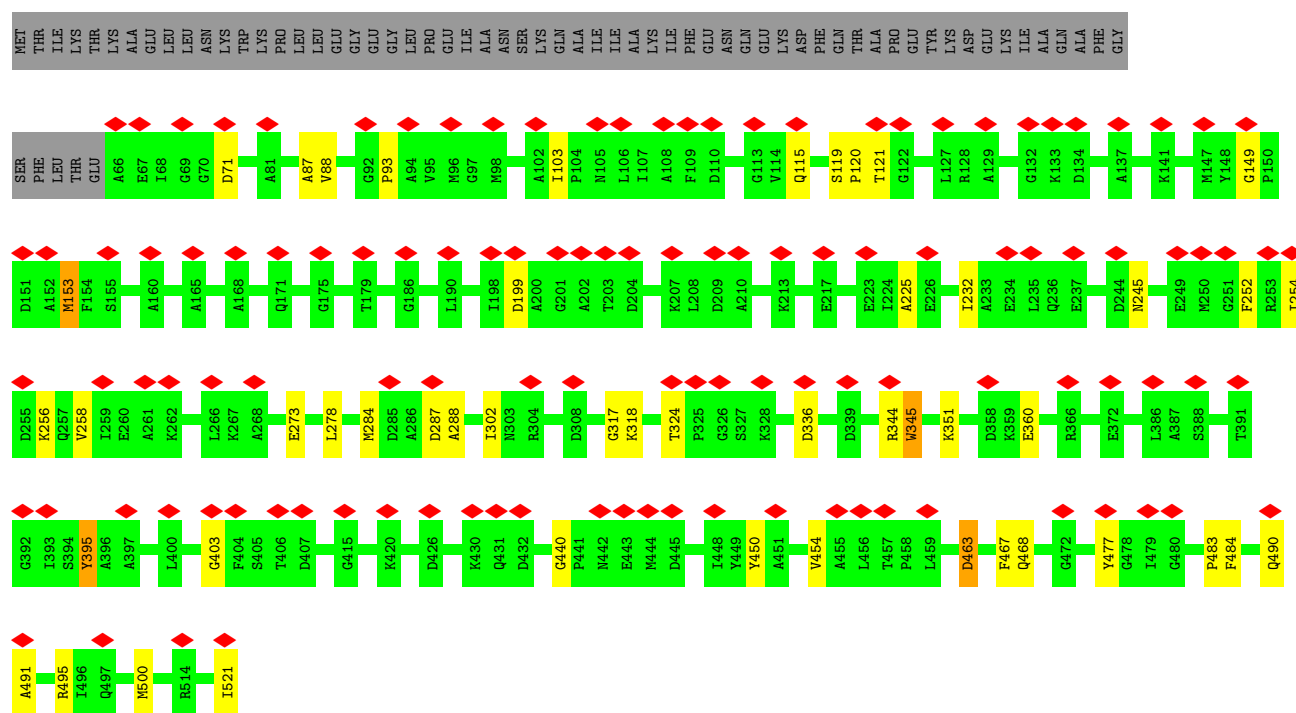
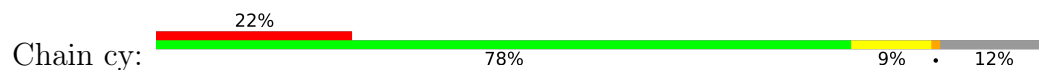
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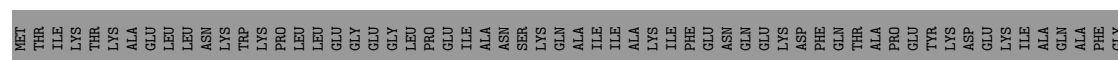
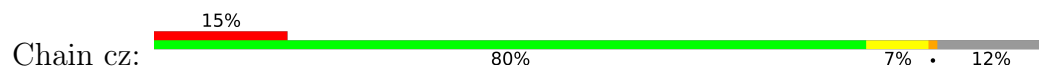
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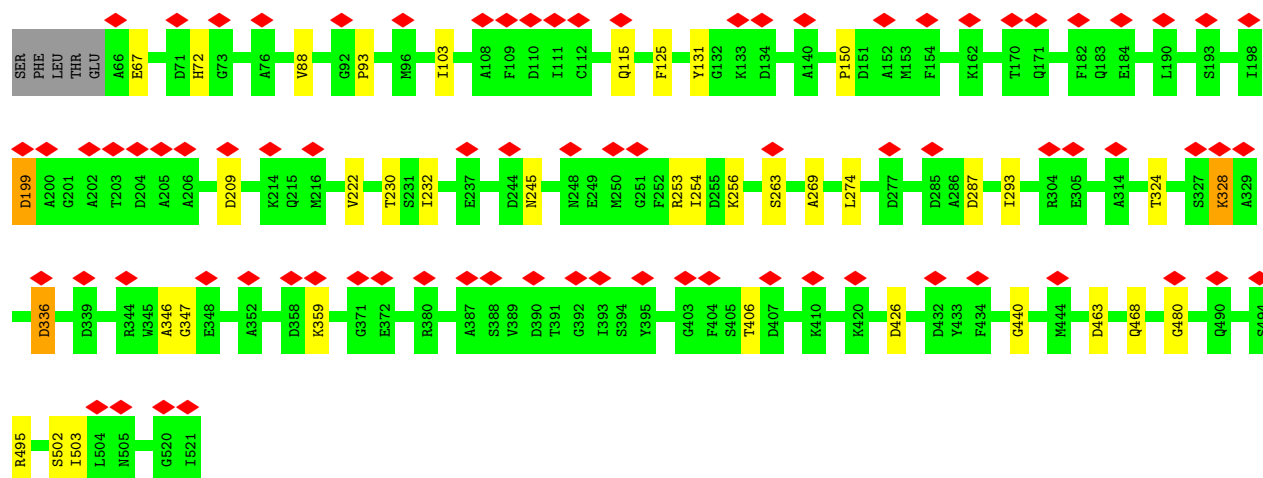


• Molecule 1: Major capsid protein

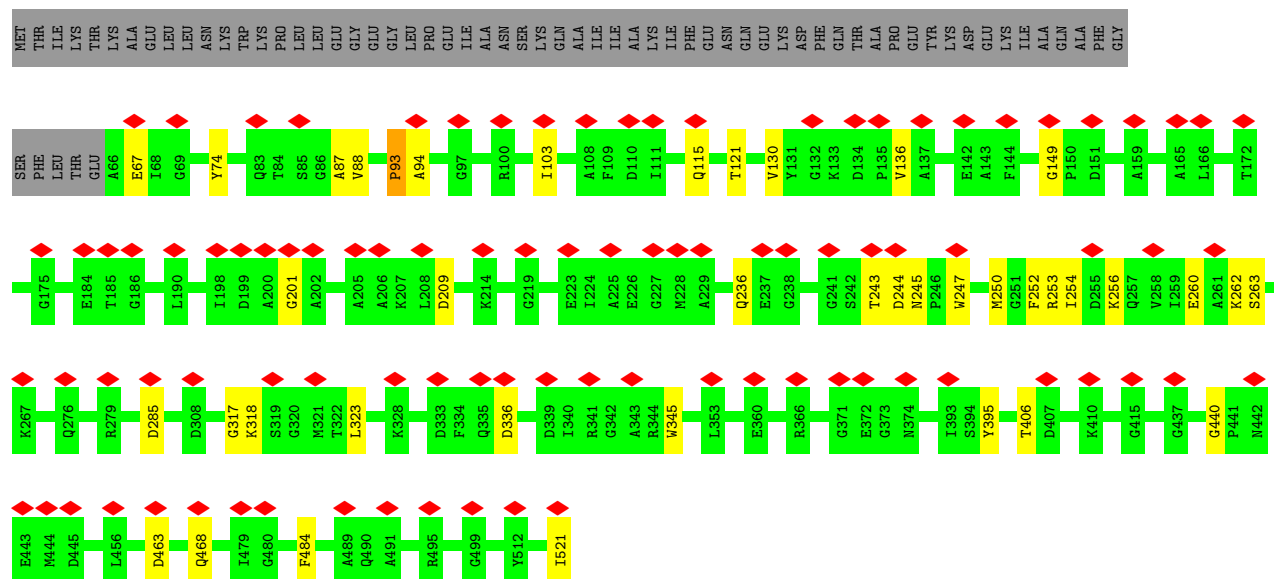
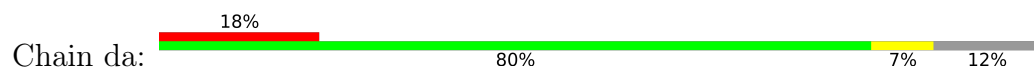


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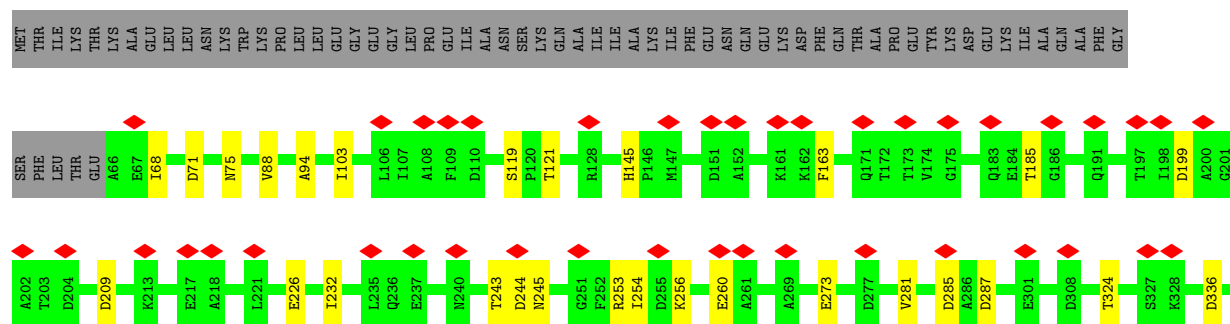
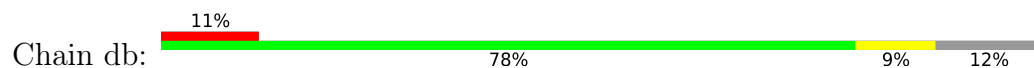


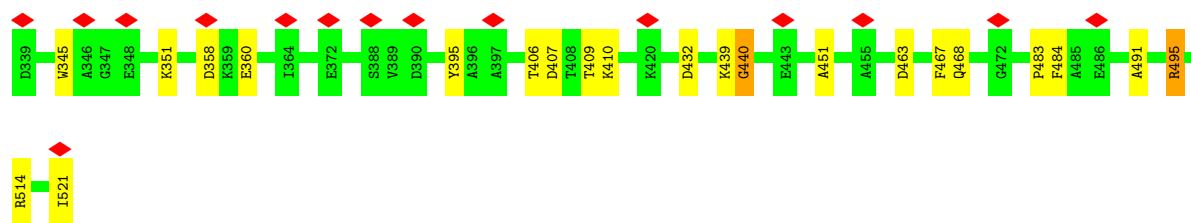


• Molecule 1: Major capsid protein

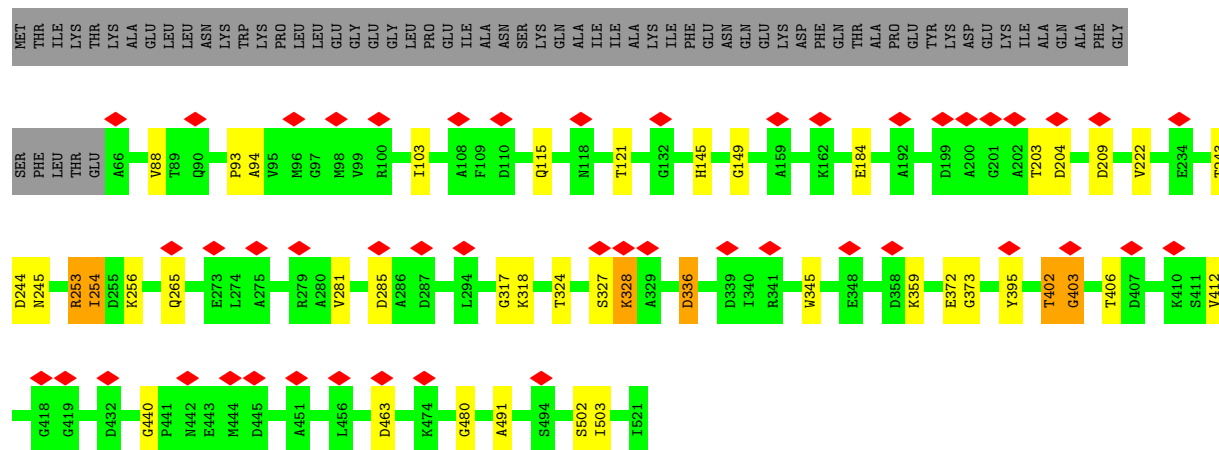
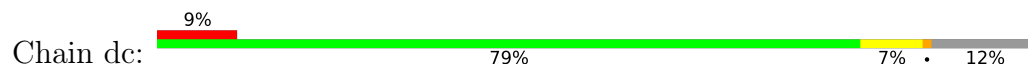


• Molecule 1: Major capsid protein

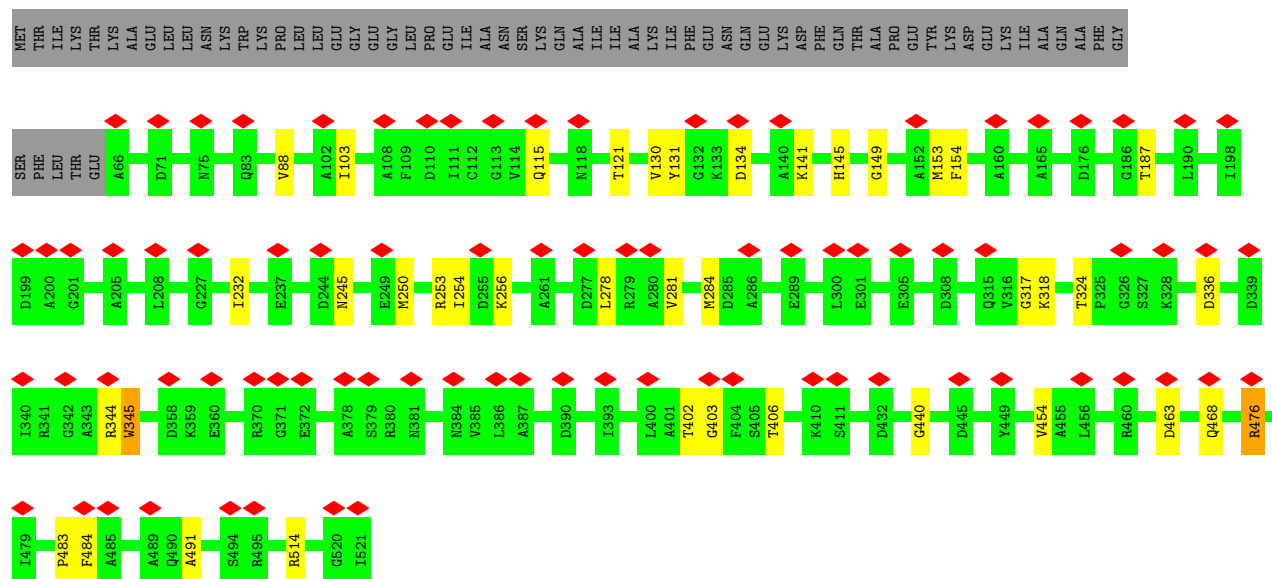
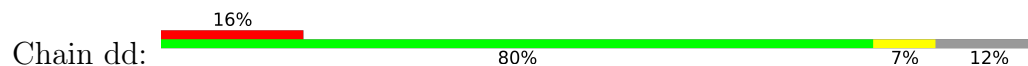




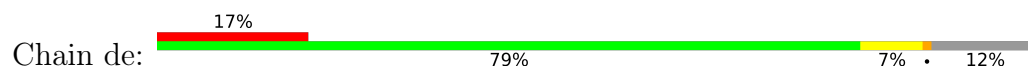
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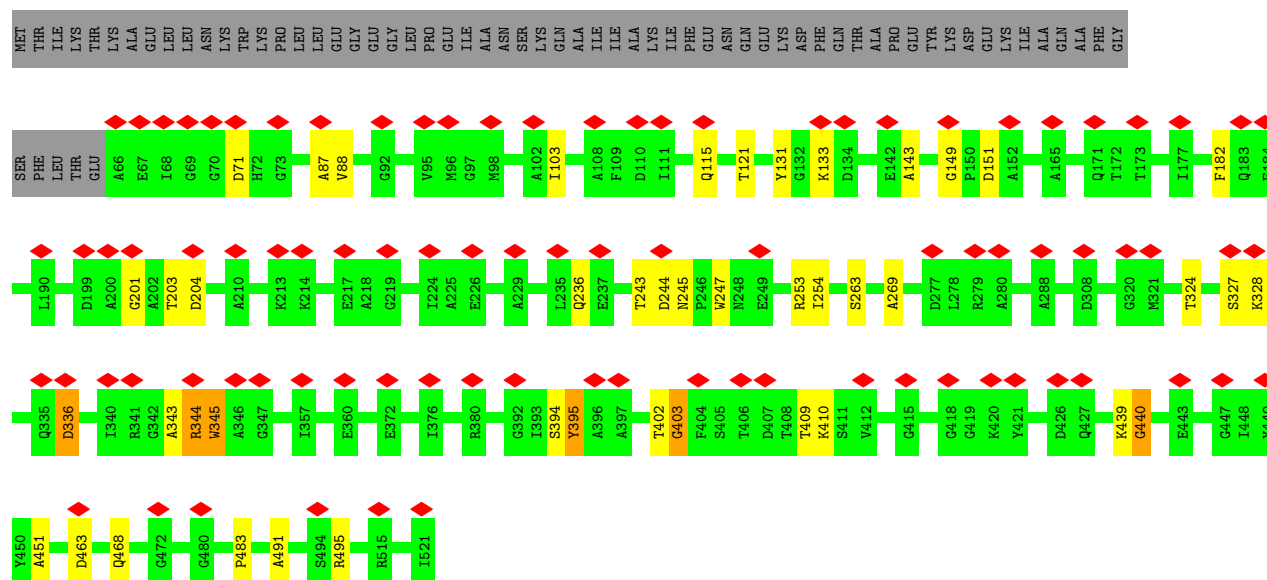


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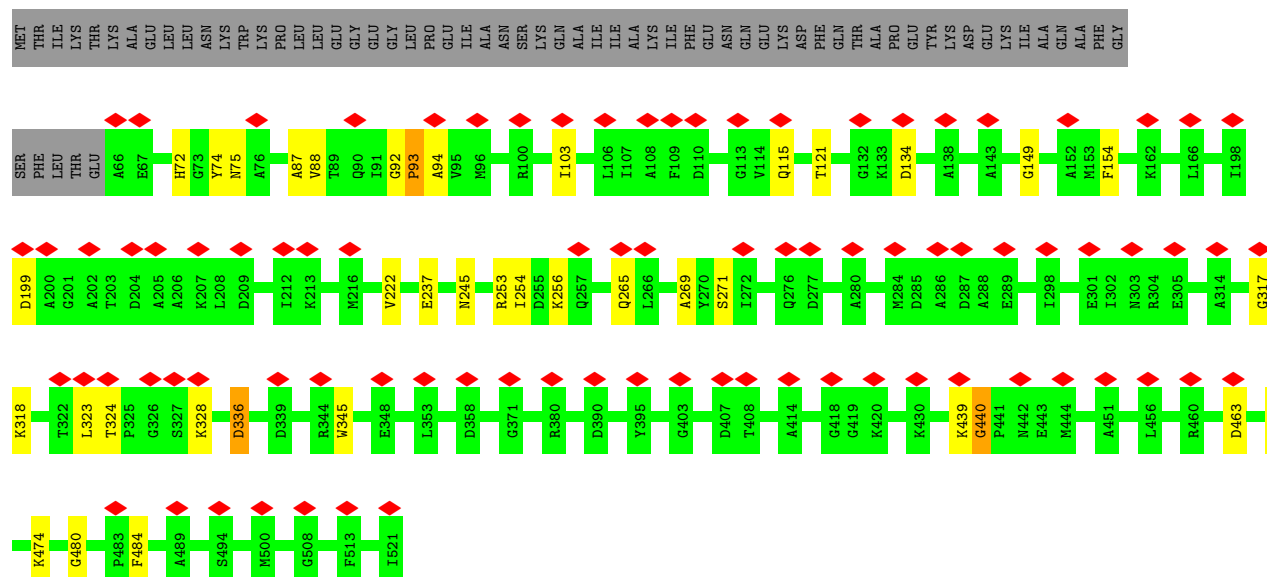
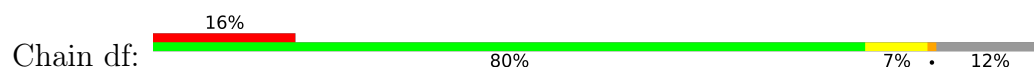


- Molecule 1: Major capsid protein

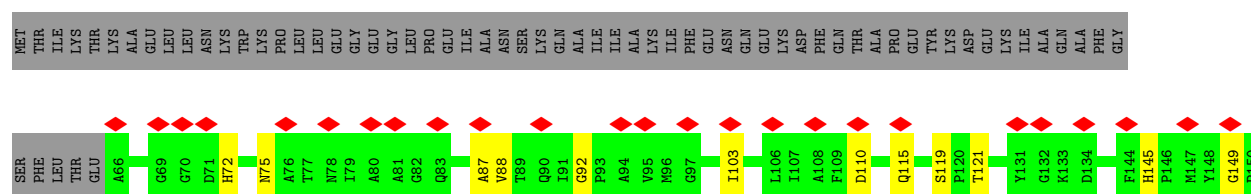
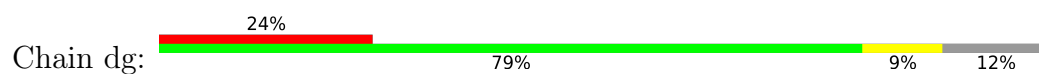




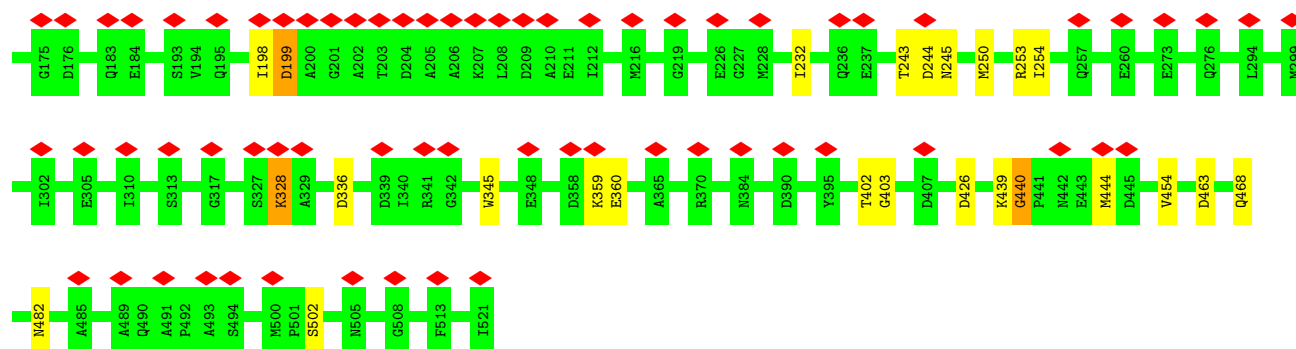
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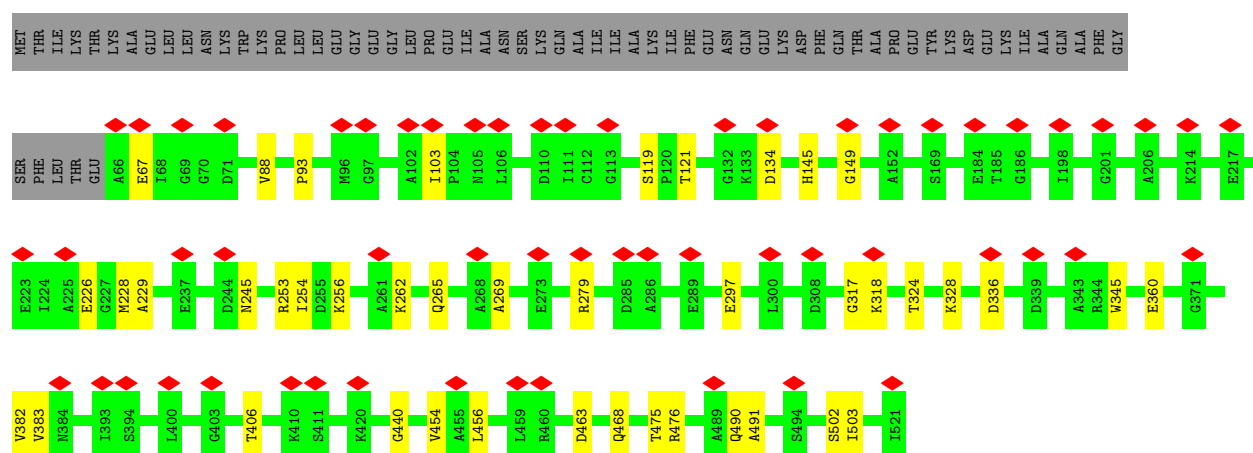
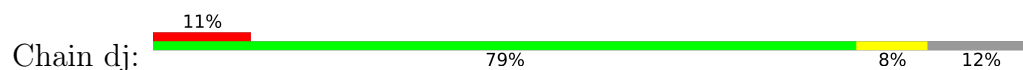
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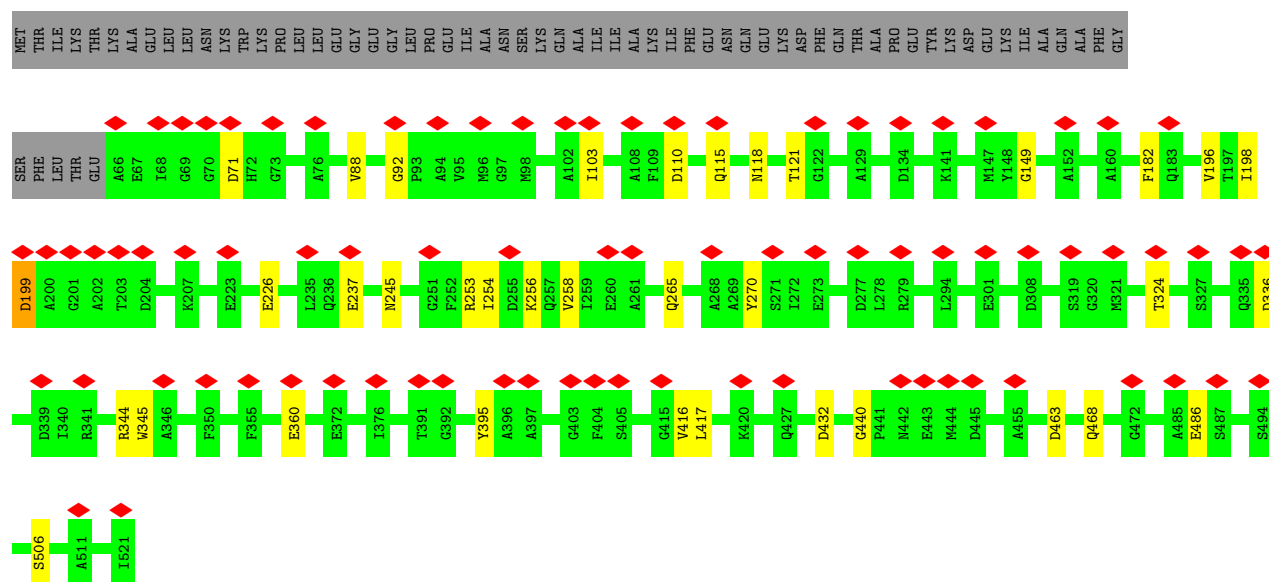
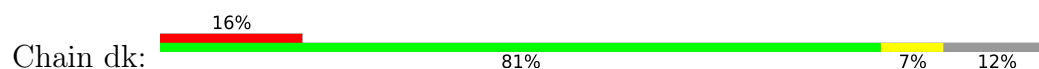




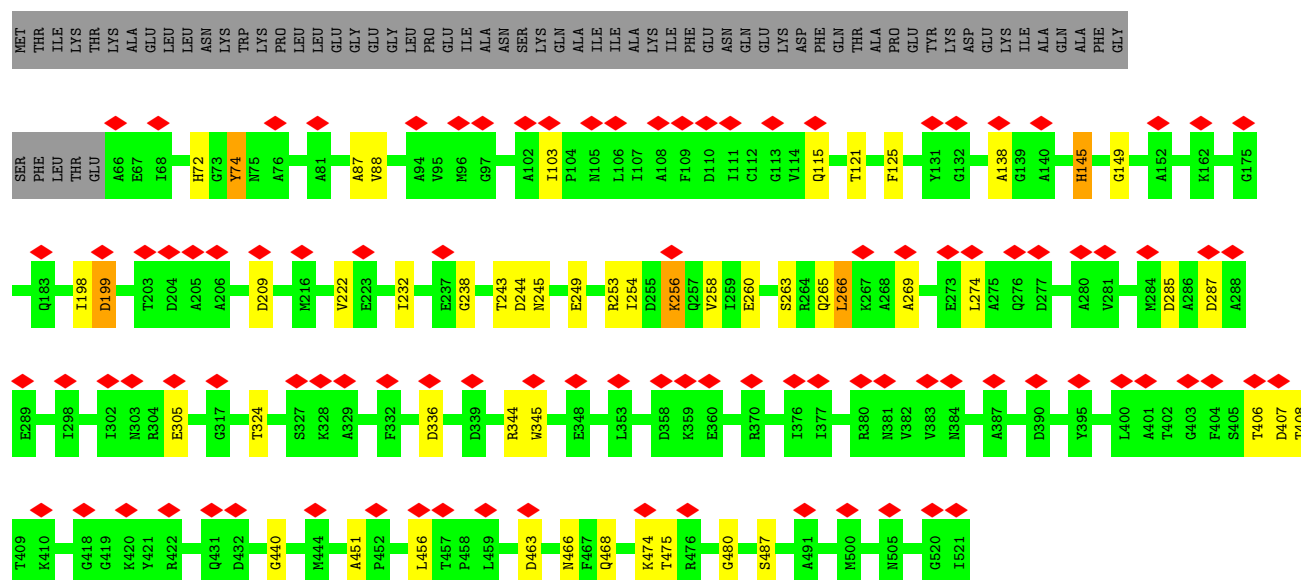
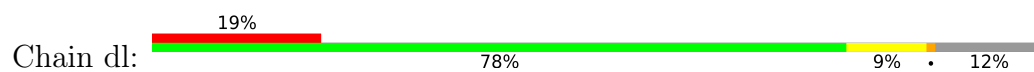
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

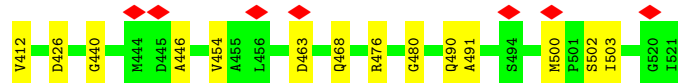
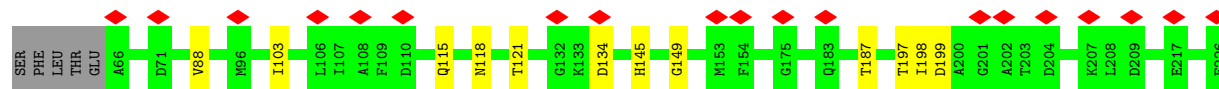
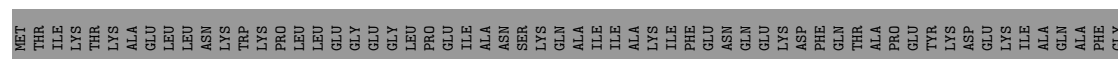
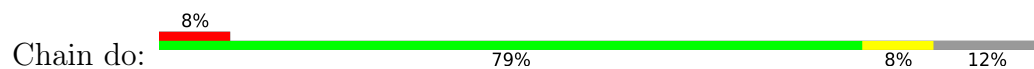


- Molecule 1: Major capsid protein

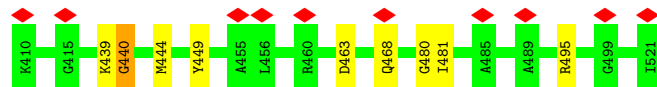
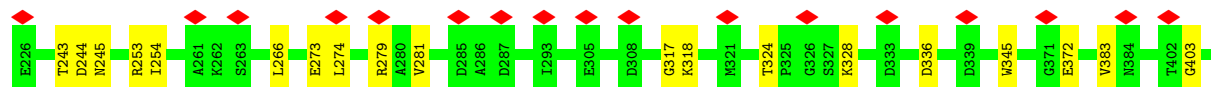
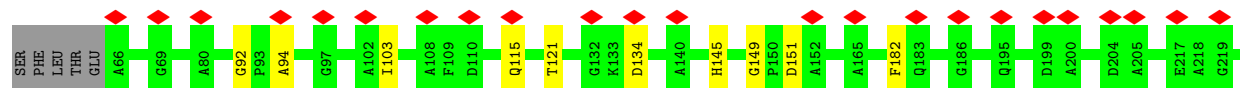
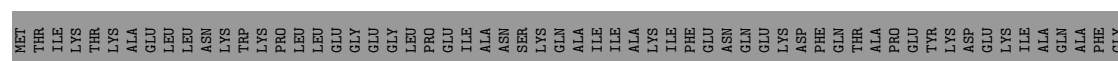
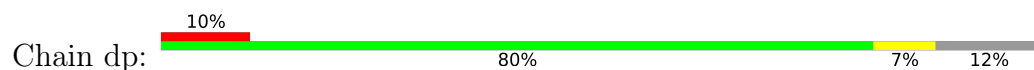




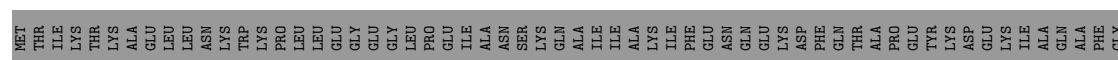
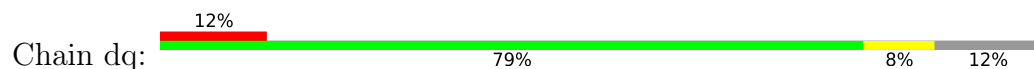
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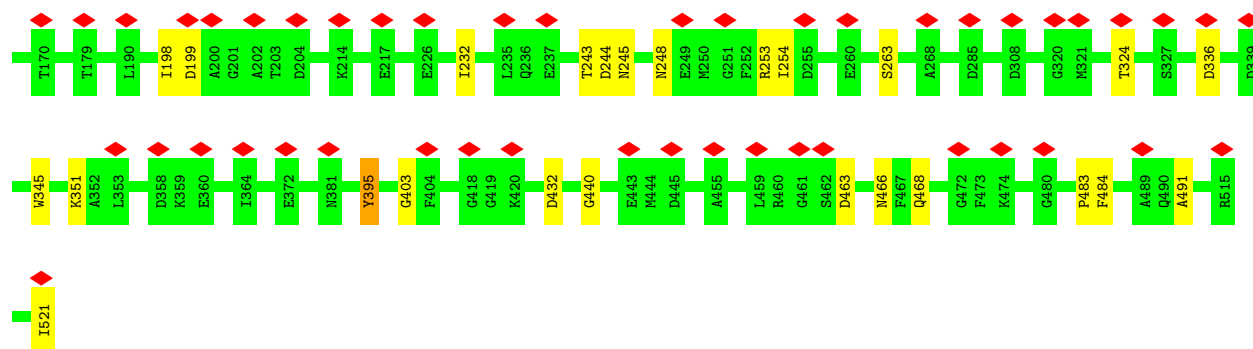


- Molecule 1: Major capsid protein

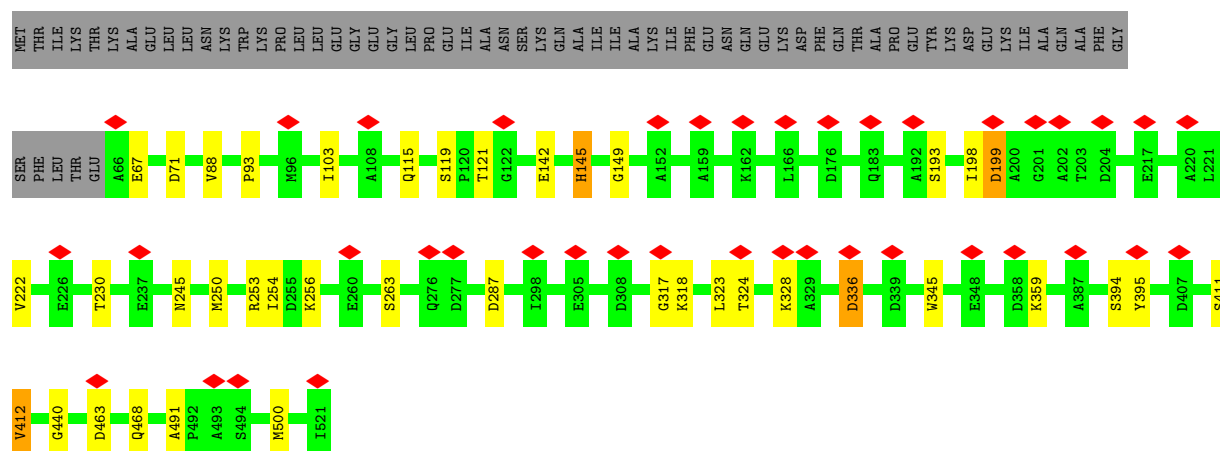
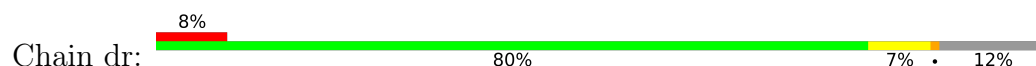


- Molecule 1: Major capsid protein

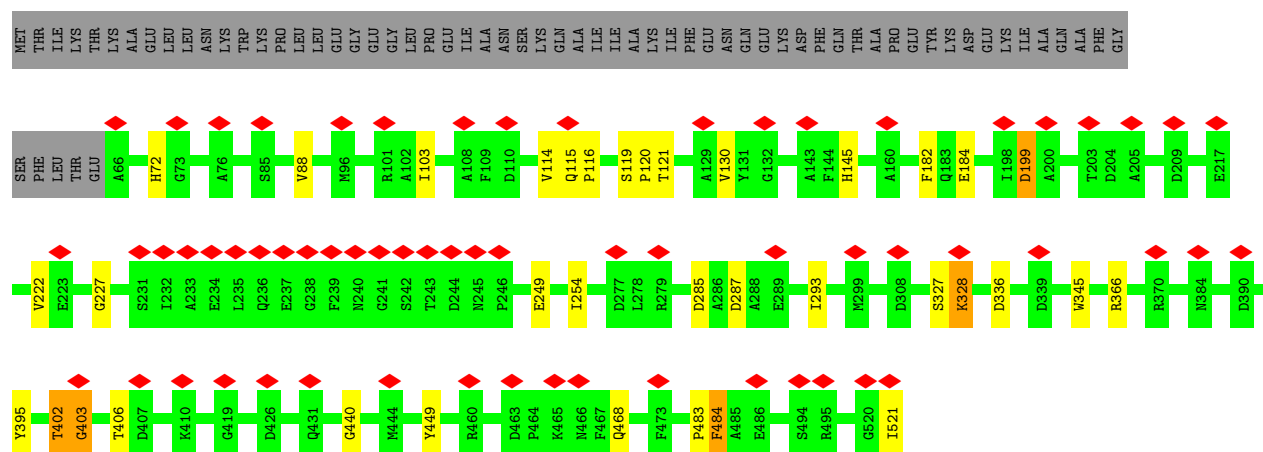
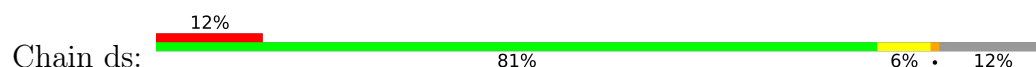




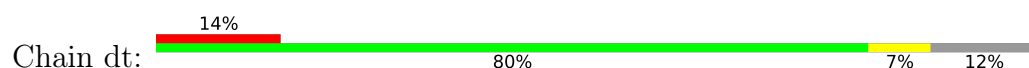
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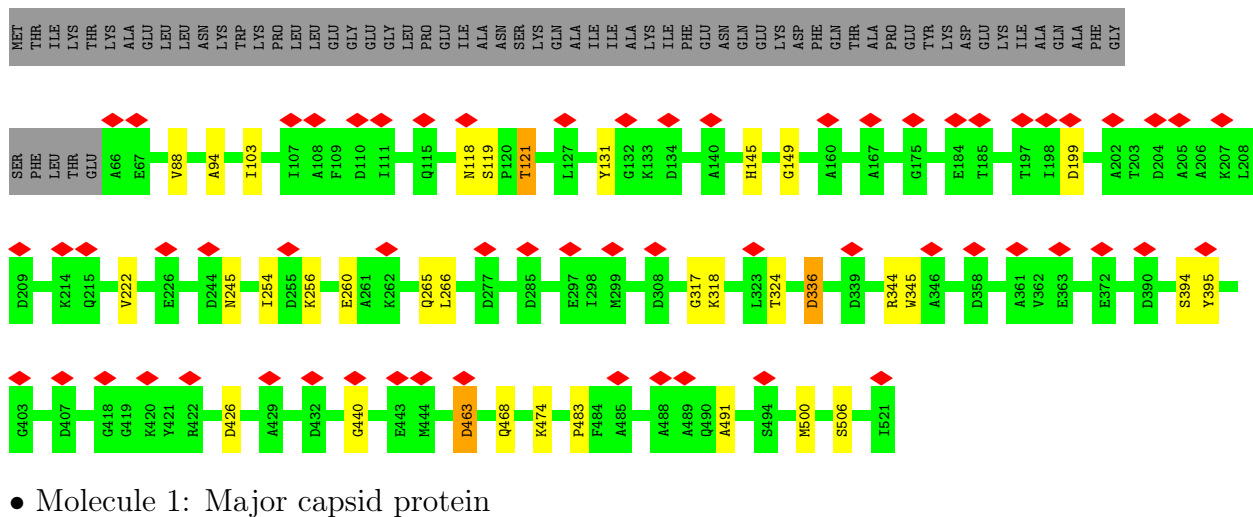
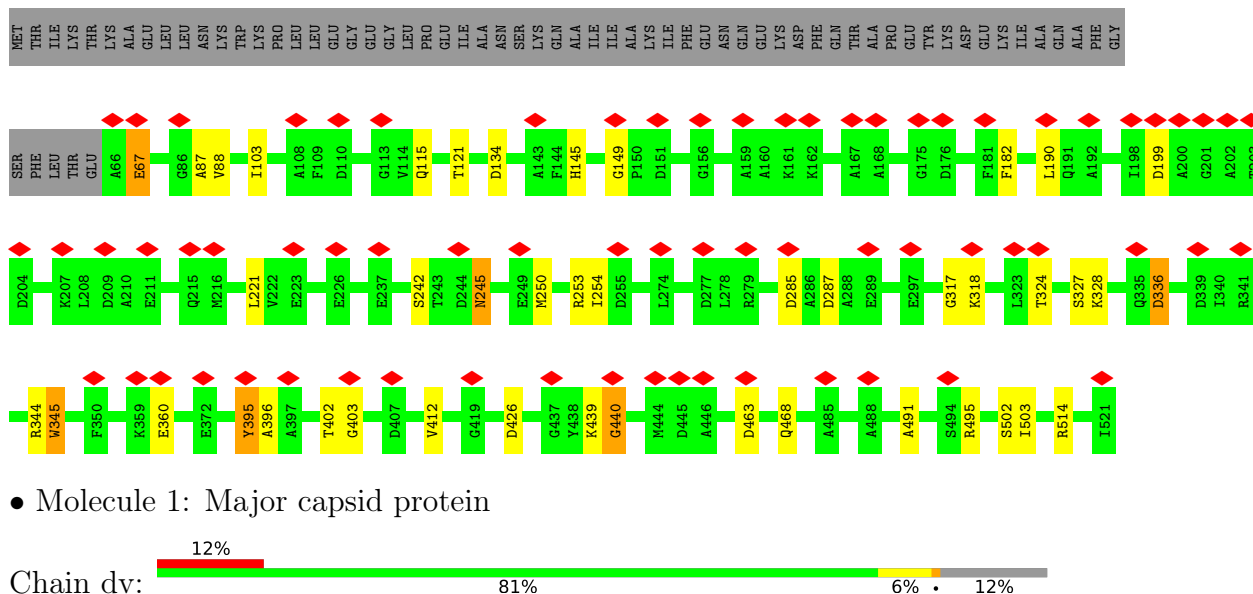
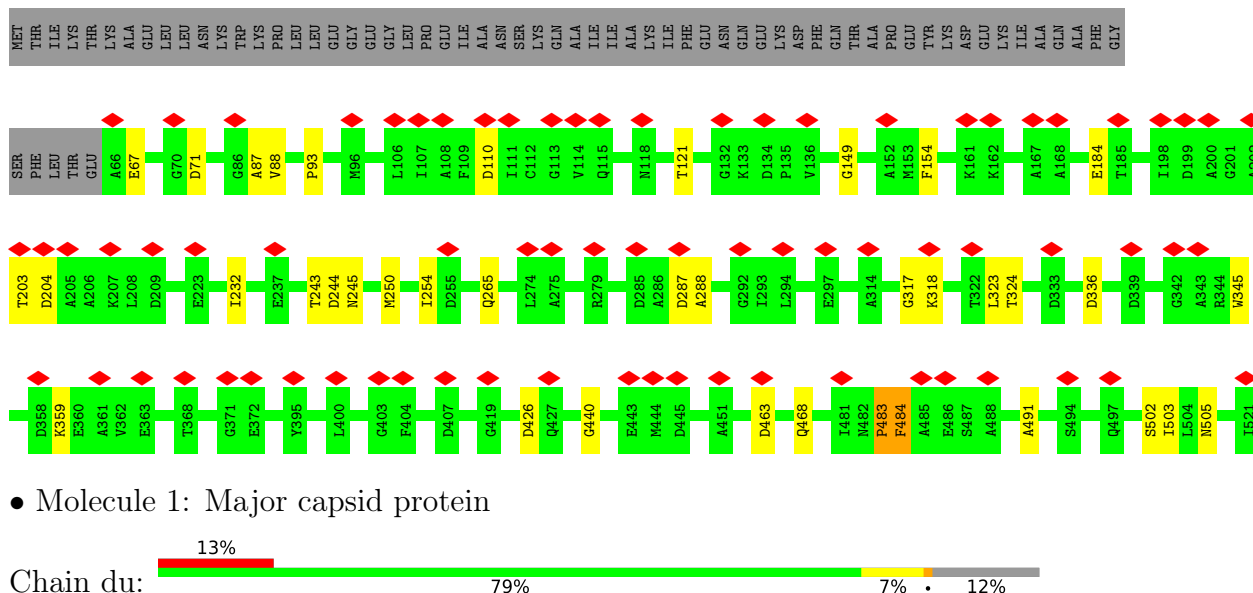


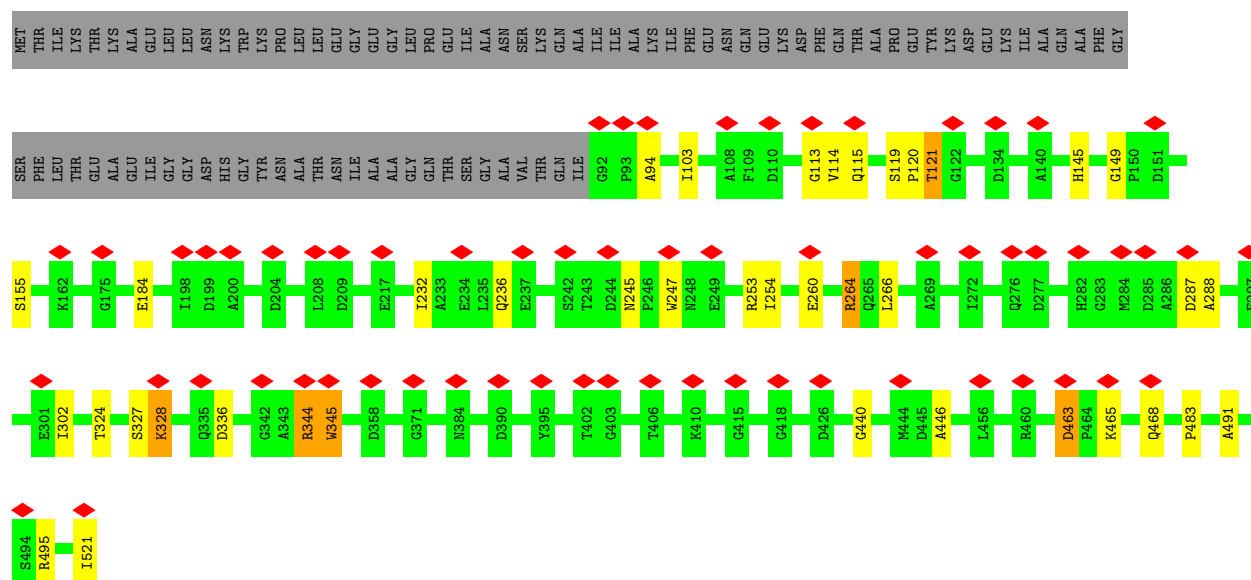
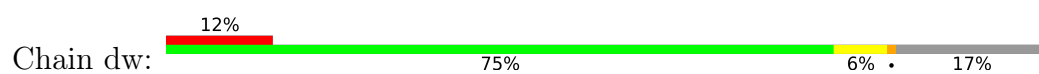
- Molecule 1: Major capsid protein



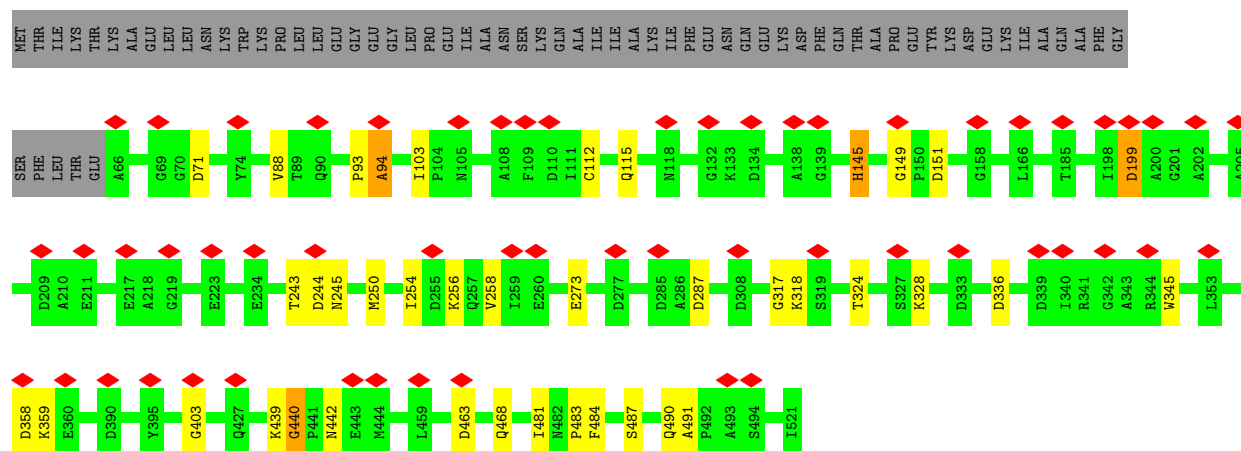
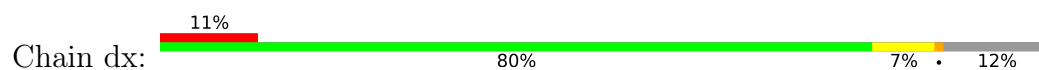
- Molecule 1: Major capsid protein



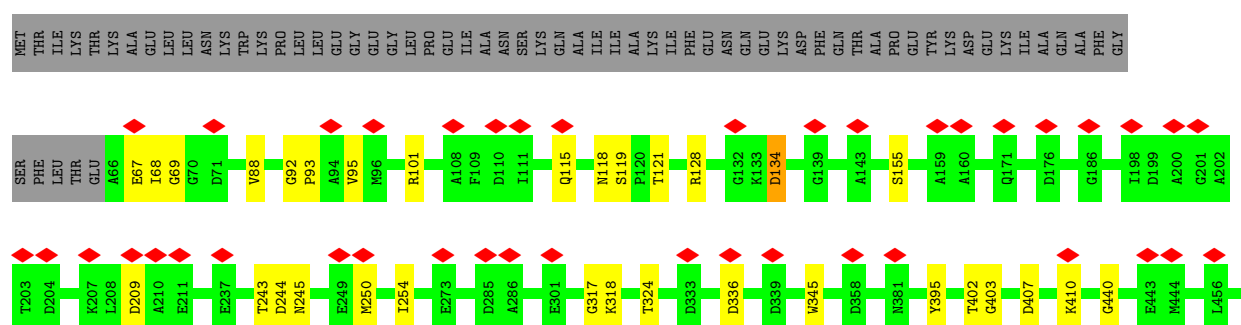
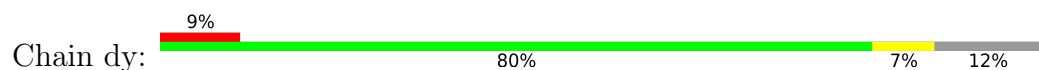


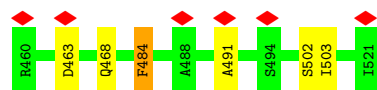


• Molecule 1: Major capsid protein

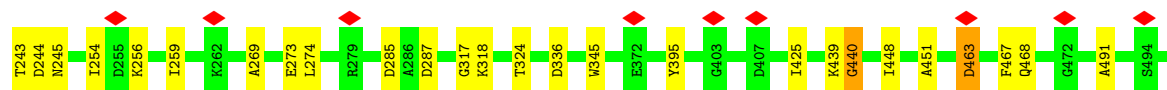
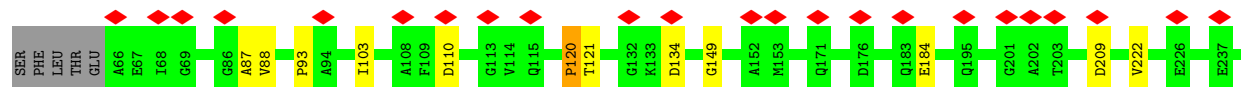
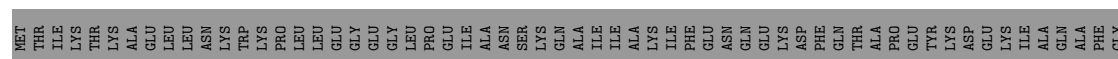
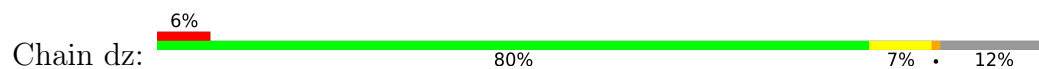


• Molecule 1: Major capsid protein

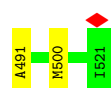
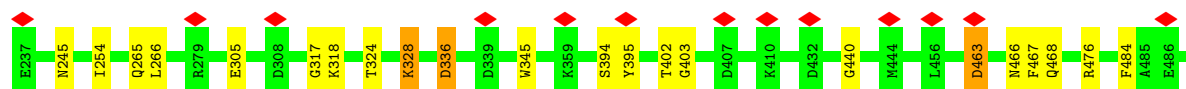
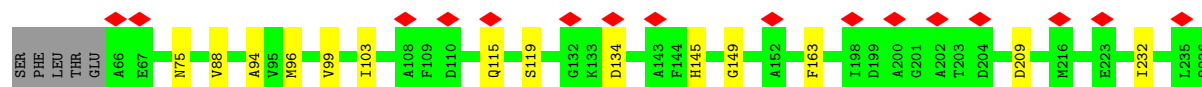
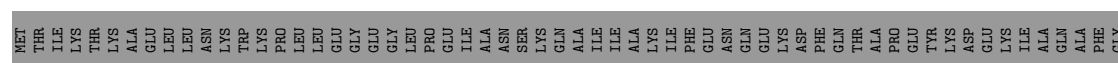
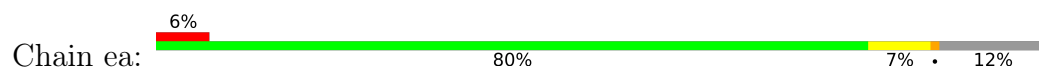




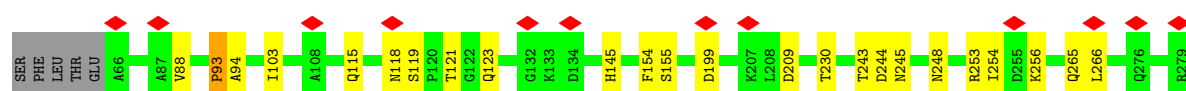
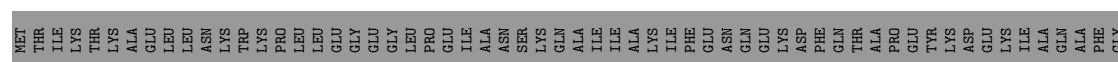
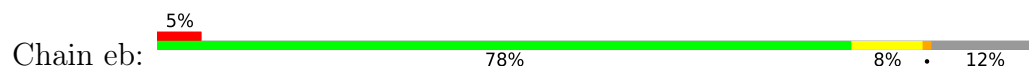
- Molecule 1: Major capsid protein

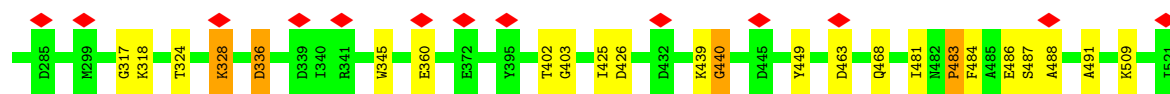


- Molecule 1: Major capsid protein

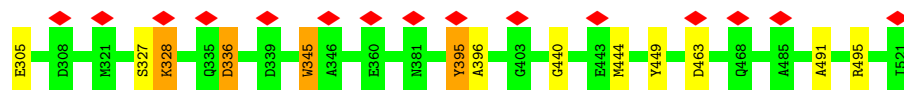
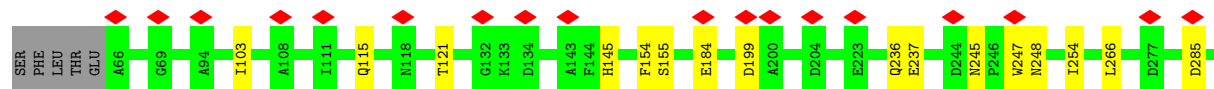
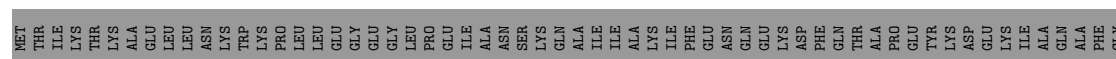
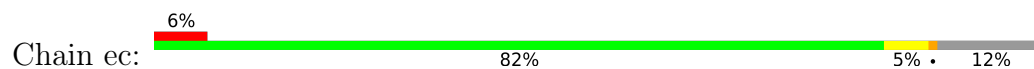


- Molecule 1: Major capsid protein

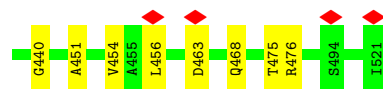
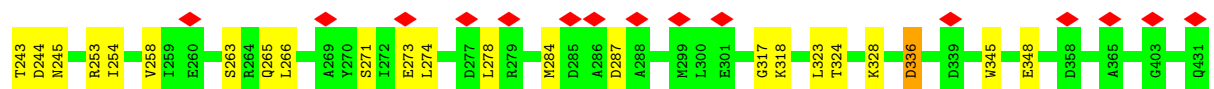
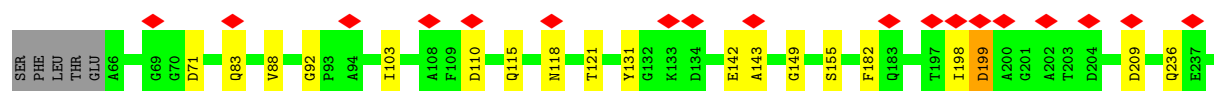
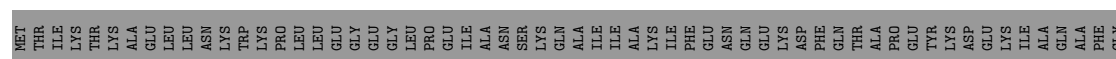
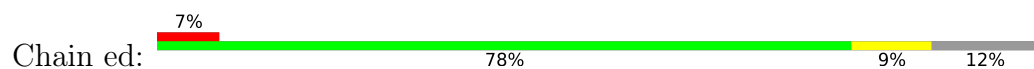




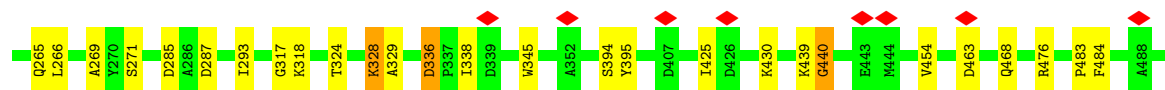
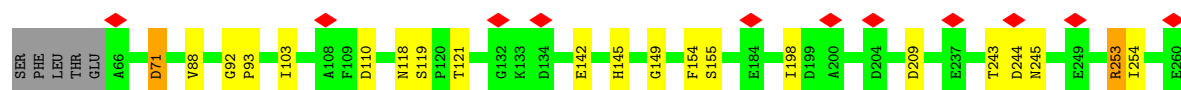
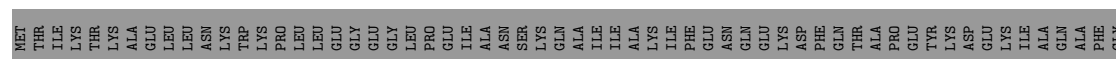
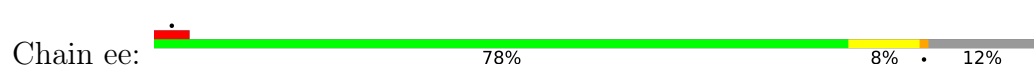
• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein



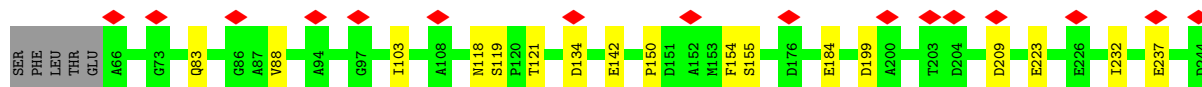
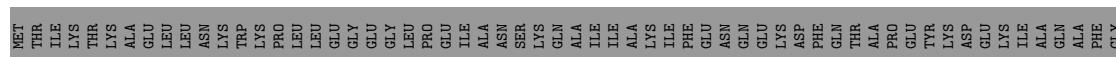
• Molecule 1: Major capsid protein





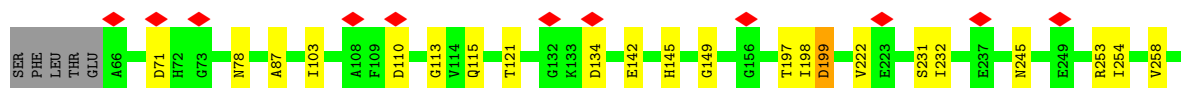
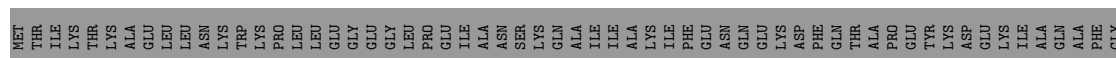
- Molecule 1: Major capsid protein

Chain ef: 80% 7% 12%



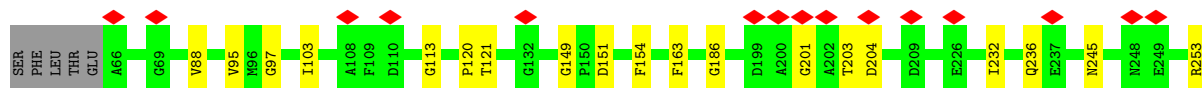
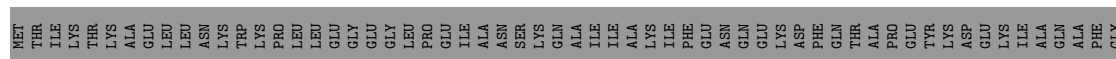
- Molecule 1: Major capsid protein

Chain eg: 78% 8% 12%



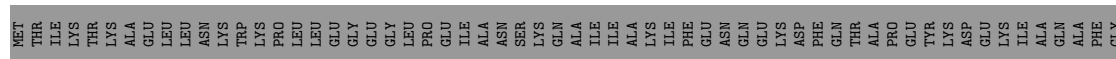
- Molecule 1: Major capsid protein

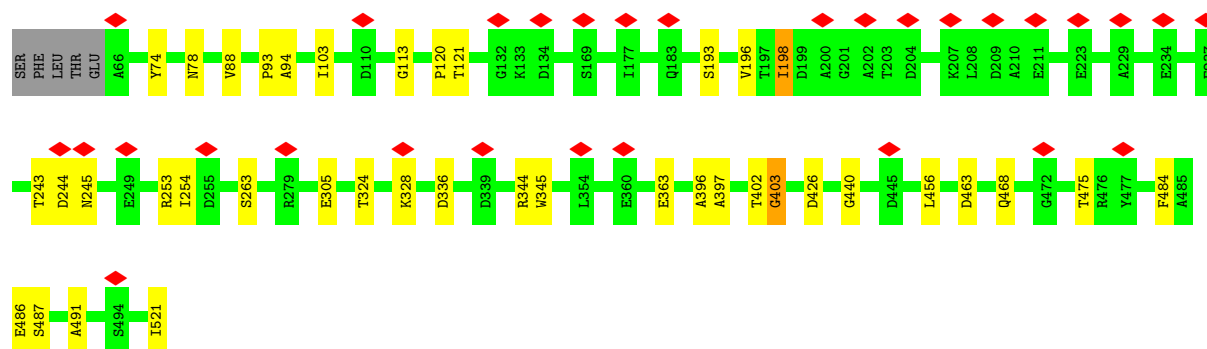
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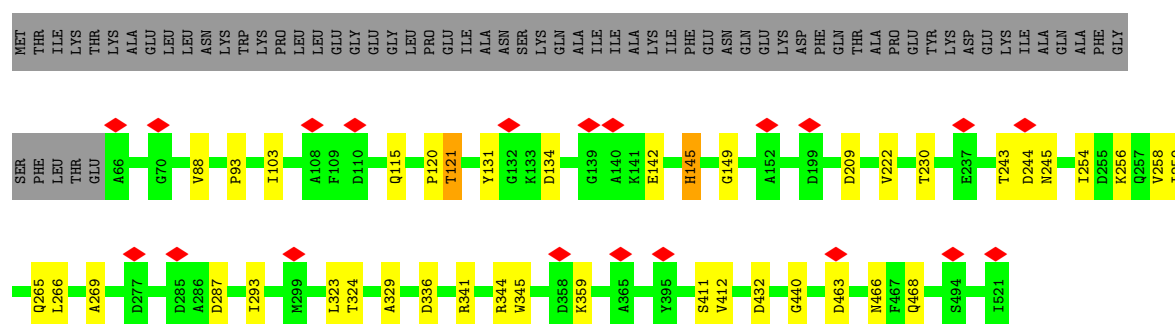
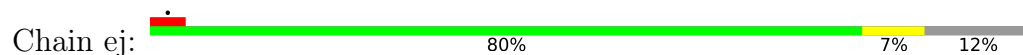
- Molecule 1: Major capsid protein

Chain ei: 6% 80% 7% 12%

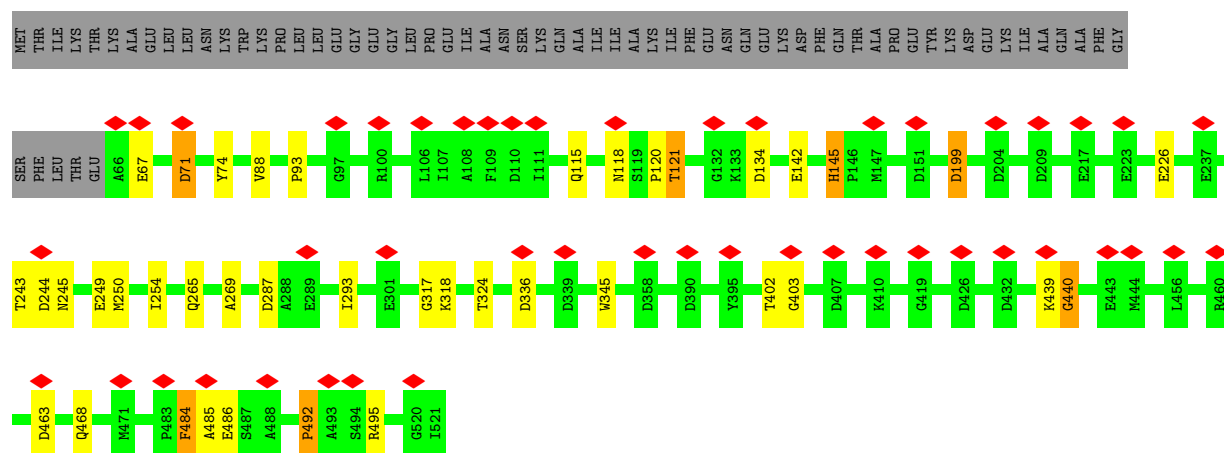
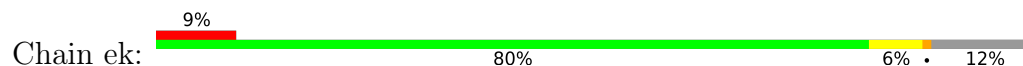




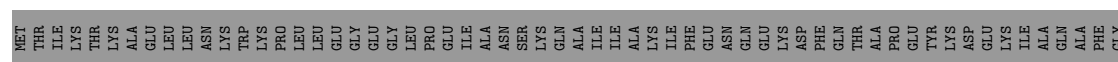
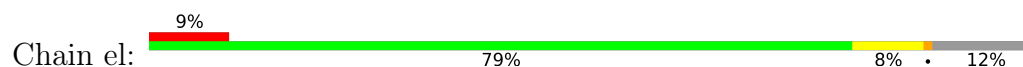
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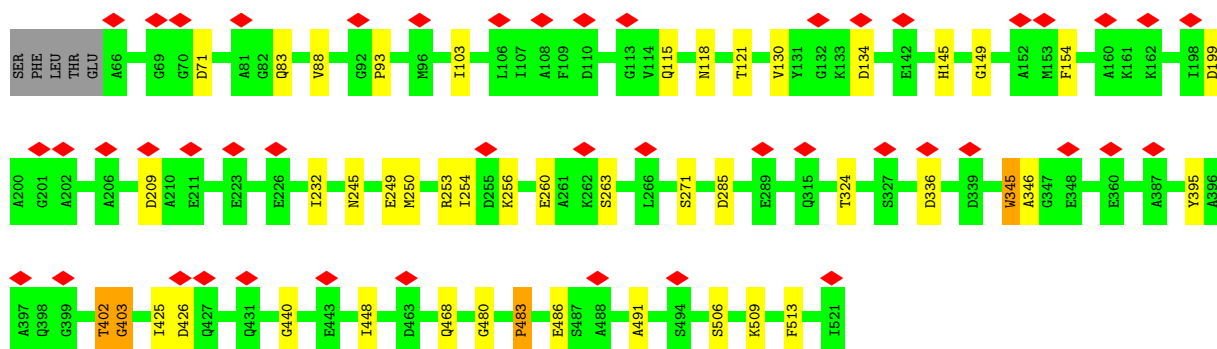


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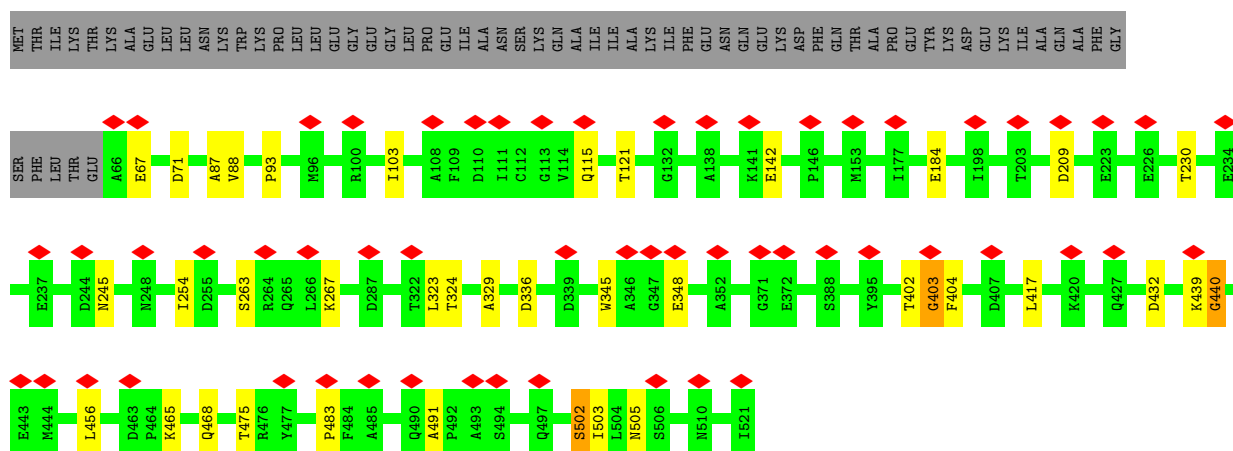
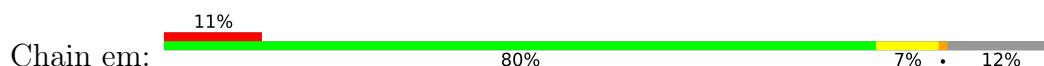


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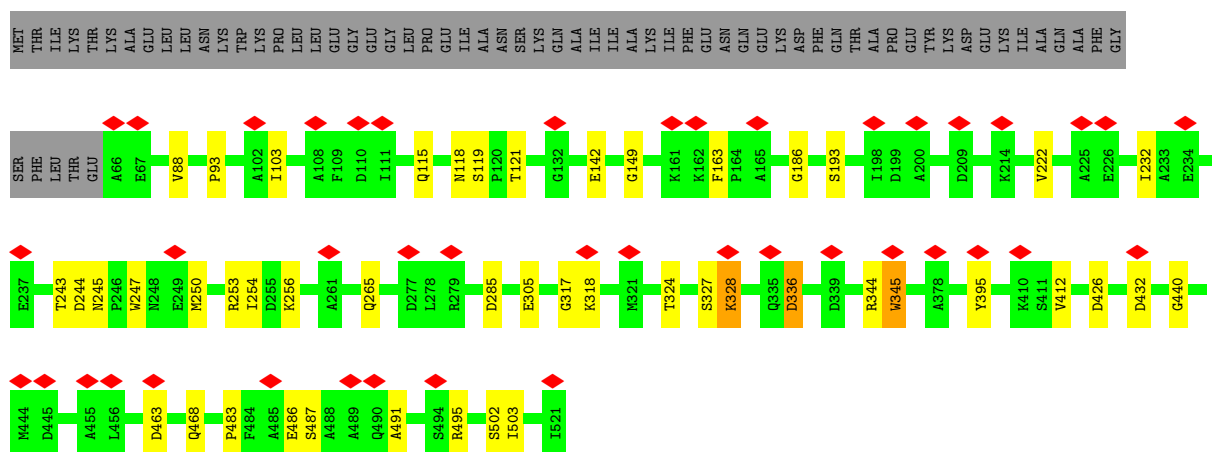
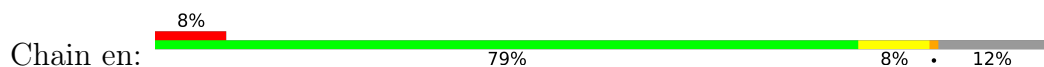




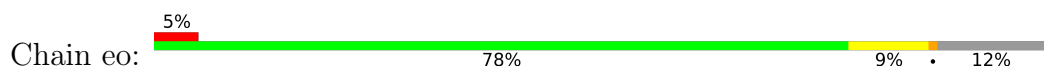
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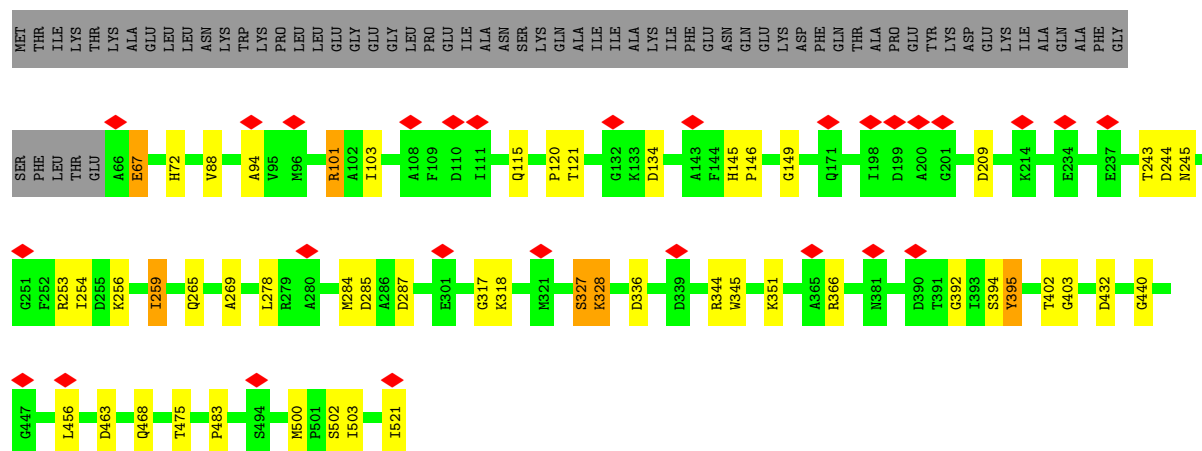


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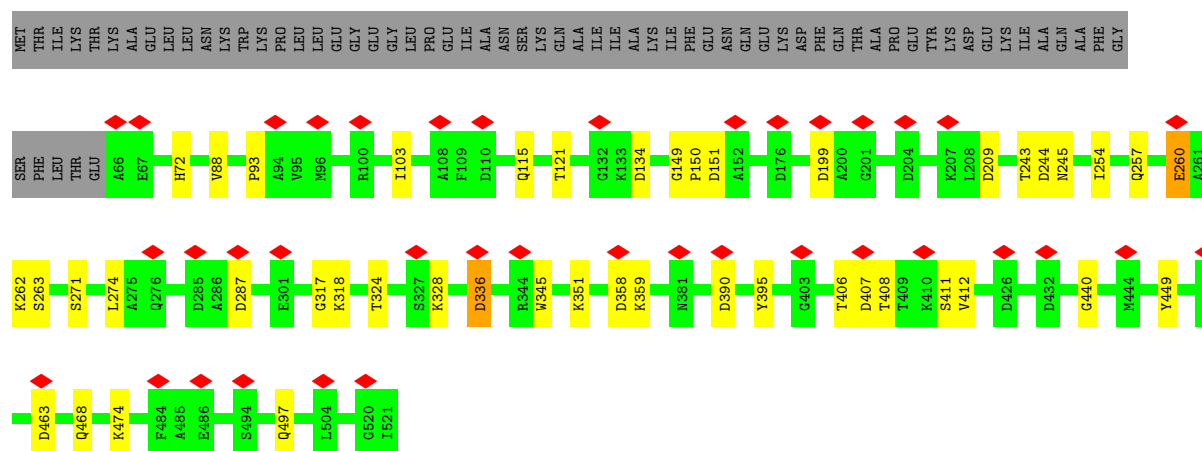
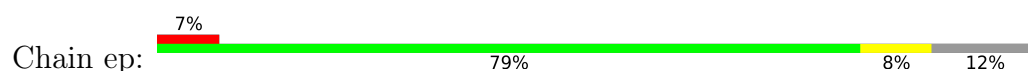


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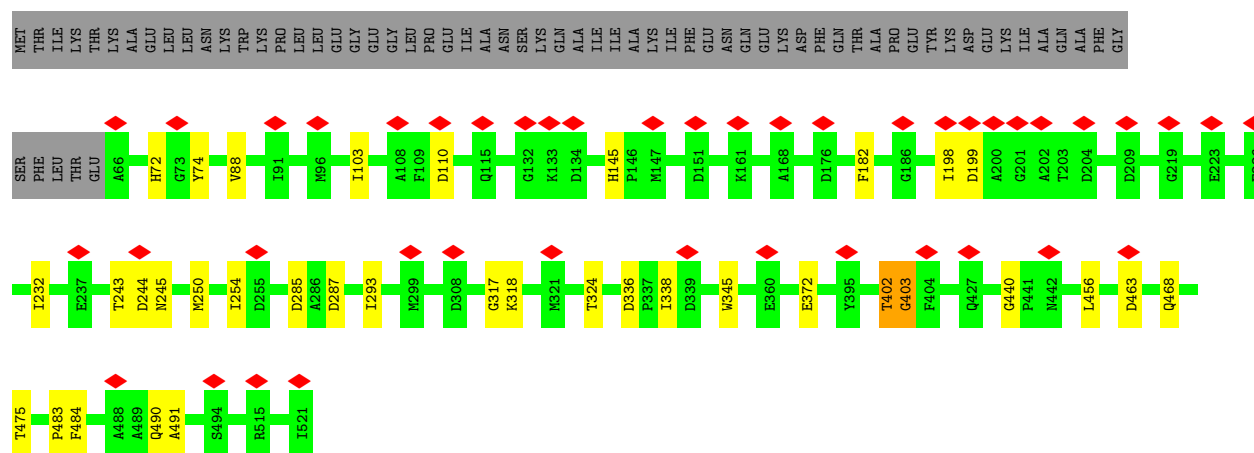
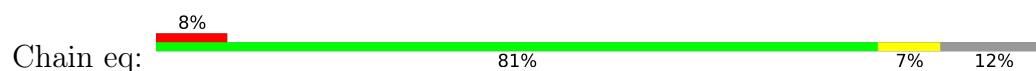




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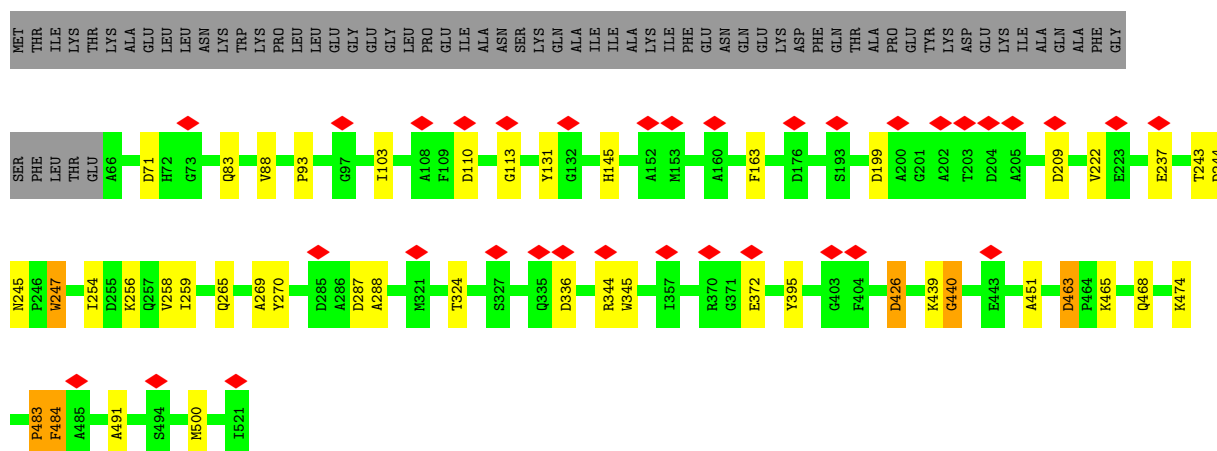


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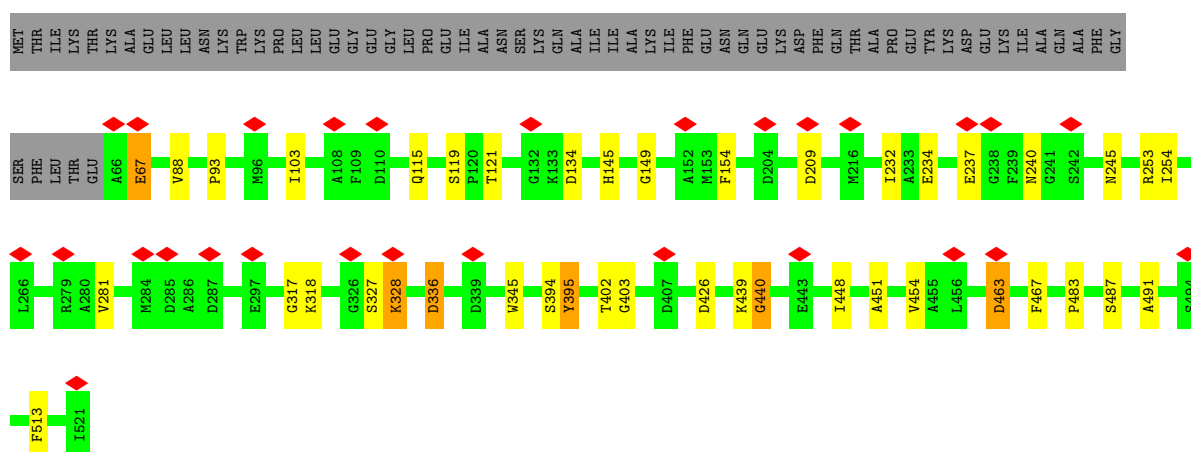
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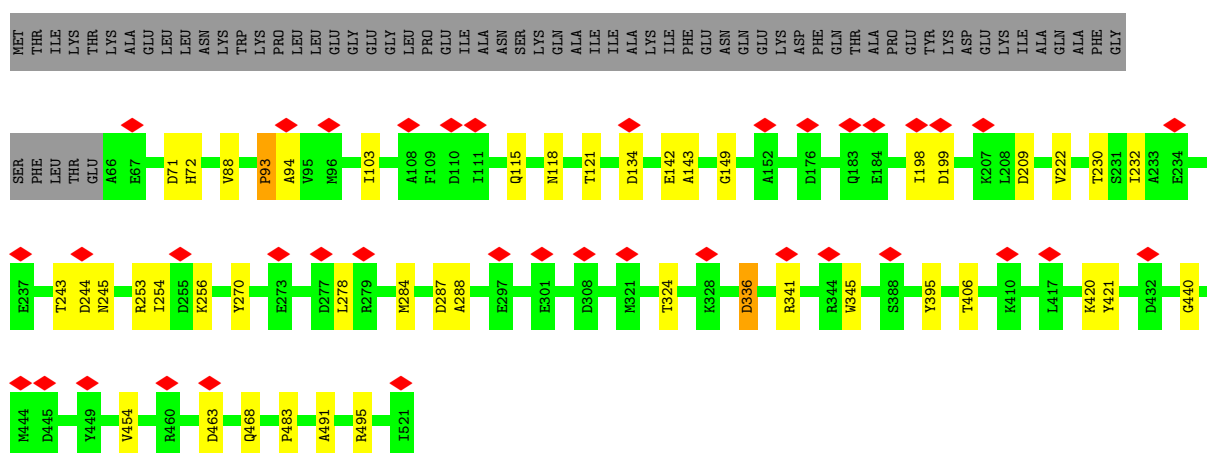
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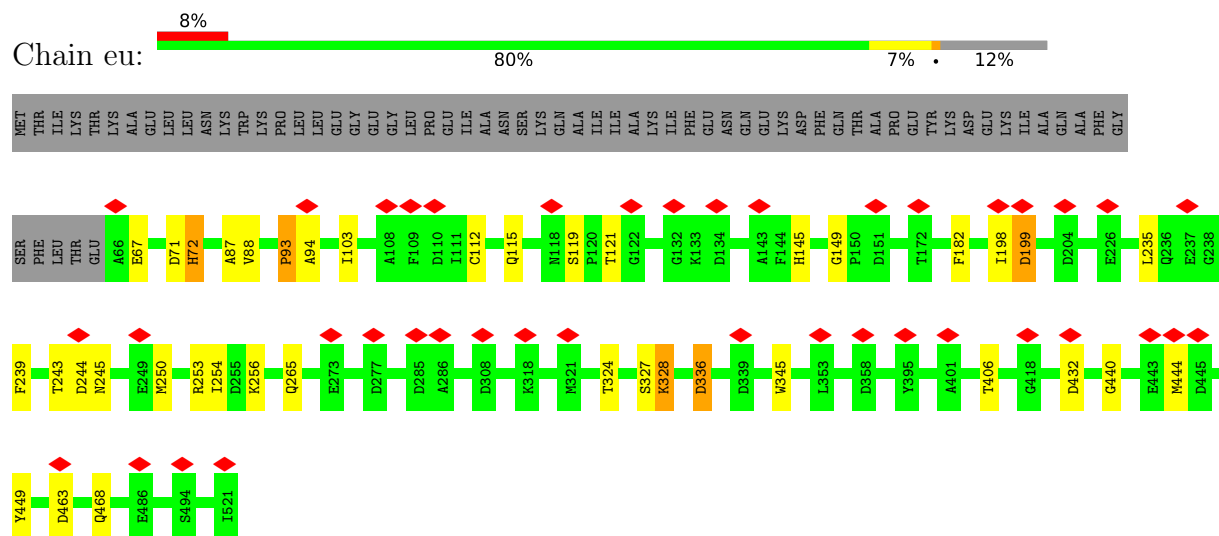


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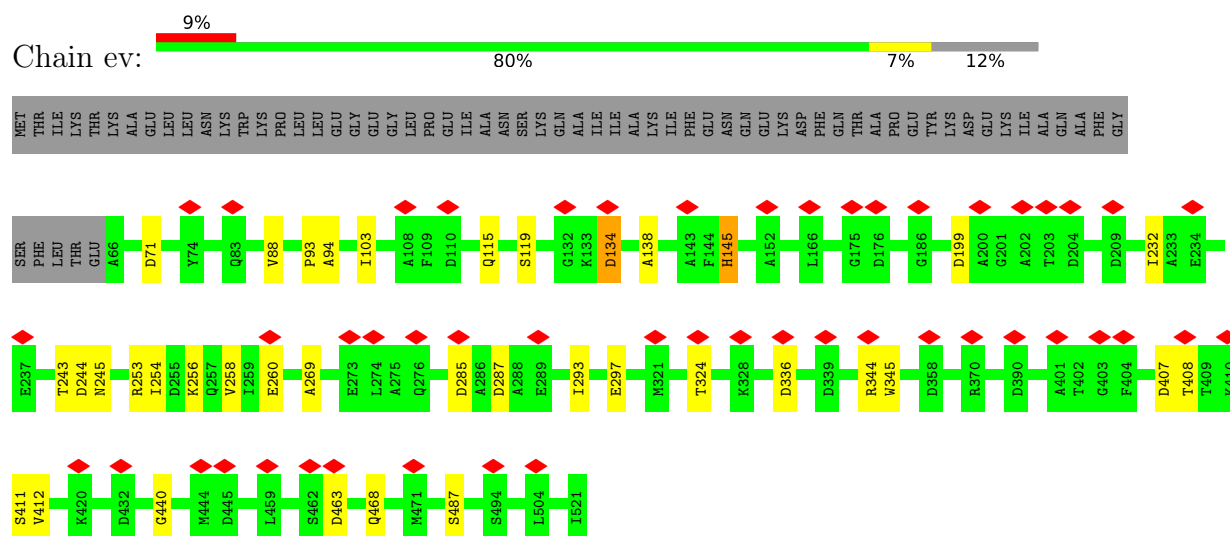
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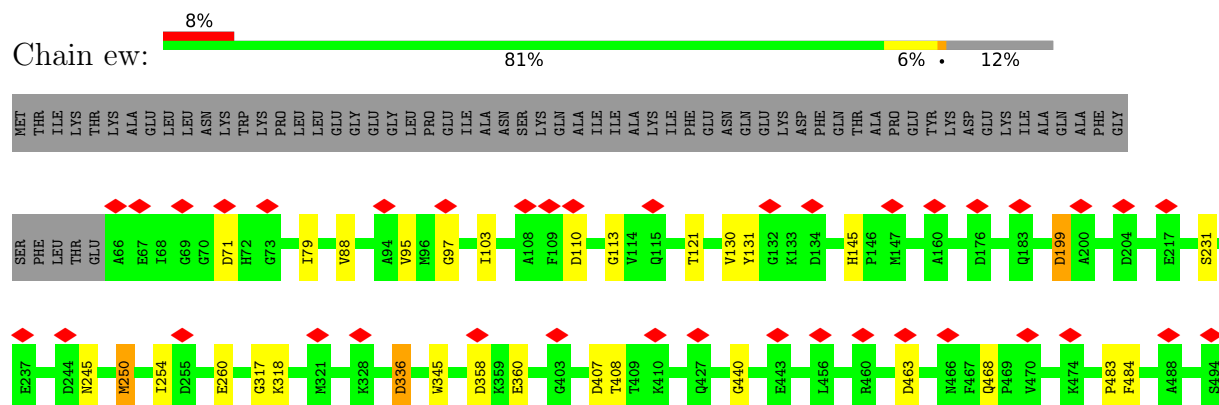
- Molecule 1: Major capsid protein

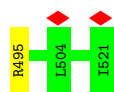


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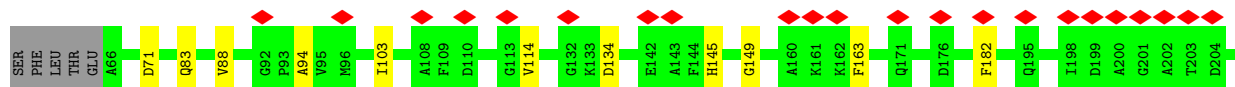
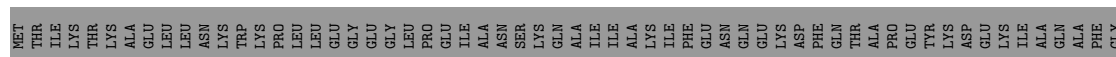
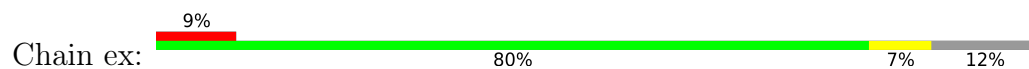


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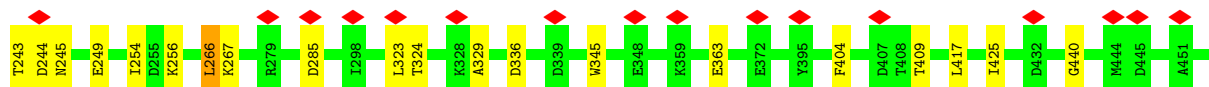
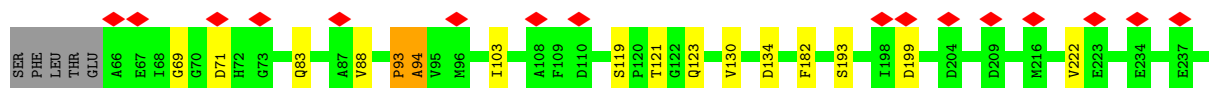
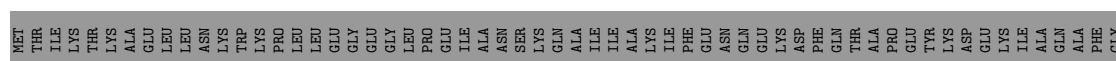
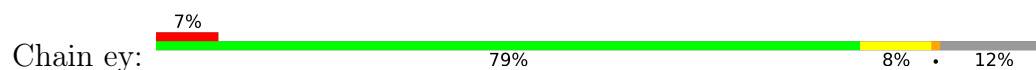




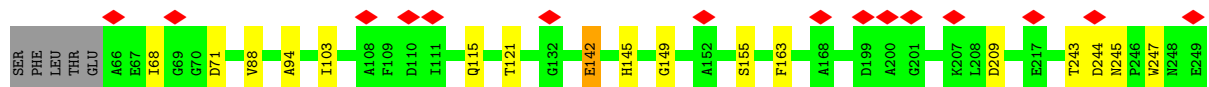
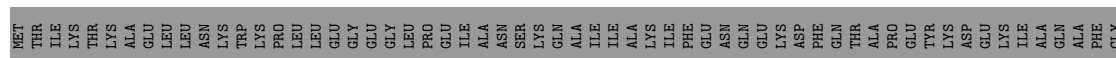
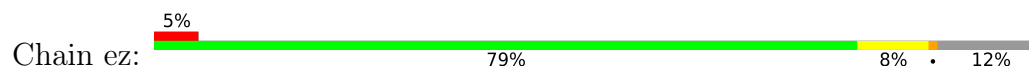
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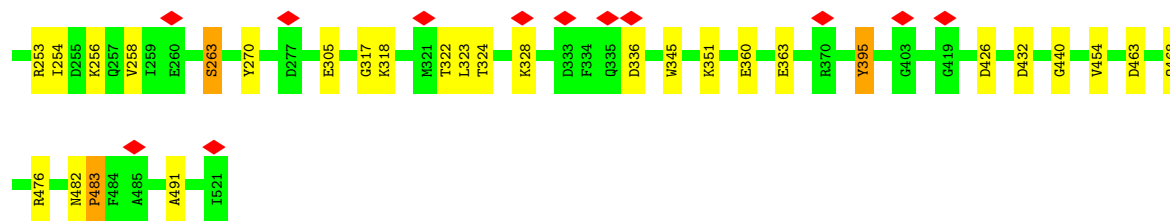


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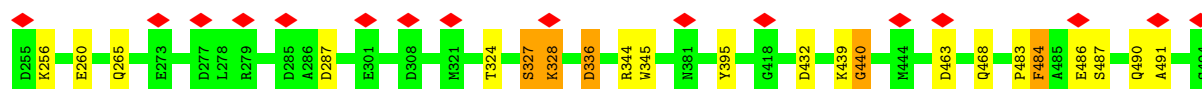
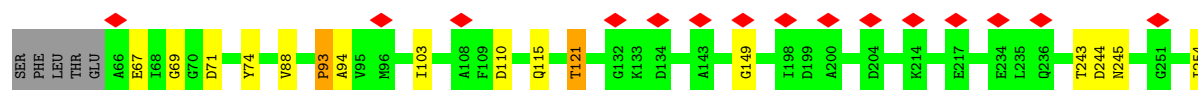
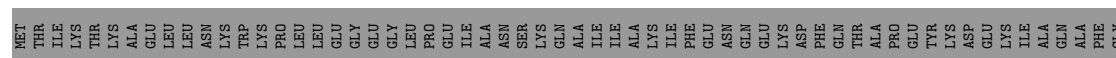
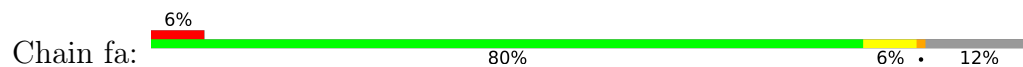


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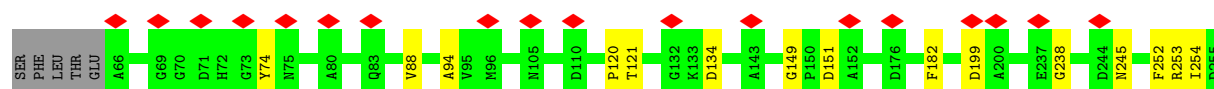
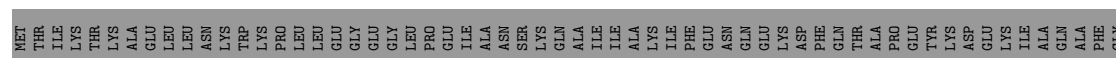
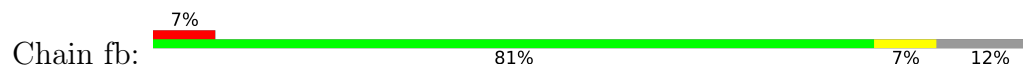




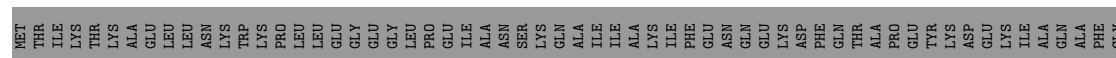
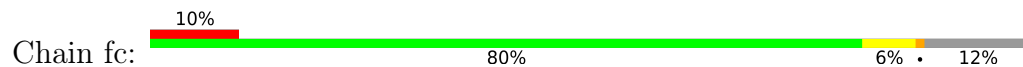
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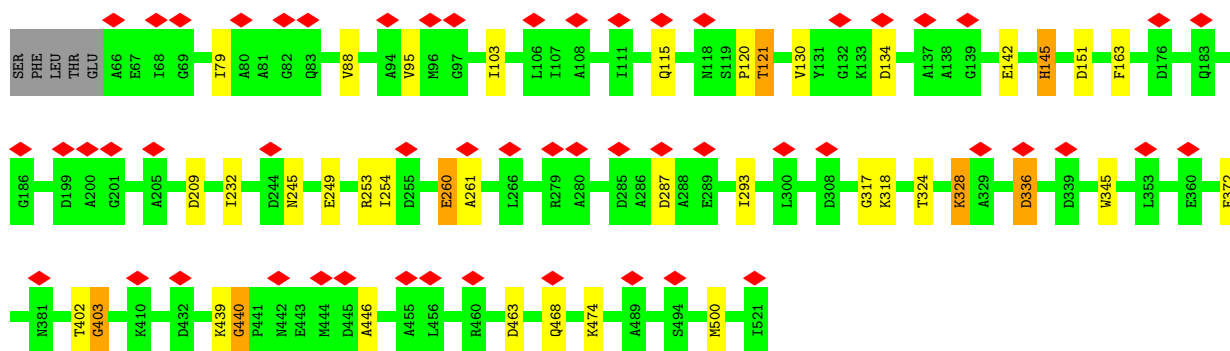


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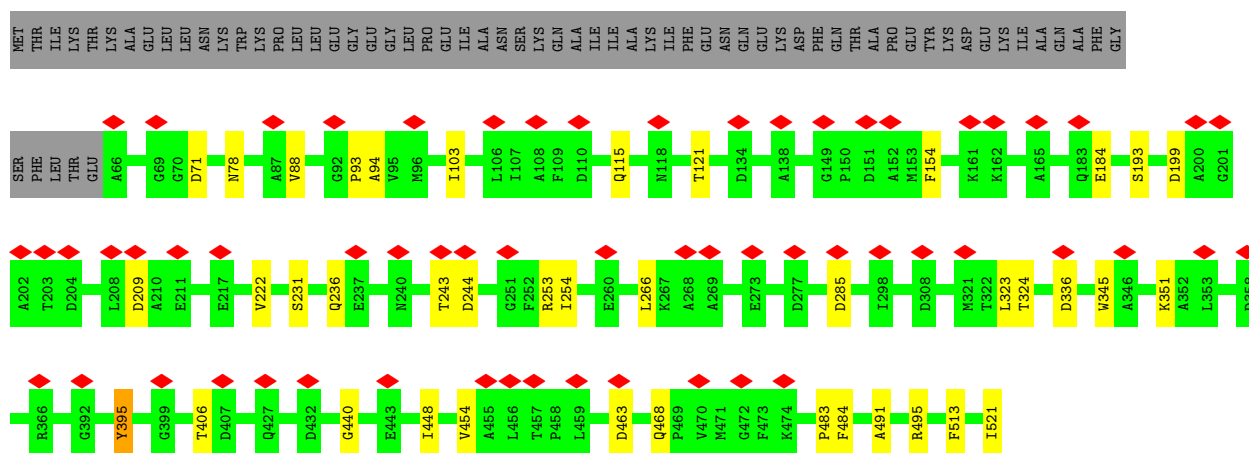
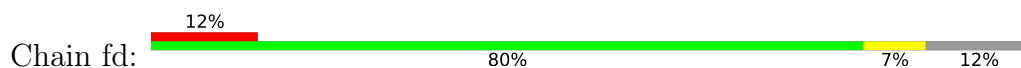


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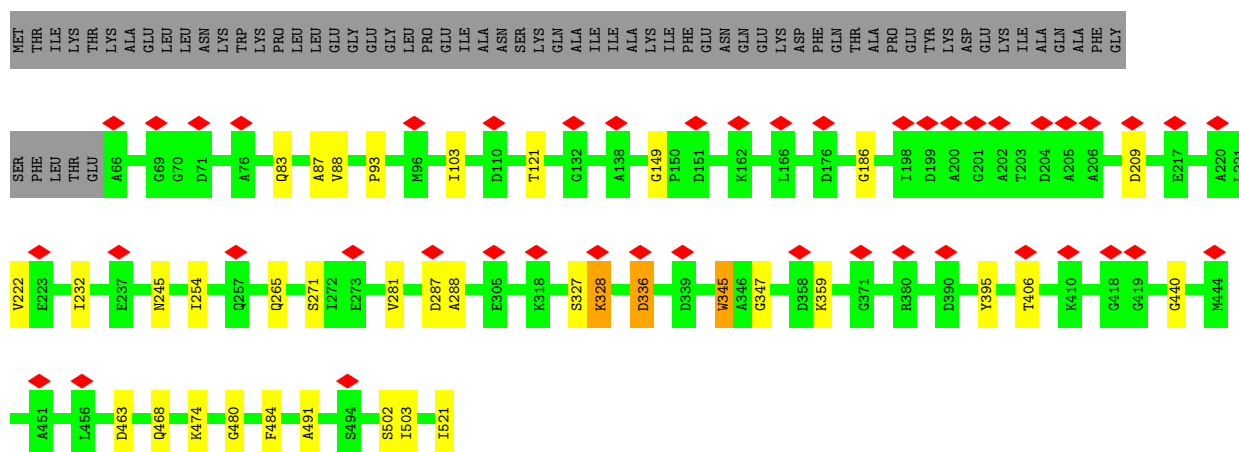
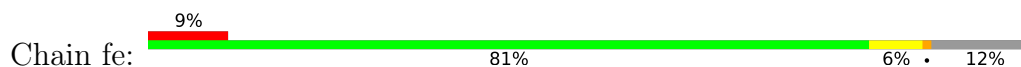




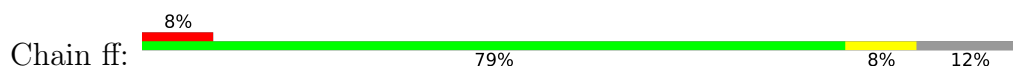
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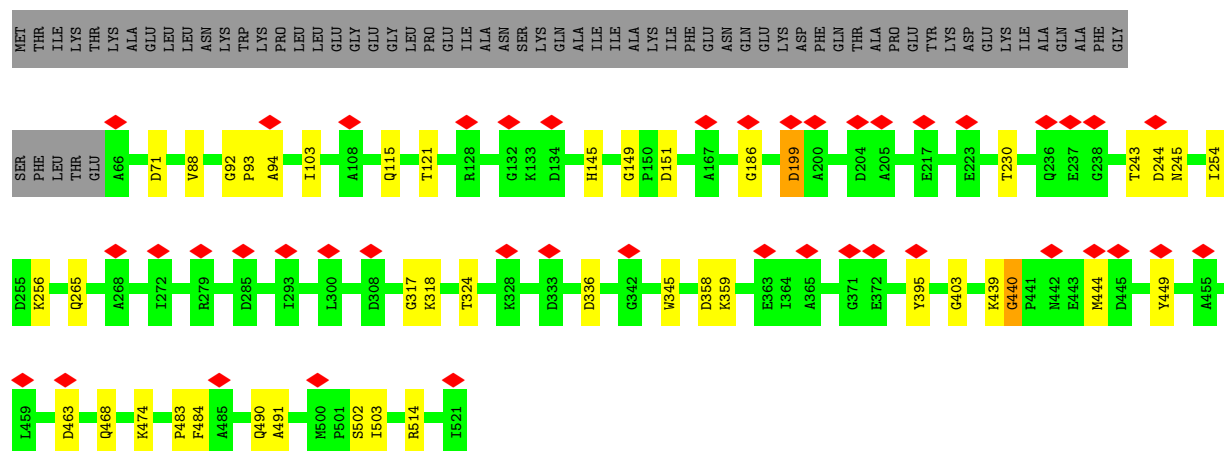


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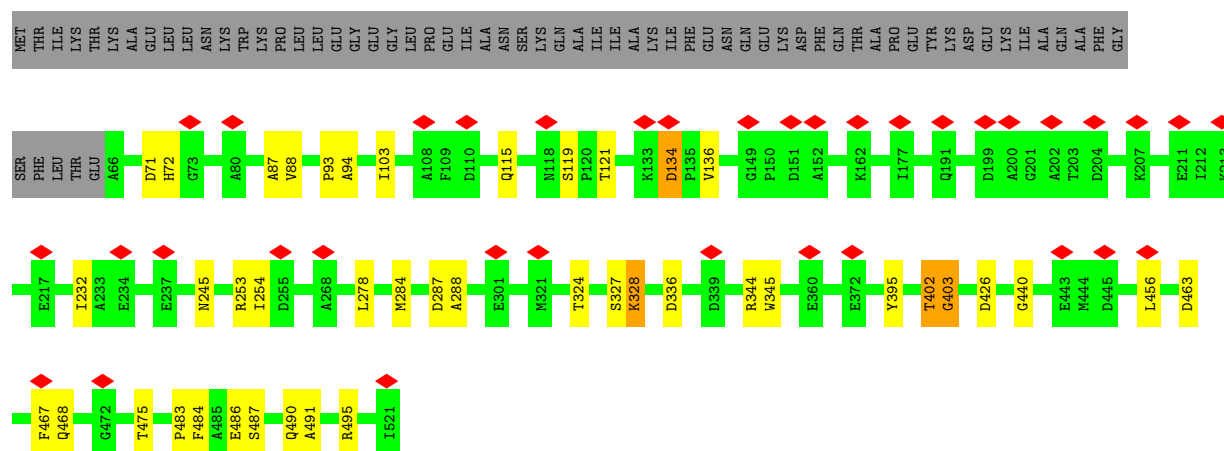
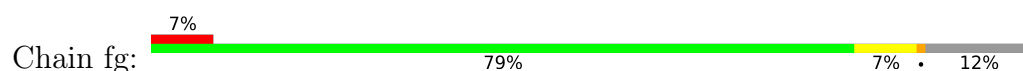


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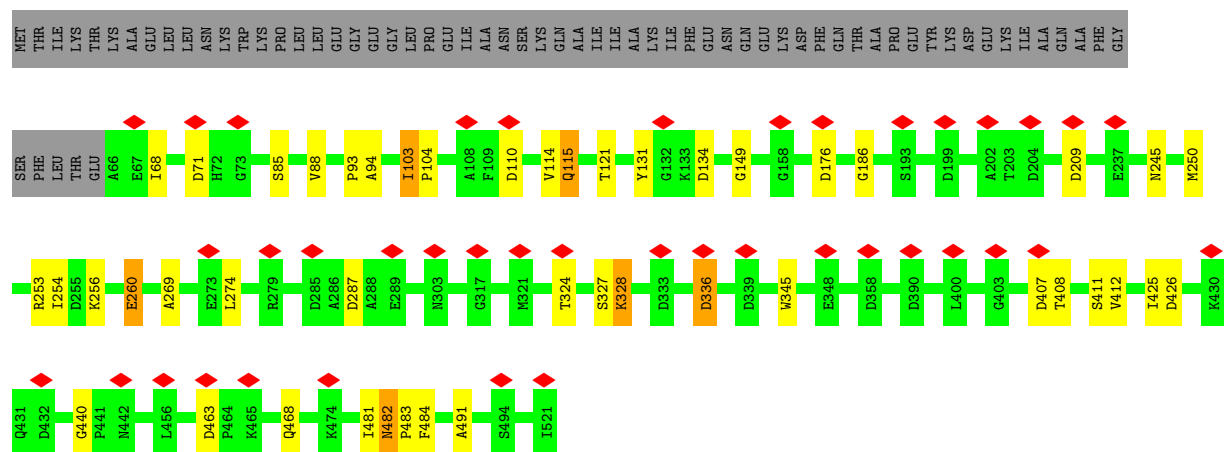
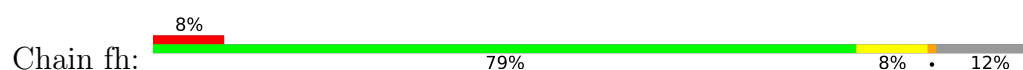




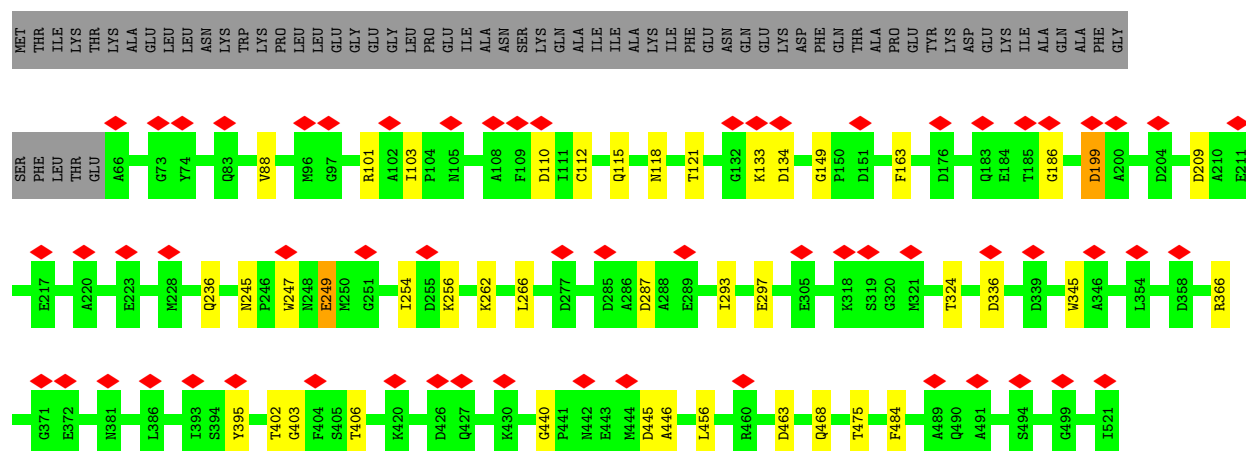
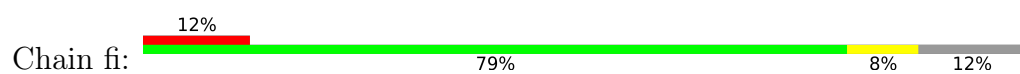
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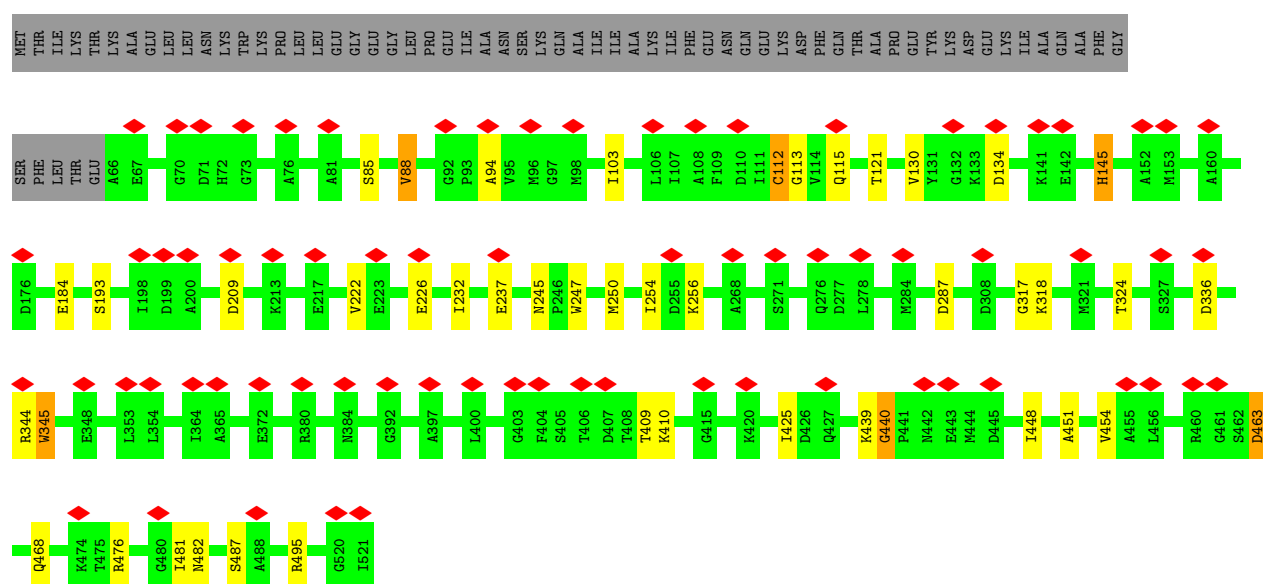
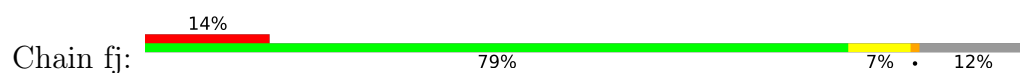
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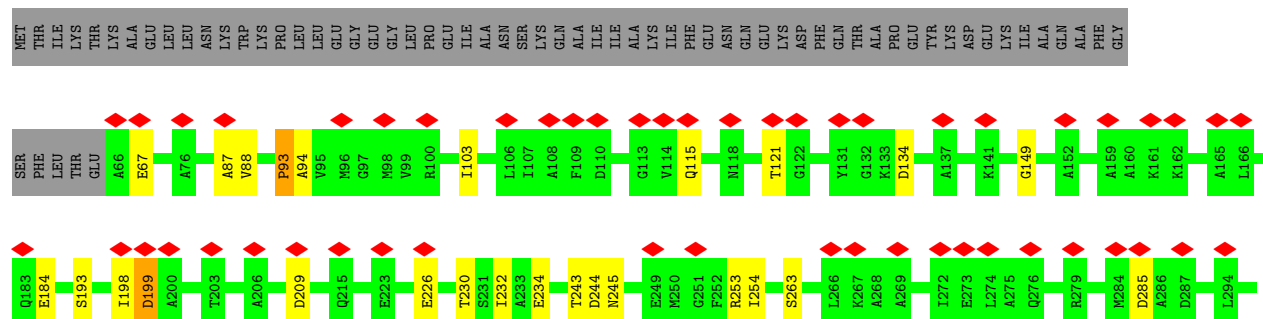
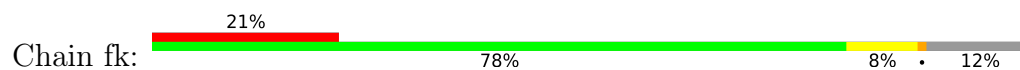
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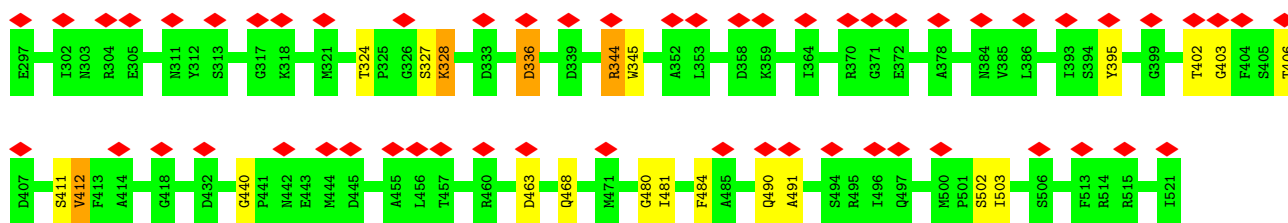


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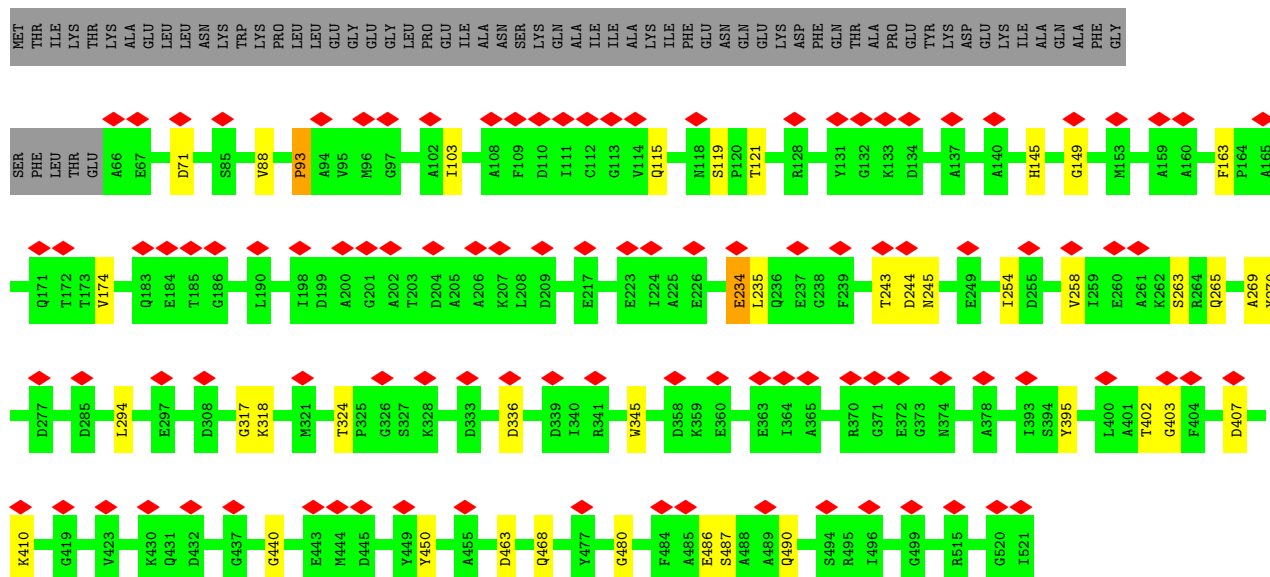
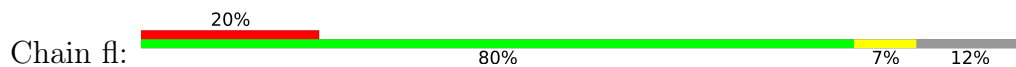


• Molecule 1: Major capsid protein

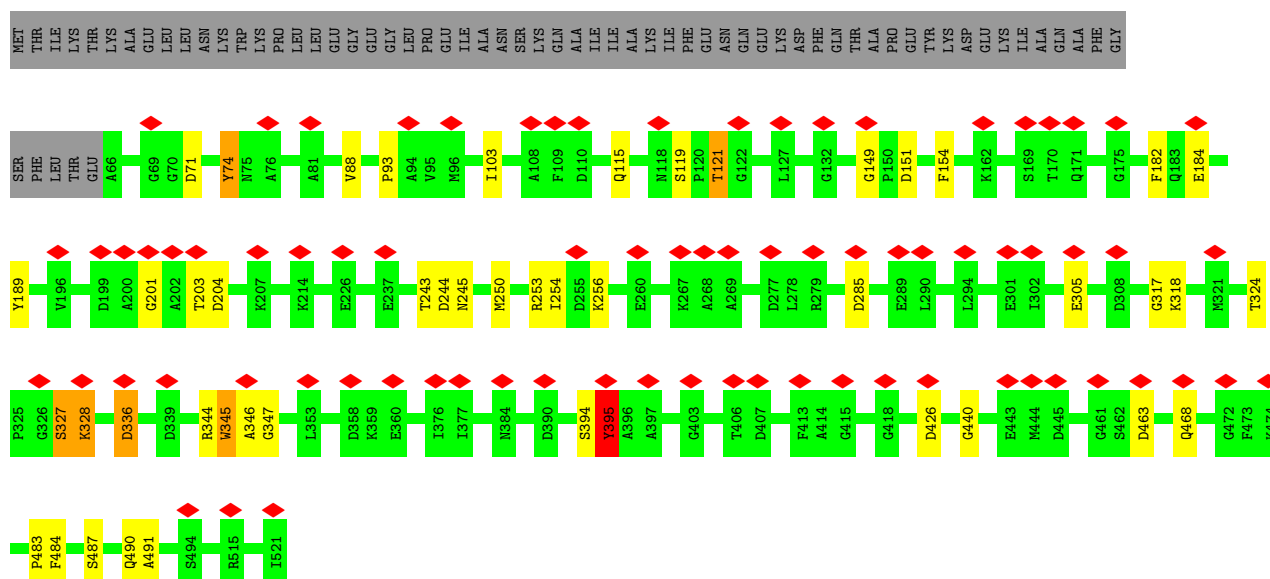
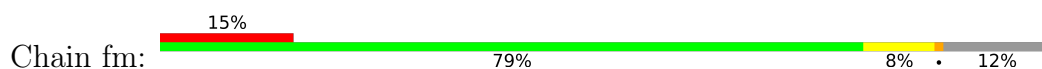




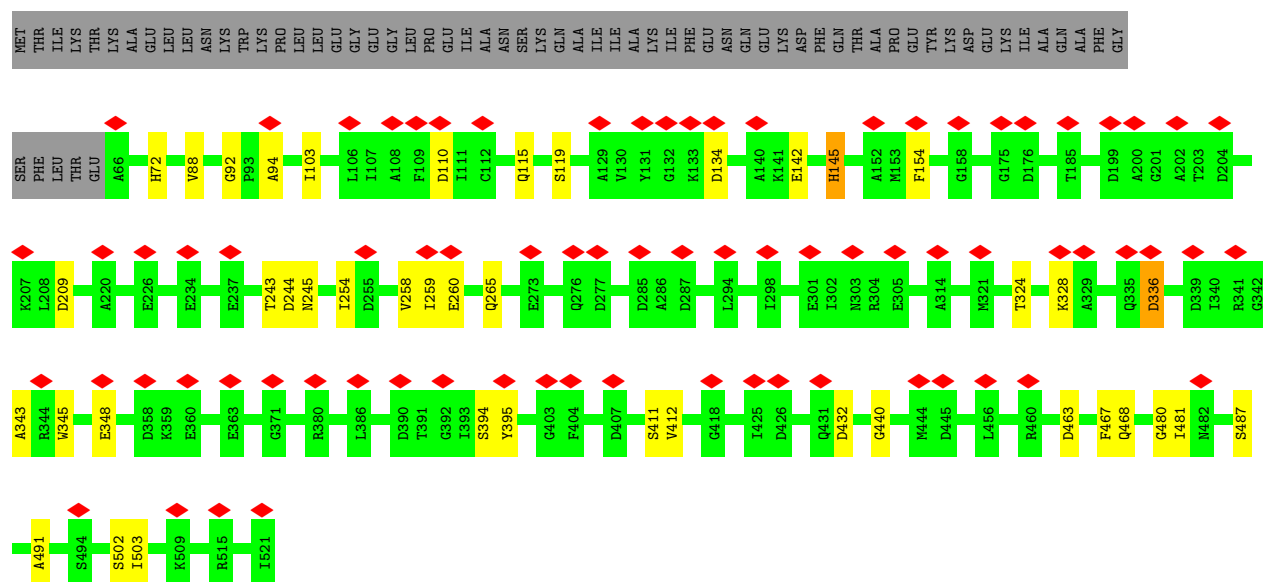
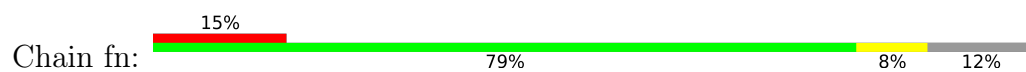
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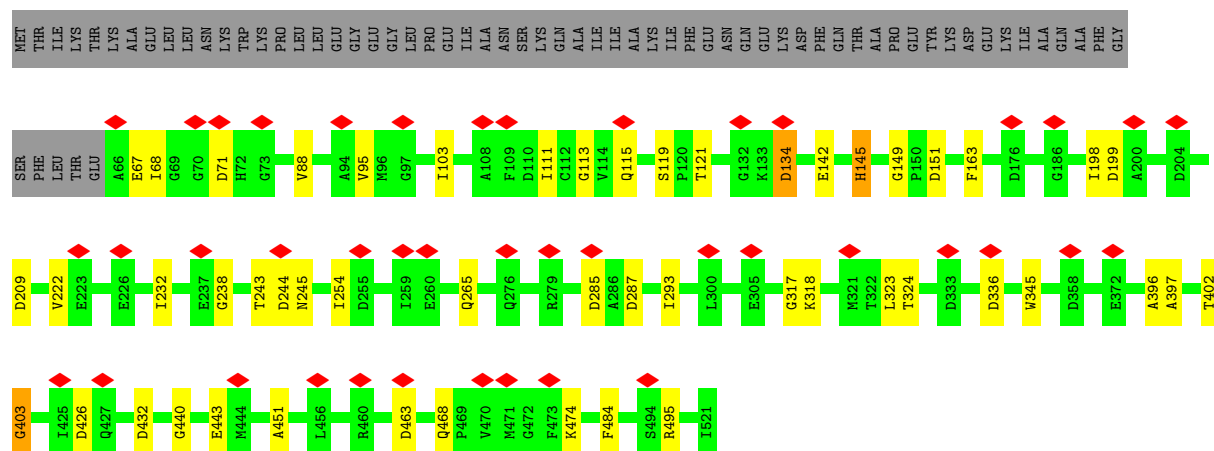
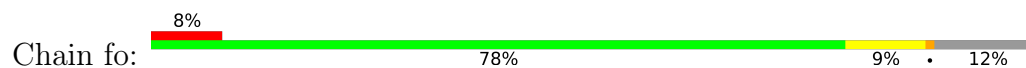
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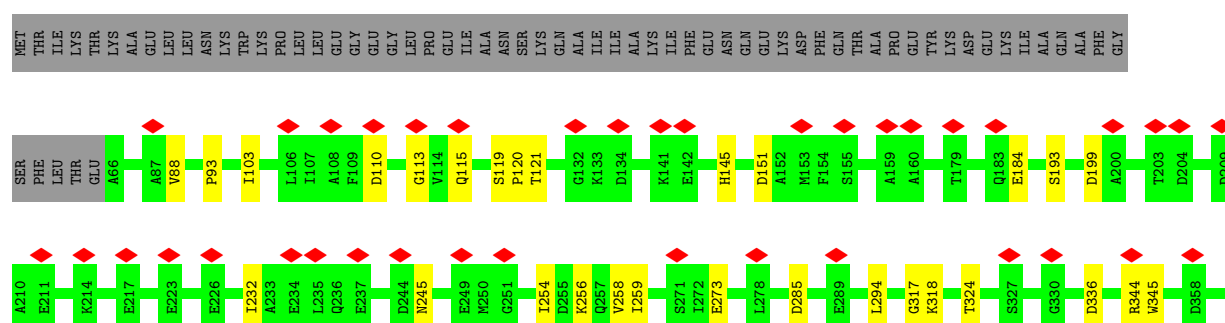
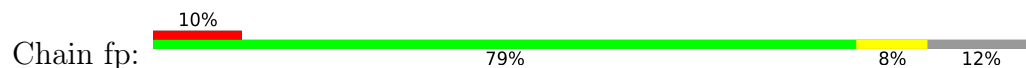
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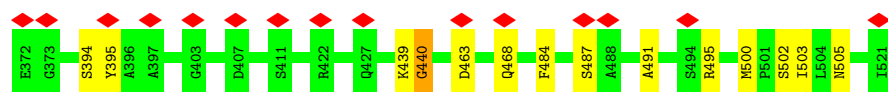


• Molecule 1: Major capsid protein

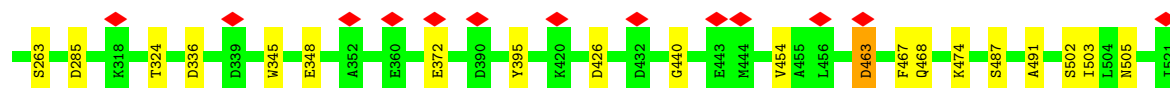
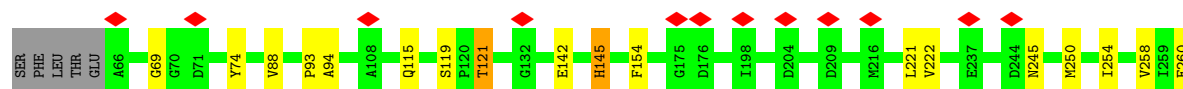
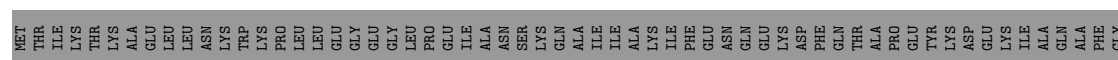
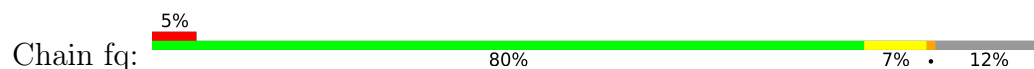


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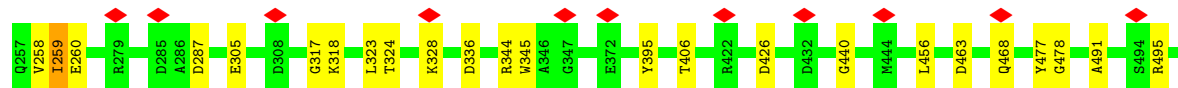
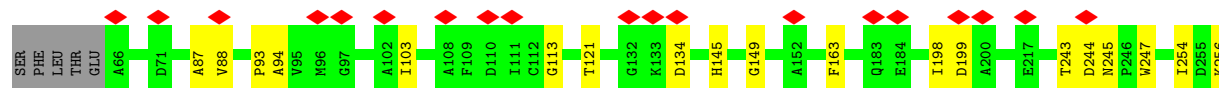
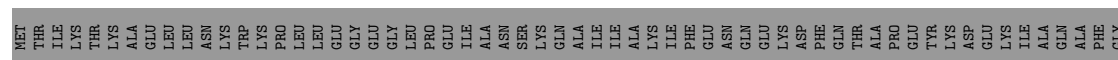
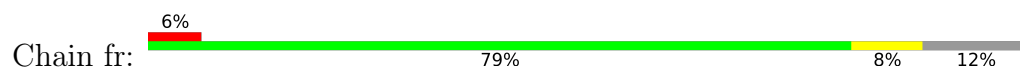




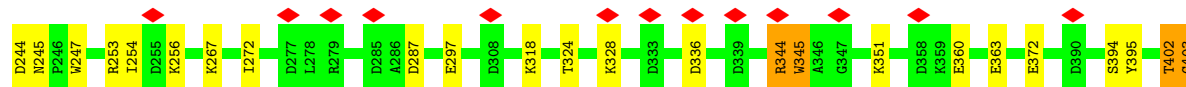
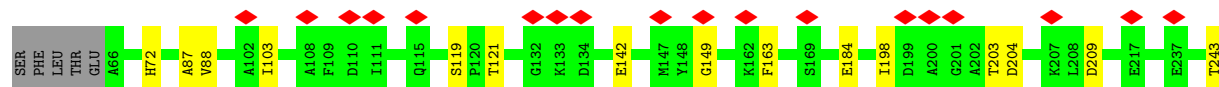
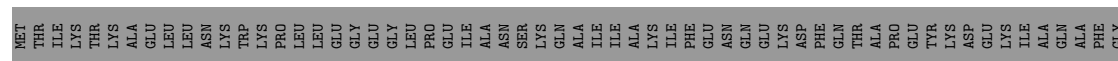
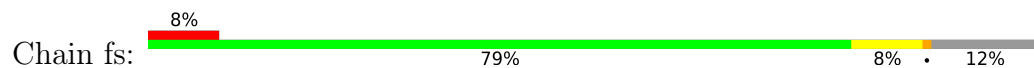
• Molecule 1: Major capsid protein

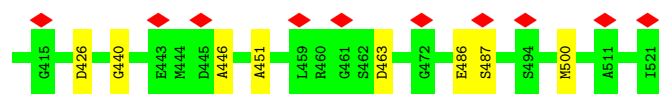


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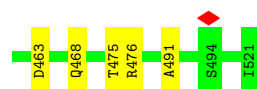
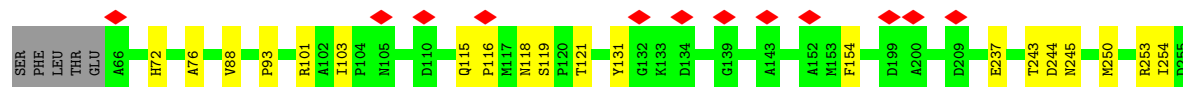
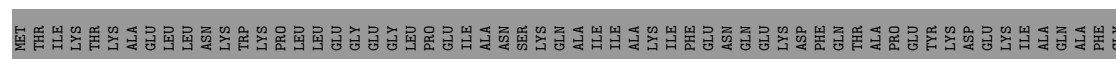
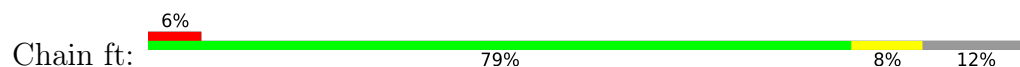


• Molecule 1: Major capsid protein

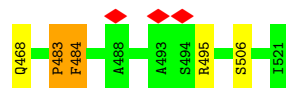
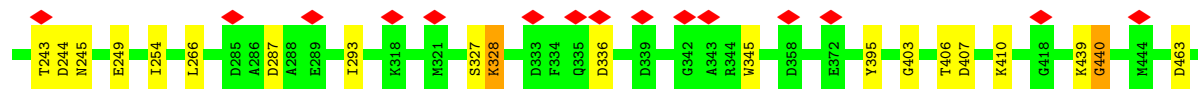
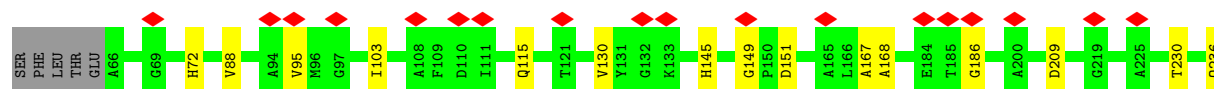
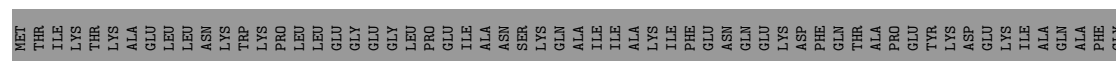
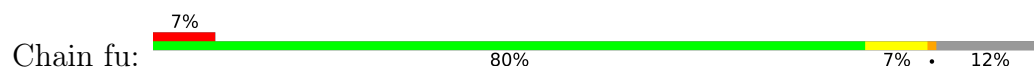




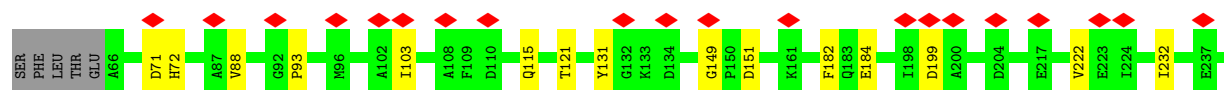
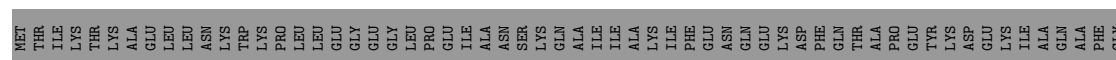
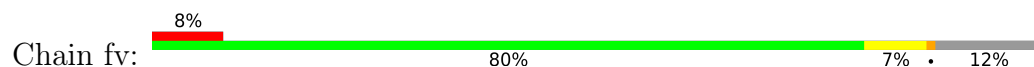
• Molecule 1: Major capsid protein

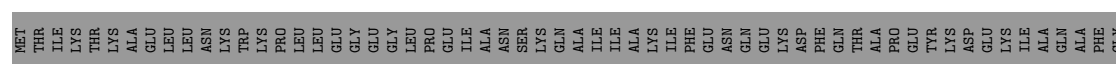


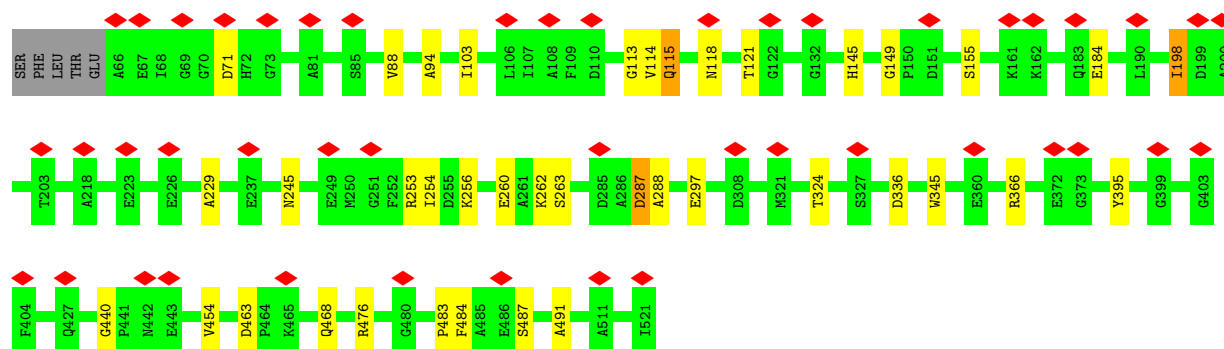
• Molecule 1: Major capsid protein



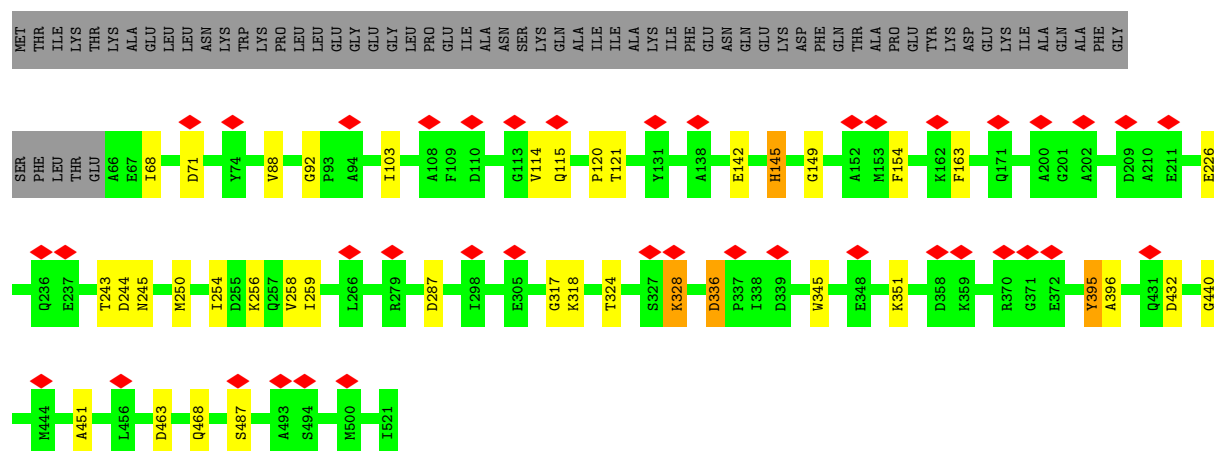
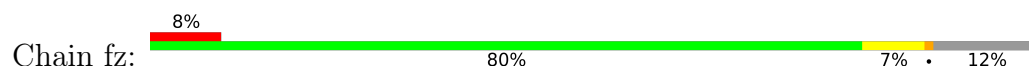
• Molecule 1: Major capsid protein



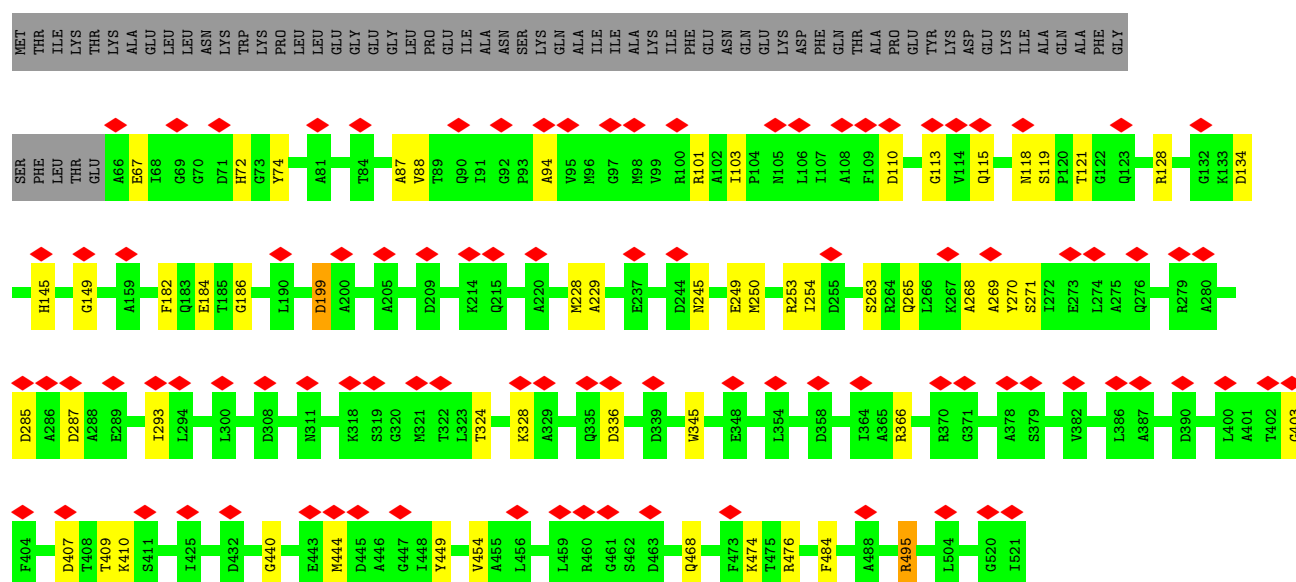
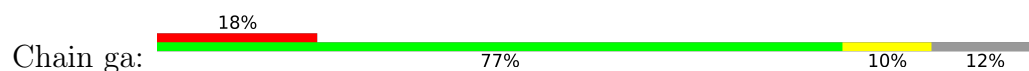




- Molecule 1: Major capsid protein

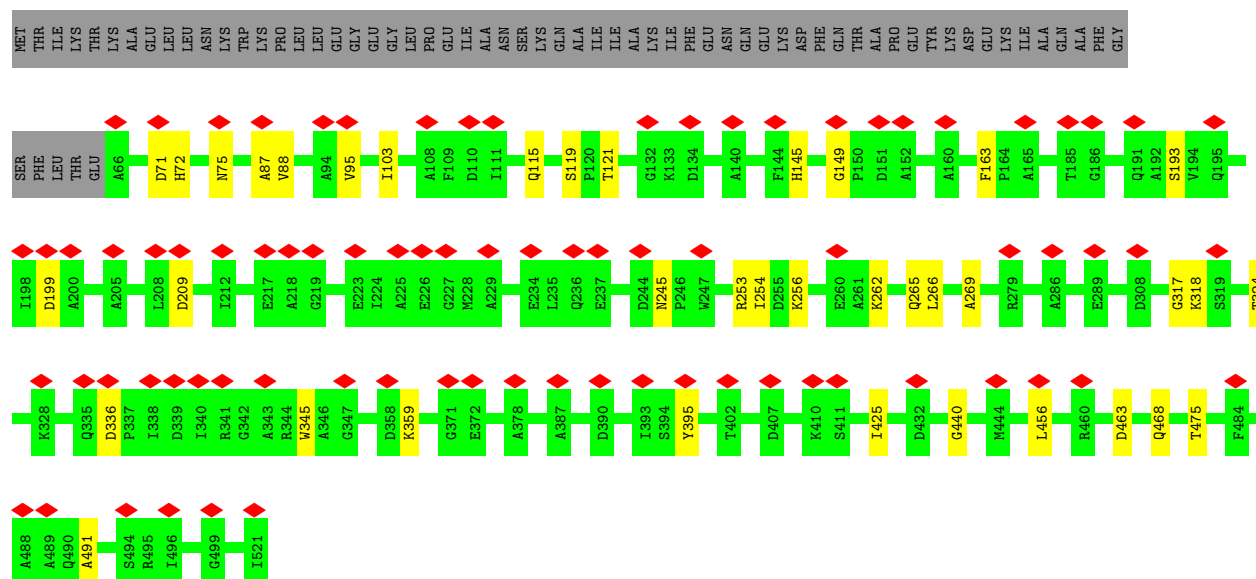
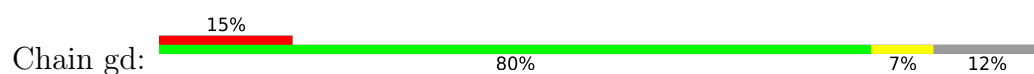


- Molecule 1: Major capsid protein

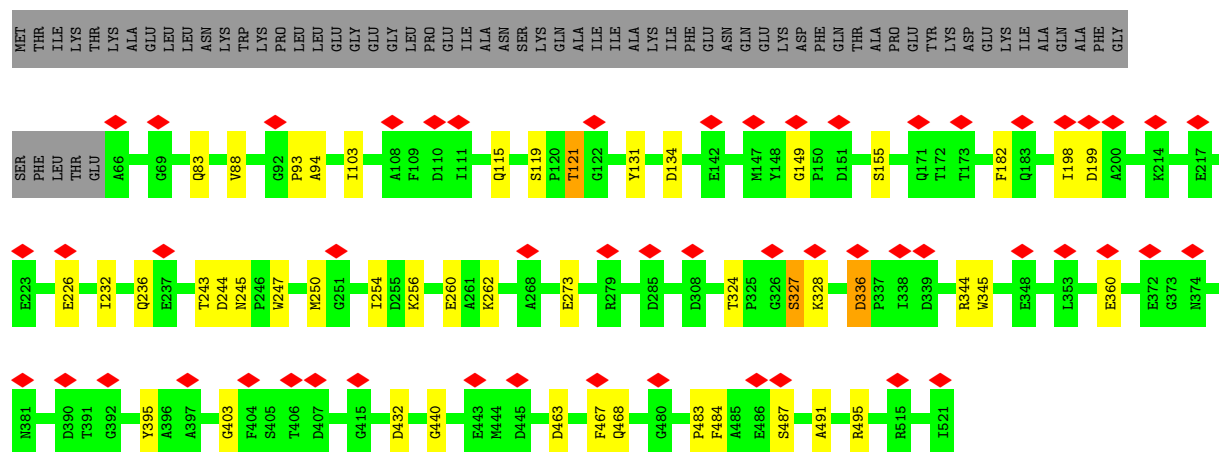
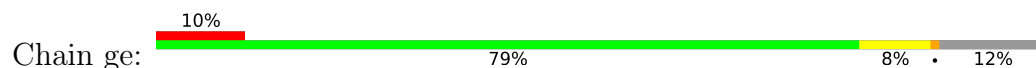


- Molecule 1: Major capsid protein

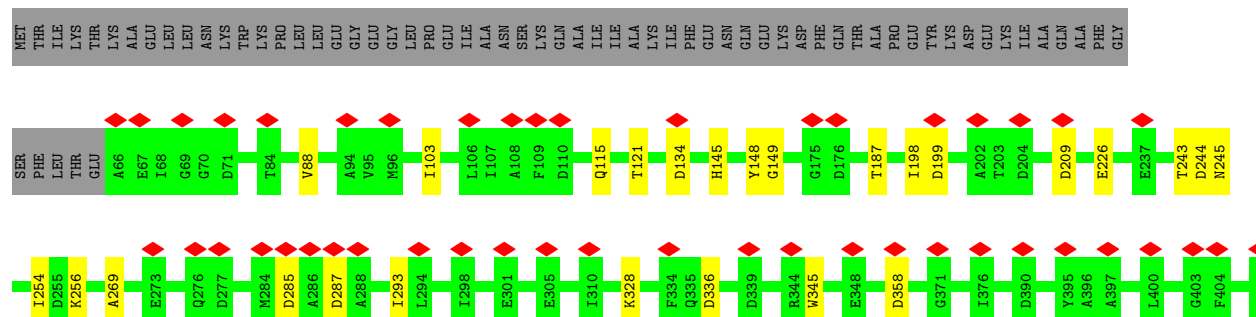
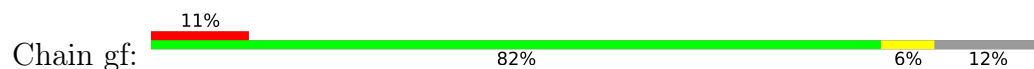


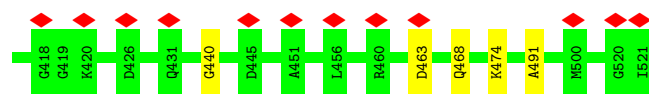


- Molecule 1: Major capsid protein

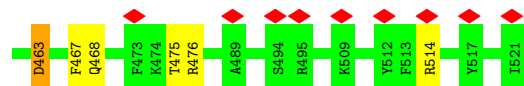
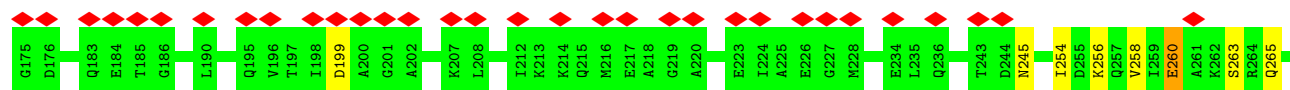
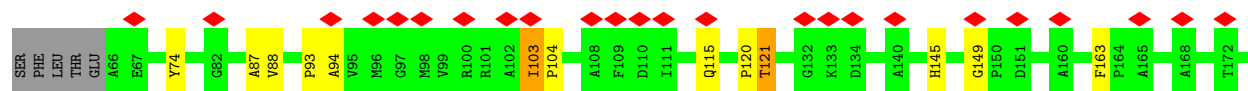
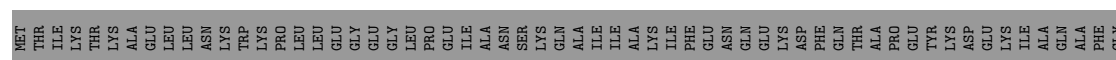
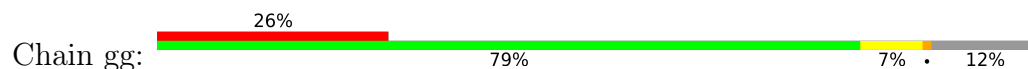


- Molecule 1: Major capsid protein

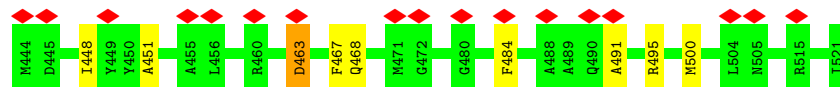
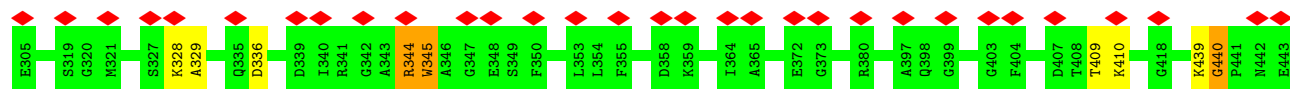
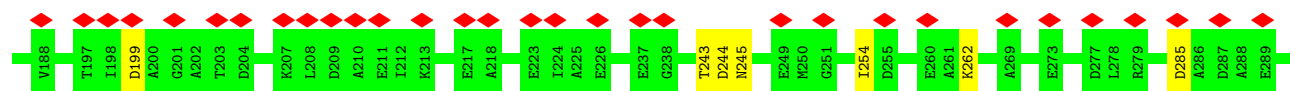
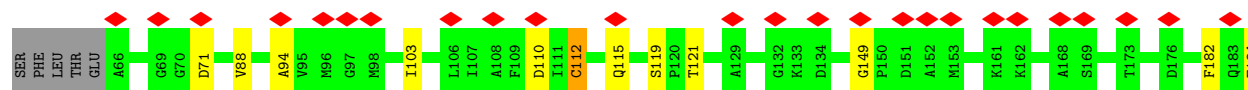
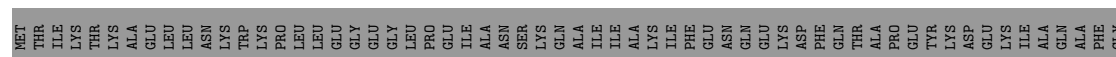
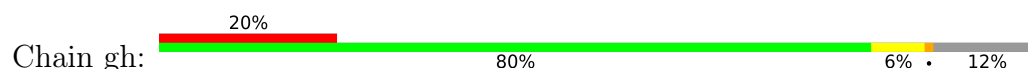




• Molecule 1: Major capsid protein

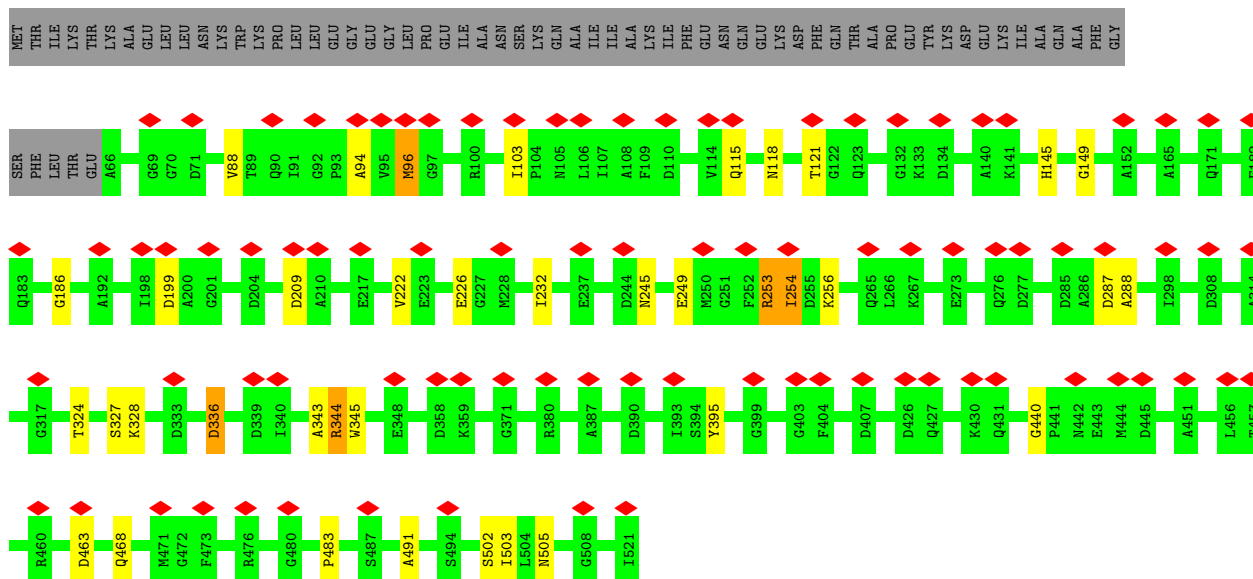


• Molecule 1: Major capsid protein



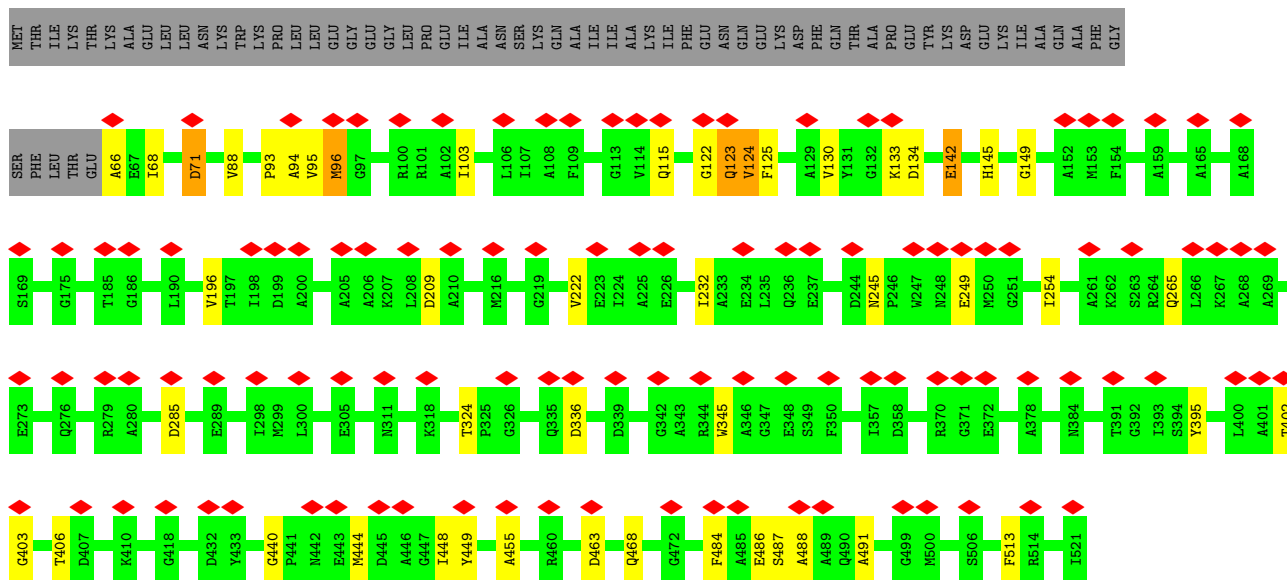
• Molecule 1: Major capsid protein

Chain gi: 



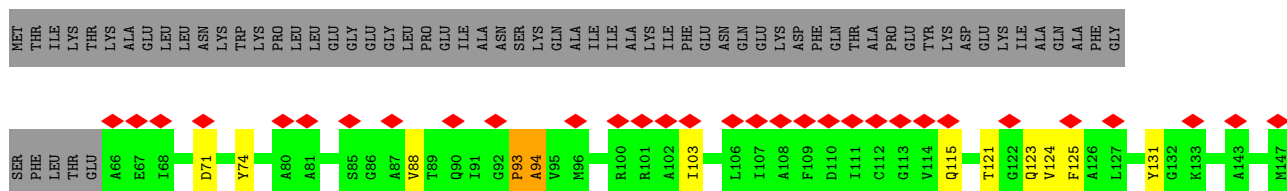
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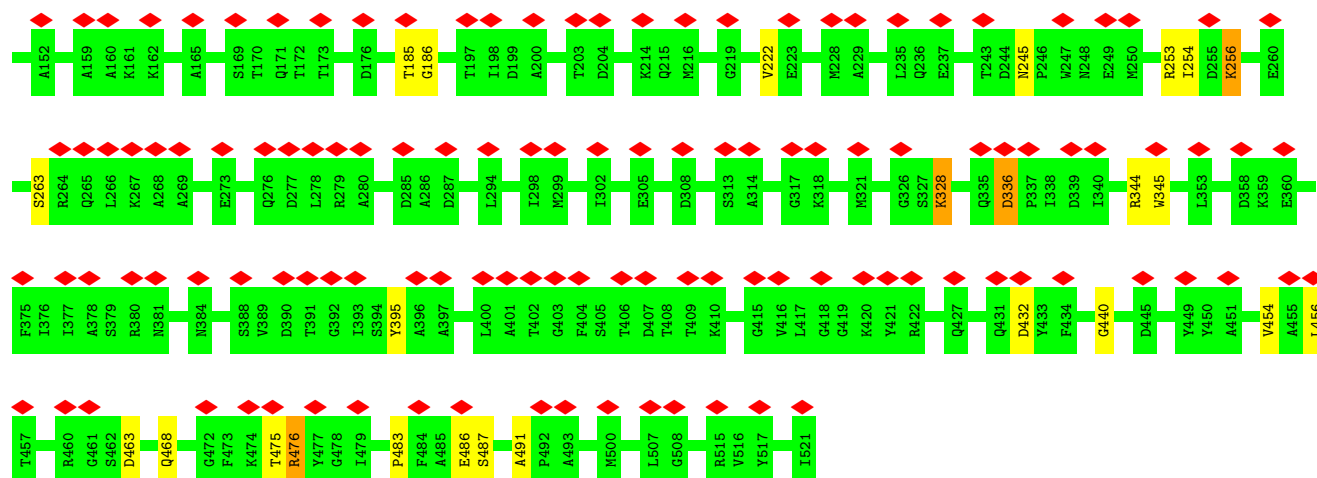
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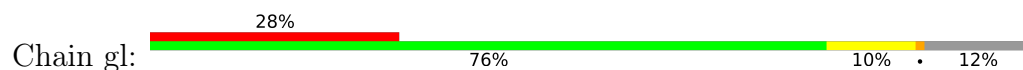
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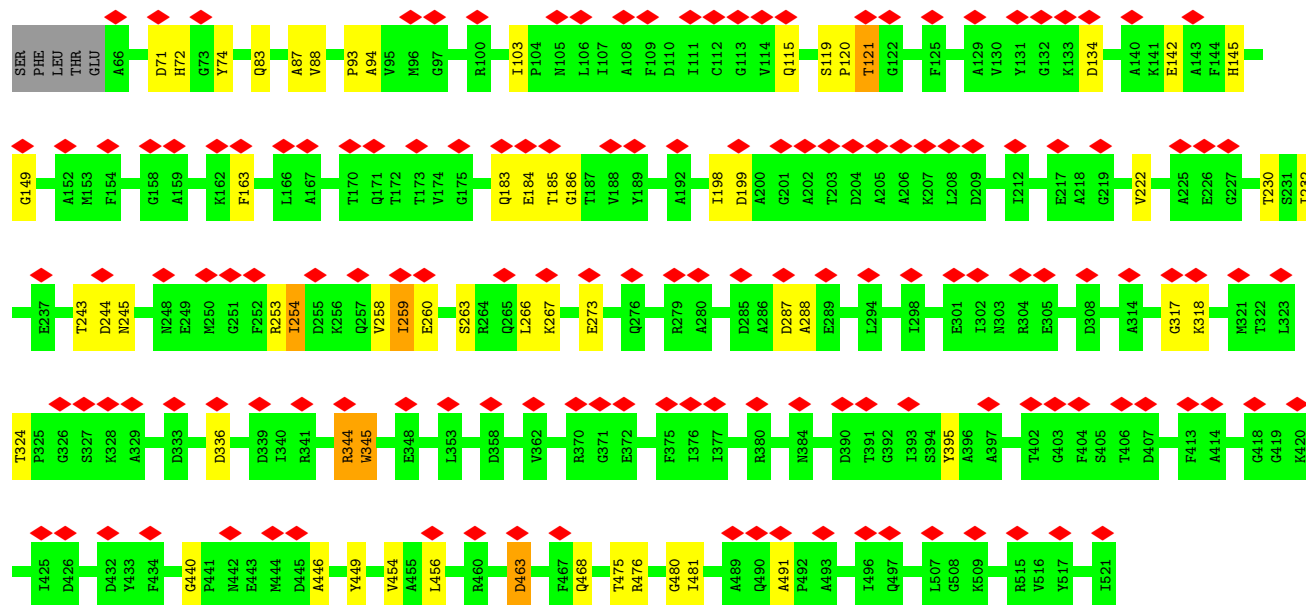




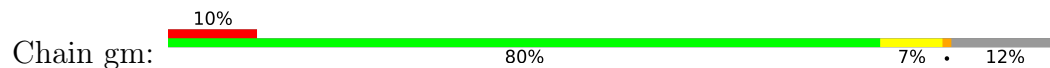
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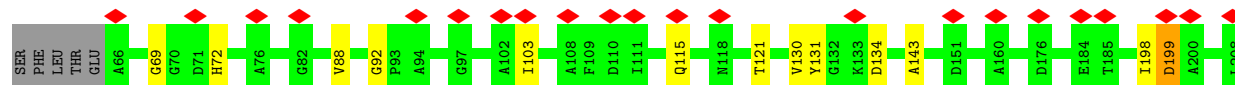
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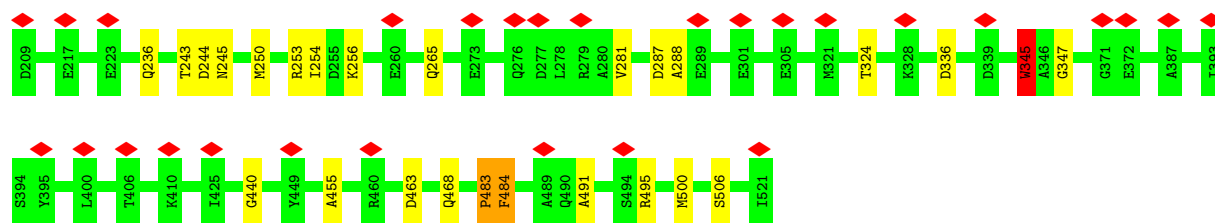


• Molecule 1: Major capsid protein

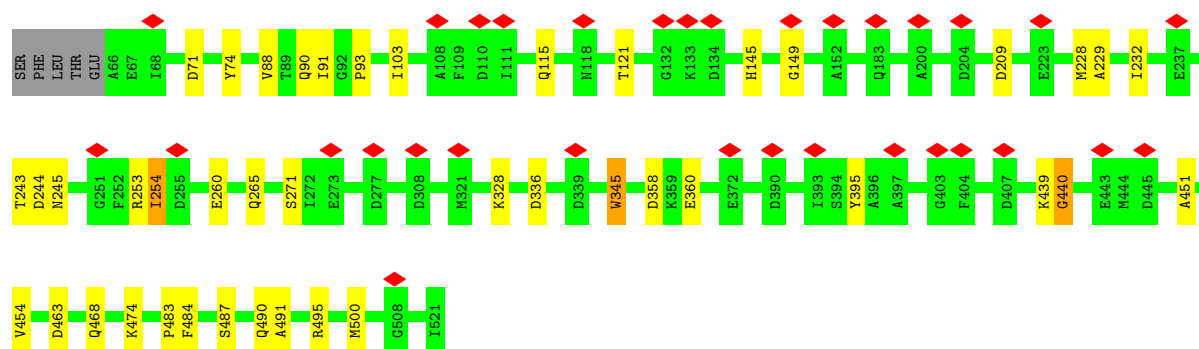
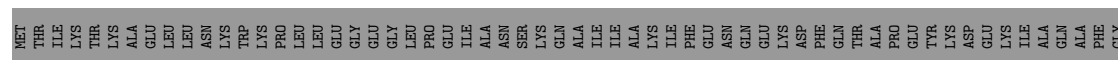
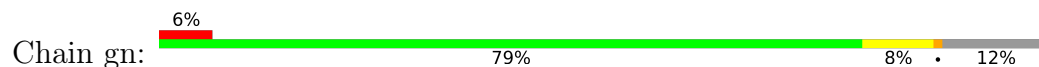


MET THR ILE LYS THR LYS ALA GLU LEU ASN TRP LYS PRO LEU LEU GLY GLY GLY PRO LEU ILE ALA ASN SER LYS GLN ALA ILE ILE ILE ALA ASP PHE GLN THR PRO GLU TYR LYS ASP GLU LYS ILE ALA GLN PHE GLY

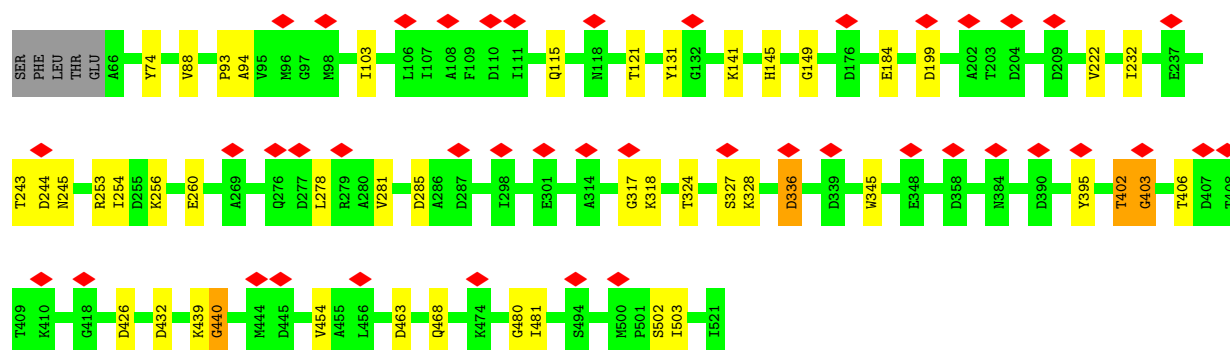
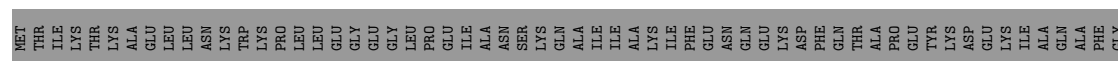
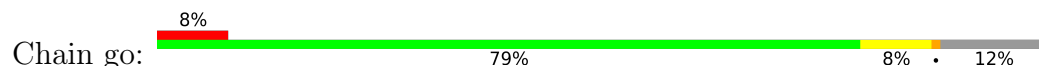




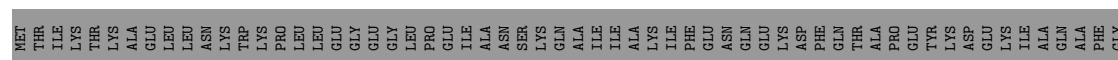
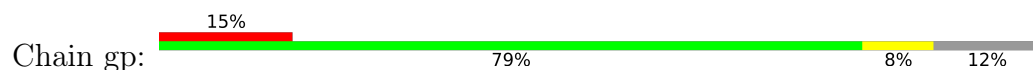
• Molecule 1: Major capsid protein

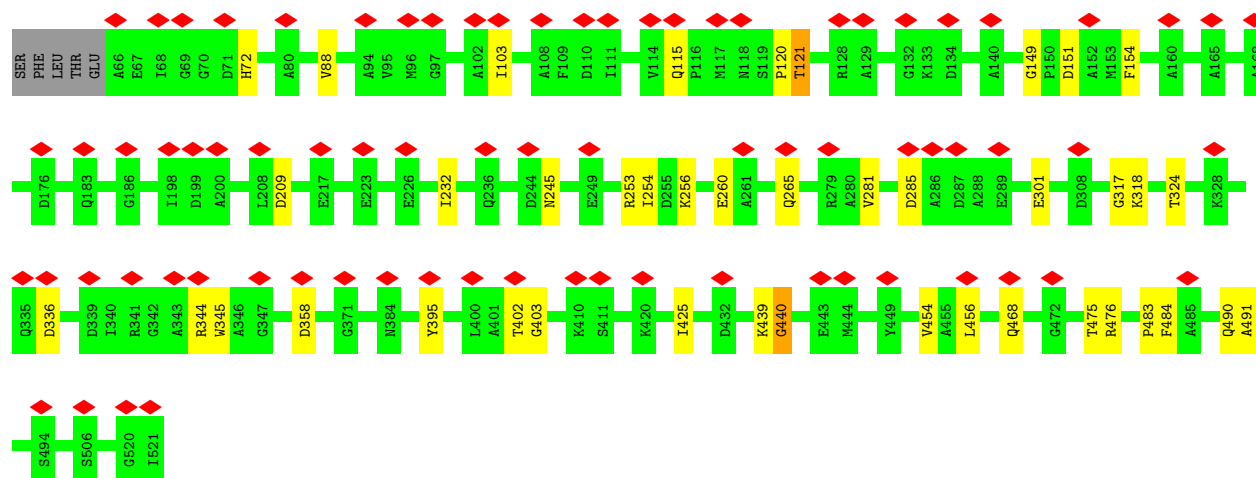


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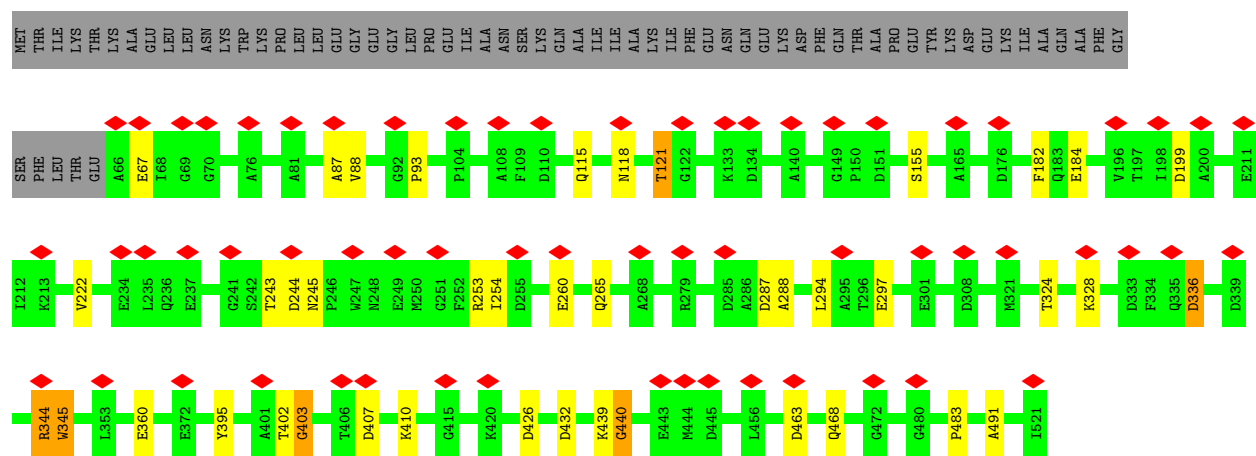
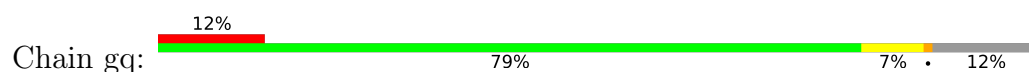


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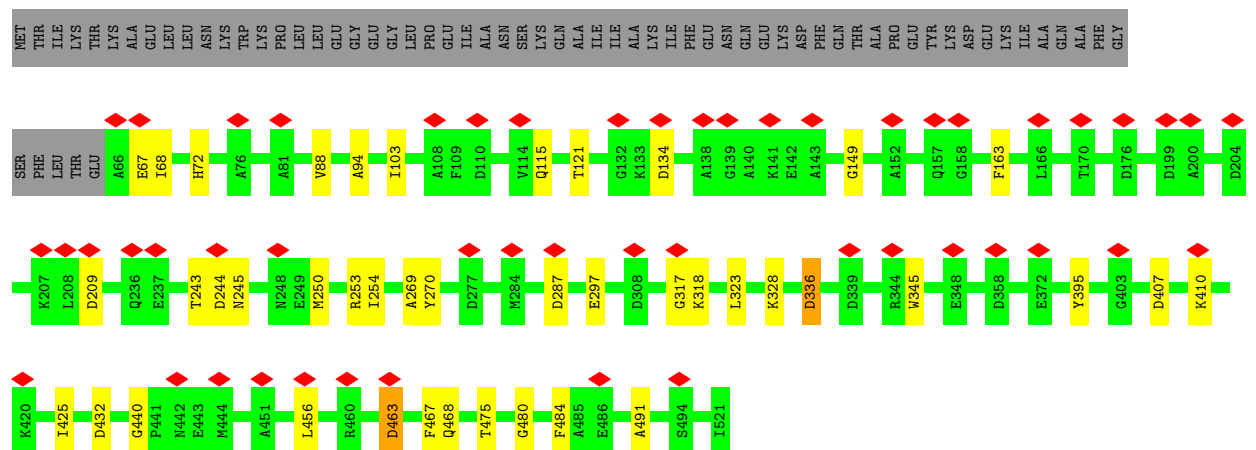
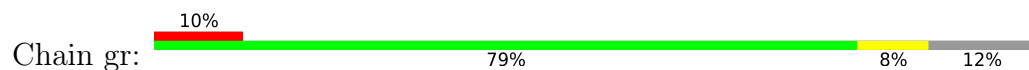




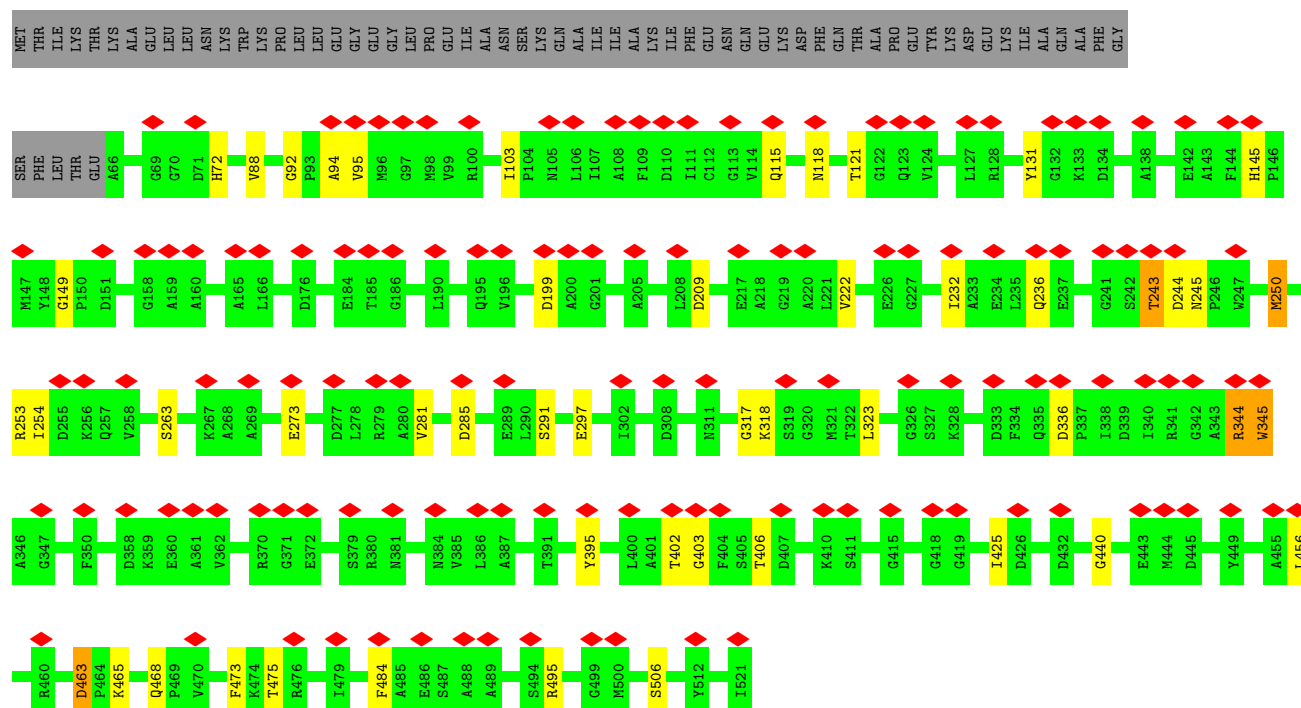
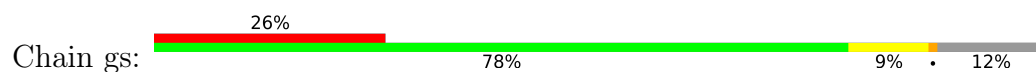
- Molecule 1: Major capsid protein



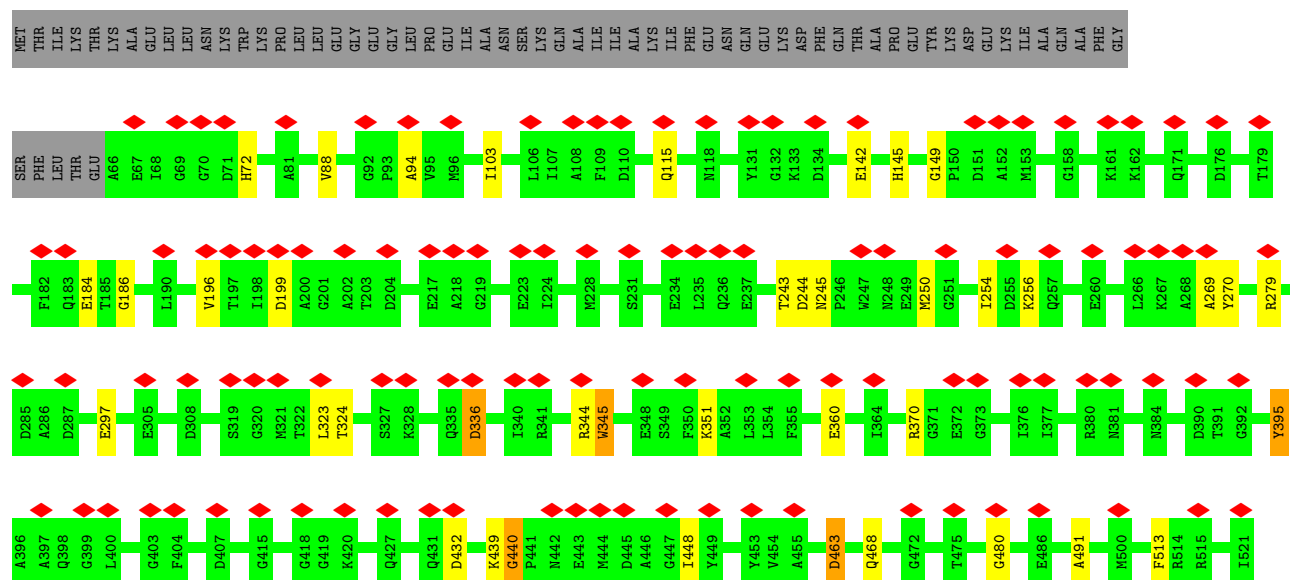
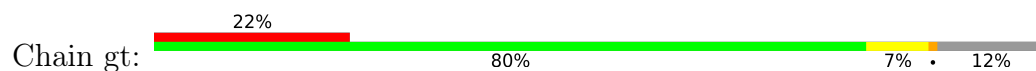
- Molecule 1: Major capsid protein



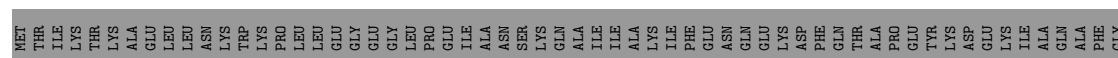
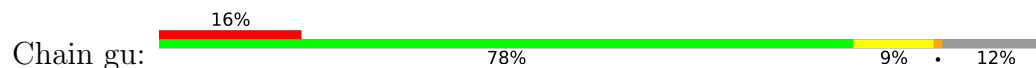
- Molecule 1: Major capsid protein

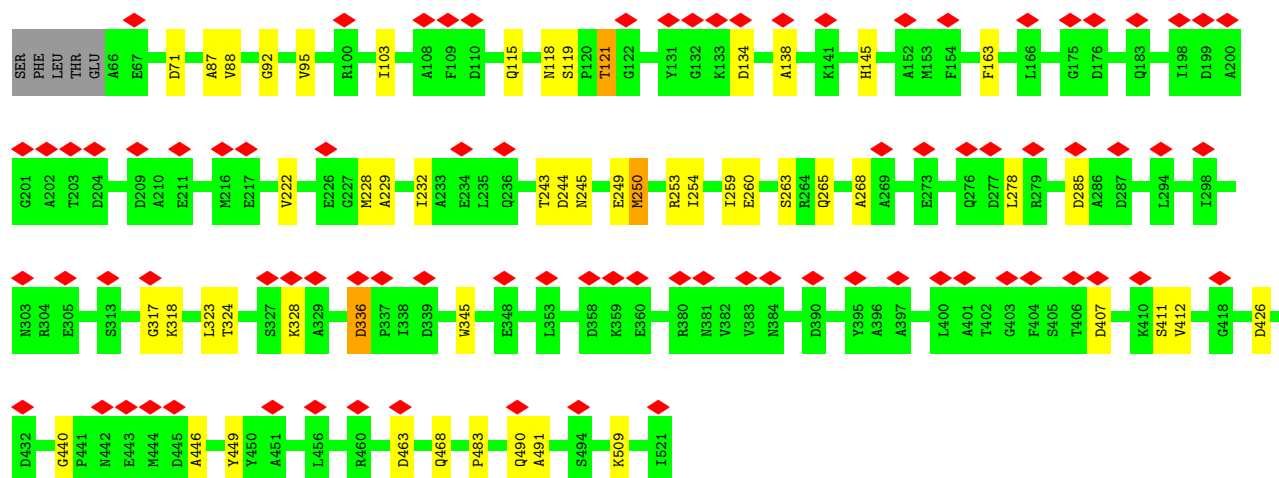


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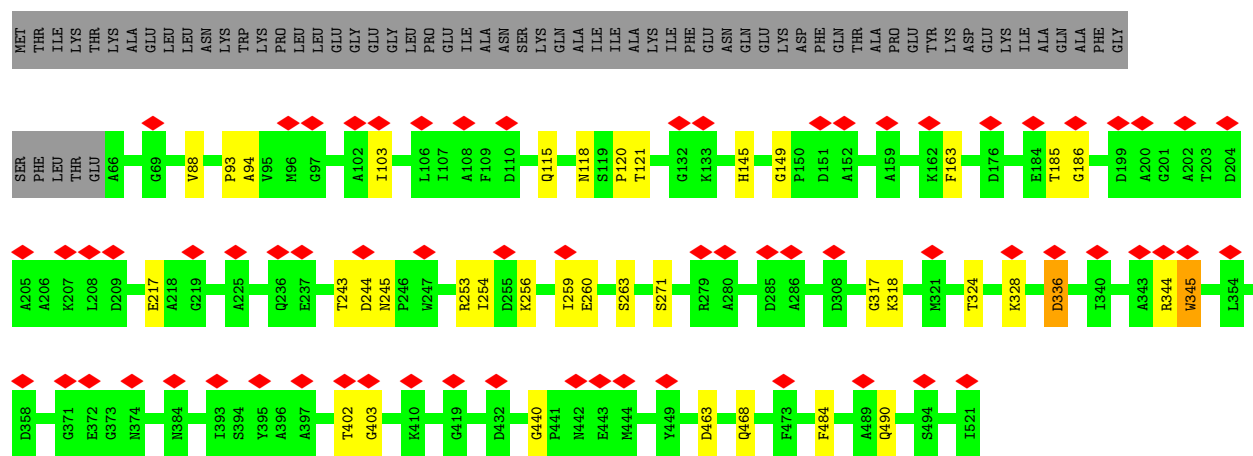
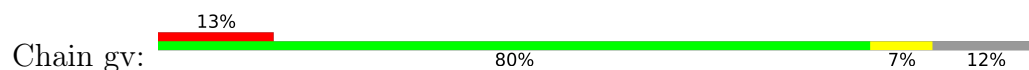


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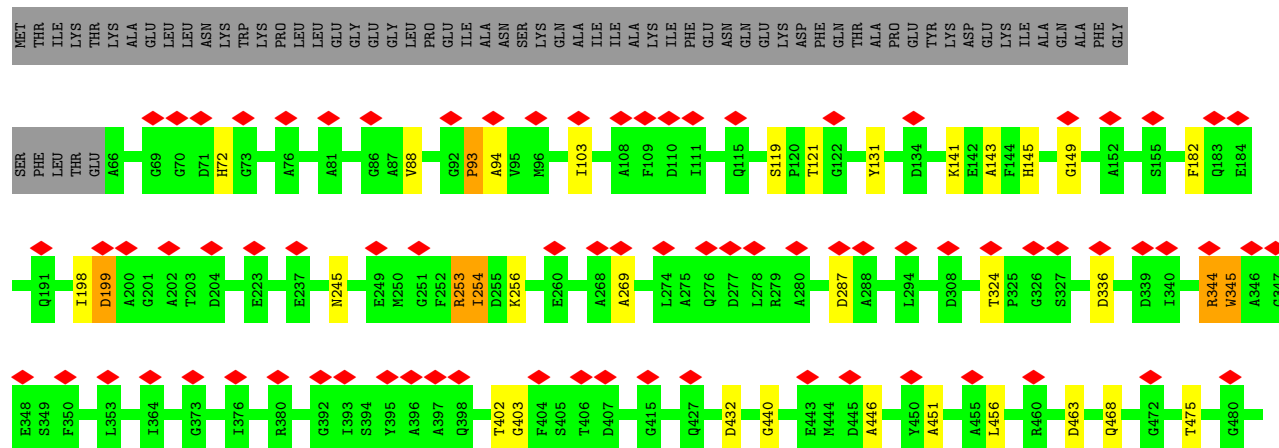
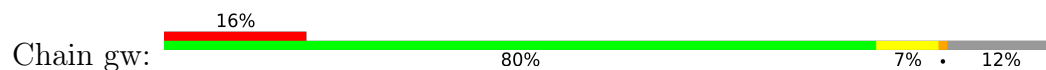


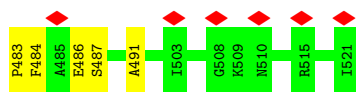


• Molecule 1: Major capsid protein



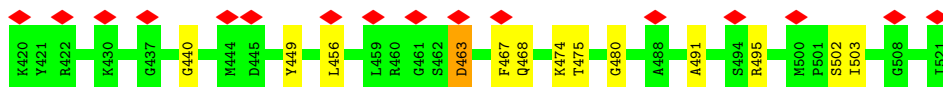
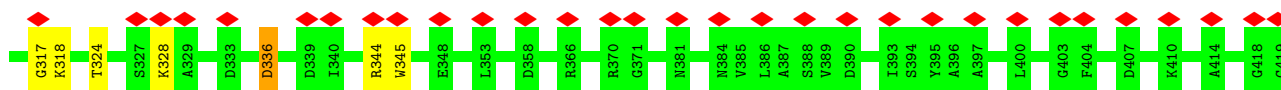
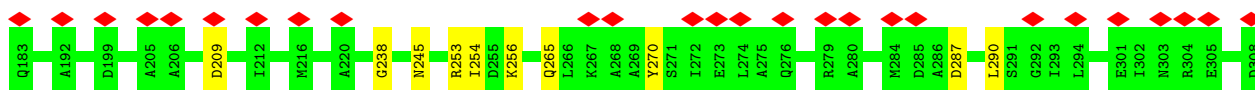
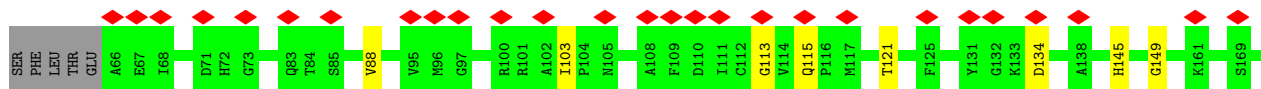
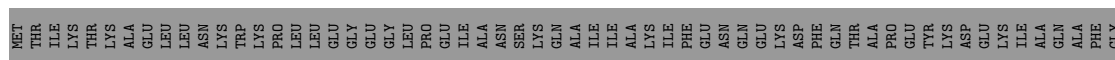
• Molecule 1: Major capsid protein





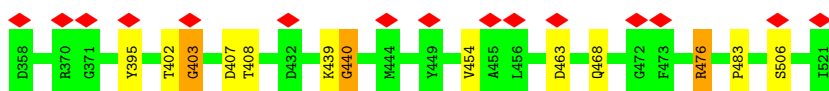
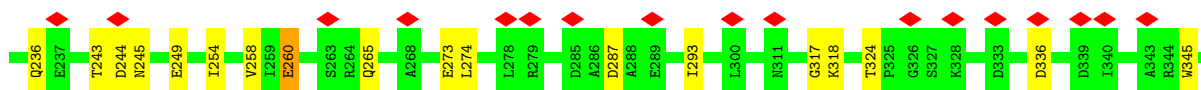
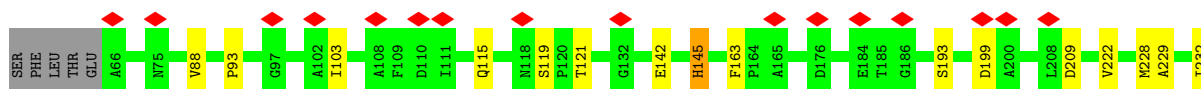
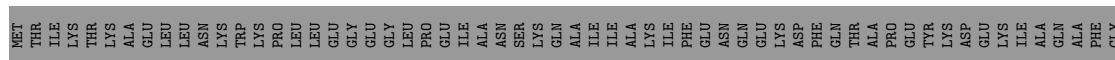
- Molecule 1: Major capsid protein

Chain gx:
19% 80% 7% 12%



- Molecule 1: Major capsid protein

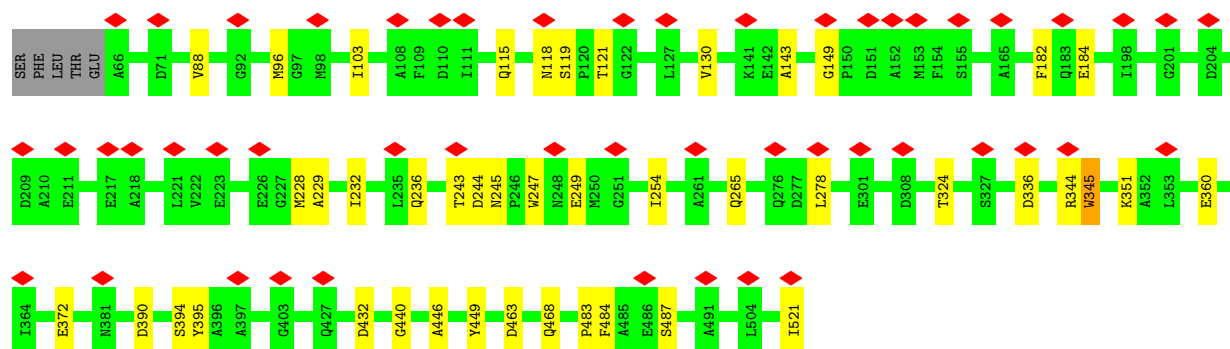
Chain gy:
9% 79% 8% 12%



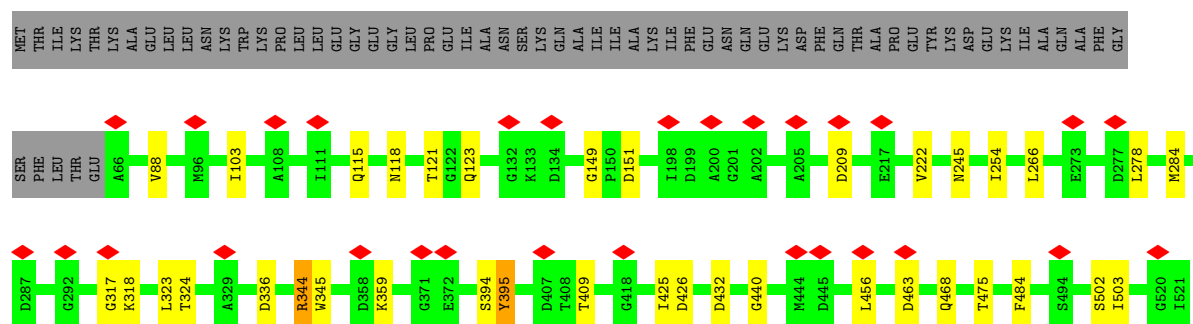
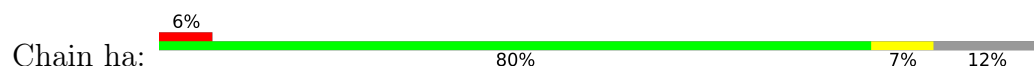
- Molecule 1: Major capsid protein

Chain gz:
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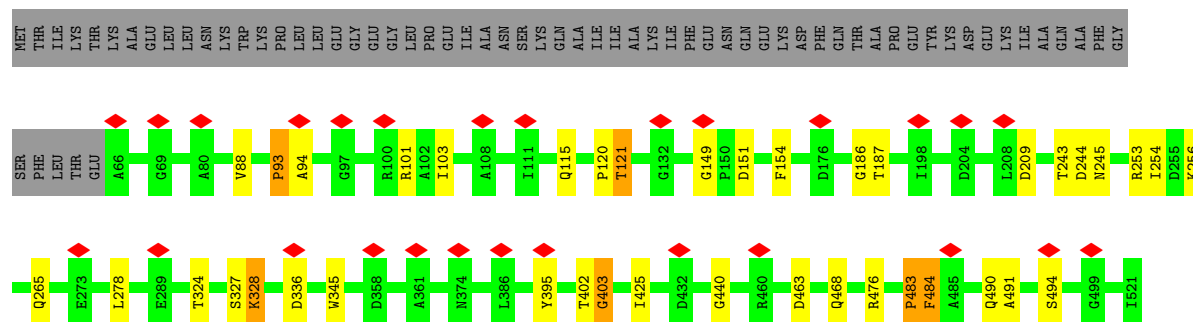
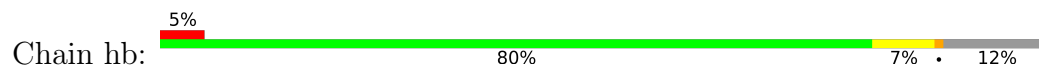




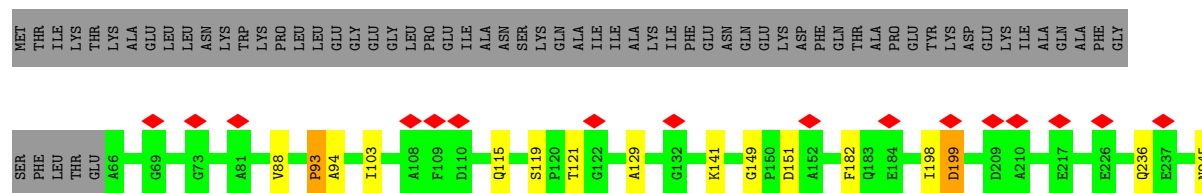
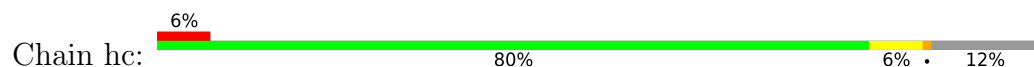
• Molecule 1: Major capsid protein

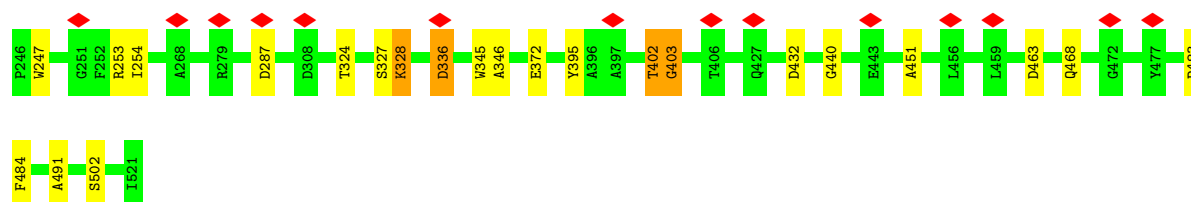


• Molecule 1: Major capsid protein

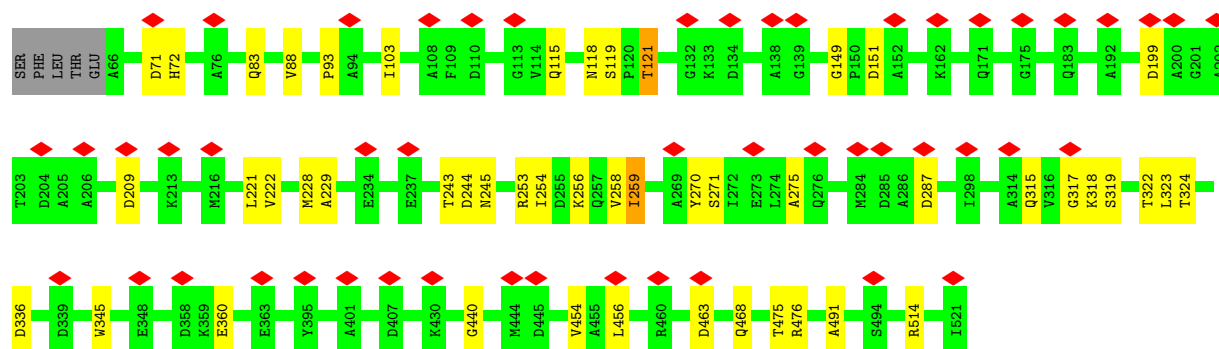
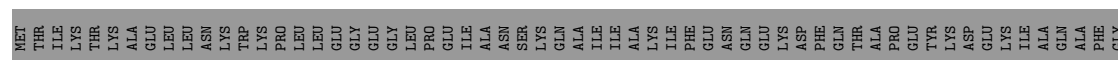
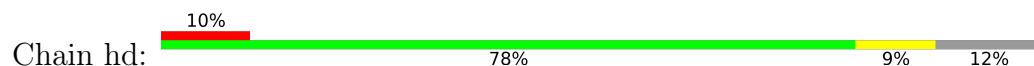


• Molecule 1: Major capsid protein

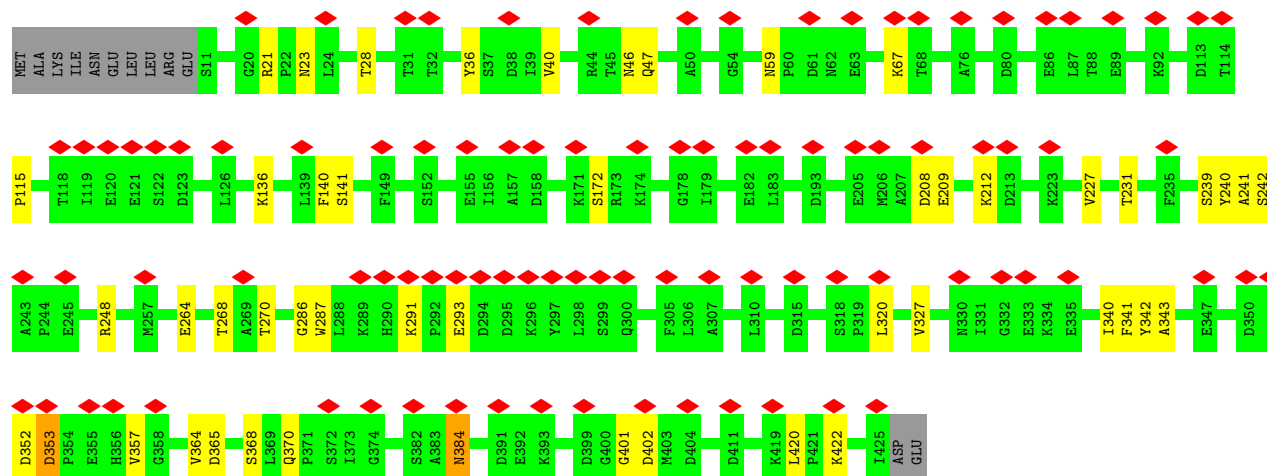
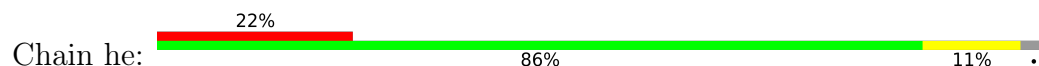




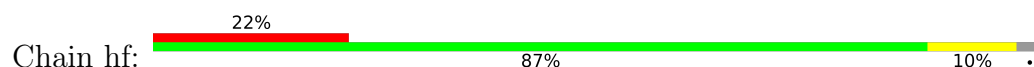
• Molecule 1: Major capsid protein

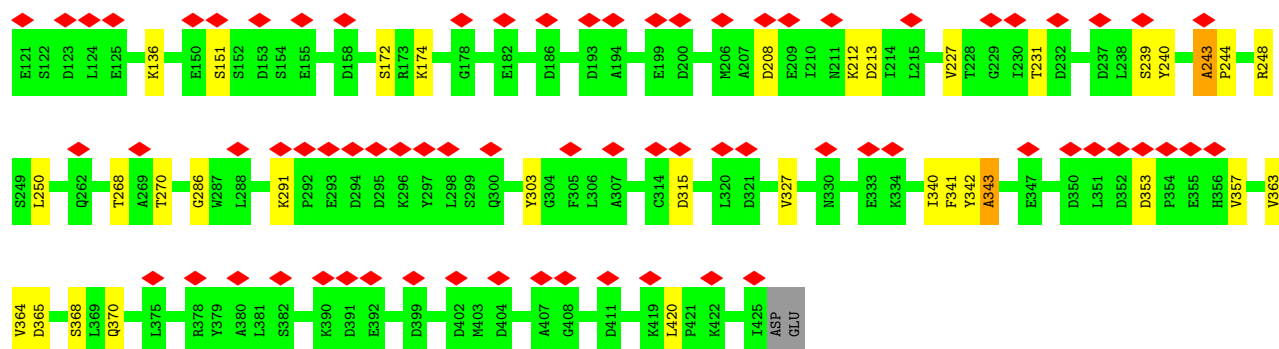


• Molecule 2: Capsid vertex protein

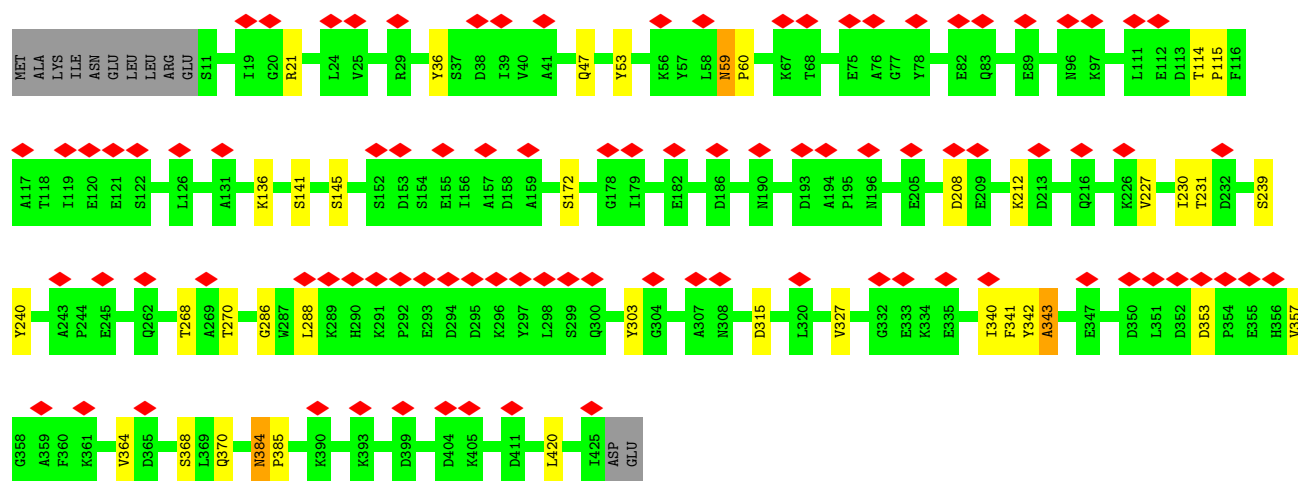
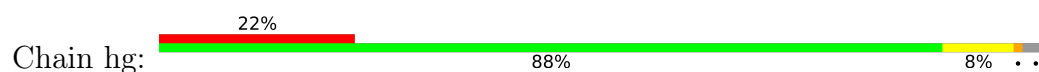


• Molecule 2: Capsid vertex protein

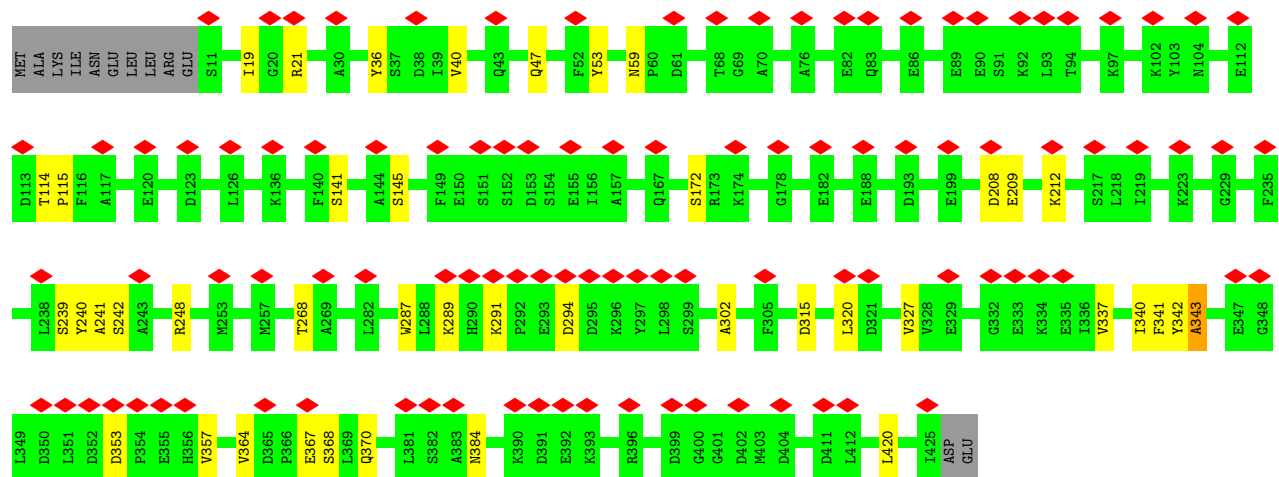
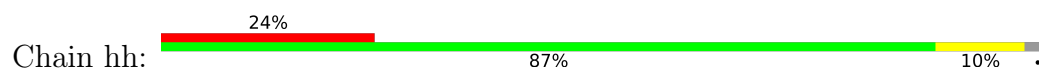




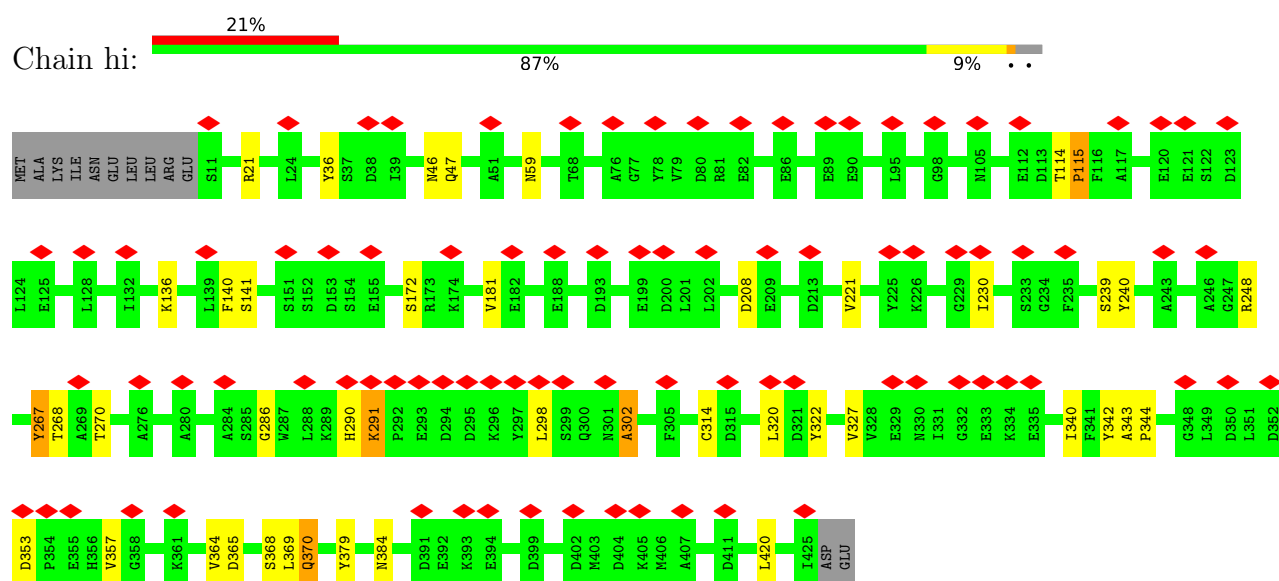
• Molecule 2: Capsid vertex protein



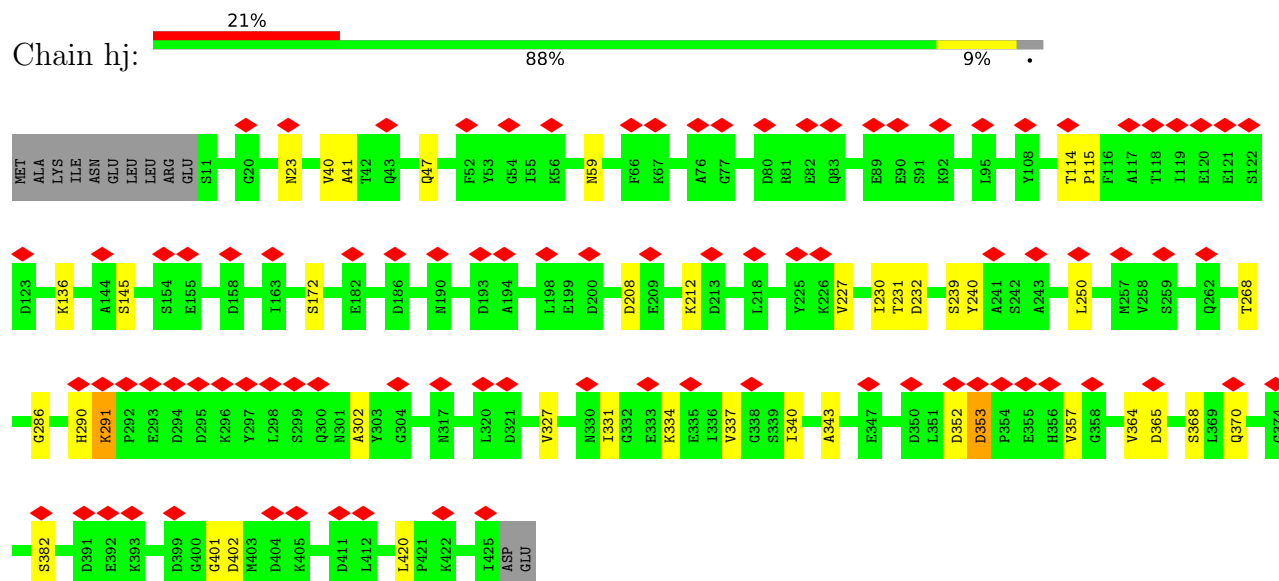
• Molecule 2: Capsid vertex protein



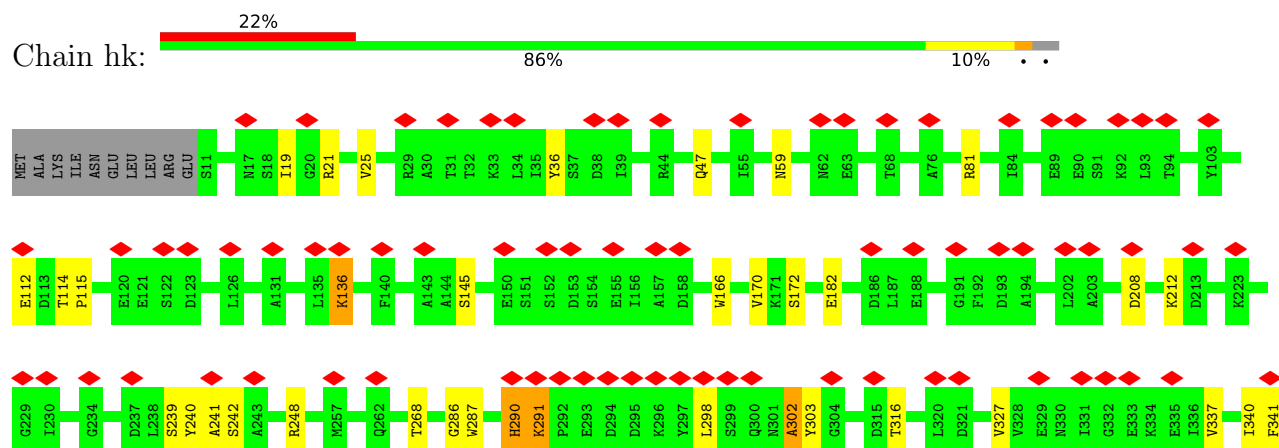
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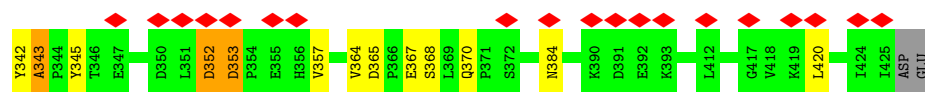


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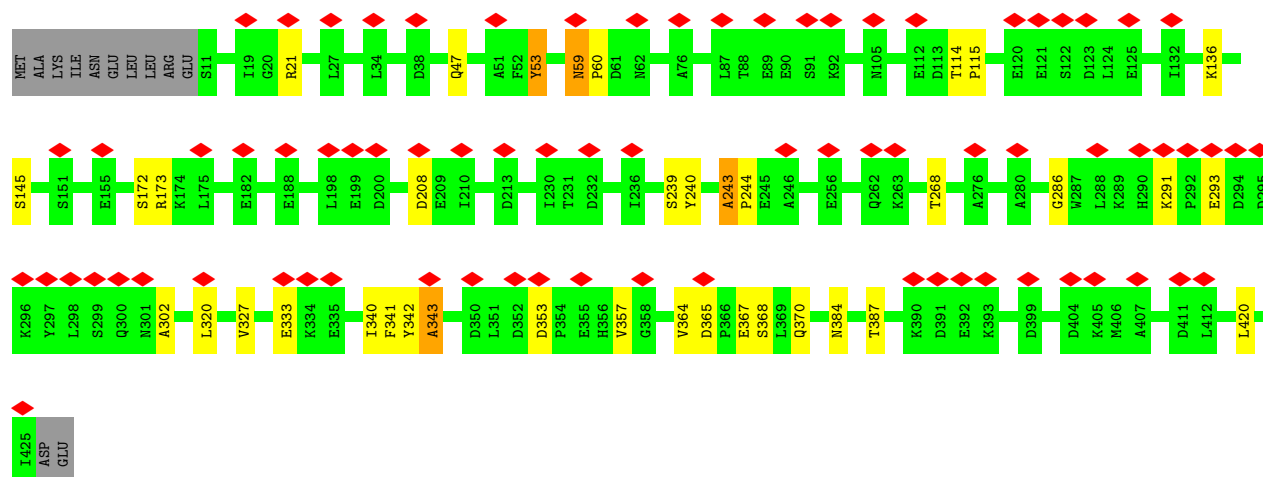
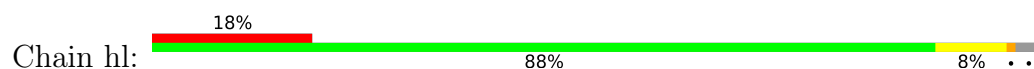


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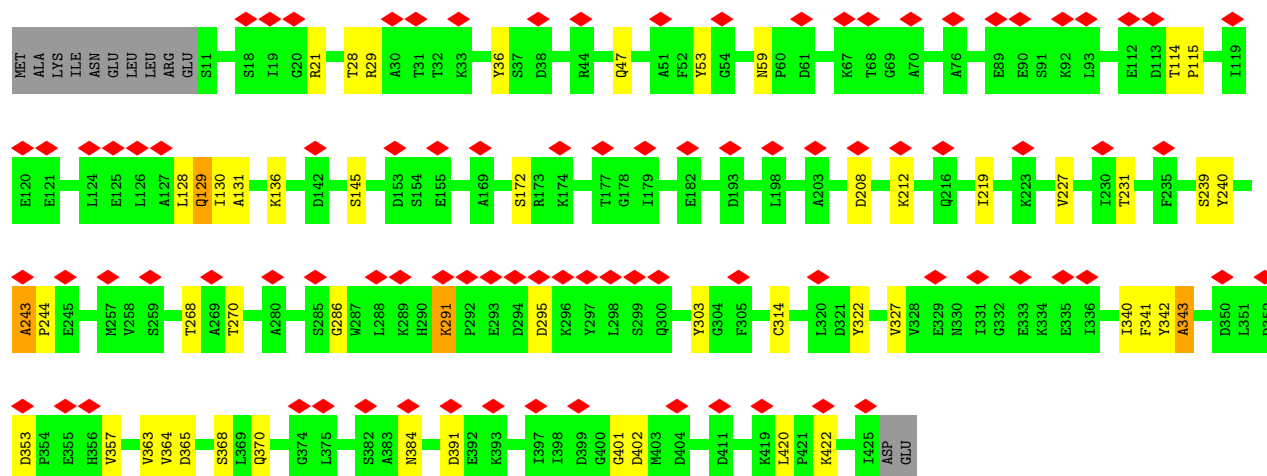
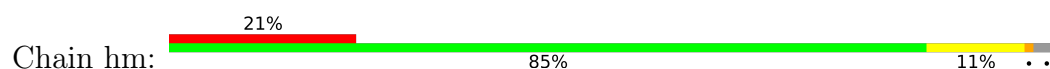




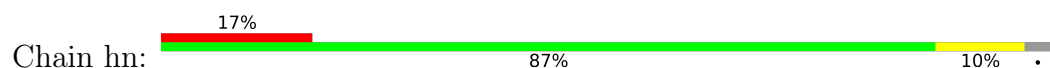
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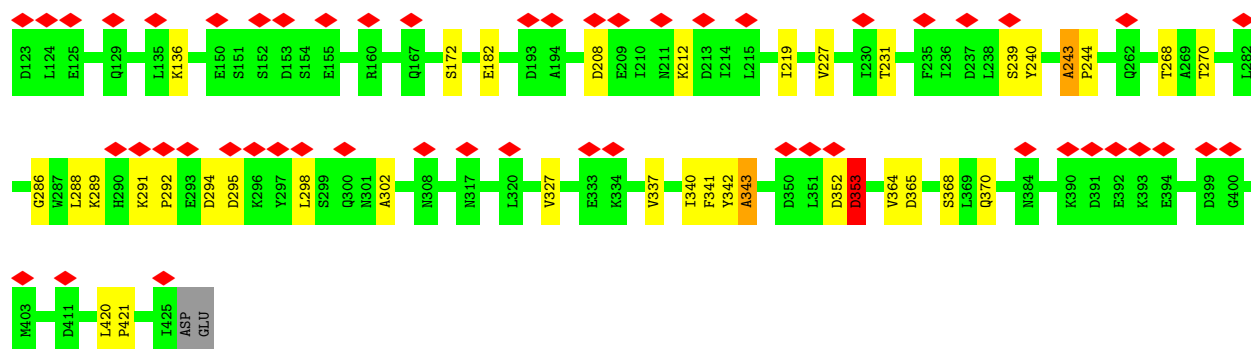


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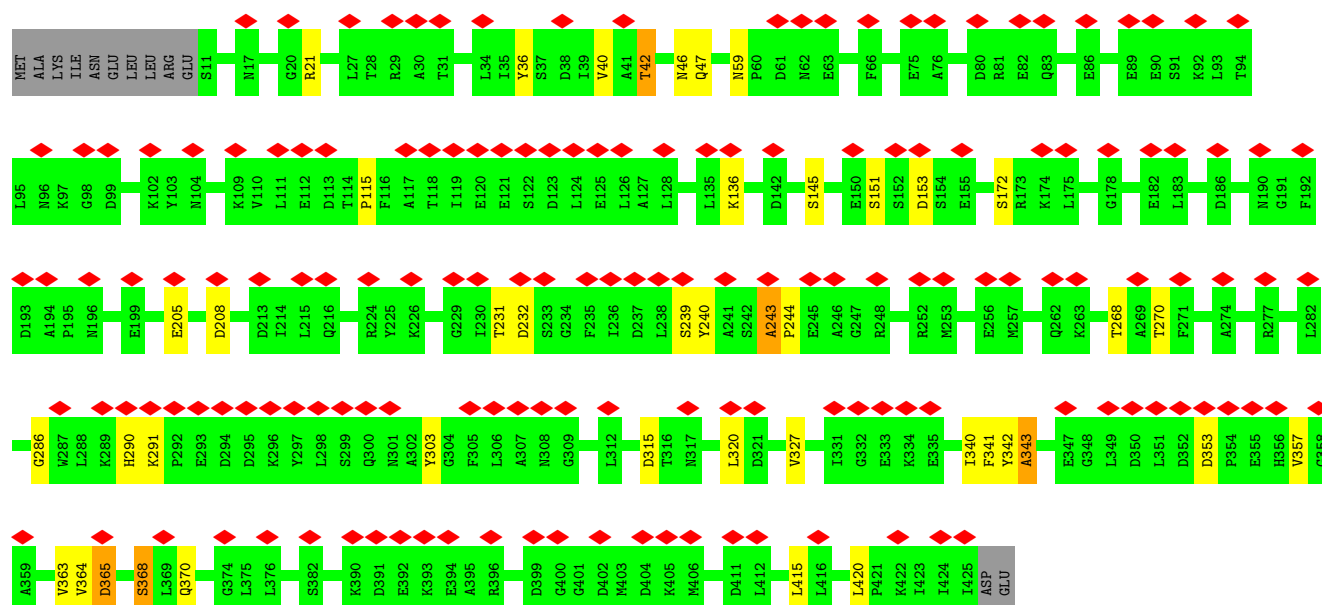
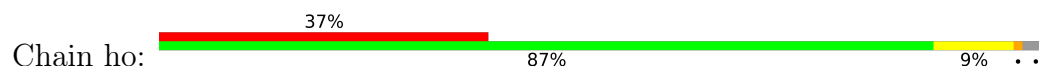


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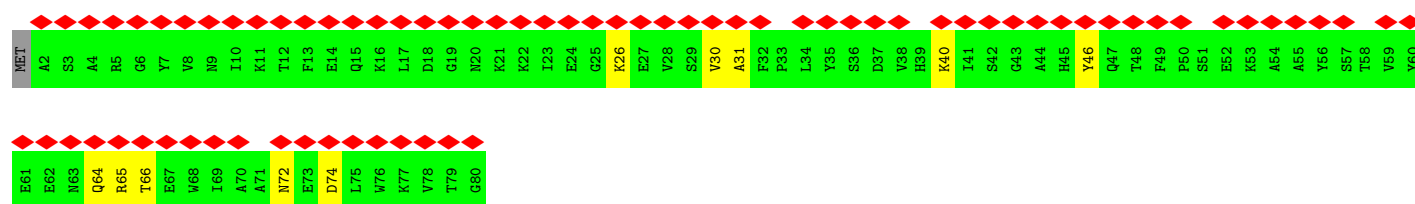
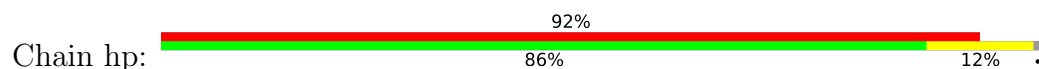




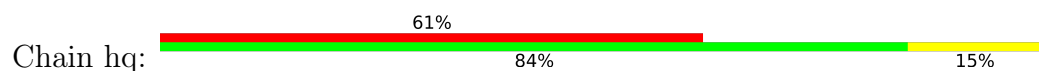
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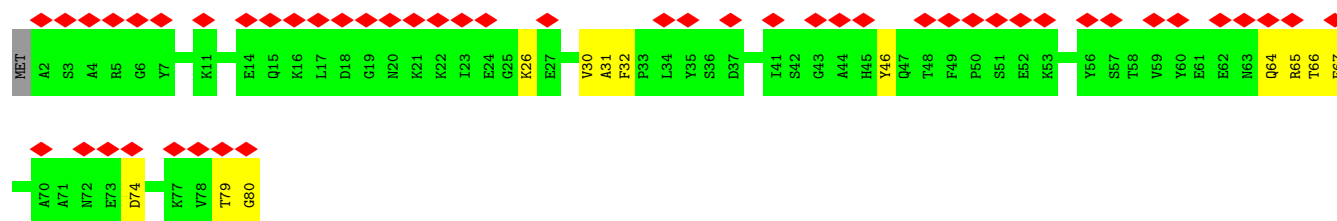


• Molecule 3: Small outer capsid protein

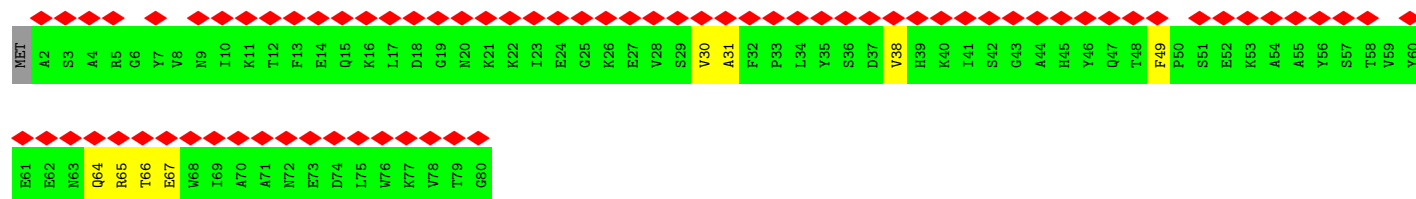
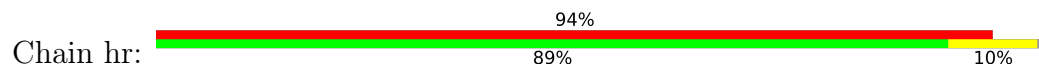


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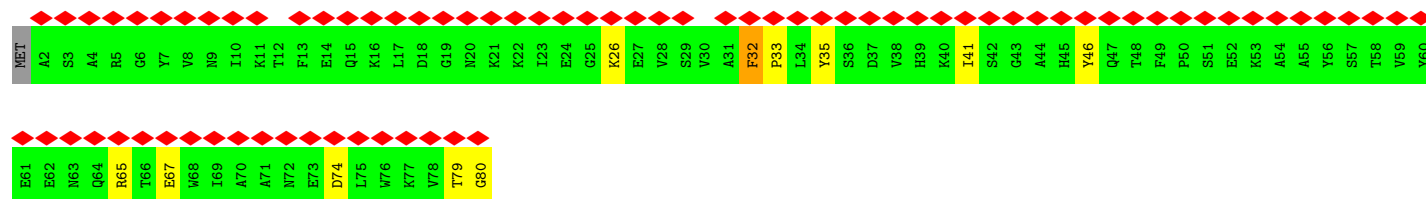
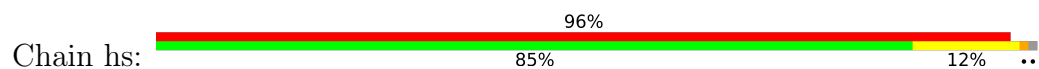




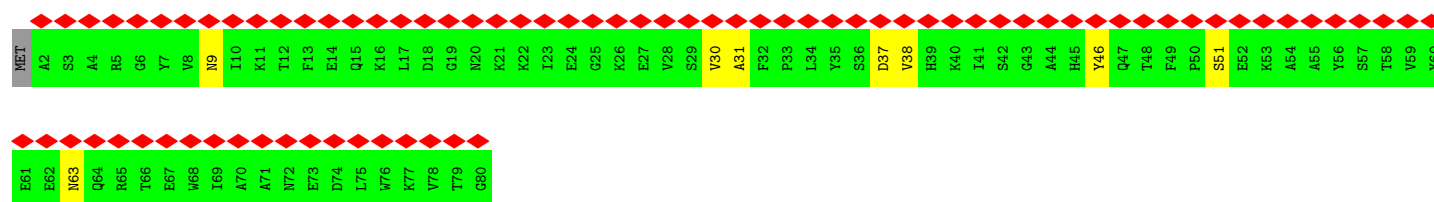
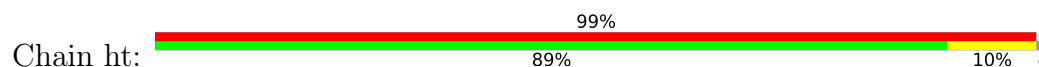
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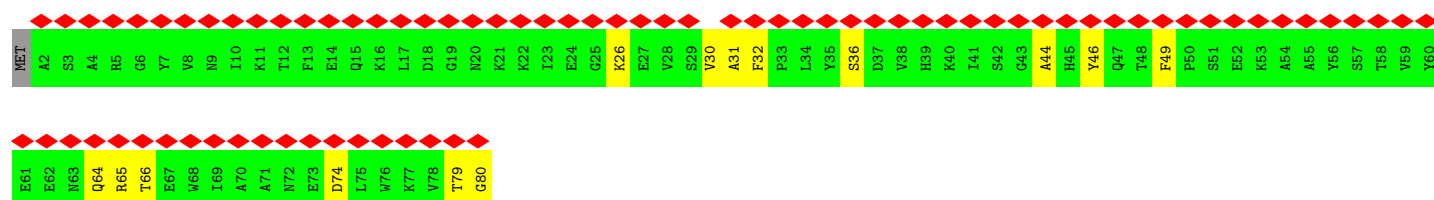
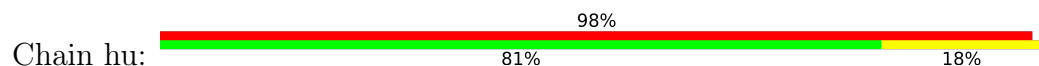
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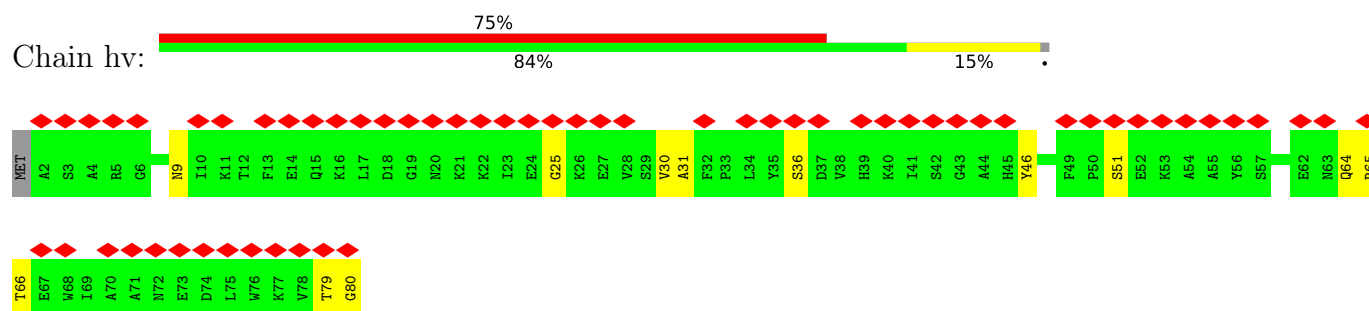
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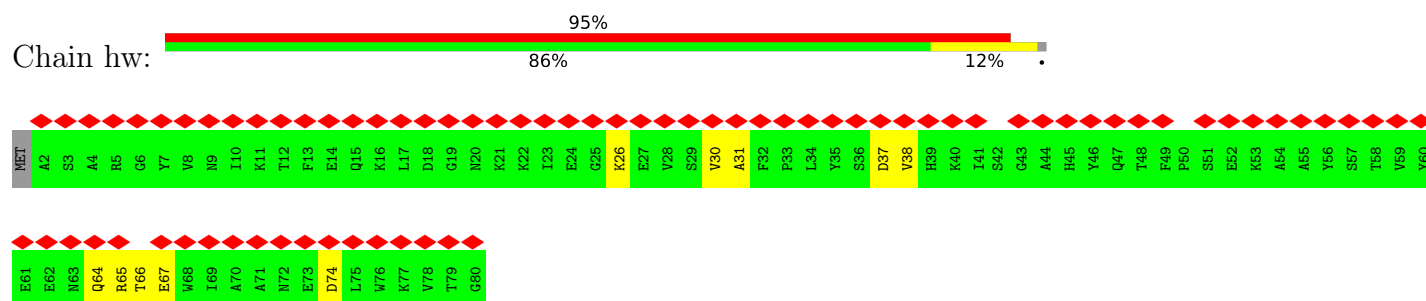
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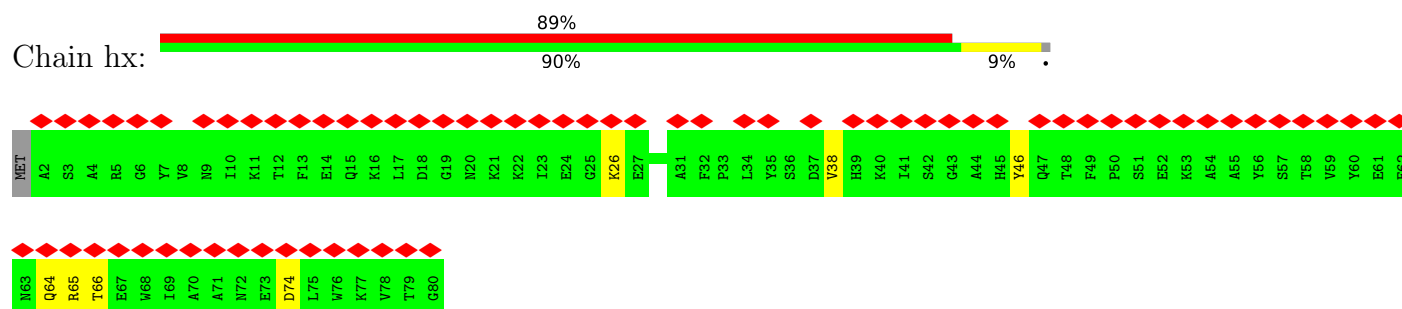
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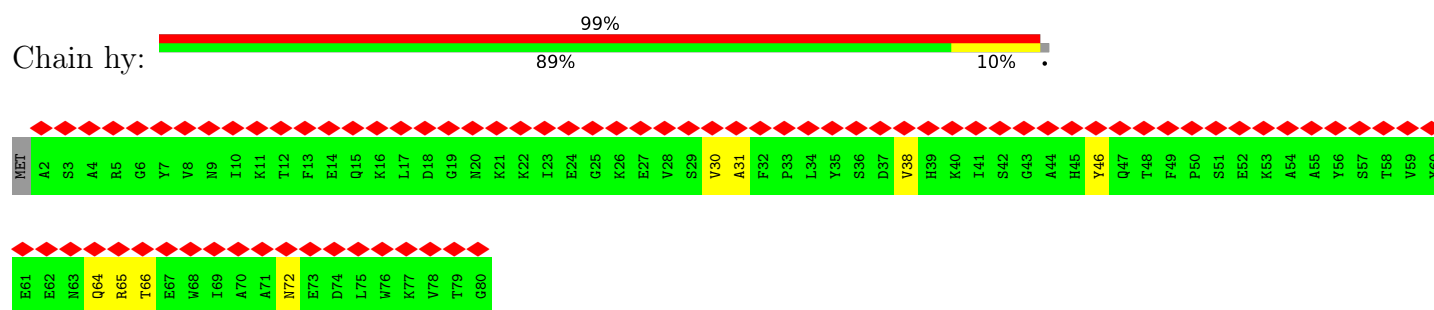
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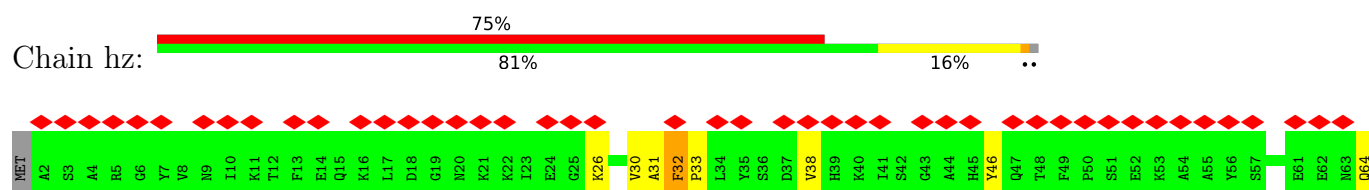
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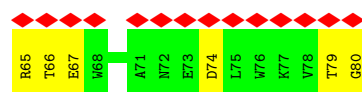


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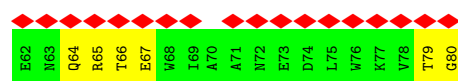
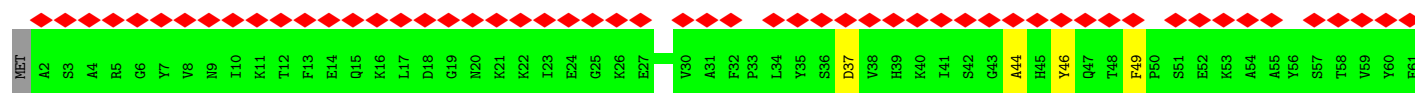
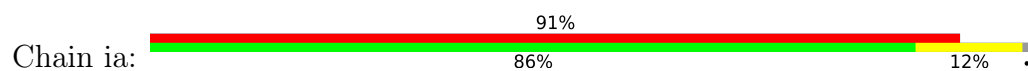


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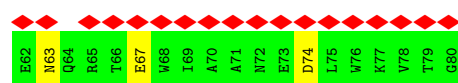
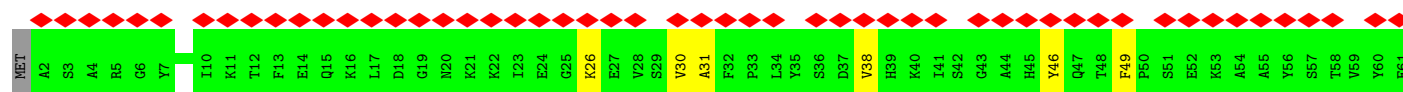
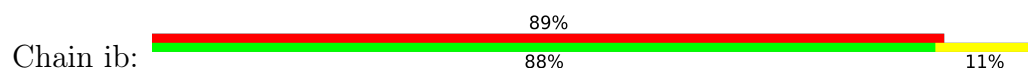




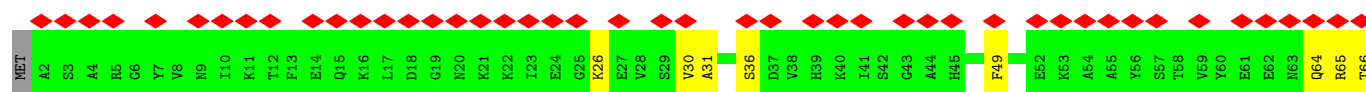
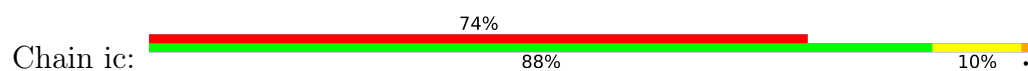
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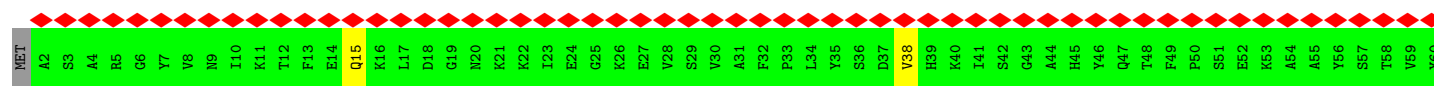
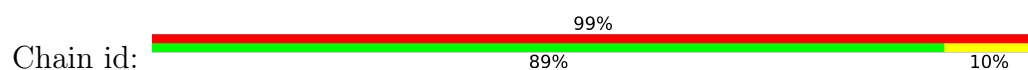
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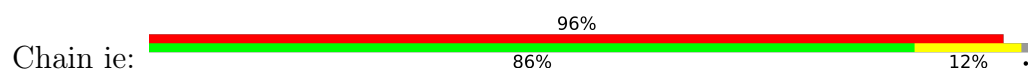
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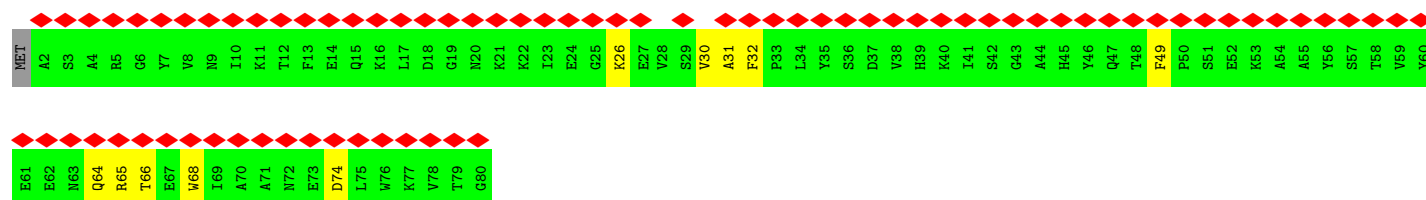


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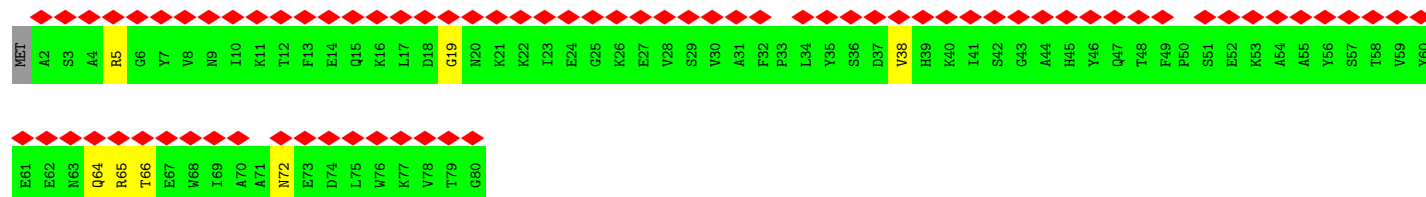
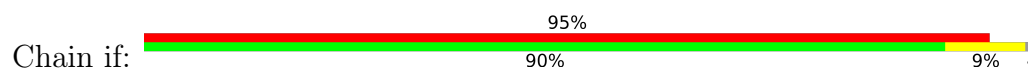


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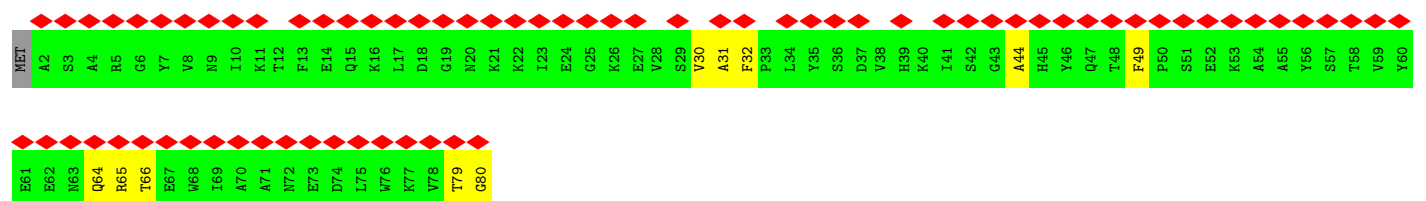
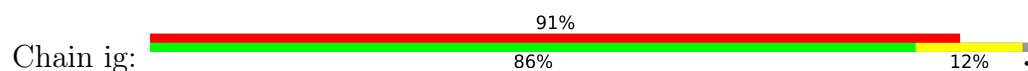




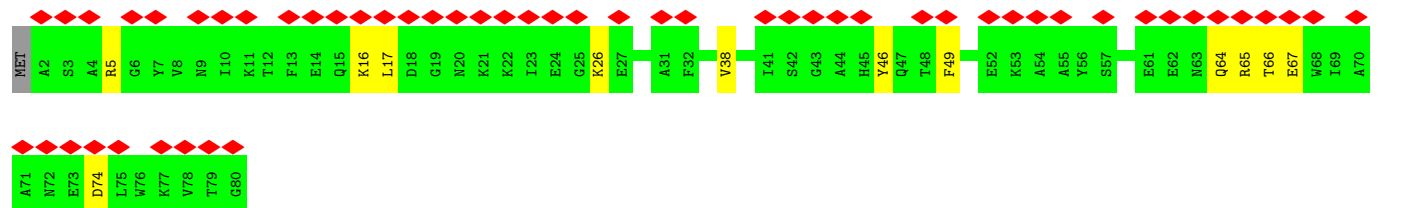
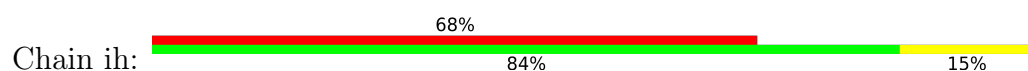
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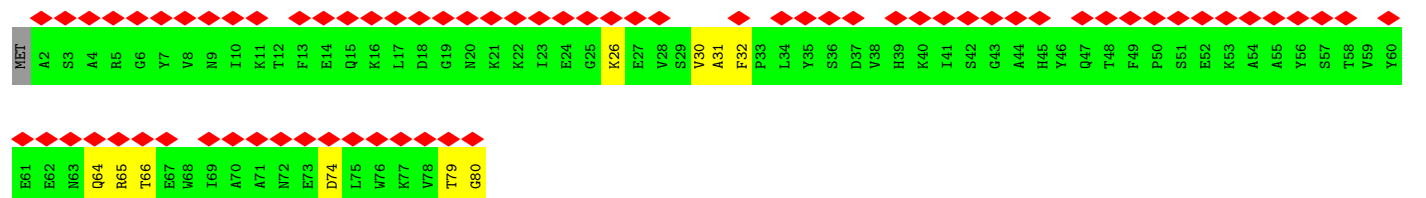
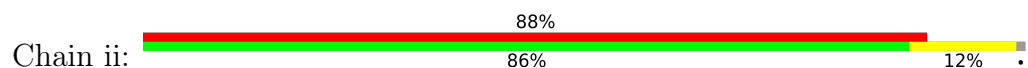
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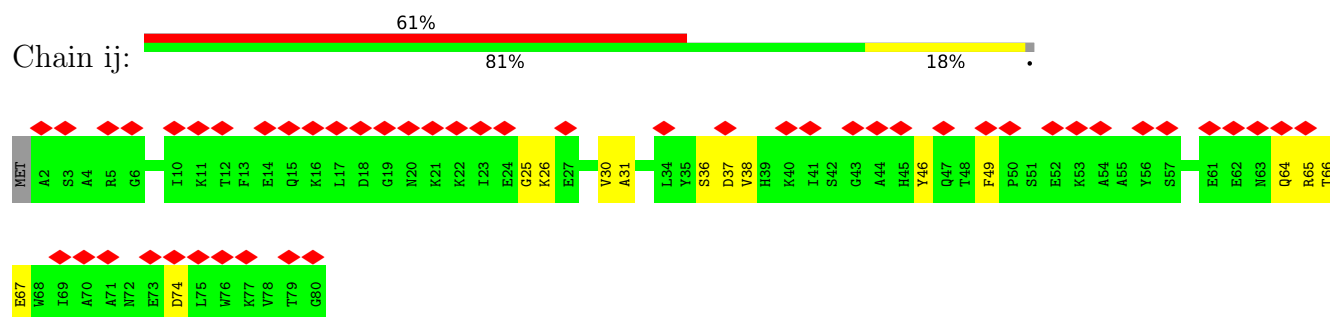
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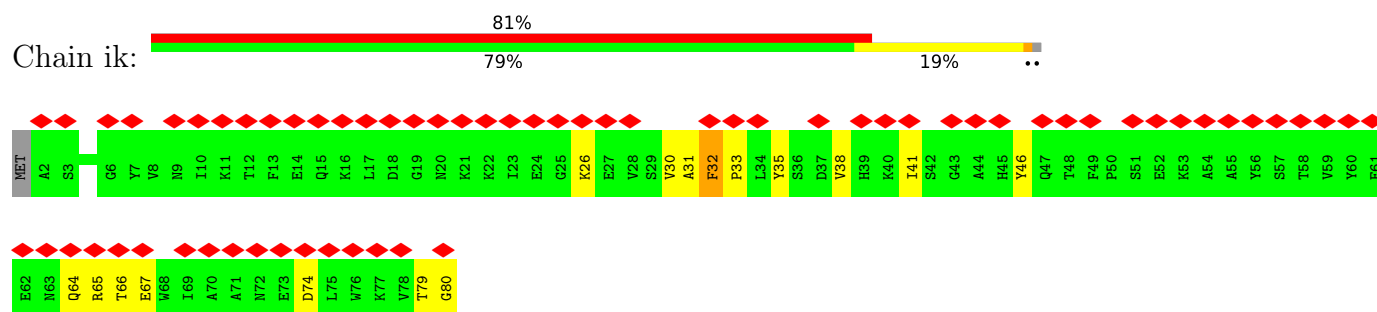
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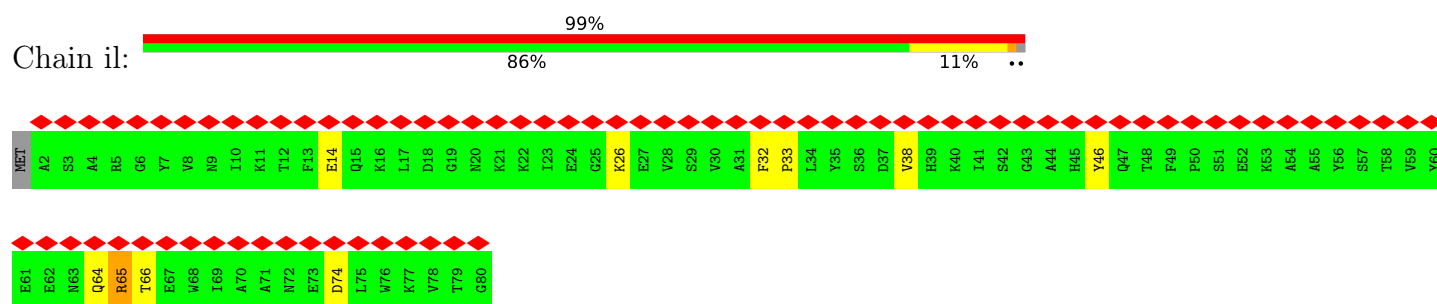
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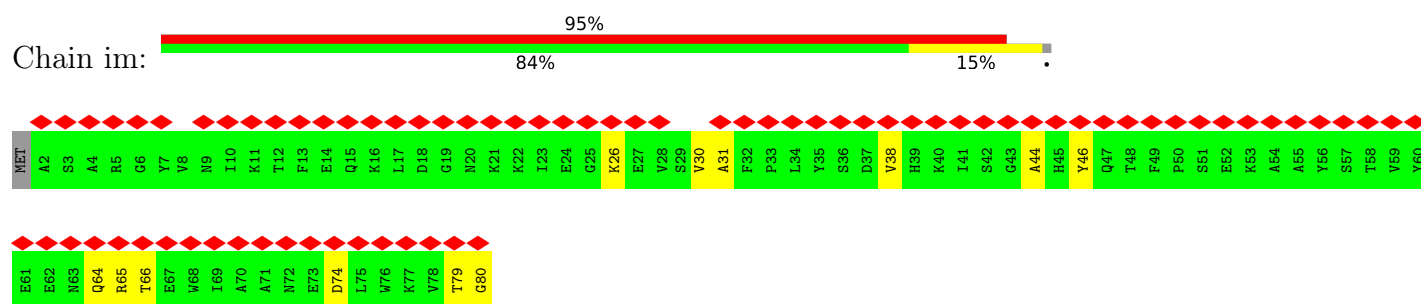
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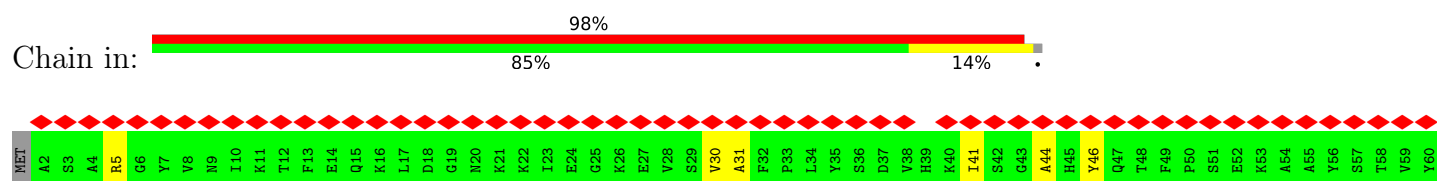
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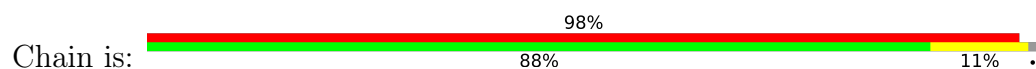


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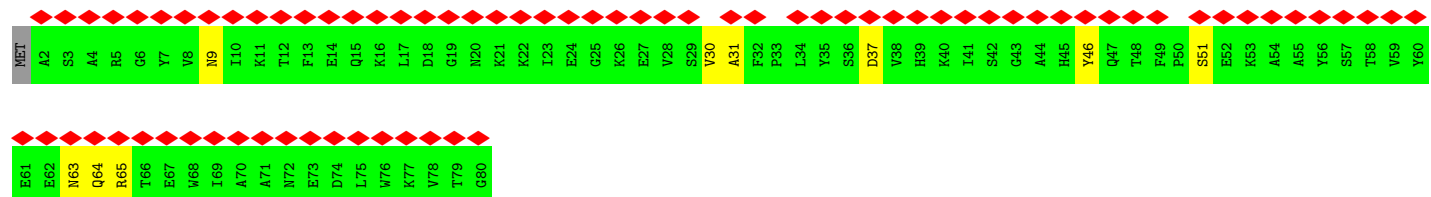
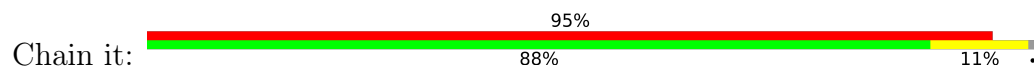
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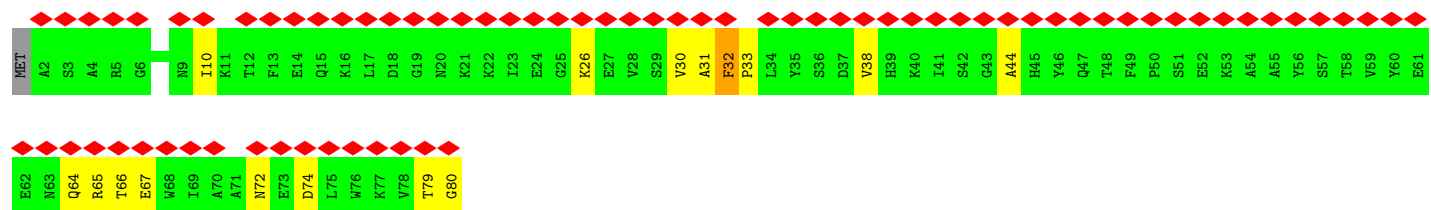
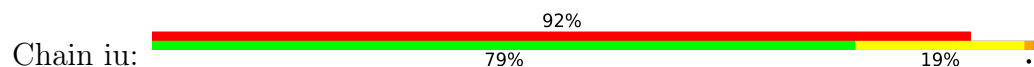




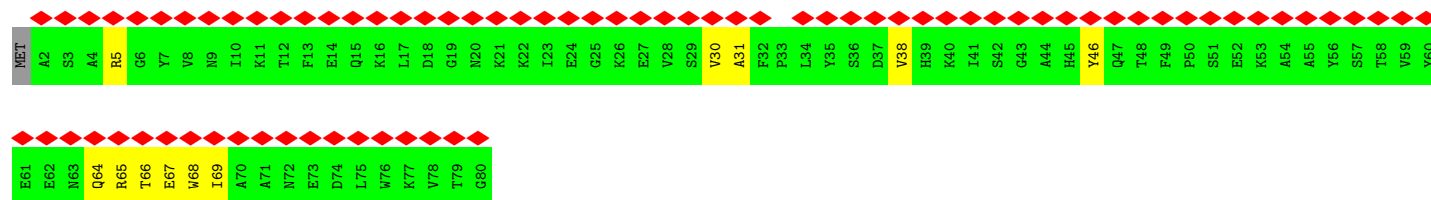
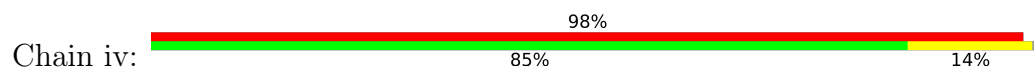
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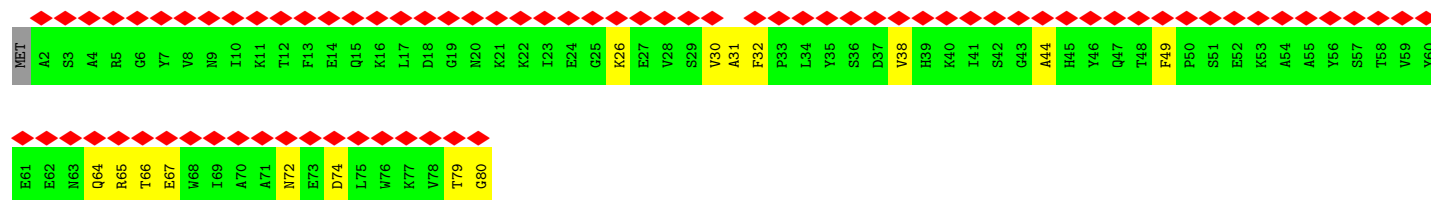
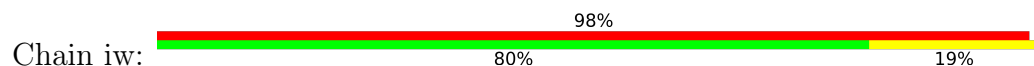
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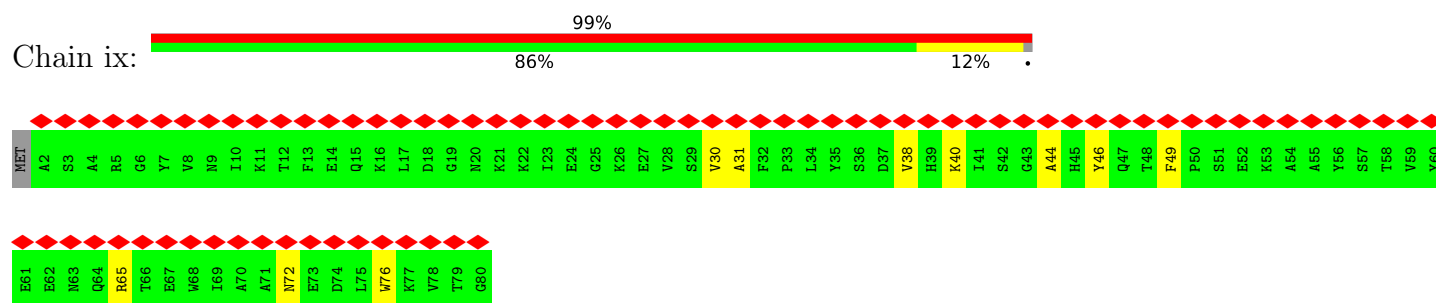
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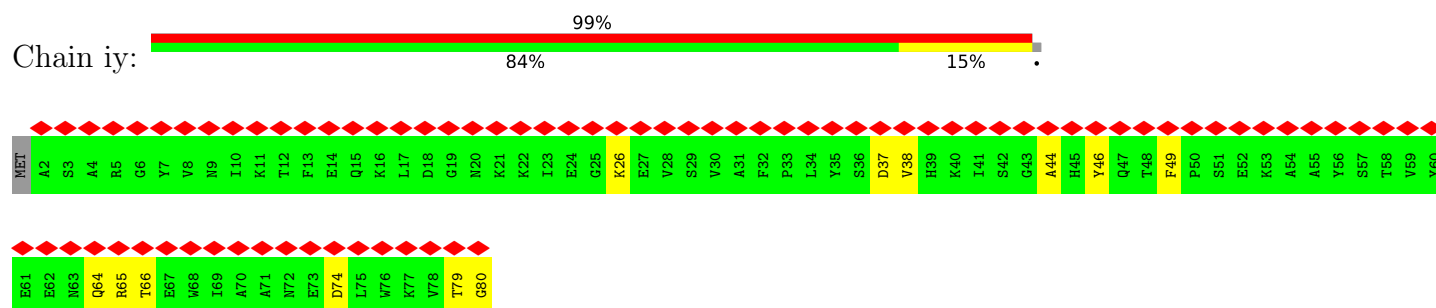
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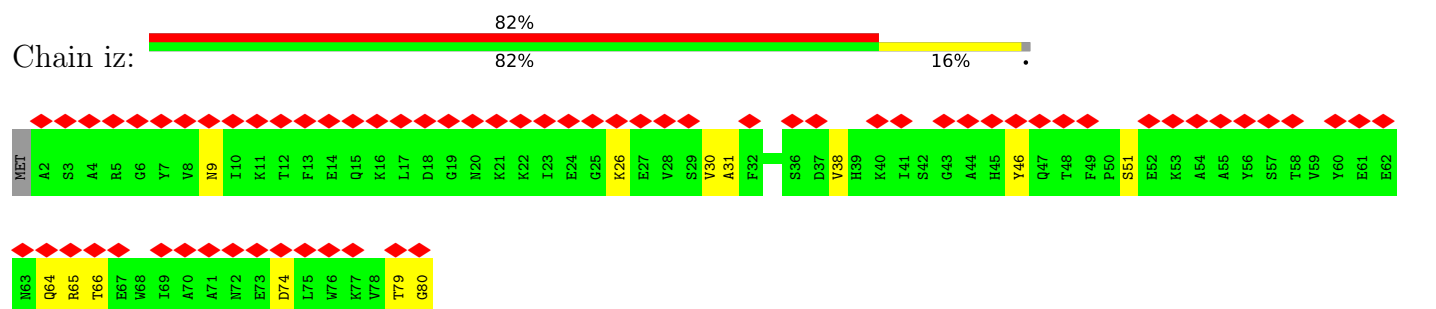
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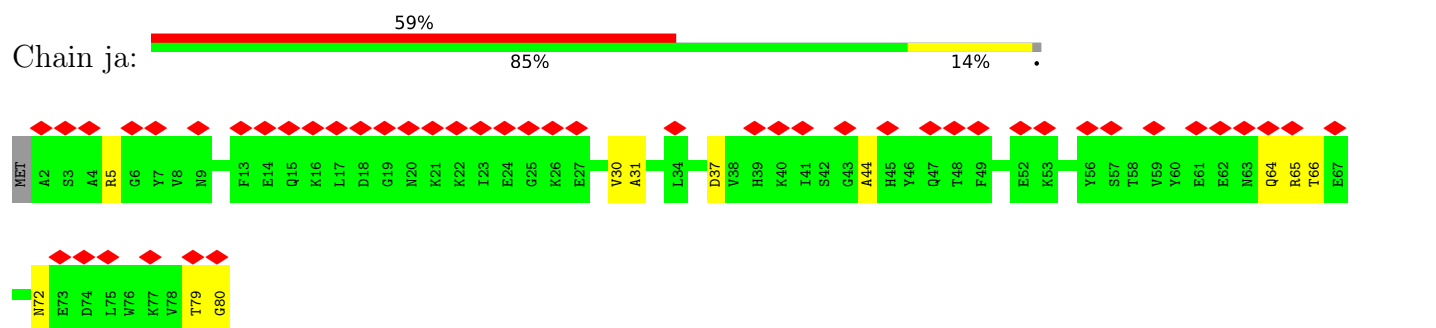
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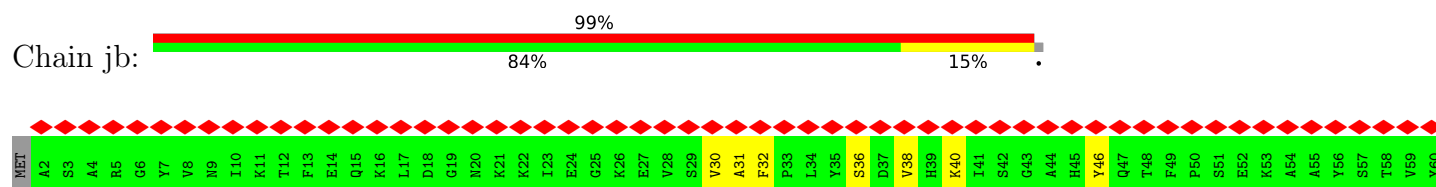
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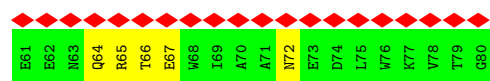


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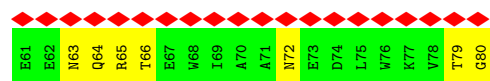
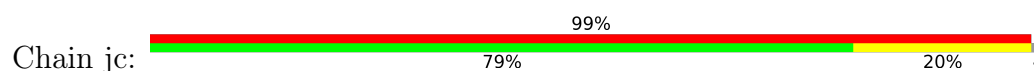


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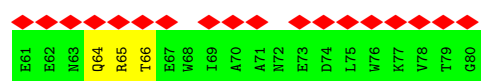
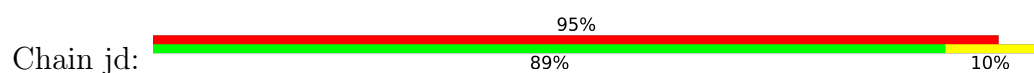




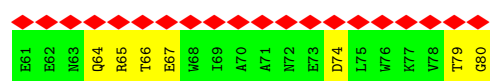
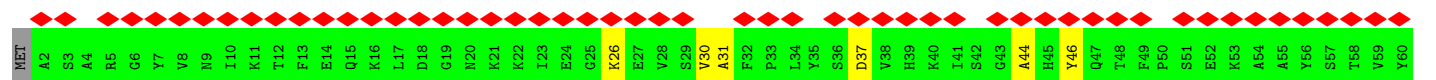
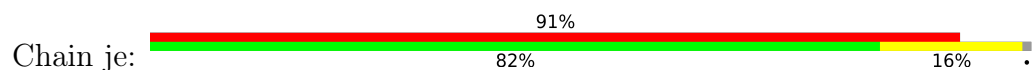
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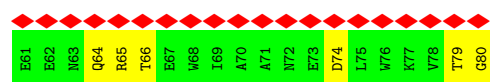
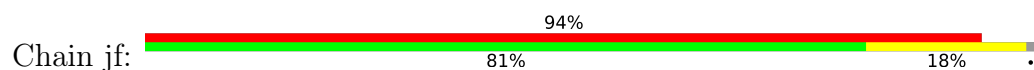
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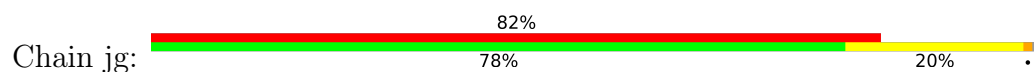
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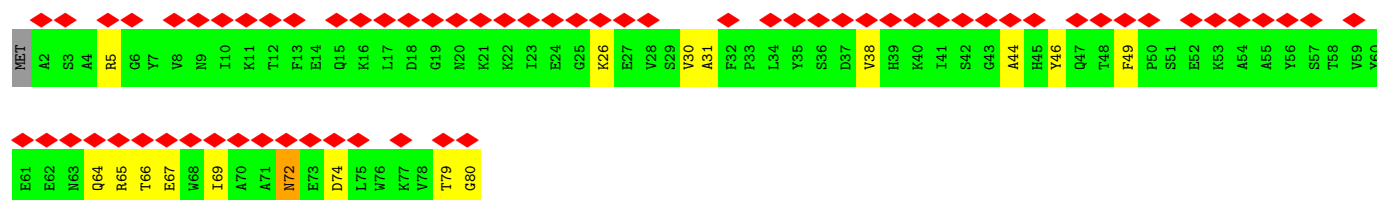


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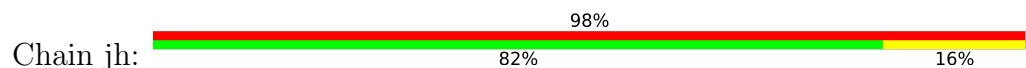


- Molecule 3: Small outer capsid protein

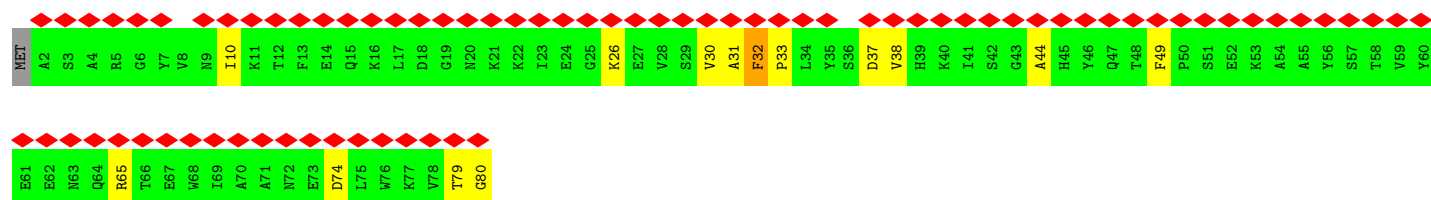
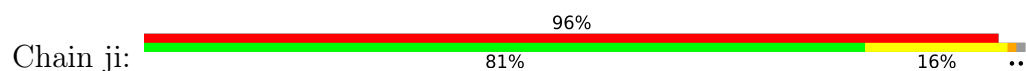




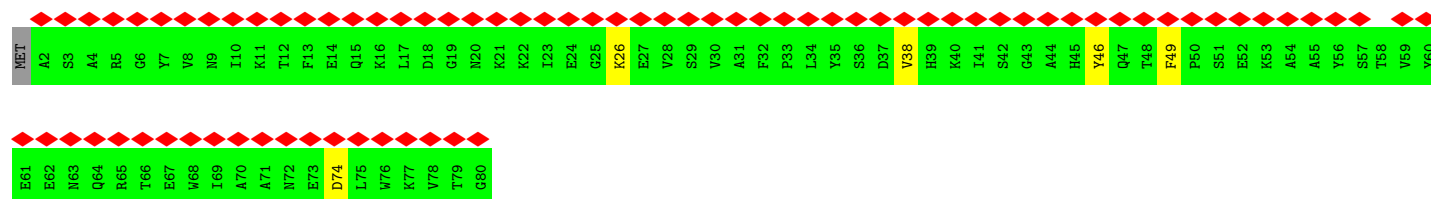
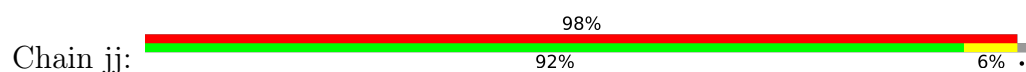
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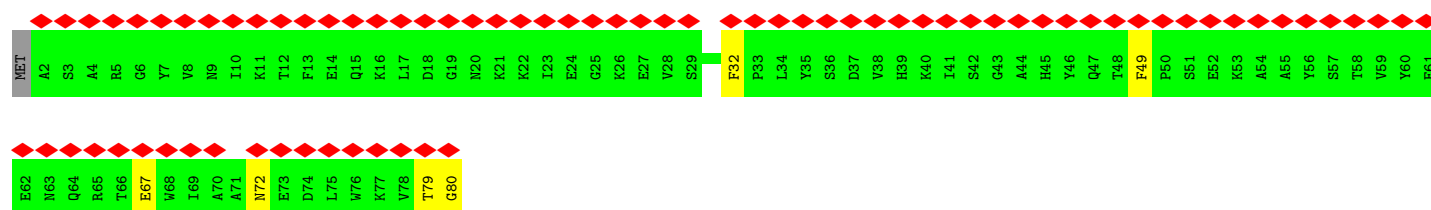
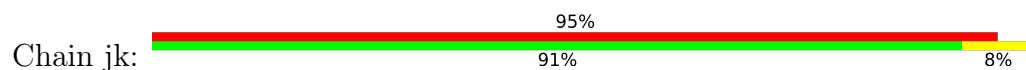
• Molecule 3: Small outer capsid protein



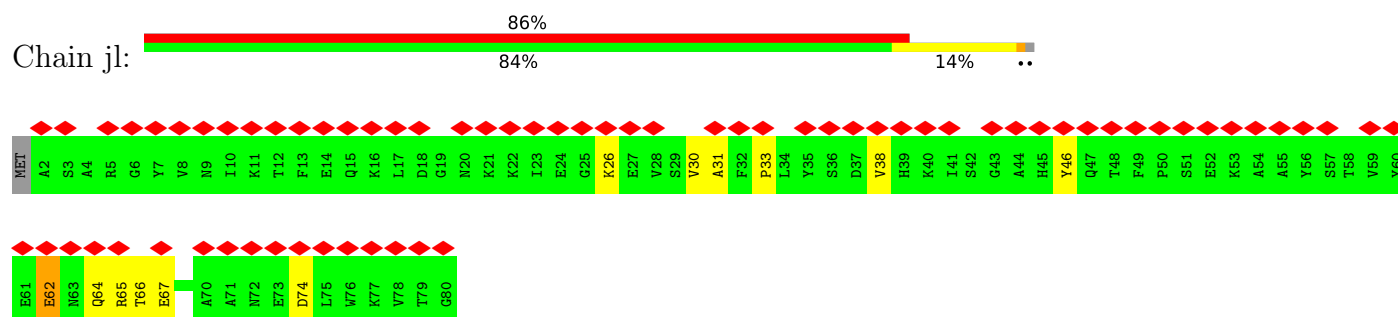
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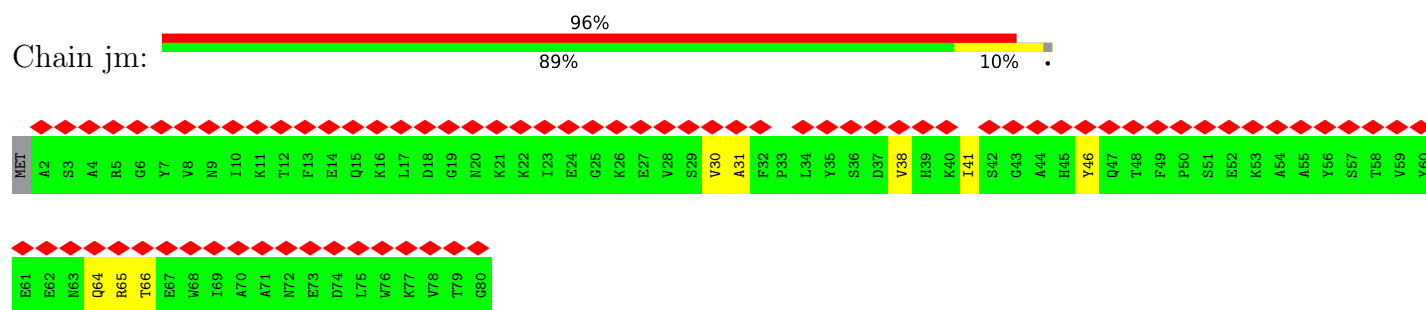
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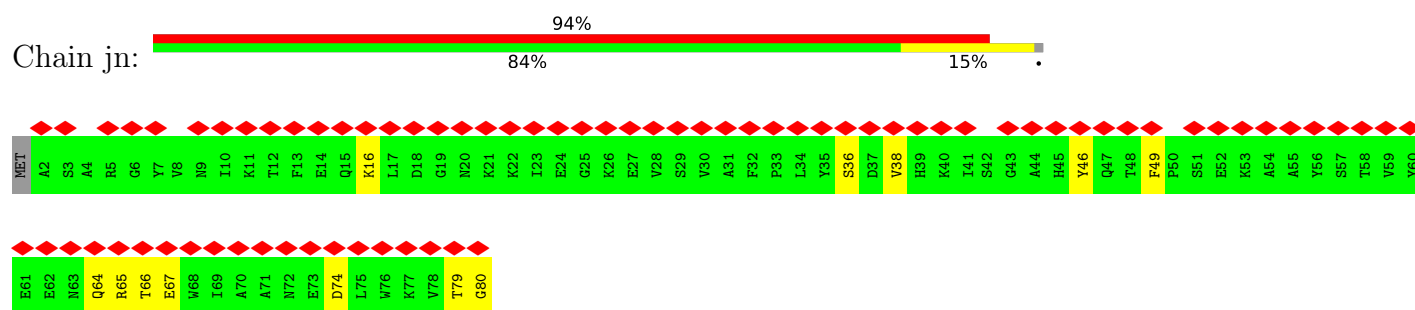
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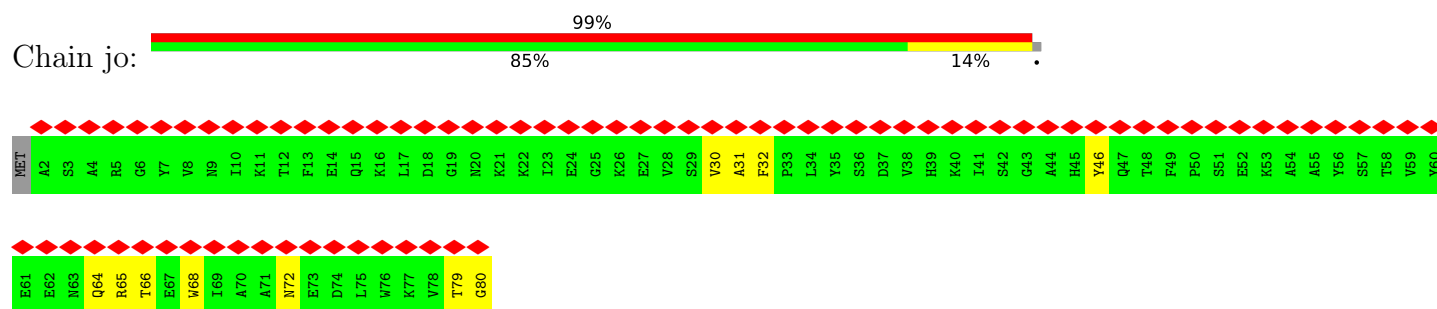
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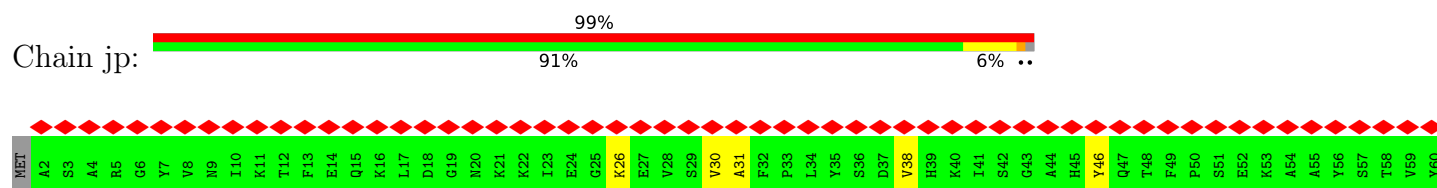
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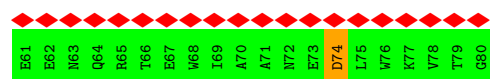


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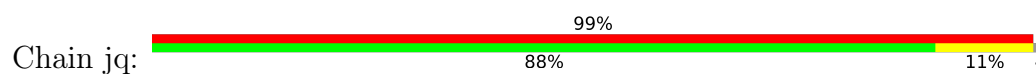


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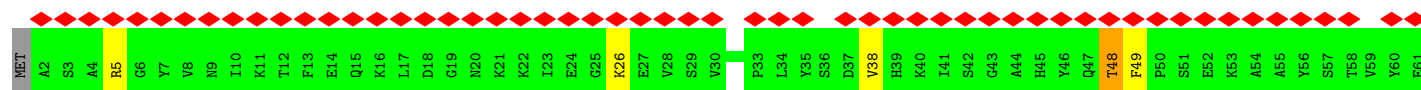
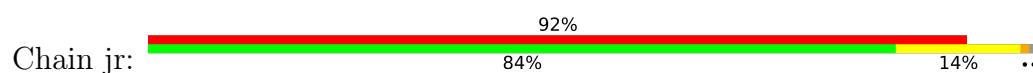




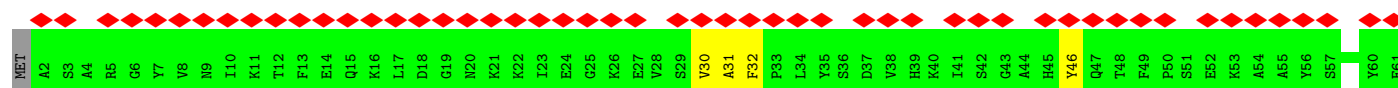
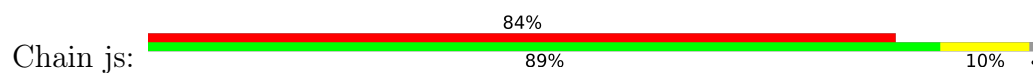
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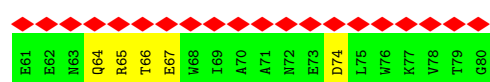
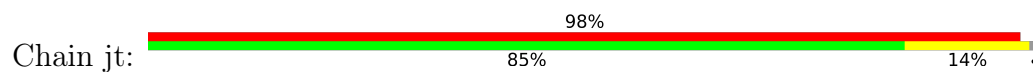
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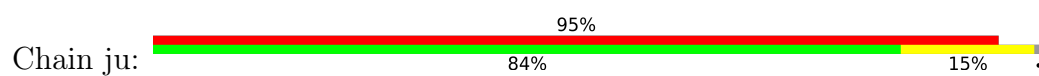
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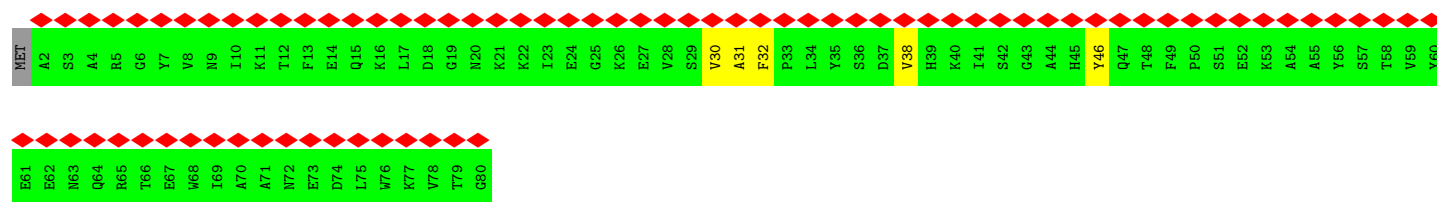
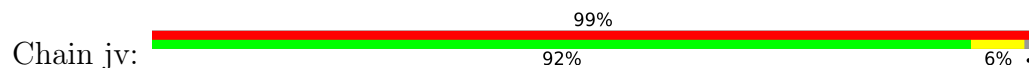
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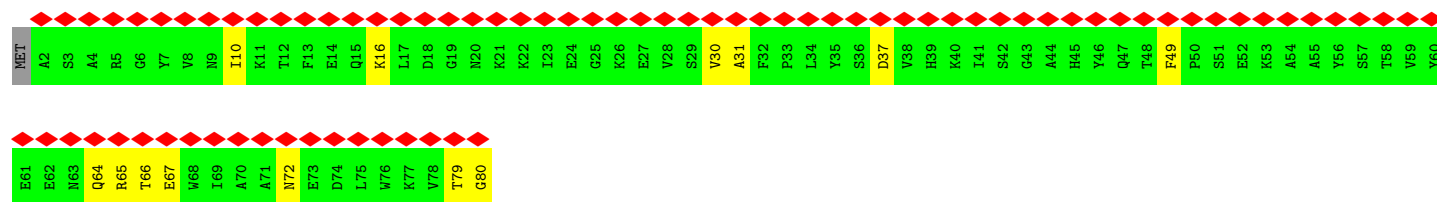
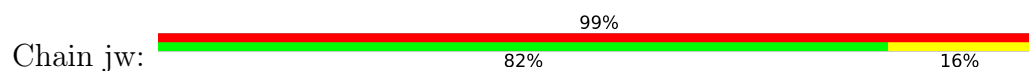
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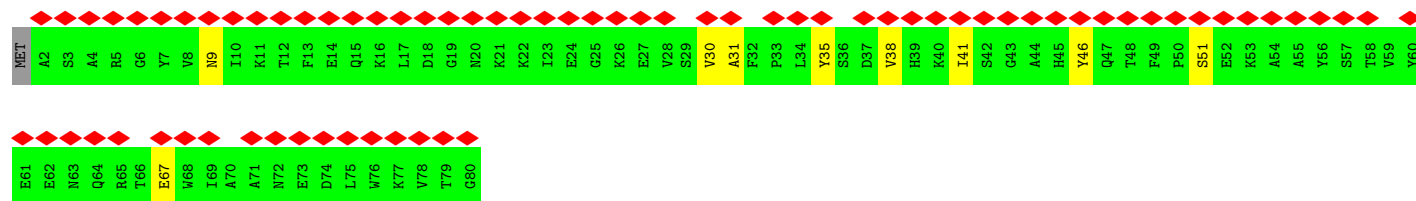
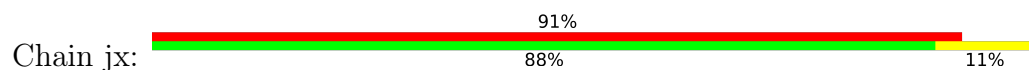
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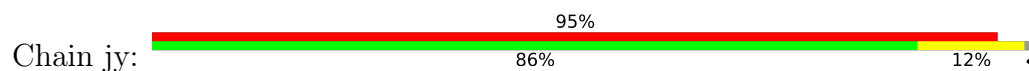
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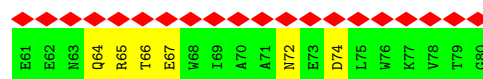
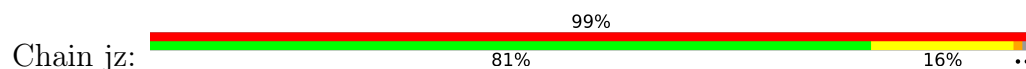


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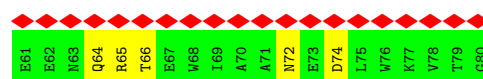
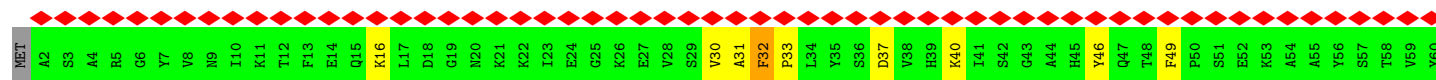
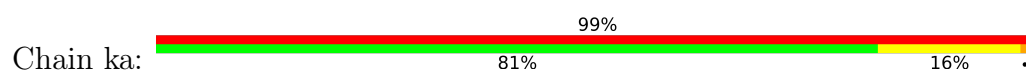




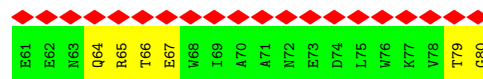
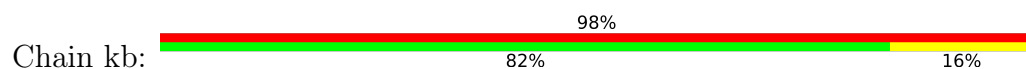
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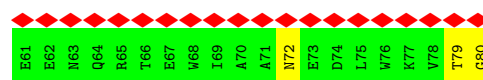
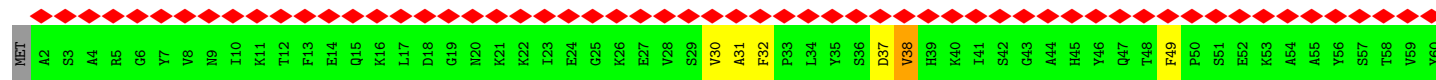
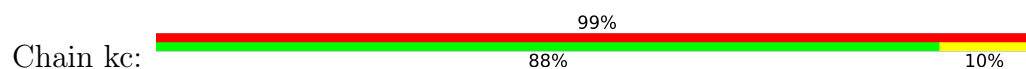
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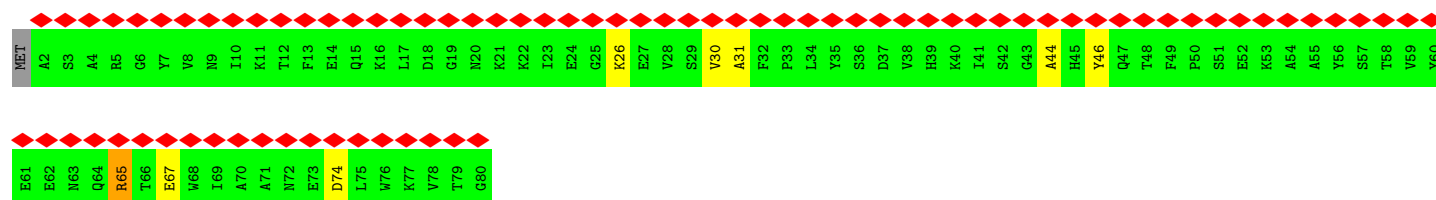


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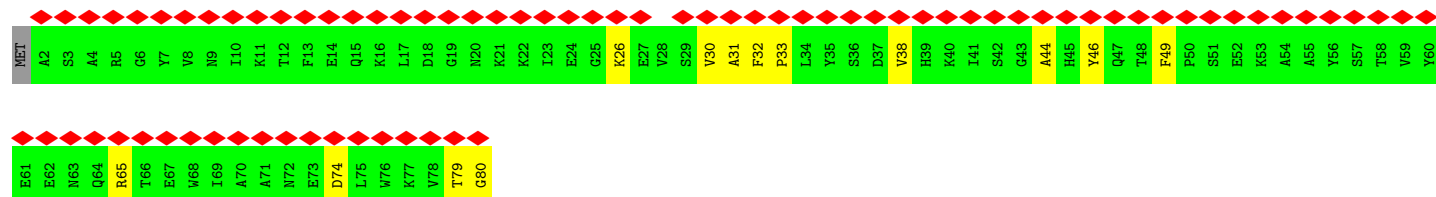
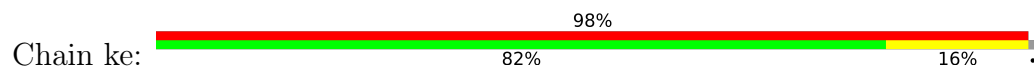


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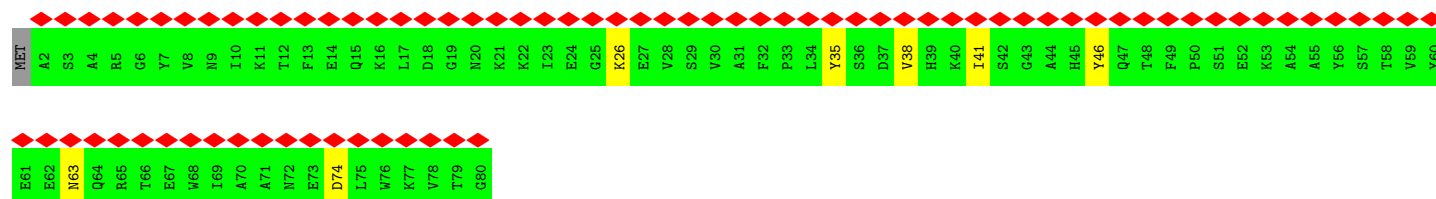
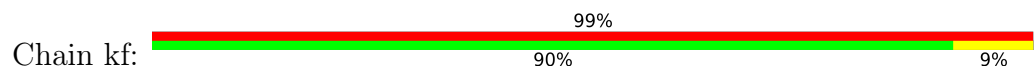




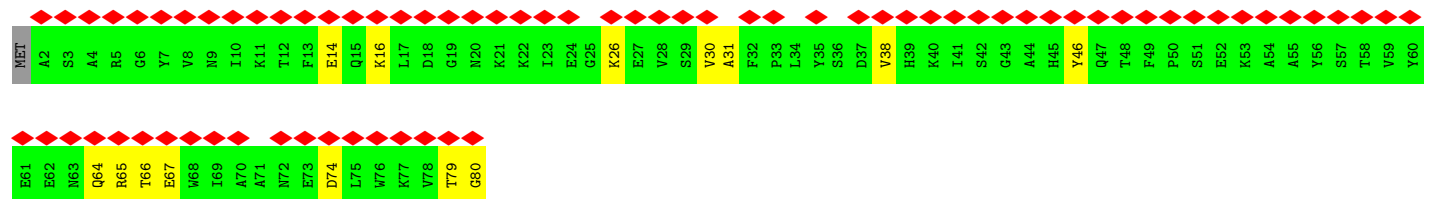
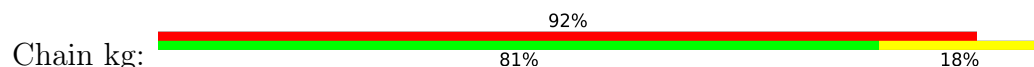
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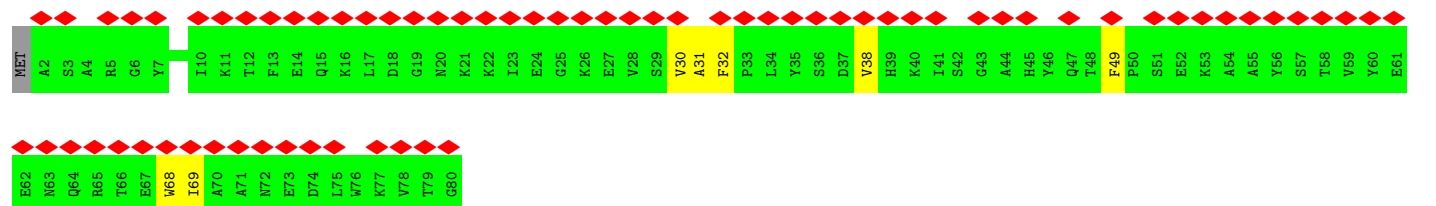
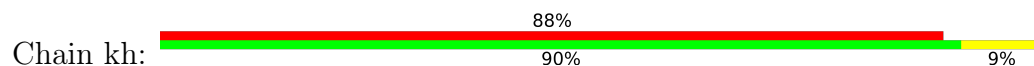
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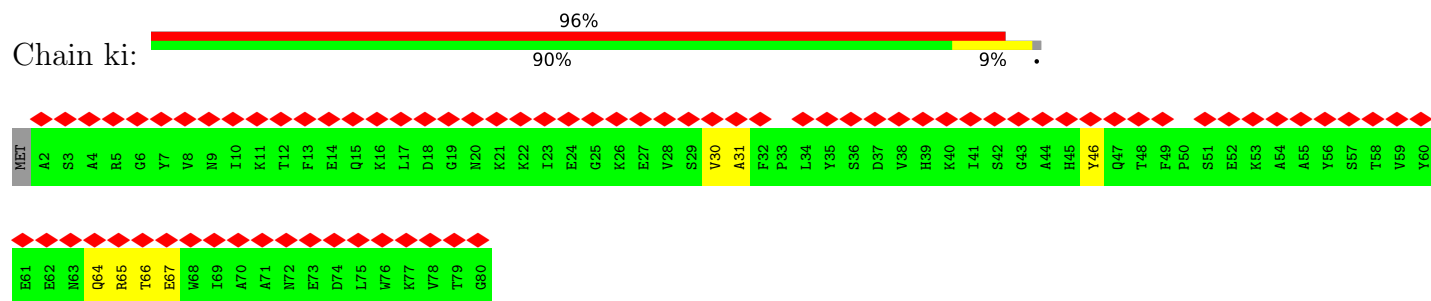
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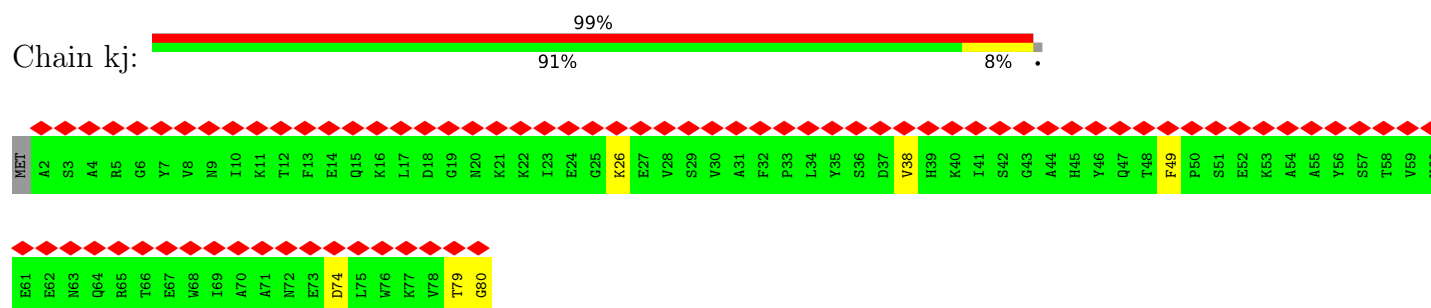
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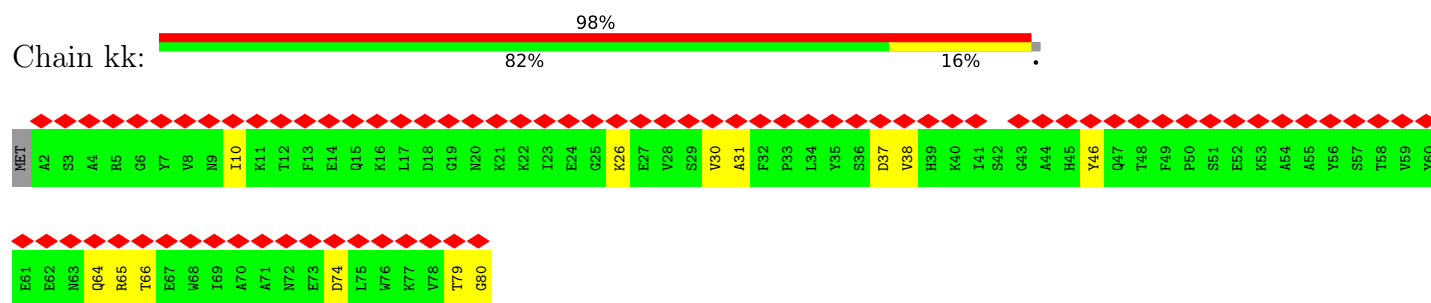
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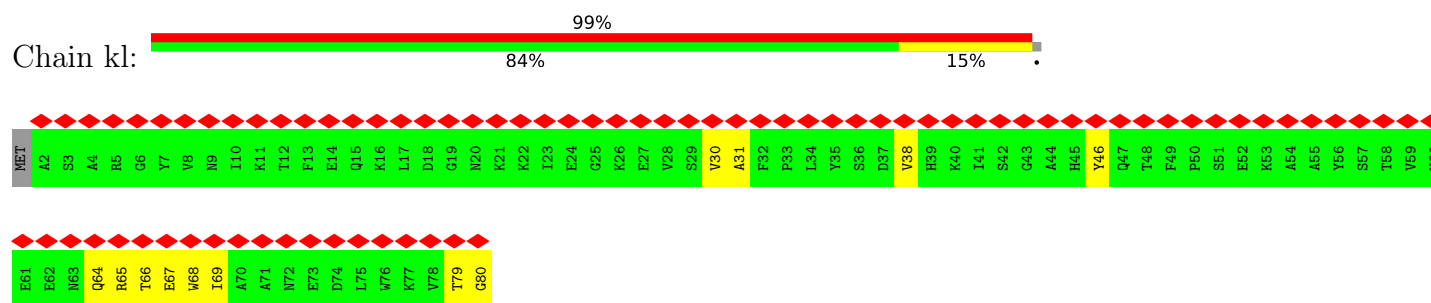
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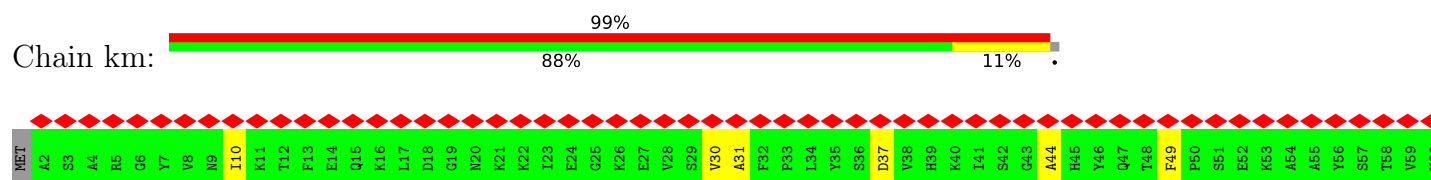
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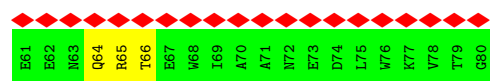


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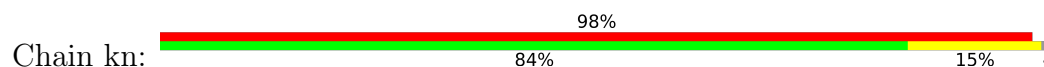


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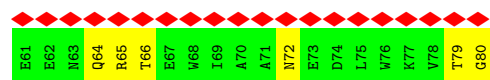
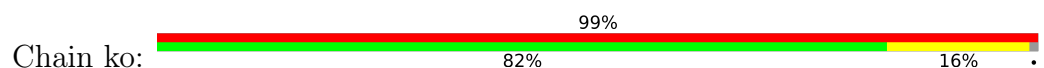




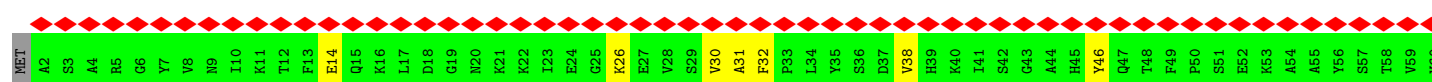
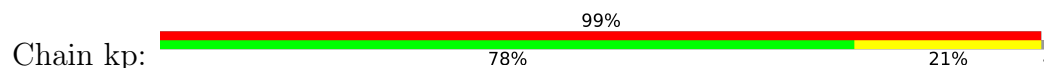
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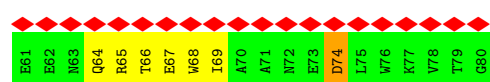
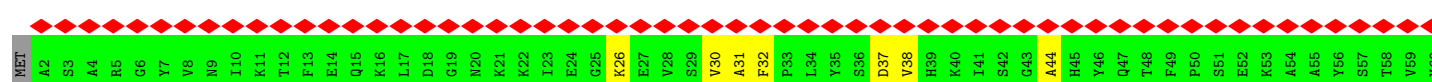
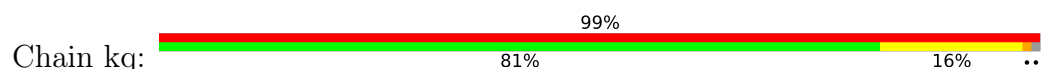
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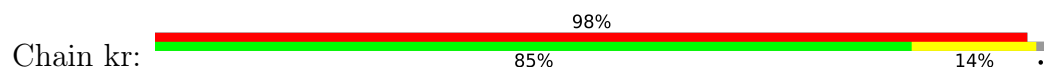
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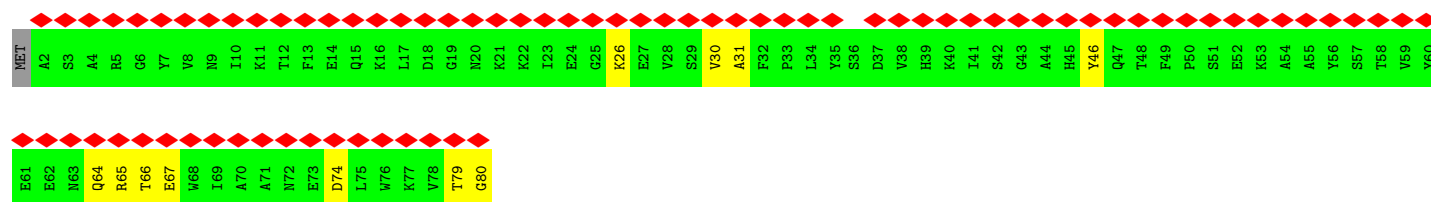


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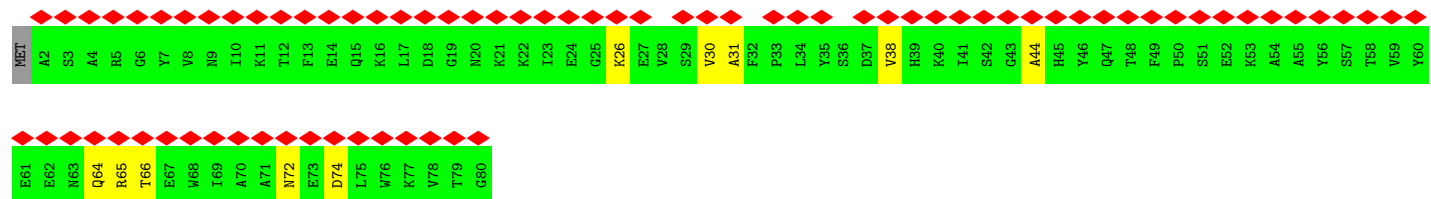
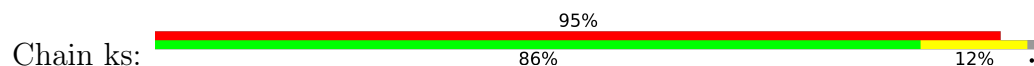


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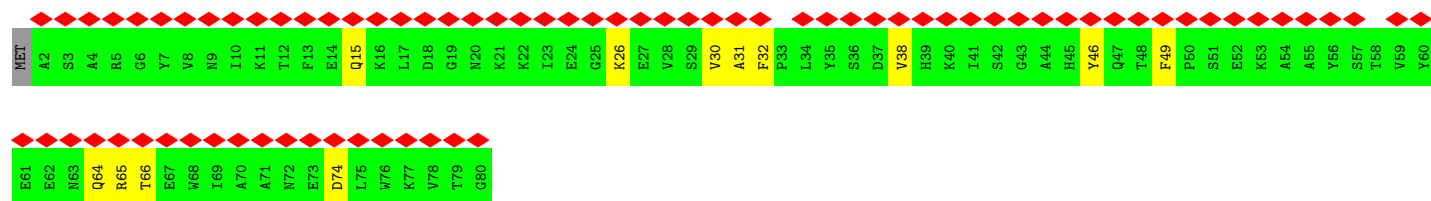
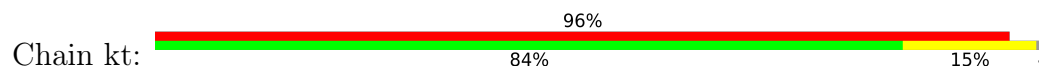




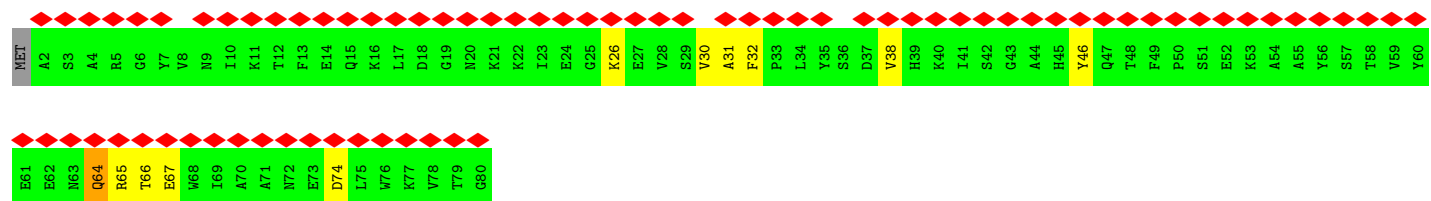
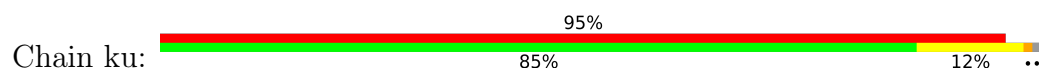
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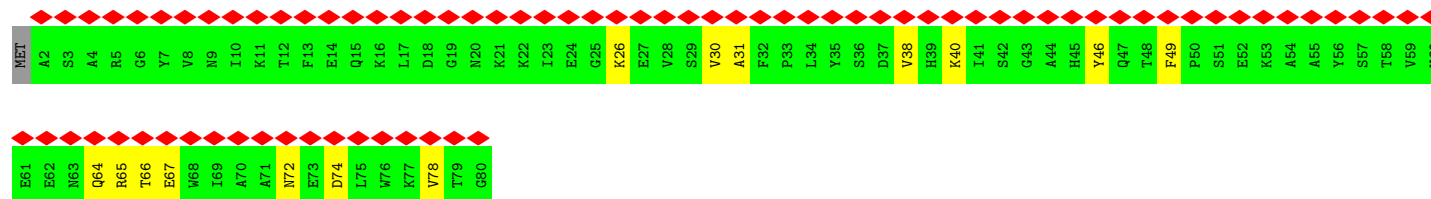
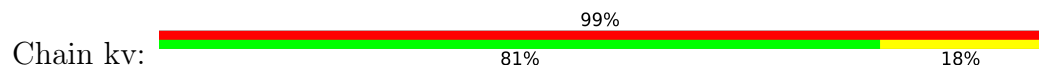
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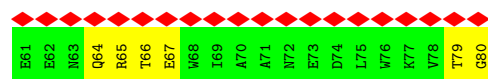
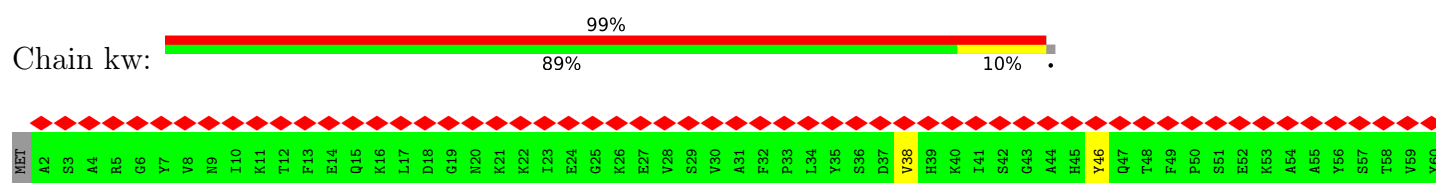
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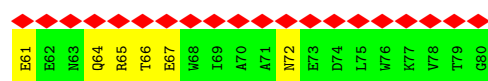
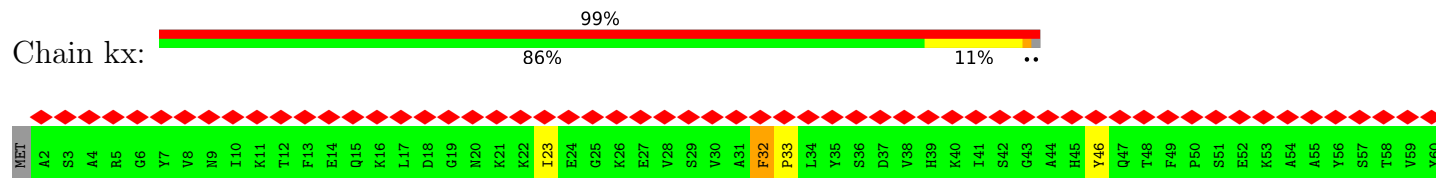
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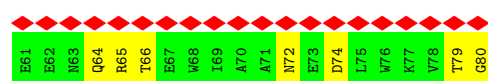
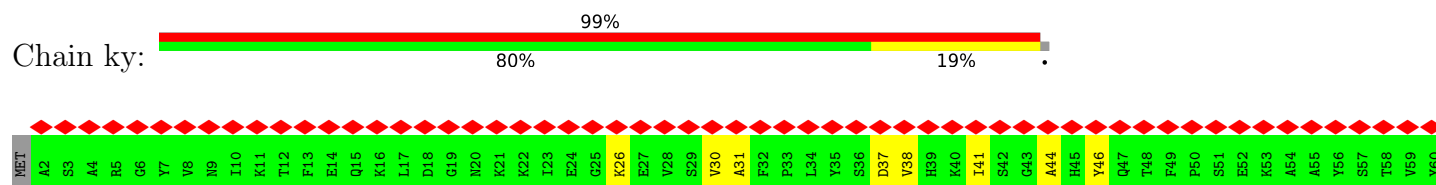
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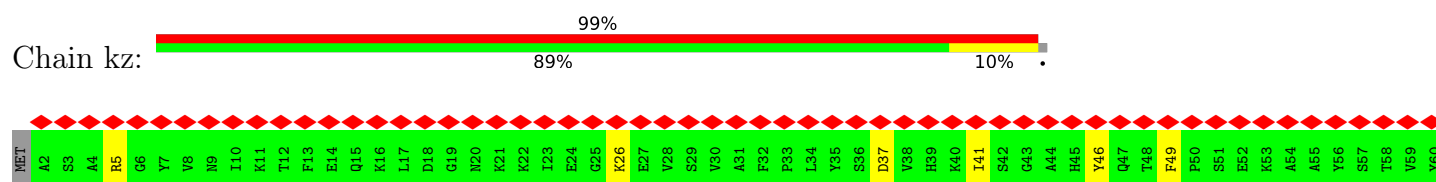
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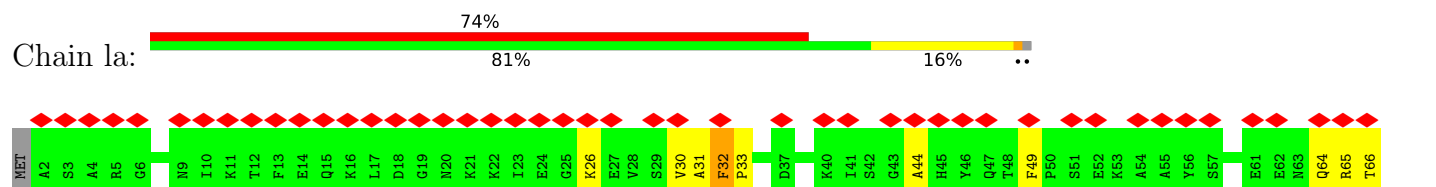
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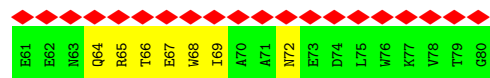
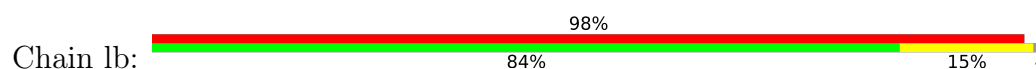


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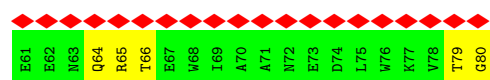
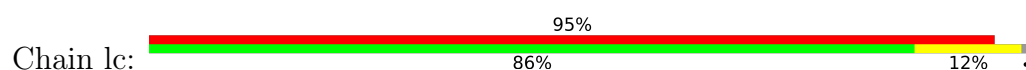




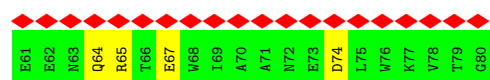
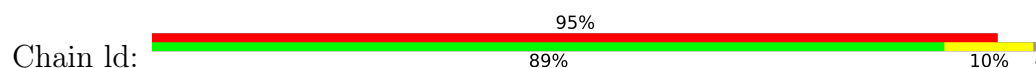
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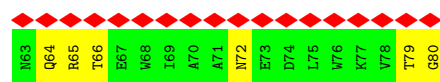
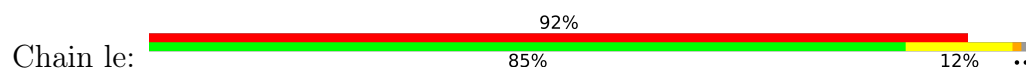
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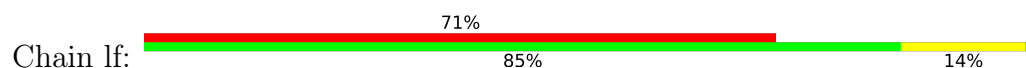
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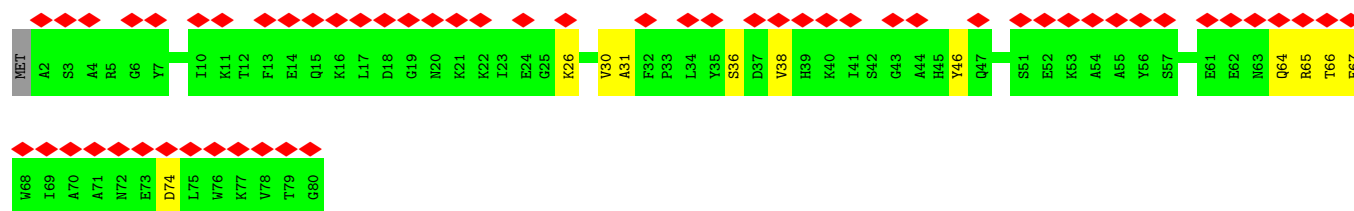


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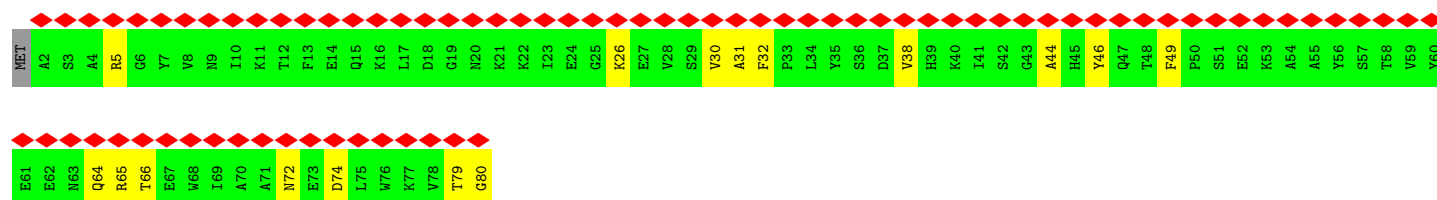
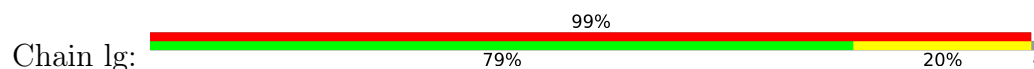


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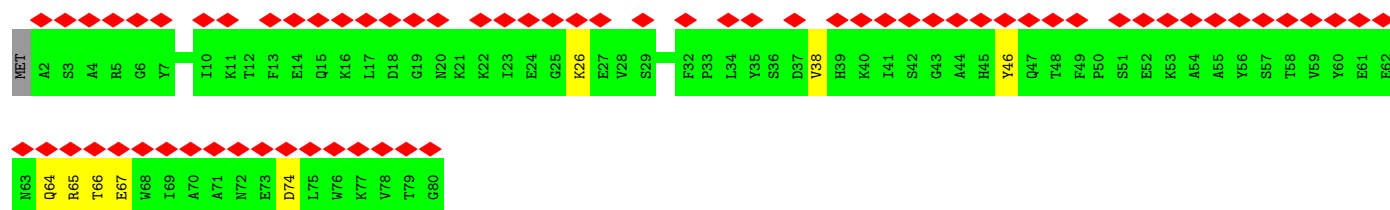
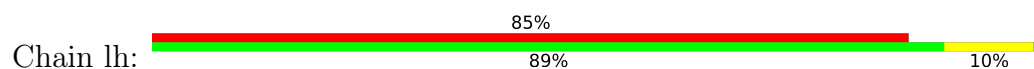




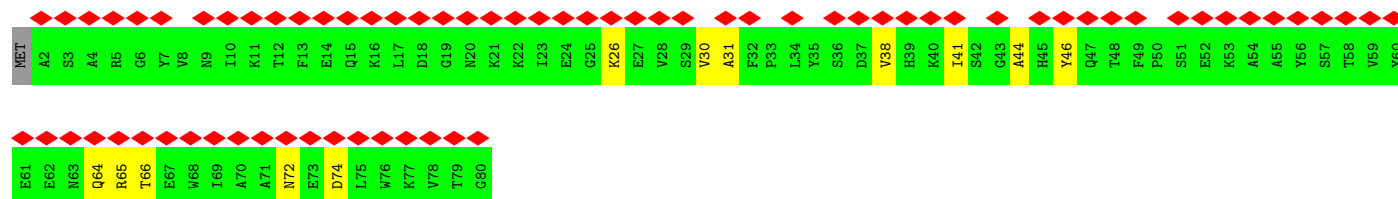
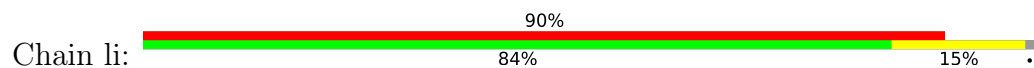
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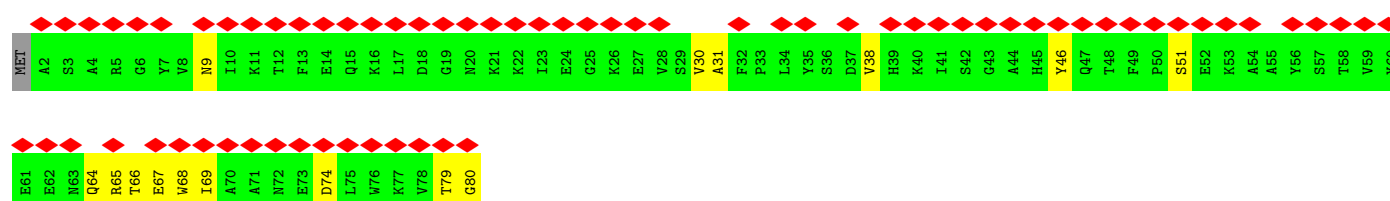
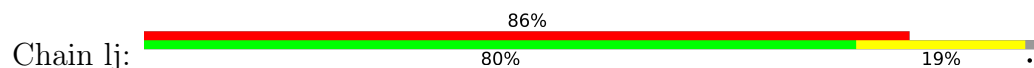
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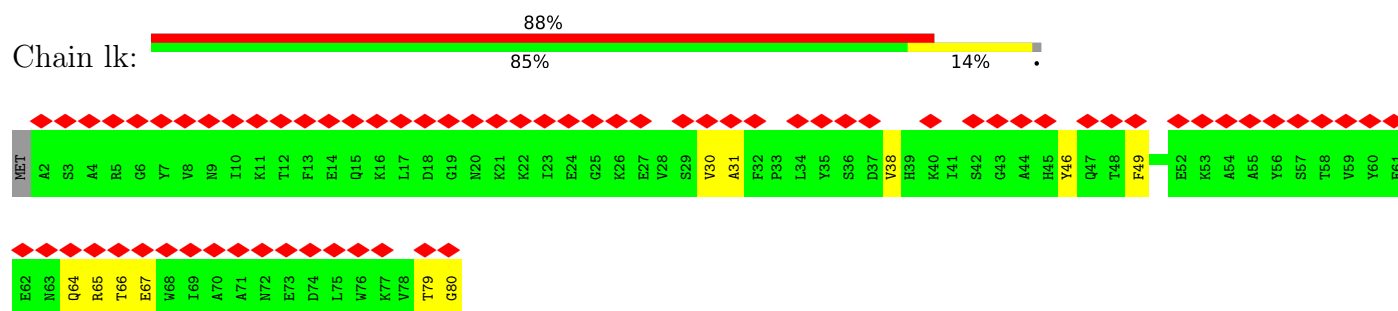
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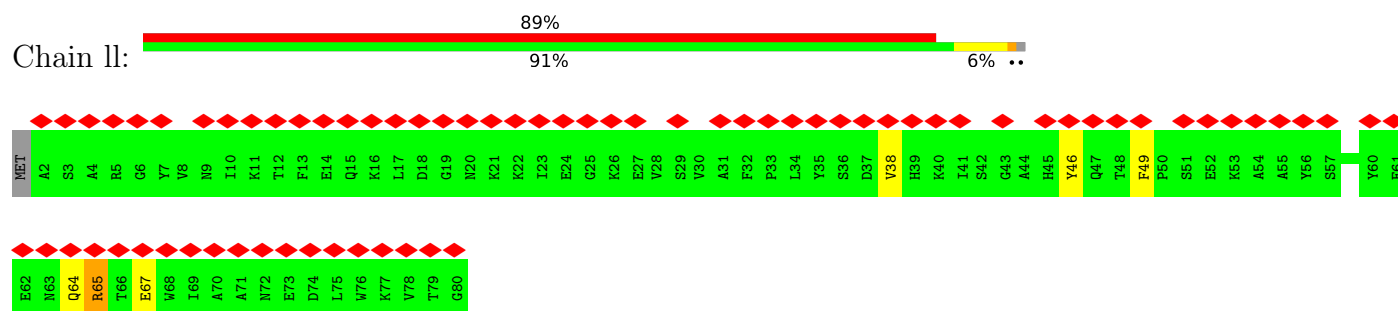
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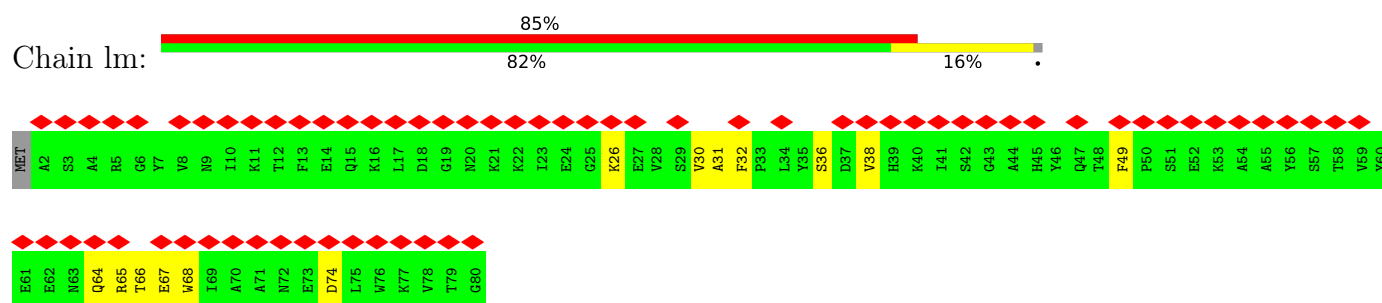
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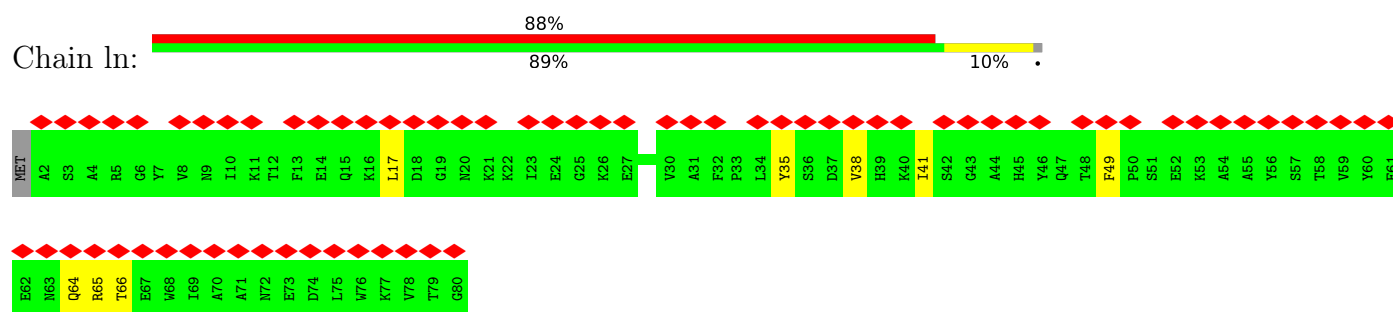
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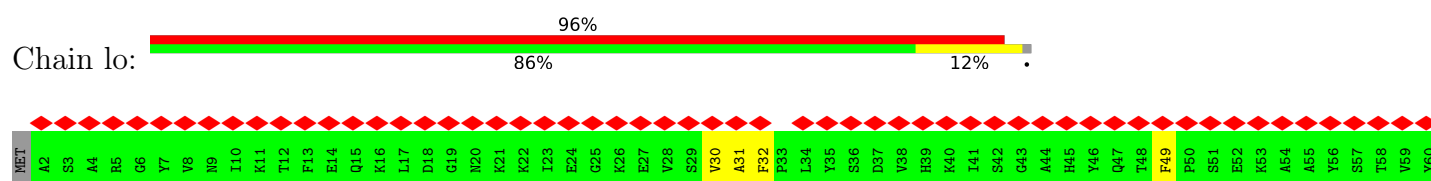
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• Molecule 3: Small outer capsid protein

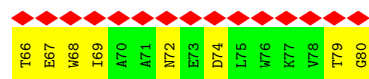
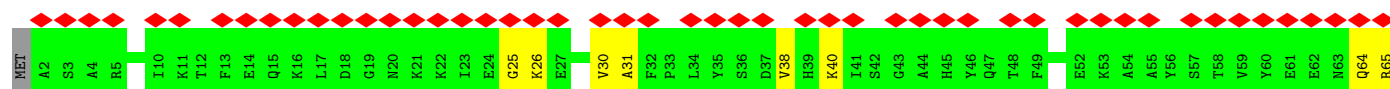
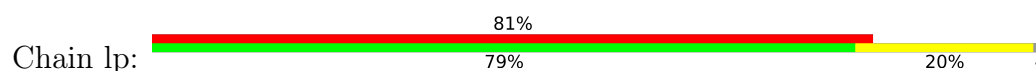


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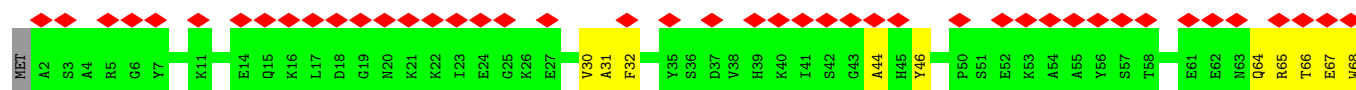
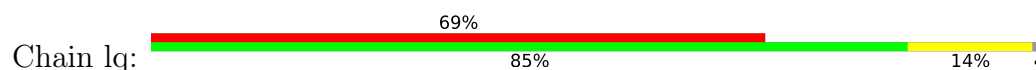




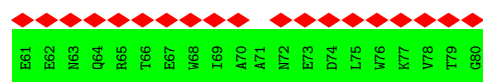
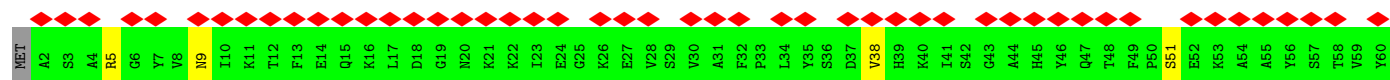
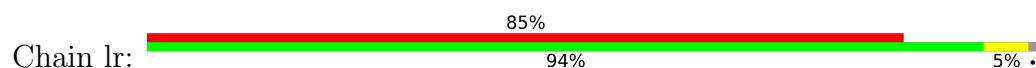
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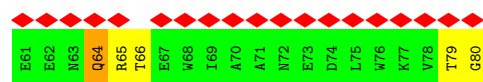
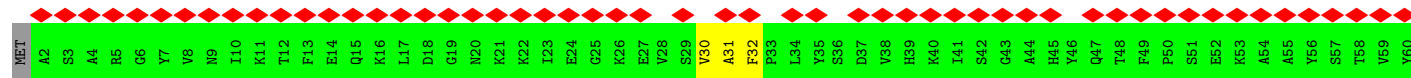
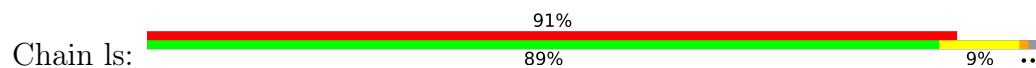
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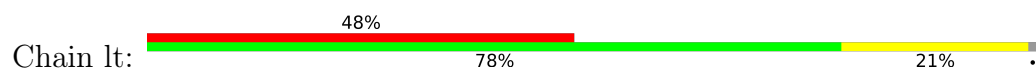
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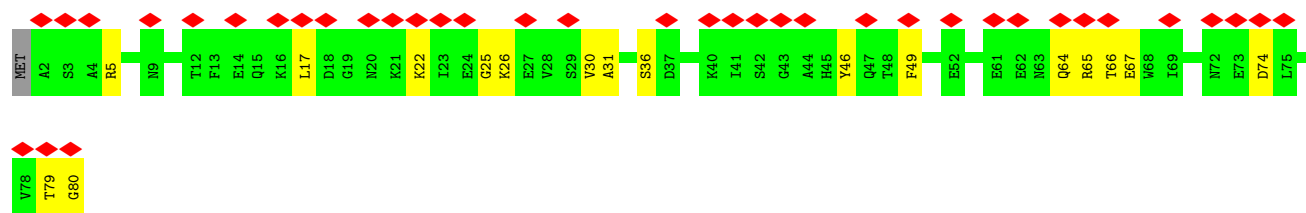


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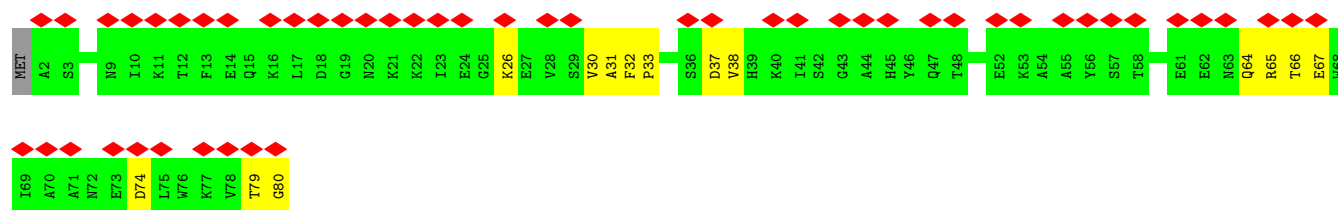
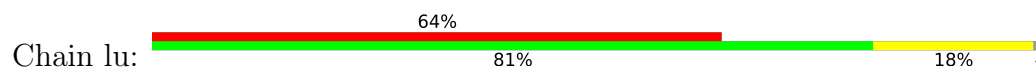


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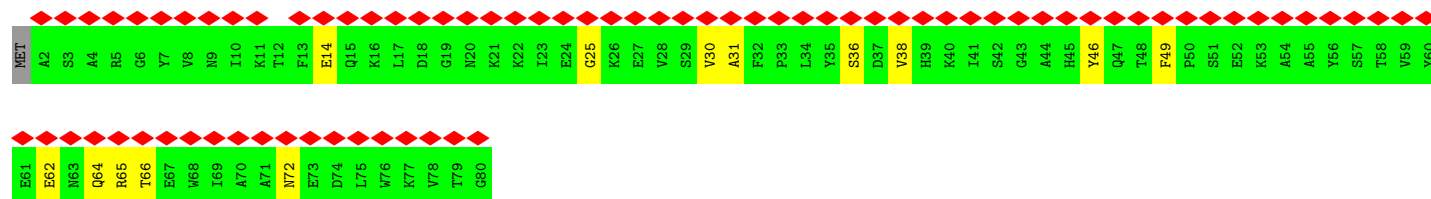
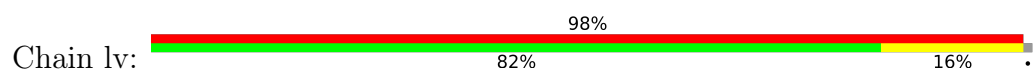




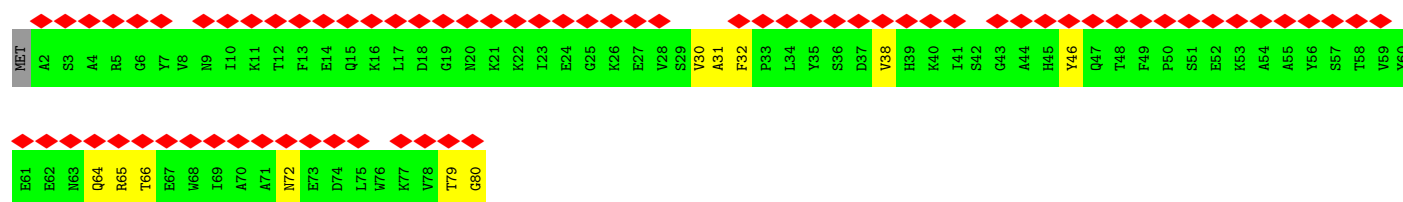
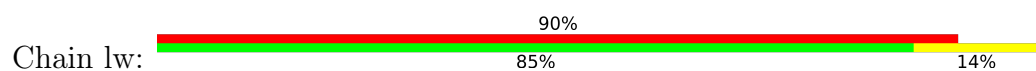
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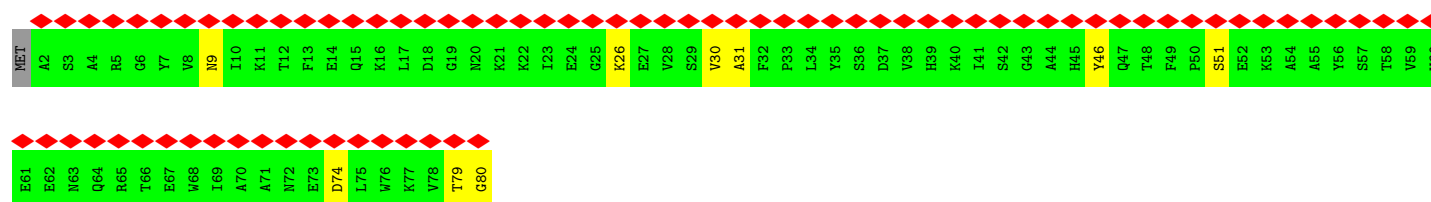
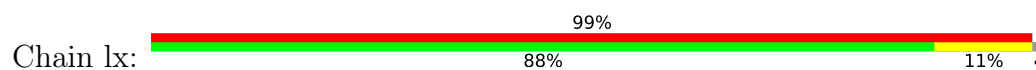
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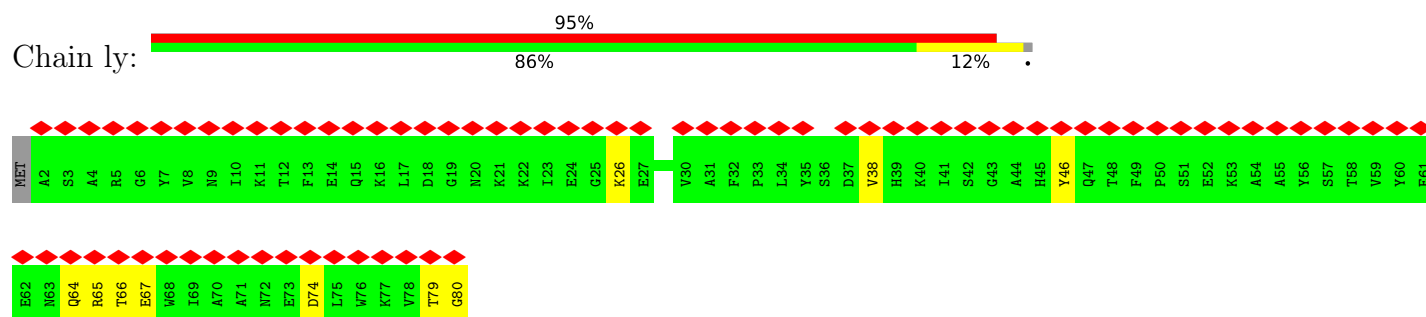
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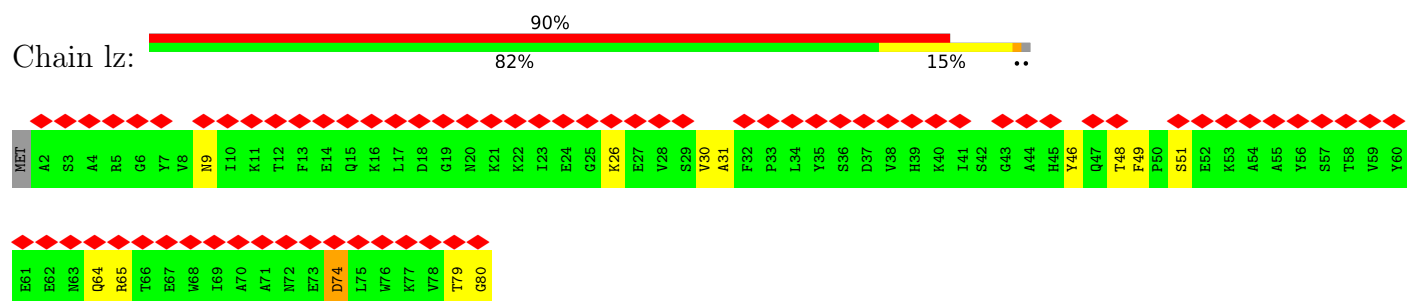
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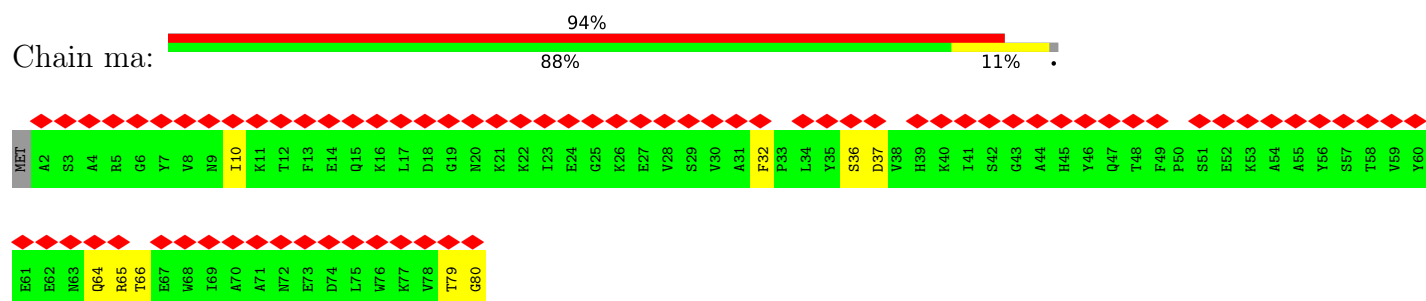
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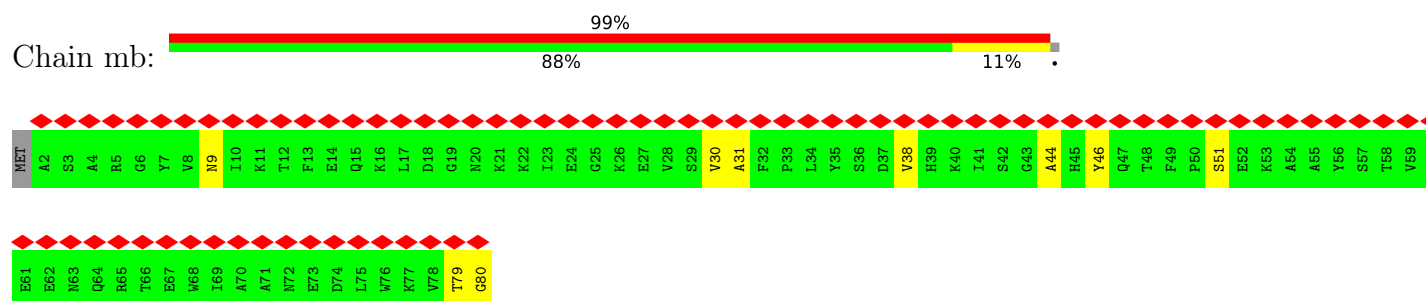
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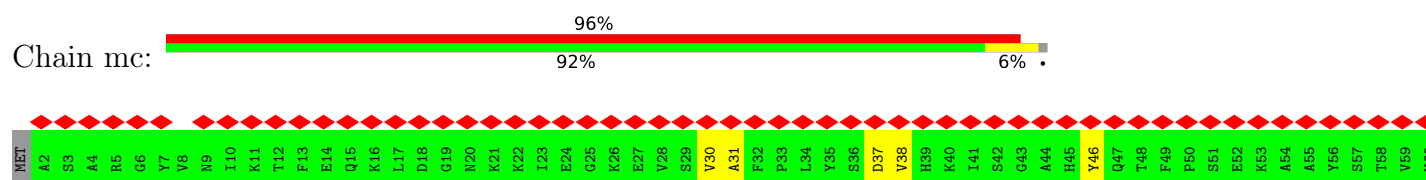
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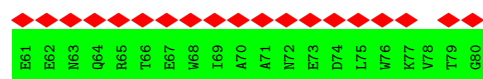


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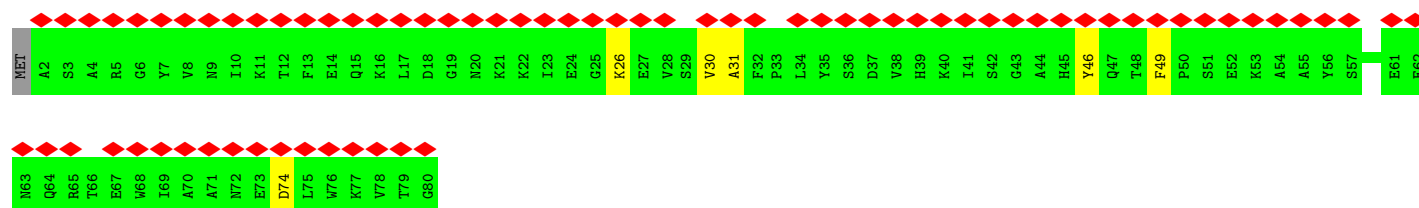


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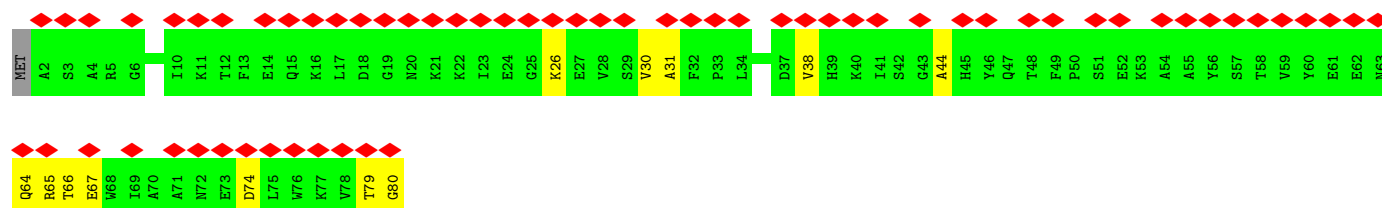
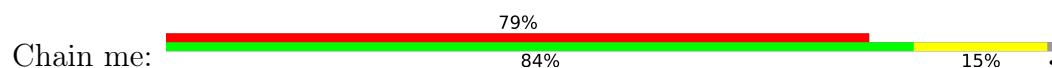




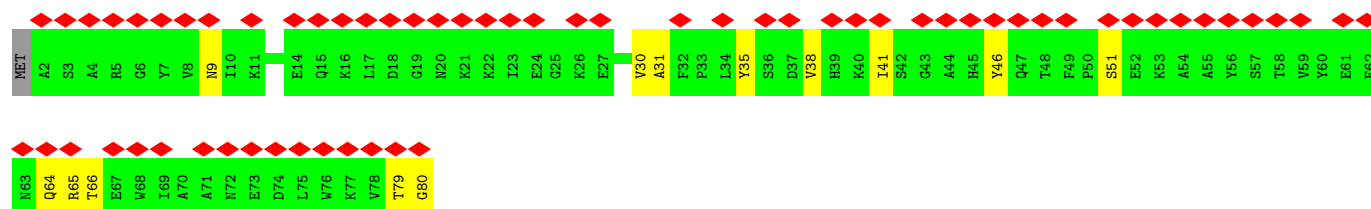
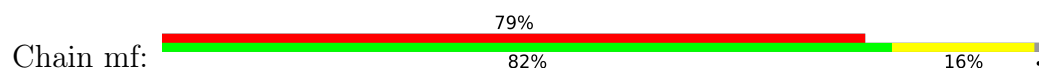
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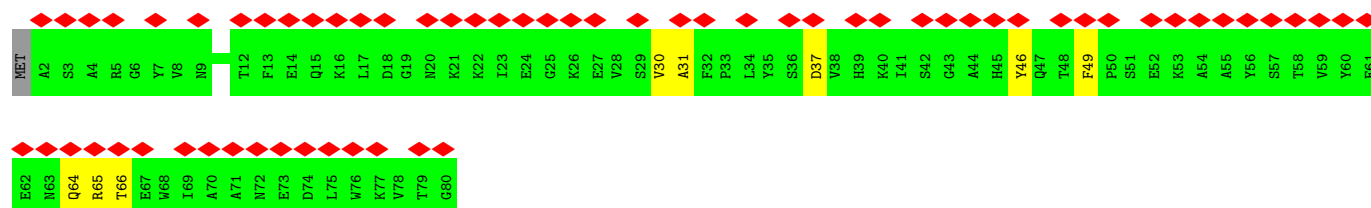
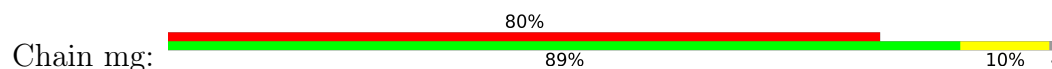
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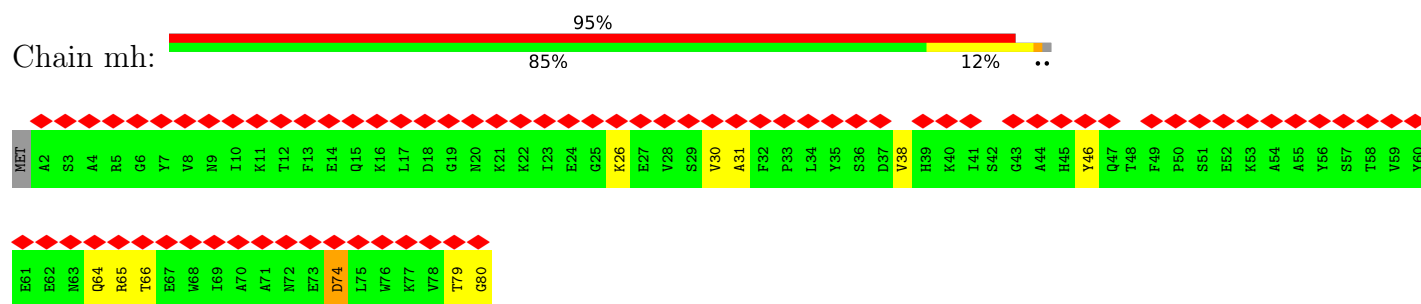
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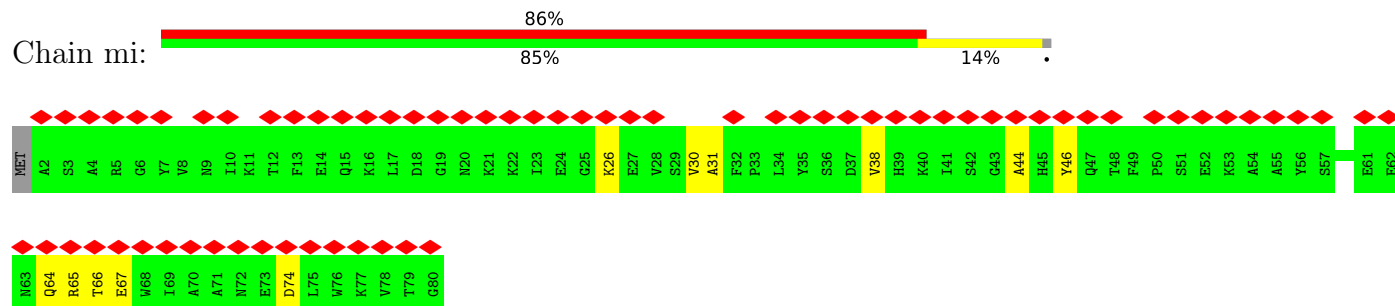
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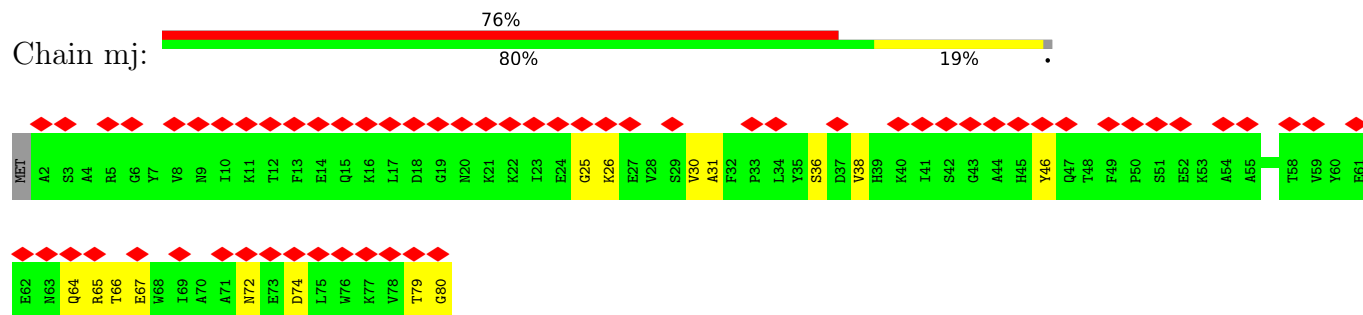
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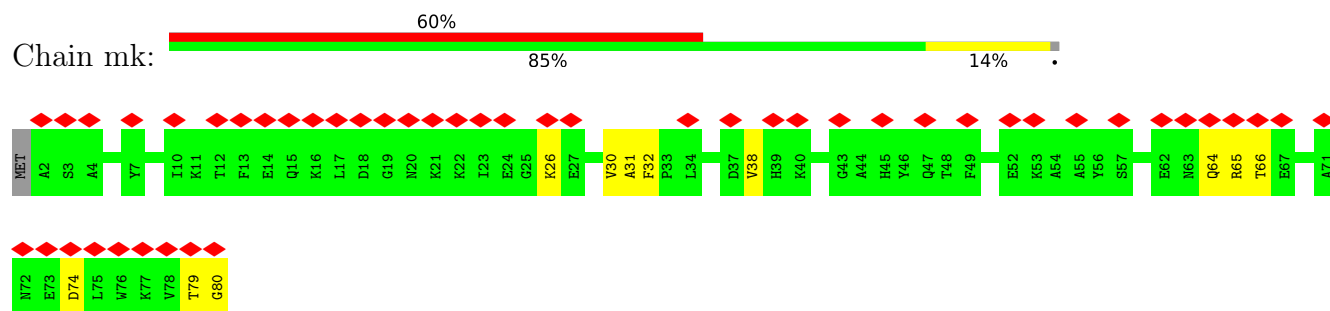
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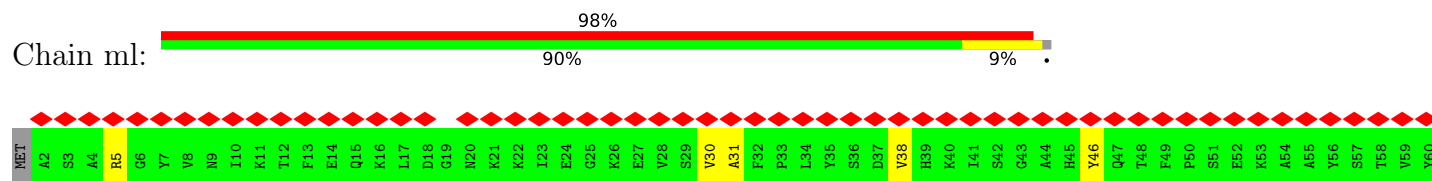
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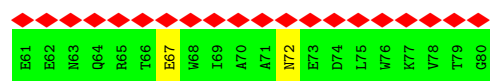


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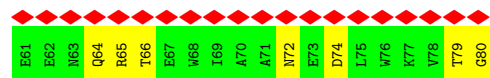
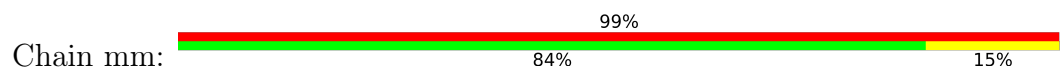


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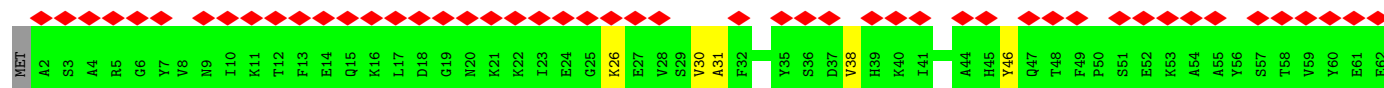
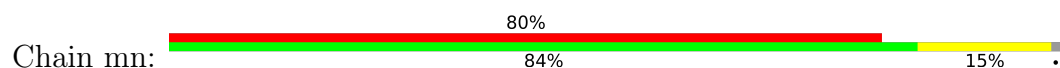




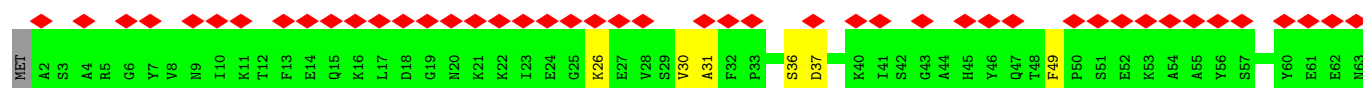
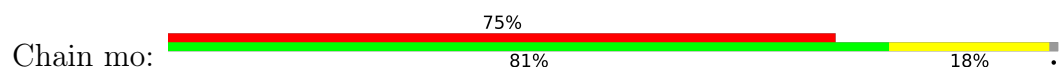
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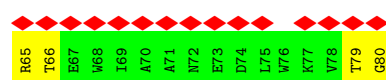
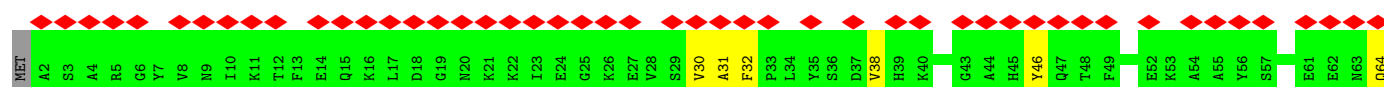
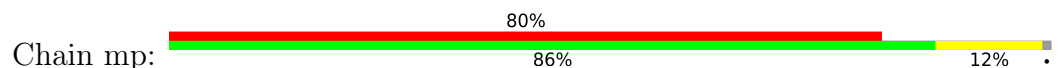
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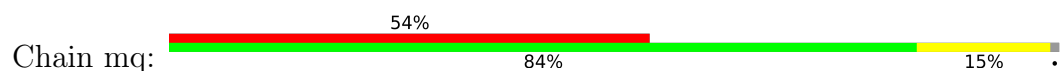
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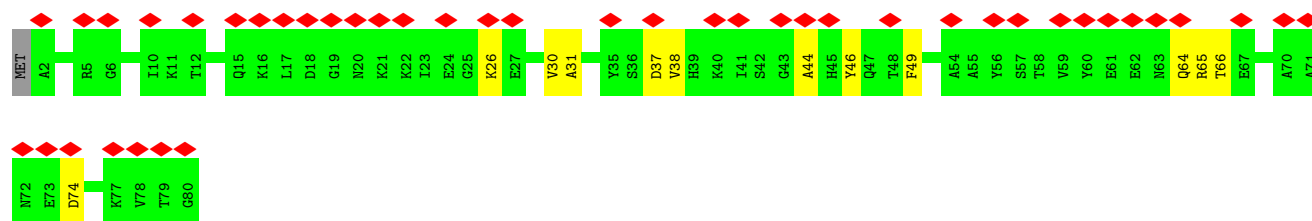


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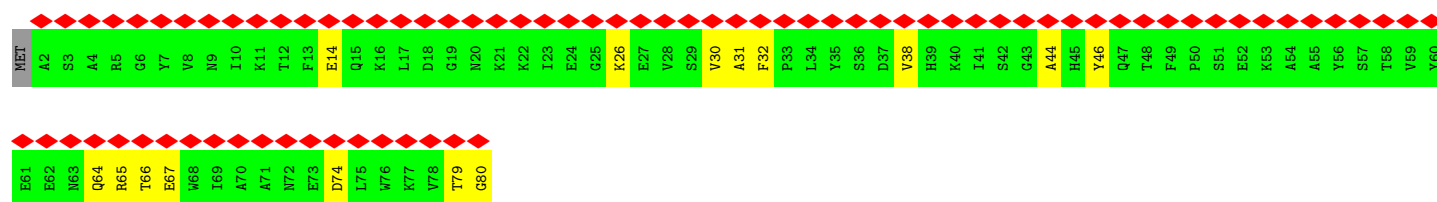
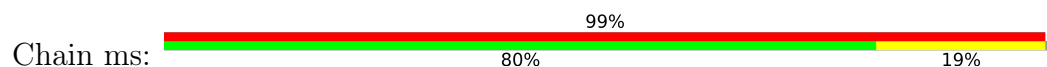


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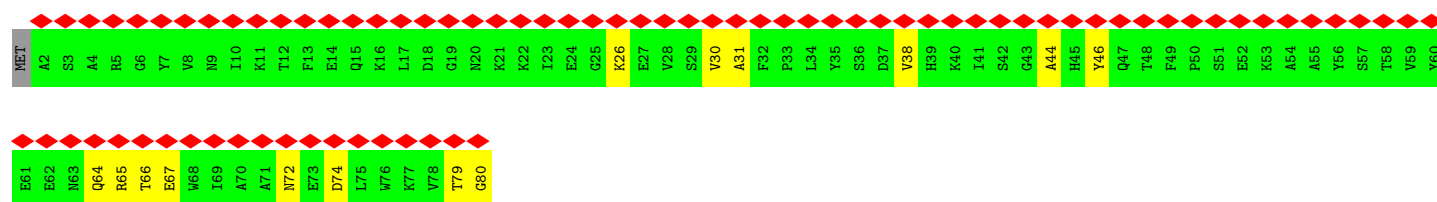
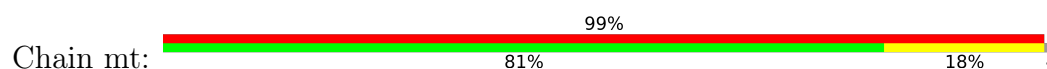




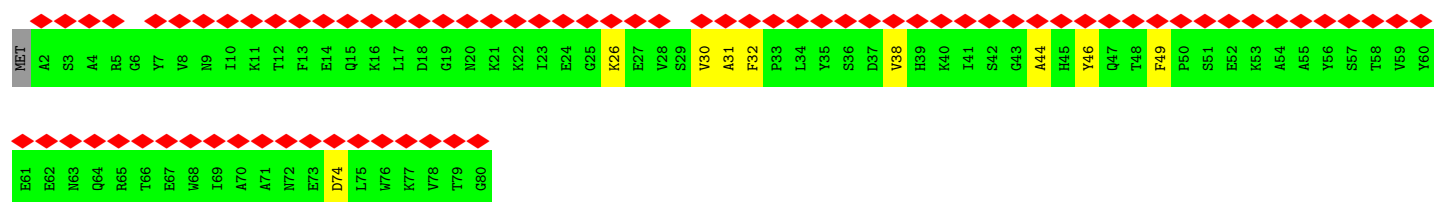
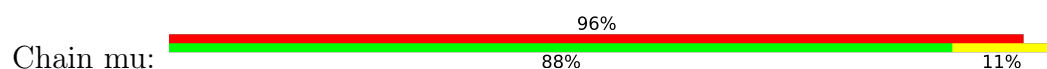
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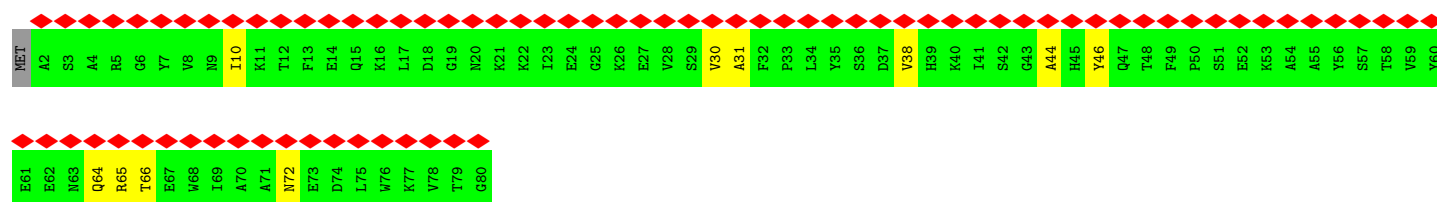
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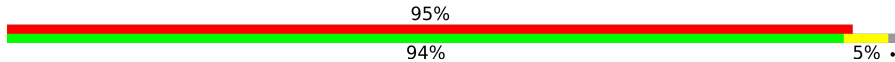
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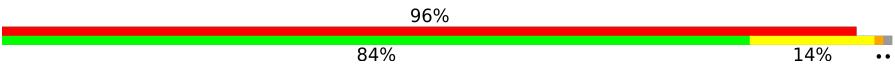


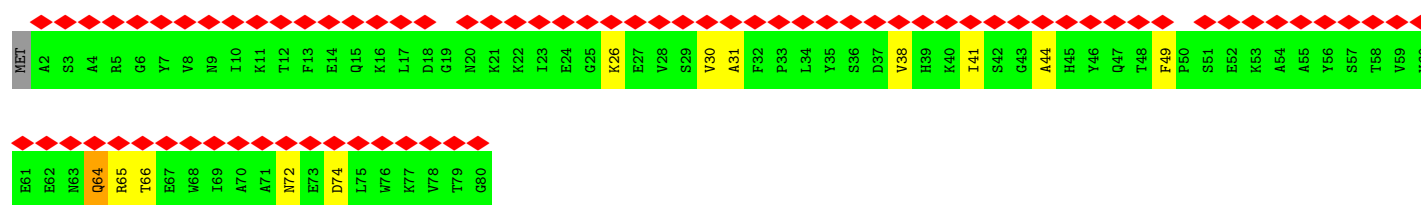
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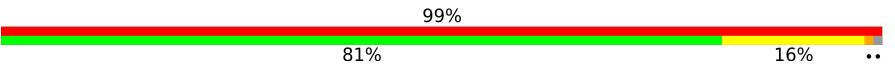


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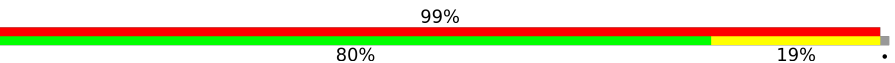


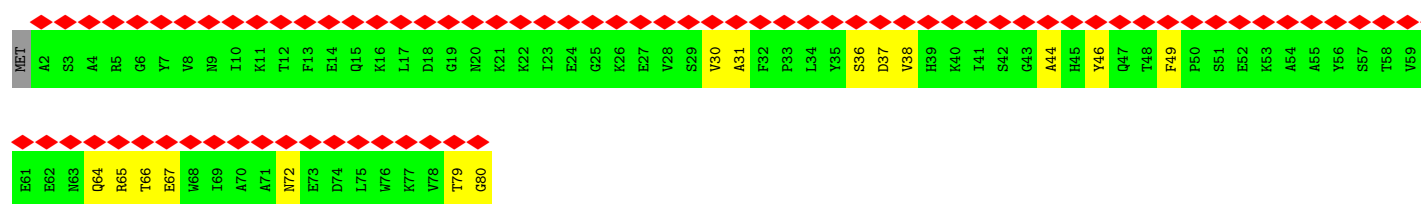
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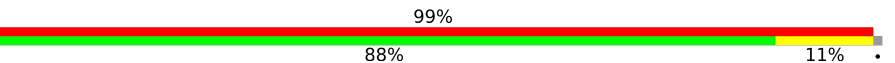


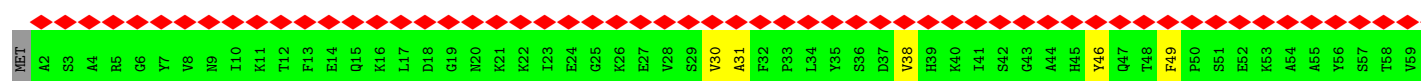
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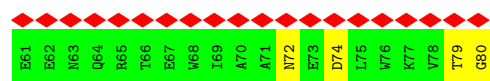
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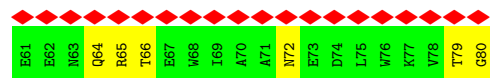
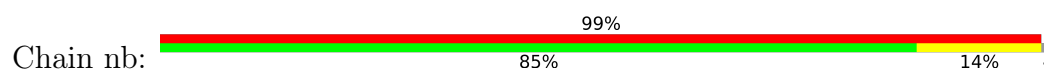
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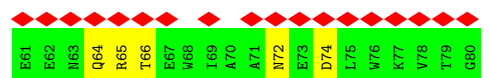
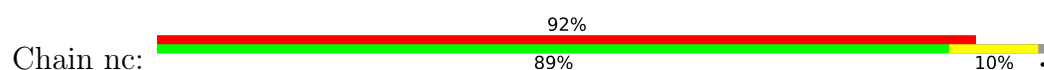




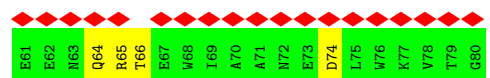
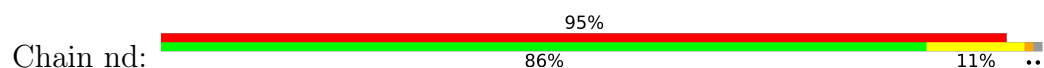
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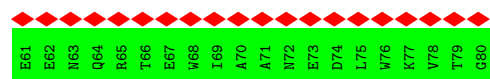
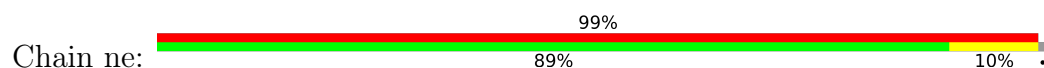
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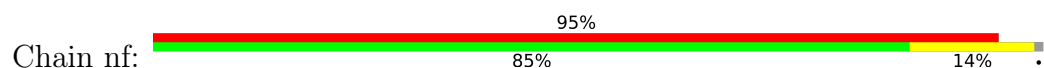
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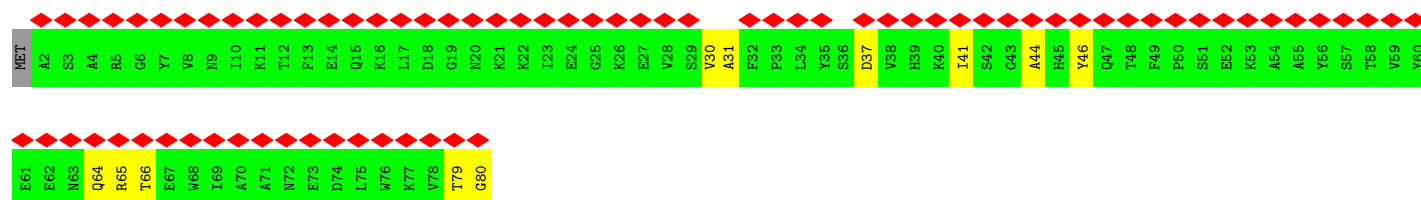


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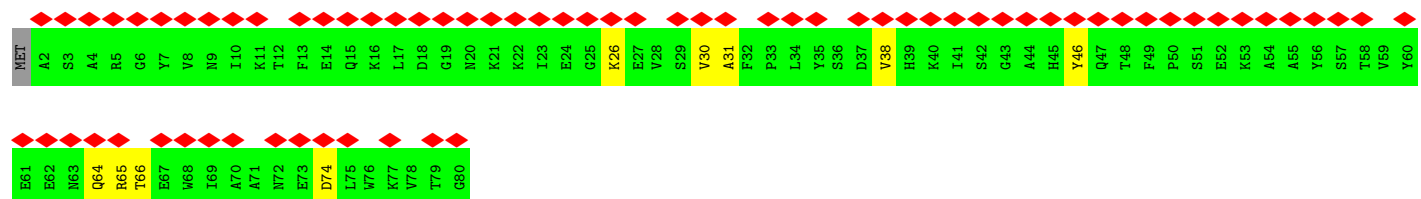
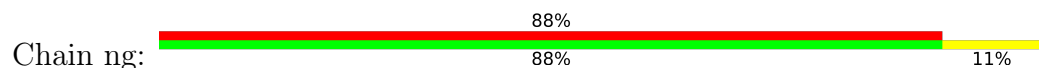


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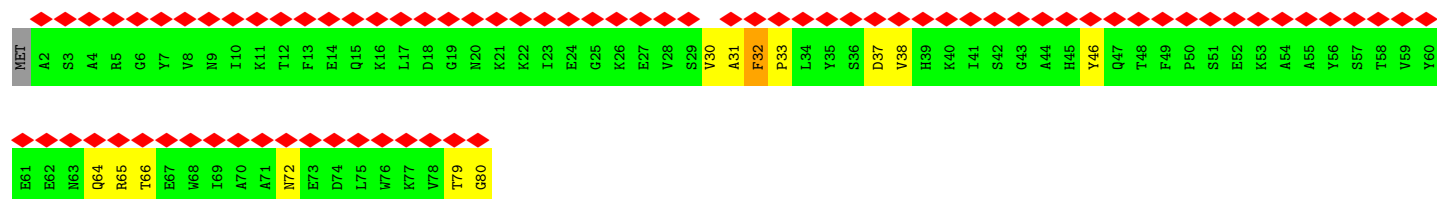
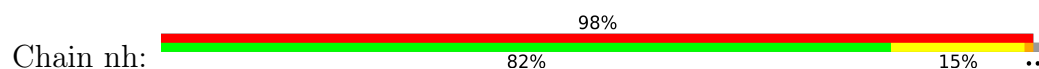




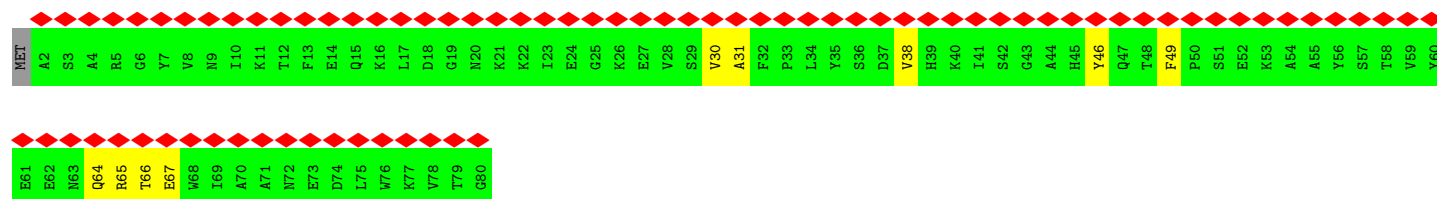
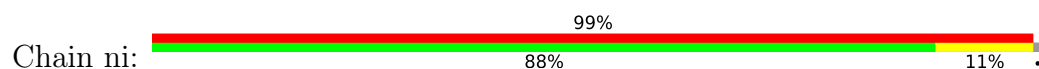
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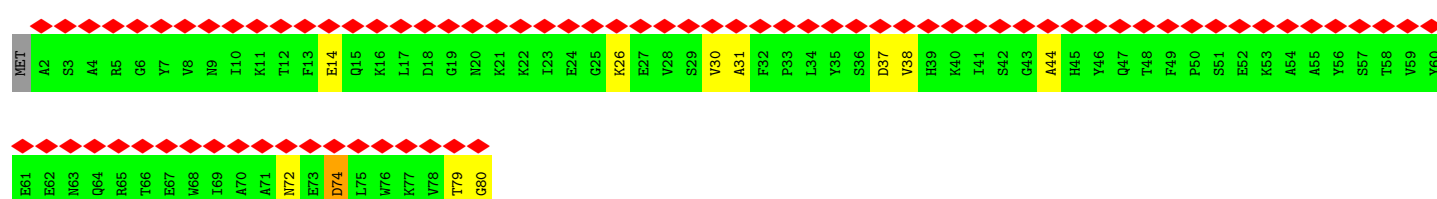
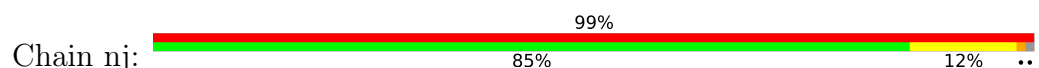
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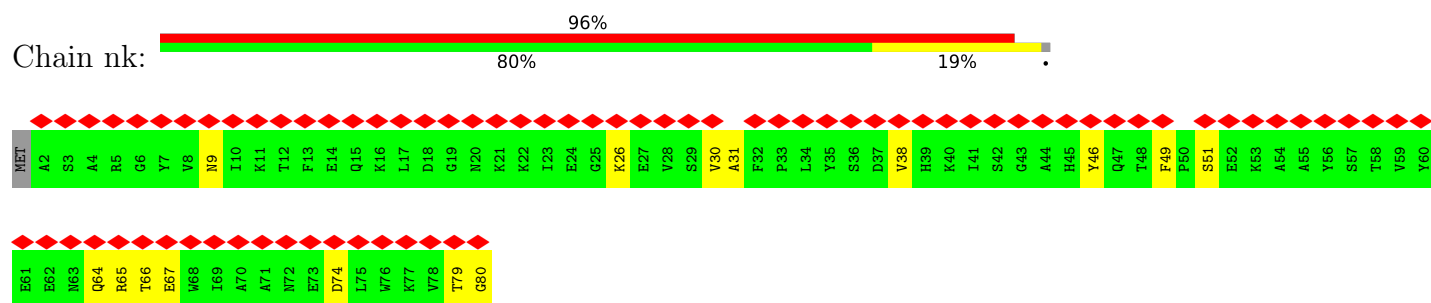
• Molecule 3: Small outer capsid protein



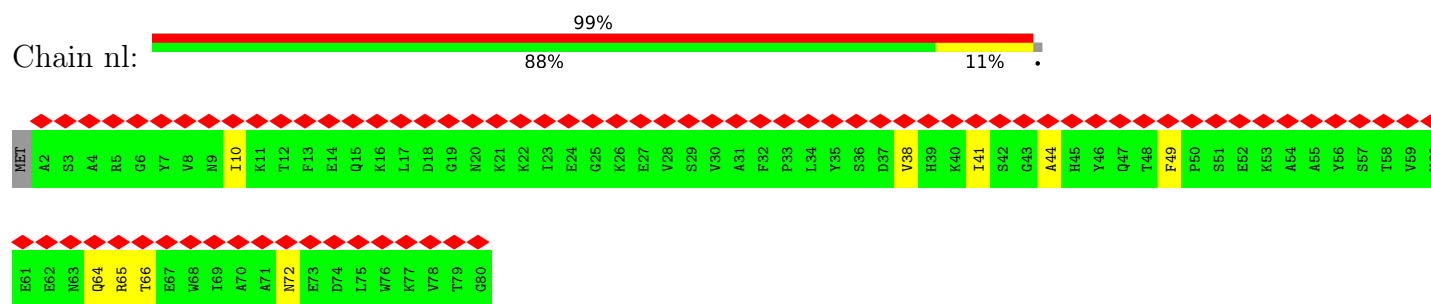
• Molecule 3: Small outer capsid protein



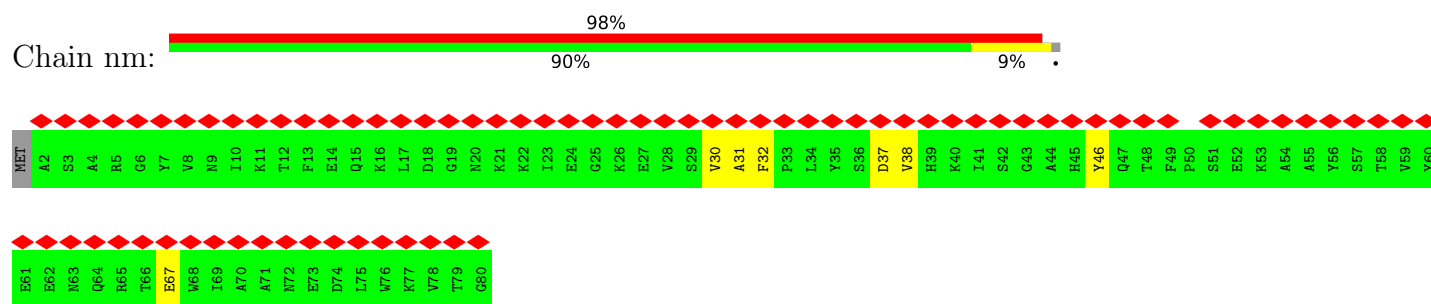
• Molecule 3: Small outer capsid protein



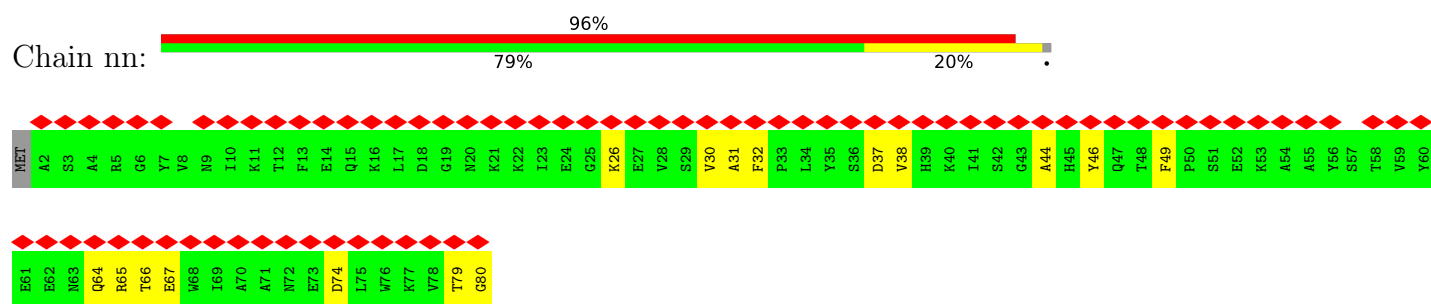
• Molecule 3: Small outer capsid protein



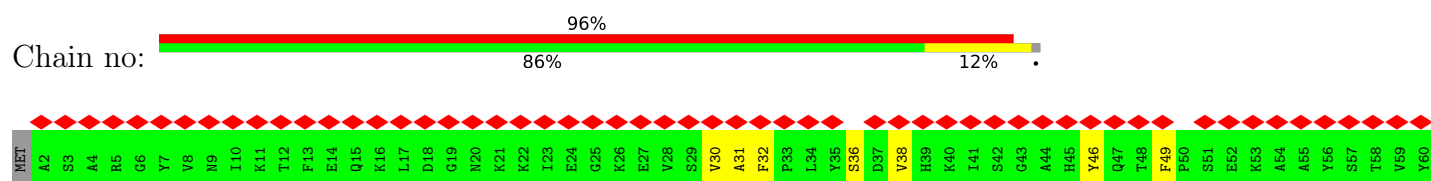
• Molecule 3: Small outer capsid protein

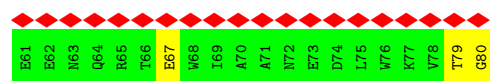


• Molecule 3: Small outer capsid protein

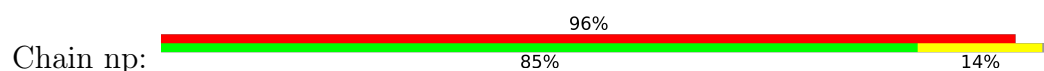


• Molecule 3: Small outer capsid protein

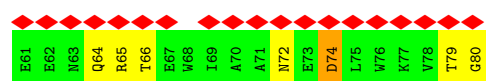
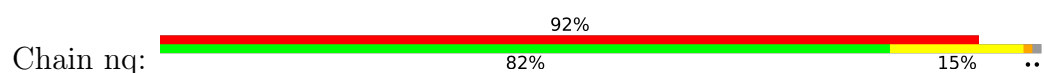




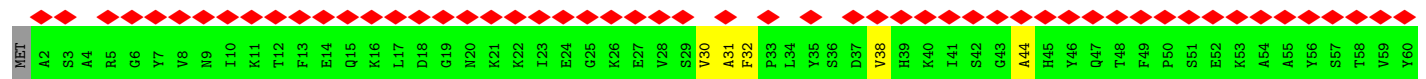
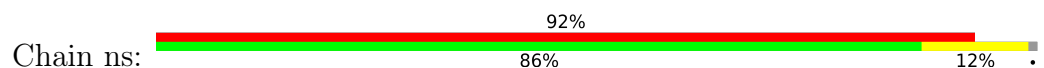
• Molecule 3: Small outer capsid protein



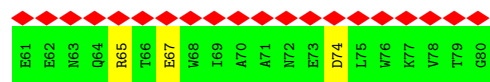
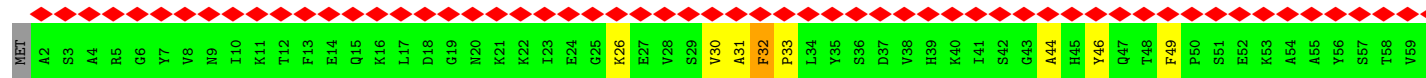
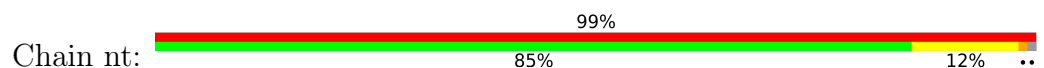
• Molecule 3: Small outer capsid protein



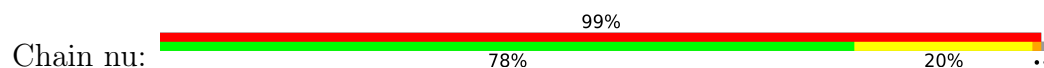
• Molecule 3: Small outer capsid protein

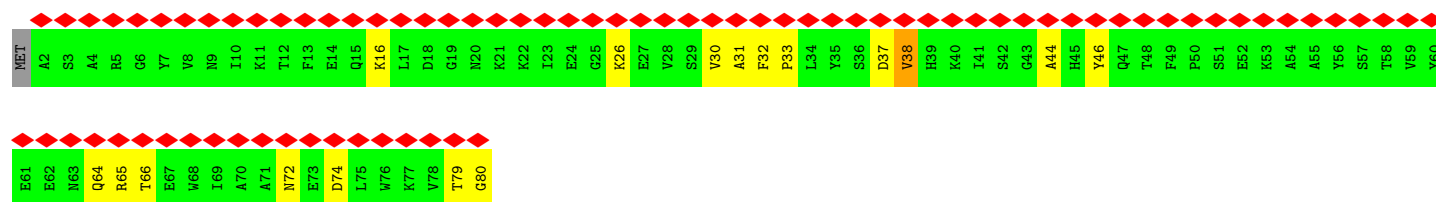


• Molecule 3: Small outer capsid protein

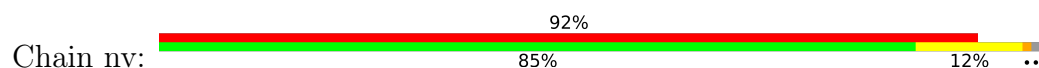


• Molecule 3: Small outer capsid protein

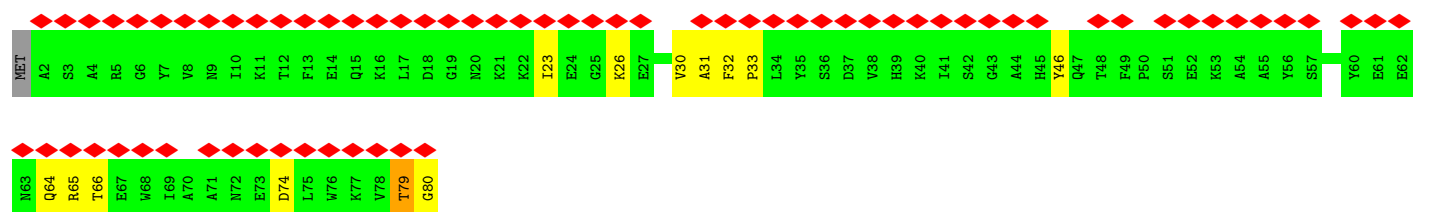
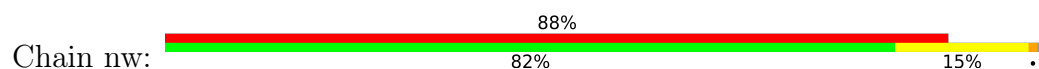




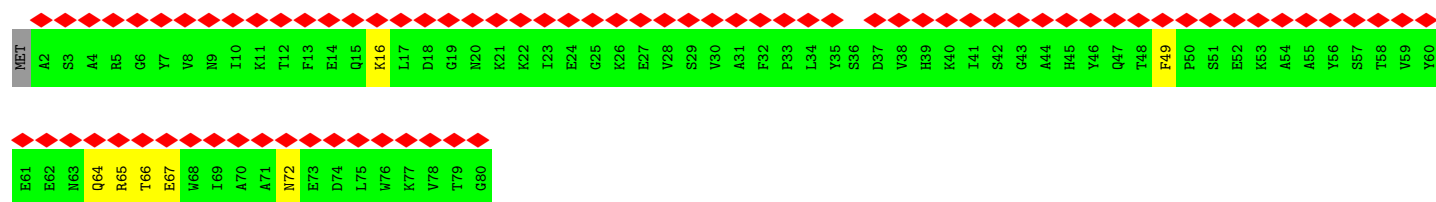
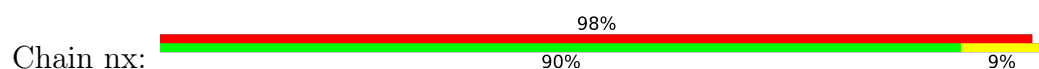
• Molecule 3: Small outer capsid protein



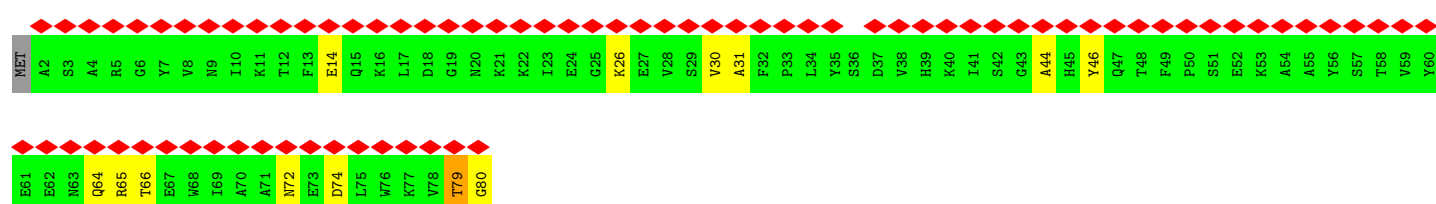
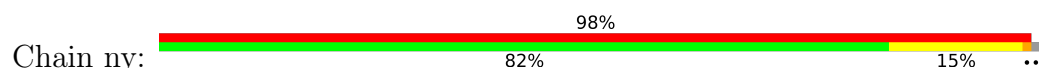
• Molecule 3: Small outer capsid protein



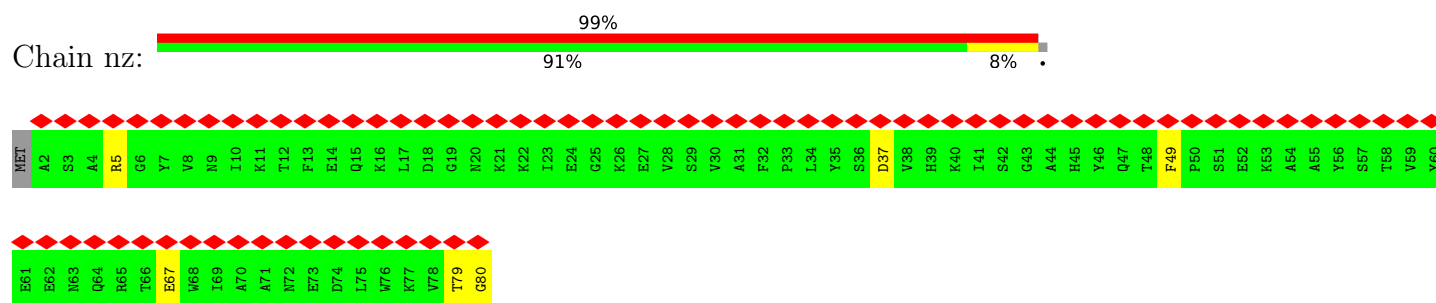
• Molecule 3: Small outer capsid protein



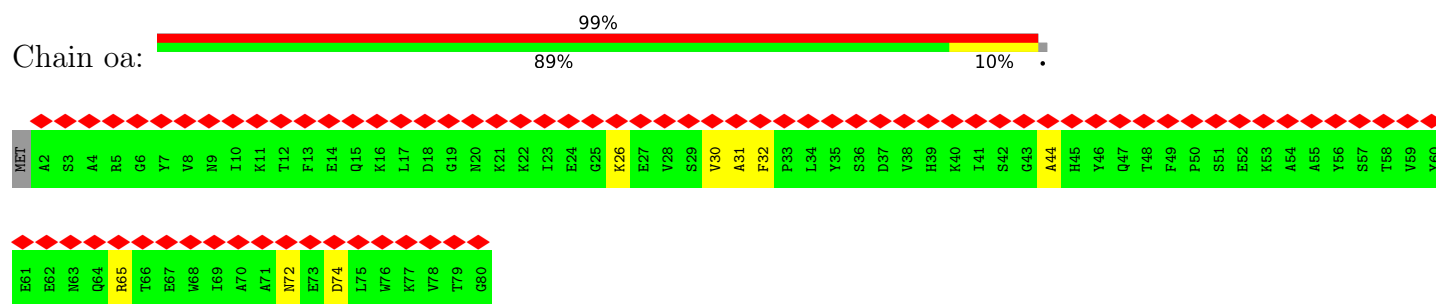
• Molecule 3: Small outer capsid protein



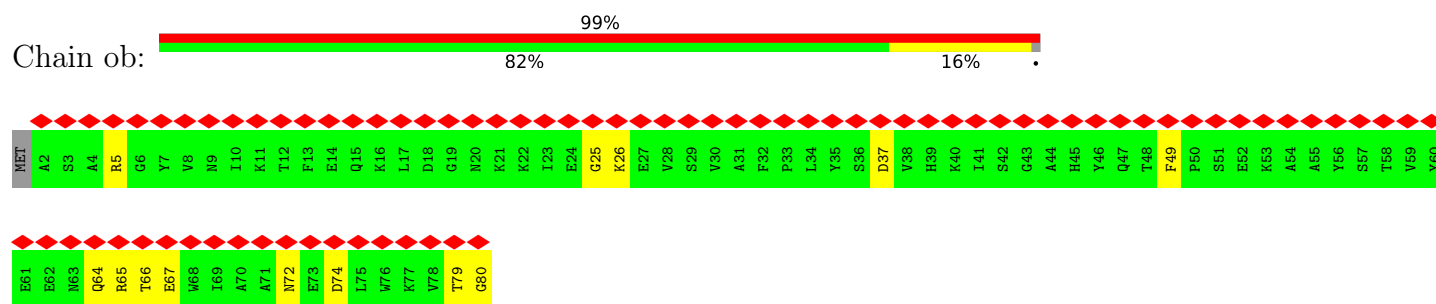
• Molecule 3: Small outer capsid protein



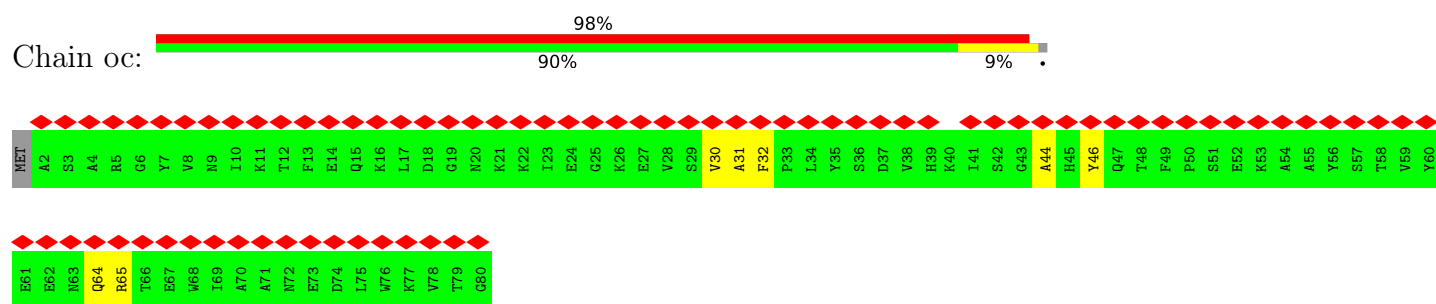
• Molecule 3: Small outer capsid protein



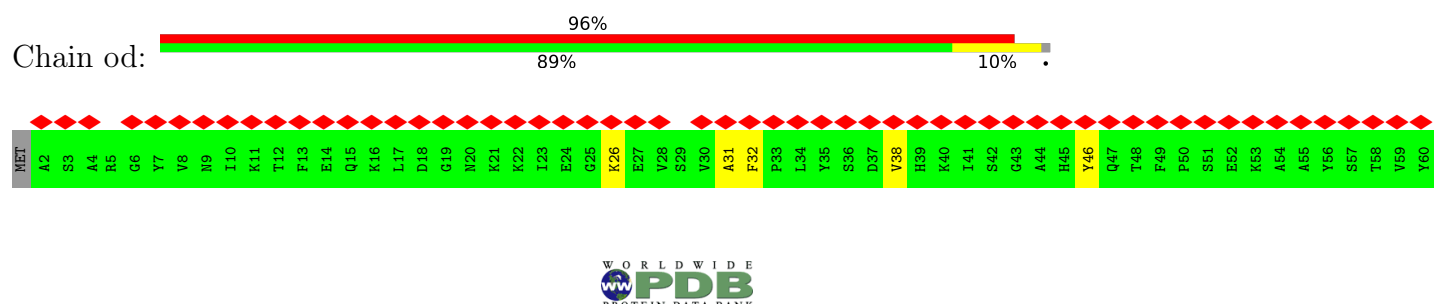
• Molecule 3: Small outer capsid protein

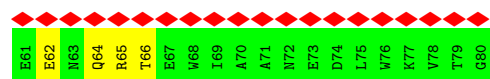


• Molecule 3: Small outer capsid protein



• Molecule 3: Small outer capsid protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	53608	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	23.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.990	Depositor
Minimum map value	-0.745	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	1382.4, 1382.4, 1382.4	wwPDB
Map dimensions	960, 960, 960	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.44, 1.44, 1.44	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	aa	0.98	0/3493	1.33	31/4731 (0.7%)
1	ab	0.96	0/3493	1.34	30/4731 (0.6%)
1	ac	0.95	0/3493	1.32	38/4731 (0.8%)
1	ad	0.96	0/3493	1.36	32/4731 (0.7%)
1	ae	0.98	0/3493	1.37	40/4731 (0.8%)
1	af	0.96	0/3493	1.33	35/4731 (0.7%)
1	ag	0.96	1/3493 (0.0%)	1.35	35/4731 (0.7%)
1	ah	0.95	0/3493	1.33	34/4731 (0.7%)
1	ai	0.96	1/3493 (0.0%)	1.32	32/4731 (0.7%)
1	aj	0.94	1/3493 (0.0%)	1.33	32/4731 (0.7%)
1	ak	0.95	0/3493	1.32	29/4731 (0.6%)
1	al	0.98	1/3493 (0.0%)	1.36	35/4731 (0.7%)
1	am	0.95	0/3493	1.37	44/4731 (0.9%)
1	an	0.98	1/3493 (0.0%)	1.35	38/4731 (0.8%)
1	ao	0.97	1/3493 (0.0%)	1.33	29/4731 (0.6%)
1	ap	0.95	0/3493	1.34	38/4731 (0.8%)
1	aq	0.96	0/3493	1.33	25/4731 (0.5%)
1	ar	0.95	0/3493	1.33	36/4731 (0.8%)
1	as	1.00	0/3493	1.37	36/4731 (0.8%)
1	at	0.98	2/3493 (0.1%)	1.38	50/4731 (1.1%)
1	au	0.98	3/3493 (0.1%)	1.33	35/4731 (0.7%)
1	av	0.94	0/3493	1.35	31/4731 (0.7%)
1	aw	0.97	2/3493 (0.1%)	1.39	39/4731 (0.8%)
1	ax	0.97	0/3493	1.35	37/4731 (0.8%)
1	ay	0.96	1/3493 (0.0%)	1.34	33/4731 (0.7%)
1	az	0.96	1/3493 (0.0%)	1.33	35/4731 (0.7%)
1	ba	0.97	1/3493 (0.0%)	1.35	35/4731 (0.7%)
1	bb	0.97	0/3493	1.36	38/4731 (0.8%)
1	bc	0.94	0/3493	1.33	31/4731 (0.7%)
1	bd	0.96	0/3493	1.33	40/4731 (0.8%)
1	be	0.97	0/3493	1.37	33/4731 (0.7%)
1	bf	1.00	2/3493 (0.1%)	1.35	31/4731 (0.7%)
1	bg	0.97	0/3493	1.35	41/4731 (0.9%)
1	bh	0.94	0/3493	1.36	34/4731 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	bi	0.97	0/3493	1.36	38/4731 (0.8%)
1	bj	0.97	0/3493	1.33	34/4731 (0.7%)
1	bk	0.97	0/3493	1.32	33/4731 (0.7%)
1	bl	0.96	1/3493 (0.0%)	1.35	35/4731 (0.7%)
1	bm	0.96	1/3493 (0.0%)	1.33	39/4731 (0.8%)
1	bn	0.99	0/3493	1.32	28/4731 (0.6%)
1	bo	0.97	1/3493 (0.0%)	1.35	44/4731 (0.9%)
1	bp	0.95	0/3493	1.35	46/4731 (1.0%)
1	bq	0.94	0/3493	1.35	38/4731 (0.8%)
1	br	0.96	1/3493 (0.0%)	1.36	43/4731 (0.9%)
1	bs	0.97	1/3493 (0.0%)	1.35	32/4731 (0.7%)
1	bt	0.95	0/3493	1.35	37/4731 (0.8%)
1	bu	0.98	0/3493	1.39	37/4731 (0.8%)
1	bv	0.97	0/3493	1.33	24/4731 (0.5%)
1	bw	0.94	0/3493	1.38	40/4731 (0.8%)
1	bx	0.97	1/3493 (0.0%)	1.33	38/4731 (0.8%)
1	by	0.98	0/3493	1.37	36/4731 (0.8%)
1	bz	0.98	2/3493 (0.1%)	1.36	27/4731 (0.6%)
1	ca	0.96	0/3493	1.36	40/4731 (0.8%)
1	cb	0.97	0/3493	1.35	31/4731 (0.7%)
1	cc	0.97	0/3493	1.35	42/4731 (0.9%)
1	cd	0.95	0/3493	1.32	33/4731 (0.7%)
1	ce	0.99	0/3493	1.34	43/4731 (0.9%)
1	cf	0.95	0/3493	1.32	28/4731 (0.6%)
1	cg	0.95	1/3493 (0.0%)	1.32	33/4731 (0.7%)
1	ch	0.97	1/3493 (0.0%)	1.34	33/4731 (0.7%)
1	ci	0.97	1/3493 (0.0%)	1.40	51/4731 (1.1%)
1	cj	0.96	0/3493	1.36	45/4731 (1.0%)
1	ck	0.97	1/3493 (0.0%)	1.37	41/4731 (0.9%)
1	cl	0.97	0/3493	1.33	32/4731 (0.7%)
1	cm	0.97	0/3493	1.36	32/4731 (0.7%)
1	cn	0.96	2/3493 (0.1%)	1.36	41/4731 (0.9%)
1	co	0.97	0/3493	1.36	41/4731 (0.9%)
1	cp	0.96	0/3493	1.32	27/4731 (0.6%)
1	cq	0.96	0/3493	1.38	42/4731 (0.9%)
1	cr	0.96	1/3493 (0.0%)	1.34	33/4731 (0.7%)
1	cs	0.93	1/3493 (0.0%)	1.37	43/4731 (0.9%)
1	ct	0.95	1/3493 (0.0%)	1.34	38/4731 (0.8%)
1	cu	0.95	0/3493	1.33	34/4731 (0.7%)
1	cv	0.95	1/3493 (0.0%)	1.33	35/4731 (0.7%)
1	cw	0.95	0/3493	1.35	42/4731 (0.9%)
1	cx	0.94	1/3493 (0.0%)	1.35	40/4731 (0.8%)
1	cy	0.96	0/3493	1.34	37/4731 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	cz	0.94	0/3493	1.36	36/4731 (0.8%)
1	da	0.95	1/3493 (0.0%)	1.35	32/4731 (0.7%)
1	db	0.97	1/3493 (0.0%)	1.35	37/4731 (0.8%)
1	dc	0.94	0/3493	1.35	41/4731 (0.9%)
1	dd	0.95	0/3493	1.35	40/4731 (0.8%)
1	de	0.95	0/3493	1.37	38/4731 (0.8%)
1	df	0.97	1/3493 (0.0%)	1.35	38/4731 (0.8%)
1	dg	0.96	0/3493	1.37	42/4731 (0.9%)
1	dh	0.98	1/3493 (0.0%)	1.36	34/4731 (0.7%)
1	di	0.97	1/3493 (0.0%)	1.37	31/4731 (0.7%)
1	dj	0.98	0/3493	1.32	33/4731 (0.7%)
1	dk	0.98	0/3493	1.38	36/4731 (0.8%)
1	dl	0.96	2/3493 (0.1%)	1.37	44/4731 (0.9%)
1	dm	0.95	0/3493	1.38	40/4731 (0.8%)
1	dn	0.96	0/3493	1.33	31/4731 (0.7%)
1	do	0.98	1/3493 (0.0%)	1.34	39/4731 (0.8%)
1	dp	0.94	1/3493 (0.0%)	1.35	31/4731 (0.7%)
1	dq	0.96	1/3493 (0.0%)	1.34	37/4731 (0.8%)
1	dr	0.98	2/3493 (0.1%)	1.33	39/4731 (0.8%)
1	ds	0.94	0/3493	1.36	30/4731 (0.6%)
1	dt	0.97	1/3493 (0.0%)	1.34	30/4731 (0.6%)
1	du	0.98	1/3493 (0.0%)	1.34	35/4731 (0.7%)
1	dv	0.95	0/3493	1.33	33/4731 (0.7%)
1	dw	0.95	1/3315 (0.0%)	1.33	31/4488 (0.7%)
1	dx	0.97	0/3493	1.34	34/4731 (0.7%)
1	dy	0.98	0/3493	1.37	36/4731 (0.8%)
1	dz	0.96	0/3493	1.36	35/4731 (0.7%)
1	ea	0.98	1/3493 (0.0%)	1.31	38/4731 (0.8%)
1	eb	0.97	1/3493 (0.0%)	1.36	36/4731 (0.8%)
1	ec	0.95	1/3493 (0.0%)	1.31	20/4731 (0.4%)
1	ed	0.95	1/3493 (0.0%)	1.34	35/4731 (0.7%)
1	ee	1.01	0/3493	1.38	39/4731 (0.8%)
1	ef	1.02	0/3493	1.33	31/4731 (0.7%)
1	eg	0.99	2/3493 (0.1%)	1.35	44/4731 (0.9%)
1	eh	0.97	0/3493	1.35	36/4731 (0.8%)
1	ei	0.98	0/3493	1.35	31/4731 (0.7%)
1	ej	0.98	0/3493	1.33	41/4731 (0.9%)
1	ek	0.97	0/3493	1.38	35/4731 (0.7%)
1	el	0.94	0/3493	1.37	48/4731 (1.0%)
1	em	0.98	1/3493 (0.0%)	1.32	28/4731 (0.6%)
1	en	0.93	1/3493 (0.0%)	1.36	39/4731 (0.8%)
1	eo	0.98	0/3493	1.36	41/4731 (0.9%)
1	ep	0.95	0/3493	1.33	31/4731 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	eq	0.97	0/3493	1.33	34/4731 (0.7%)
1	er	0.98	1/3493 (0.0%)	1.34	39/4731 (0.8%)
1	es	0.96	0/3493	1.33	39/4731 (0.8%)
1	et	0.94	0/3493	1.33	38/4731 (0.8%)
1	eu	0.96	2/3493 (0.1%)	1.36	34/4731 (0.7%)
1	ev	0.95	1/3493 (0.0%)	1.33	30/4731 (0.6%)
1	ew	0.98	0/3493	1.35	26/4731 (0.5%)
1	ex	0.98	1/3493 (0.0%)	1.35	38/4731 (0.8%)
1	ey	0.97	1/3493 (0.0%)	1.36	43/4731 (0.9%)
1	ez	0.96	1/3493 (0.0%)	1.34	36/4731 (0.8%)
1	fa	0.95	0/3493	1.34	36/4731 (0.8%)
1	fb	0.99	0/3493	1.32	26/4731 (0.5%)
1	fc	0.97	0/3493	1.35	37/4731 (0.8%)
1	fd	0.95	1/3493 (0.0%)	1.35	35/4731 (0.7%)
1	fe	0.94	0/3493	1.35	35/4731 (0.7%)
1	ff	0.96	0/3493	1.33	38/4731 (0.8%)
1	fg	0.97	0/3493	1.35	39/4731 (0.8%)
1	fh	0.96	0/3493	1.36	41/4731 (0.9%)
1	fi	0.95	0/3493	1.36	40/4731 (0.8%)
1	fj	0.98	1/3493 (0.0%)	1.35	29/4731 (0.6%)
1	fk	0.95	0/3493	1.37	50/4731 (1.1%)
1	fl	0.95	0/3493	1.35	39/4731 (0.8%)
1	fm	0.94	0/3493	1.35	45/4731 (1.0%)
1	fn	0.98	1/3493 (0.0%)	1.35	39/4731 (0.8%)
1	fo	0.98	1/3493 (0.0%)	1.40	52/4731 (1.1%)
1	fp	0.98	1/3493 (0.0%)	1.32	37/4731 (0.8%)
1	fq	0.99	1/3493 (0.0%)	1.33	32/4731 (0.7%)
1	fr	0.98	3/3493 (0.1%)	1.34	34/4731 (0.7%)
1	fs	0.98	1/3493 (0.0%)	1.36	44/4731 (0.9%)
1	ft	0.98	0/3493	1.37	33/4731 (0.7%)
1	fu	0.95	0/3493	1.35	36/4731 (0.8%)
1	fv	0.96	0/3493	1.34	38/4731 (0.8%)
1	fw	0.96	0/3493	1.32	28/4731 (0.6%)
1	fx	0.94	0/3493	1.34	37/4731 (0.8%)
1	fy	0.95	1/3493 (0.0%)	1.30	30/4731 (0.6%)
1	fz	0.98	1/3493 (0.0%)	1.34	32/4731 (0.7%)
1	ga	0.94	0/3493	1.38	49/4731 (1.0%)
1	gb	0.92	0/3493	1.33	40/4731 (0.8%)
1	gc	0.94	0/3493	1.37	42/4731 (0.9%)
1	gd	0.96	0/3493	1.36	40/4731 (0.8%)
1	ge	0.95	0/3493	1.35	35/4731 (0.7%)
1	gf	0.96	0/3493	1.35	34/4731 (0.7%)
1	gg	0.95	0/3493	1.36	36/4731 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	gh	0.95	0/3493	1.36	36/4731 (0.8%)
1	gi	0.97	0/3493	1.33	37/4731 (0.8%)
1	gj	0.98	2/3493 (0.1%)	1.41	50/4731 (1.1%)
1	gk	0.95	0/3493	1.36	32/4731 (0.7%)
1	gl	0.95	0/3493	1.40	54/4731 (1.1%)
1	gm	0.96	0/3493	1.34	39/4731 (0.8%)
1	gn	0.97	1/3493 (0.0%)	1.35	41/4731 (0.9%)
1	go	0.95	1/3493 (0.0%)	1.34	37/4731 (0.8%)
1	gp	0.94	0/3493	1.34	36/4731 (0.8%)
1	gq	0.93	0/3493	1.34	29/4731 (0.6%)
1	gr	0.94	1/3493 (0.0%)	1.33	35/4731 (0.7%)
1	gs	0.93	1/3493 (0.0%)	1.36	46/4731 (1.0%)
1	gt	0.95	3/3493 (0.1%)	1.34	28/4731 (0.6%)
1	gu	0.95	1/3493 (0.0%)	1.36	48/4731 (1.0%)
1	gv	0.93	1/3493 (0.0%)	1.34	36/4731 (0.8%)
1	gw	0.97	1/3493 (0.0%)	1.36	42/4731 (0.9%)
1	gx	0.99	0/3493	1.34	36/4731 (0.8%)
1	gy	0.97	0/3493	1.34	40/4731 (0.8%)
1	gz	0.94	0/3493	1.34	28/4731 (0.6%)
1	ha	0.99	1/3493 (0.0%)	1.33	29/4731 (0.6%)
1	hb	0.97	0/3493	1.31	38/4731 (0.8%)
1	hc	0.96	0/3493	1.34	39/4731 (0.8%)
1	hd	0.99	1/3493 (0.0%)	1.35	35/4731 (0.7%)
2	he	0.92	0/3263	1.27	32/4430 (0.7%)
2	hf	0.94	0/3263	1.29	34/4430 (0.8%)
2	hg	0.94	0/3263	1.28	31/4430 (0.7%)
2	hh	0.94	0/3263	1.28	37/4430 (0.8%)
2	hi	0.94	0/3263	1.28	40/4430 (0.9%)
2	hj	0.95	0/3263	1.31	37/4430 (0.8%)
2	hk	0.96	1/3263 (0.0%)	1.30	40/4430 (0.9%)
2	hl	0.96	1/3263 (0.0%)	1.28	33/4430 (0.7%)
2	hm	0.96	0/3263	1.30	39/4430 (0.9%)
2	hn	0.94	1/3263 (0.0%)	1.27	32/4430 (0.7%)
2	ho	0.96	1/3263 (0.0%)	1.30	37/4430 (0.8%)
3	hp	0.83	0/648	1.18	1/876 (0.1%)
3	hq	0.85	0/648	1.19	4/876 (0.5%)
3	hr	0.87	0/648	1.19	4/876 (0.5%)
3	hs	0.84	0/648	1.18	4/876 (0.5%)
3	ht	0.88	0/648	1.18	3/876 (0.3%)
3	hu	0.89	0/648	1.16	6/876 (0.7%)
3	hv	0.88	0/648	1.21	2/876 (0.2%)
3	hw	0.86	0/648	1.21	3/876 (0.3%)
3	hx	0.85	0/648	1.20	2/876 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	hy	0.84	0/648	1.24	3/876 (0.3%)
3	hz	0.90	0/648	1.24	5/876 (0.6%)
3	ia	0.89	0/648	1.17	6/876 (0.7%)
3	ib	0.87	0/648	1.21	5/876 (0.6%)
3	ic	0.89	0/648	1.19	3/876 (0.3%)
3	id	0.85	0/648	1.20	3/876 (0.3%)
3	ie	0.82	0/648	1.13	4/876 (0.5%)
3	if	0.87	0/648	1.31	3/876 (0.3%)
3	ig	0.86	0/648	1.20	5/876 (0.6%)
3	ih	0.88	0/648	1.25	9/876 (1.0%)
3	ii	0.86	0/648	1.16	2/876 (0.2%)
3	ij	0.89	0/648	1.23	7/876 (0.8%)
3	ik	0.87	0/648	1.14	5/876 (0.6%)
3	il	0.88	0/648	1.18	3/876 (0.3%)
3	im	0.91	0/648	1.17	3/876 (0.3%)
3	in	0.85	0/648	1.23	5/876 (0.6%)
3	io	0.84	0/648	1.22	5/876 (0.6%)
3	ip	0.87	0/648	1.27	9/876 (1.0%)
3	iq	0.89	1/648 (0.2%)	1.18	4/876 (0.5%)
3	ir	0.89	0/648	1.18	6/876 (0.7%)
3	is	0.84	0/648	1.18	4/876 (0.5%)
3	it	0.86	0/648	1.18	2/876 (0.2%)
3	iu	0.89	1/648 (0.2%)	1.23	6/876 (0.7%)
3	iv	0.92	1/648 (0.2%)	1.22	3/876 (0.3%)
3	iw	0.85	0/648	1.21	8/876 (0.9%)
3	ix	0.86	0/648	1.17	4/876 (0.5%)
3	iy	0.86	0/648	1.21	6/876 (0.7%)
3	iz	0.89	0/648	1.19	2/876 (0.2%)
3	ja	0.94	2/648 (0.3%)	1.19	2/876 (0.2%)
3	jb	0.88	0/648	1.25	5/876 (0.6%)
3	jc	0.87	1/648 (0.2%)	1.19	5/876 (0.6%)
3	jd	0.87	0/648	1.17	3/876 (0.3%)
3	je	0.86	0/648	1.17	4/876 (0.5%)
3	jf	0.89	0/648	1.19	2/876 (0.2%)
3	jg	0.91	1/648 (0.2%)	1.21	7/876 (0.8%)
3	jh	0.89	0/648	1.20	4/876 (0.5%)
3	ji	0.87	0/648	1.22	8/876 (0.9%)
3	jj	0.87	0/648	1.17	4/876 (0.5%)
3	jk	0.87	0/648	1.17	6/876 (0.7%)
3	jl	0.91	0/648	1.24	3/876 (0.3%)
3	jm	0.87	0/648	1.21	3/876 (0.3%)
3	jn	0.86	0/648	1.23	8/876 (0.9%)
3	jo	0.91	1/648 (0.2%)	1.18	3/876 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	jp	0.86	0/648	1.17	3/876 (0.3%)
3	jq	0.88	0/648	1.19	2/876 (0.2%)
3	jr	0.82	0/648	1.23	4/876 (0.5%)
3	js	0.83	0/648	1.16	4/876 (0.5%)
3	jt	0.84	0/648	1.21	5/876 (0.6%)
3	ju	0.89	1/648 (0.2%)	1.19	5/876 (0.6%)
3	jv	0.90	0/648	1.19	4/876 (0.5%)
3	jw	0.89	1/648 (0.2%)	1.22	5/876 (0.6%)
3	jx	0.87	0/648	1.17	3/876 (0.3%)
3	jy	0.87	0/648	1.20	3/876 (0.3%)
3	jz	0.91	0/648	1.23	10/876 (1.1%)
3	ka	0.83	0/648	1.16	7/876 (0.8%)
3	kb	0.89	0/648	1.17	3/876 (0.3%)
3	kc	0.88	0/648	1.21	7/876 (0.8%)
3	kd	0.87	0/648	1.29	4/876 (0.5%)
3	ke	0.90	0/648	1.25	5/876 (0.6%)
3	kf	0.91	0/648	1.18	2/876 (0.2%)
3	kg	0.90	0/648	1.20	3/876 (0.3%)
3	kh	0.90	0/648	1.21	5/876 (0.6%)
3	ki	0.89	0/648	1.19	2/876 (0.2%)
3	kj	0.87	0/648	1.21	3/876 (0.3%)
3	kk	0.88	0/648	1.19	4/876 (0.5%)
3	kl	0.88	0/648	1.23	3/876 (0.3%)
3	km	0.83	0/648	1.22	5/876 (0.6%)
3	kn	0.89	0/648	1.22	5/876 (0.6%)
3	ko	0.89	0/648	1.22	7/876 (0.8%)
3	kp	0.88	0/648	1.22	6/876 (0.7%)
3	kq	0.89	0/648	1.23	7/876 (0.8%)
3	kr	0.85	0/648	1.19	2/876 (0.2%)
3	ks	0.85	0/648	1.21	3/876 (0.3%)
3	kt	0.87	0/648	1.19	7/876 (0.8%)
3	ku	0.89	0/648	1.22	6/876 (0.7%)
3	0.87	0/648	1.25	8/876 (0.9%)	
3	kw	0.86	0/648	1.21	3/876 (0.3%)
3	kx	0.88	0/648	1.28	6/876 (0.7%)
3	ky	0.86	0/648	1.22	6/876 (0.7%)
3	kz	0.83	0/648	1.23	6/876 (0.7%)
3	la	0.86	0/648	1.18	6/876 (0.7%)
3	lb	0.84	0/648	1.24	5/876 (0.6%)
3	lc	0.84	0/648	1.18	4/876 (0.5%)
3	ld	0.86	0/648	1.16	4/876 (0.5%)
3	le	0.88	0/648	1.27	4/876 (0.5%)
3	lf	0.93	0/648	1.24	3/876 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	lg	0.91	1/648 (0.2%)	1.20	6/876 (0.7%)
3	lh	0.88	0/648	1.26	3/876 (0.3%)
3	li	0.89	0/648	1.23	5/876 (0.6%)
3	lj	0.89	0/648	1.24	4/876 (0.5%)
3	lk	0.87	0/648	1.15	5/876 (0.6%)
3	ll	0.87	0/648	1.18	5/876 (0.6%)
3	lm	0.88	0/648	1.20	6/876 (0.7%)
3	ln	0.85	0/648	1.20	4/876 (0.5%)
3	lo	0.79	0/648	1.17	5/876 (0.6%)
3	lp	0.91	0/648	1.21	3/876 (0.3%)
3	lq	0.88	1/648 (0.2%)	1.17	5/876 (0.6%)
3	lr	0.90	0/648	1.18	2/876 (0.2%)
3	ls	0.84	0/648	1.17	3/876 (0.3%)
3	lt	0.94	1/648 (0.2%)	1.25	7/876 (0.8%)
3	lu	0.88	0/648	1.18	3/876 (0.3%)
3	lv	0.87	0/648	1.20	5/876 (0.6%)
3	lw	0.86	0/648	1.24	5/876 (0.6%)
3	lx	0.84	0/648	1.17	1/876 (0.1%)
3	ly	0.84	0/648	1.17	3/876 (0.3%)
3	lz	0.91	0/648	1.26	5/876 (0.6%)
3	ma	0.89	0/648	1.16	4/876 (0.5%)
3	mb	0.85	0/648	1.20	3/876 (0.3%)
3	mc	0.88	0/648	1.16	3/876 (0.3%)
3	md	0.88	0/648	1.16	3/876 (0.3%)
3	me	0.89	0/648	1.21	3/876 (0.3%)
3	mf	0.91	0/648	1.19	2/876 (0.2%)
3	mg	0.86	0/648	1.20	4/876 (0.5%)
3	mh	0.82	0/648	1.12	3/876 (0.3%)
3	mi	0.86	0/648	1.25	4/876 (0.5%)
3	mj	0.88	0/648	1.26	5/876 (0.6%)
3	mk	0.91	0/648	1.16	1/876 (0.1%)
3	ml	0.91	1/648 (0.2%)	1.24	4/876 (0.5%)
3	mm	0.86	1/648 (0.2%)	1.17	2/876 (0.2%)
3	mn	0.93	0/648	1.23	2/876 (0.2%)
3	mo	0.91	1/648 (0.2%)	1.19	4/876 (0.5%)
3	mp	0.88	0/648	1.13	2/876 (0.2%)
3	mq	0.90	0/648	1.23	6/876 (0.7%)
3	ms	0.84	0/648	1.28	6/876 (0.7%)
3	mt	0.84	0/648	1.21	5/876 (0.6%)
3	mu	0.89	0/648	1.19	5/876 (0.6%)
3	mv	0.86	0/648	1.23	5/876 (0.6%)
3	mw	0.89	0/648	1.23	3/876 (0.3%)
3	mx	0.89	1/648 (0.2%)	1.23	6/876 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	my	0.88	0/648	1.25	6/876 (0.7%)
3	mz	0.89	0/648	1.24	8/876 (0.9%)
3	na	0.84	0/648	1.22	5/876 (0.6%)
3	nb	0.87	0/648	1.20	5/876 (0.6%)
3	nc	0.84	0/648	1.20	0/876
3	nd	0.86	0/648	1.15	4/876 (0.5%)
3	ne	0.85	0/648	1.17	3/876 (0.3%)
3	nf	0.88	0/648	1.22	4/876 (0.5%)
3	ng	0.89	0/648	1.19	2/876 (0.2%)
3	nh	0.88	0/648	1.18	6/876 (0.7%)
3	ni	0.84	0/648	1.20	5/876 (0.6%)
3	nj	0.82	0/648	1.24	5/876 (0.6%)
3	nk	0.88	0/648	1.21	5/876 (0.6%)
3	nl	0.87	0/648	1.22	7/876 (0.8%)
3	nm	0.91	0/648	1.24	4/876 (0.5%)
3	nn	0.88	0/648	1.22	9/876 (1.0%)
3	no	0.92	0/648	1.23	7/876 (0.8%)
3	np	0.88	0/648	1.22	4/876 (0.5%)
3	nq	0.88	0/648	1.24	6/876 (0.7%)
3	ns	0.89	0/648	1.23	4/876 (0.5%)
3	nt	0.84	0/648	1.24	7/876 (0.8%)
3	nu	0.90	0/648	1.21	5/876 (0.6%)
3	nv	0.88	0/648	1.21	5/876 (0.6%)
3	nw	0.85	0/648	1.23	3/876 (0.3%)
3	nx	0.84	0/648	1.27	5/876 (0.6%)
3	ny	0.86	0/648	1.18	4/876 (0.5%)
3	nz	0.85	0/648	1.23	5/876 (0.6%)
3	oa	0.81	0/648	1.14	4/876 (0.5%)
3	ob	0.86	0/648	1.30	8/876 (0.9%)
3	oc	0.81	0/648	1.18	5/876 (0.6%)
3	od	0.85	0/648	1.19	2/876 (0.2%)
3	oe	0.86	0/648	1.24	7/876 (0.8%)
3	of	0.87	0/648	1.22	6/876 (0.7%)
3	og	0.82	0/648	1.17	1/876 (0.1%)
All	All	0.95	114/796869 (0.0%)	1.33	7933/1079125 (0.7%)

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	aq	0	1

All (114) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	gj	96	MET	SD-CE	-9.24	1.56	1.79
1	at	483	PRO	C-N	-6.56	1.25	1.33
1	do	145	HIS	CB-CG	-6.48	1.41	1.50
1	ec	145	HIS	CB-CG	-6.41	1.41	1.50
1	fj	145	HIS	CB-CG	-6.38	1.41	1.50
1	fn	145	HIS	CB-CG	-6.33	1.41	1.50
1	bl	145	HIS	CB-CG	-6.23	1.41	1.50
1	gt	145	HIS	CB-CG	-6.22	1.41	1.50
1	gt	72	HIS	CB-CG	-6.21	1.41	1.50
1	ev	145	HIS	CB-CG	-6.20	1.41	1.50
1	db	145	HIS	CB-CG	-6.18	1.41	1.50
1	fq	145	HIS	CB-CG	-6.17	1.41	1.50
1	cs	122	GLY	CA-C	6.16	1.57	1.52
1	ai	145	HIS	CB-CG	-6.12	1.41	1.50
1	gv	145	HIS	CB-CG	-6.11	1.41	1.50
1	az	145	HIS	CB-CG	-6.10	1.41	1.50
3	lg	5	ARG	CD-NE	-6.10	1.37	1.46
1	dl	145	HIS	CB-CG	-5.96	1.41	1.50
1	bo	145	HIS	CB-CG	-5.95	1.41	1.50
1	ct	145	HIS	CB-CG	-5.95	1.41	1.50
1	ea	145	HIS	CB-CG	-5.93	1.41	1.50
1	fr	145	HIS	CB-CG	-5.91	1.41	1.50
1	ch	145	HIS	CB-CG	-5.90	1.41	1.50
3	mo	72	ASN	CB-CG	-5.89	1.37	1.52
1	fo	323	LEU	CB-CG	-5.88	1.41	1.53
2	hn	288	LEU	CB-CG	5.87	1.65	1.53
1	ao	145	HIS	CB-CG	-5.87	1.42	1.50
1	fp	145	HIS	CB-CG	-5.82	1.42	1.50
1	bm	145	HIS	CB-CG	-5.81	1.42	1.50
1	dr	145	HIS	CB-CG	-5.81	1.42	1.50
1	ba	145	HIS	CB-CG	-5.79	1.42	1.50
1	fz	145	HIS	CB-CG	-5.79	1.42	1.50
3	jg	5	ARG	CD-NE	-5.79	1.38	1.46
1	ex	145	HIS	CB-CG	-5.79	1.42	1.50
1	em	323	LEU	CB-CG	-5.76	1.42	1.53
1	gw	72	HIS	CB-CG	-5.76	1.42	1.50
1	gj	124	VAL	CA-C	5.74	1.59	1.52
3	ja	72	ASN	CB-CG	-5.73	1.37	1.52
1	bs	323	LEU	CB-CG	-5.72	1.42	1.53
1	au	145	HIS	CB-CG	-5.71	1.42	1.50
1	aw	145	HIS	CB-CG	-5.70	1.42	1.50
1	go	145	HIS	CB-CG	-5.70	1.42	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	gu	323	LEU	CB-CG	-5.68	1.42	1.53
1	cr	122	GLY	CA-C	5.67	1.57	1.52
1	cg	145	HIS	CB-CG	-5.66	1.42	1.50
1	at	483	PRO	CA-CB	-5.66	1.46	1.53
1	fy	145	HIS	CB-CG	-5.63	1.42	1.50
1	an	145	HIS	CB-CG	-5.62	1.42	1.50
2	hl	173	ARG	CD-NE	-5.61	1.38	1.46
1	ed	323	LEU	CB-CG	-5.60	1.42	1.53
1	bz	122	GLY	CA-C	5.59	1.57	1.52
1	au	323	LEU	CB-CG	-5.56	1.42	1.53
1	eg	145	HIS	CB-CG	-5.54	1.42	1.50
3	lt	5	ARG	CD-NE	-5.50	1.38	1.46
1	gn	145	HIS	CB-CG	-5.50	1.42	1.50
1	dp	145	HIS	CB-CG	-5.49	1.42	1.50
1	ha	323	LEU	CB-CG	-5.49	1.42	1.53
1	gr	323	LEU	CB-CG	-5.48	1.42	1.53
3	jo	72	ASN	CB-CG	-5.48	1.38	1.52
1	bz	145	HIS	CB-CG	-5.48	1.42	1.50
1	di	145	HIS	CB-CG	-5.42	1.42	1.50
1	er	247	TRP	NE1-CE2	-5.41	1.31	1.37
1	dw	145	HIS	CB-CG	-5.41	1.42	1.50
1	ez	323	LEU	CB-CG	-5.41	1.42	1.53
1	ey	323	LEU	CB-CG	-5.40	1.42	1.53
1	dh	145	HIS	CB-CG	-5.40	1.42	1.50
1	bx	78	ASN	C-O	-5.40	1.17	1.24
1	gt	323	LEU	CB-CG	-5.39	1.42	1.53
1	dr	323	LEU	CB-CG	-5.38	1.42	1.53
1	dq	145	HIS	CB-CG	-5.37	1.42	1.50
3	ja	5	ARG	CD-NE	-5.36	1.38	1.46
3	jw	72	ASN	CB-CG	-5.36	1.38	1.52
1	br	145	HIS	CB-CG	-5.34	1.42	1.50
1	aj	145	HIS	CB-CG	-5.32	1.42	1.50
1	eb	145	HIS	CB-CG	-5.30	1.42	1.50
1	bf	145	HIS	CB-CG	-5.30	1.42	1.50
3	iq	5	ARG	CD-NE	-5.30	1.38	1.46
1	bf	180	HIS	CB-CG	-5.29	1.42	1.50
1	eu	72	HIS	CB-CG	-5.28	1.42	1.50
1	al	323	LEU	CB-CG	-5.25	1.43	1.53
1	cx	72	HIS	CB-CG	-5.24	1.42	1.50
1	da	323	LEU	CB-CG	-5.23	1.43	1.53
2	hk	166	TRP	NE1-CE2	-5.23	1.31	1.37
1	ci	122	GLY	CA-C	5.22	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	ck	323	LEU	CB-CG	-5.22	1.43	1.53
3	ml	5	ARG	CD-NE	-5.21	1.39	1.46
3	iv	5	ARG	NE-CZ	5.20	1.38	1.33
1	dt	323	LEU	CB-CG	-5.20	1.43	1.53
1	eu	145	HIS	CB-CG	-5.19	1.42	1.50
3	jc	72	ASN	CB-CG	-5.19	1.39	1.52
1	cn	323	LEU	CB-CG	-5.19	1.43	1.53
1	cn	93	PRO	CA-C	5.18	1.57	1.52
1	fs	247	TRP	NE1-CE2	-5.18	1.31	1.37
1	ay	323	LEU	CB-CG	-5.17	1.43	1.53
3	iu	72	ASN	CB-CG	-5.16	1.39	1.52
2	ho	415	LEU	CB-CG	5.15	1.63	1.53
1	eg	396	ALA	CA-C	-5.15	1.46	1.52
1	hd	253	ARG	CA-C	5.15	1.57	1.52
1	en	483	PRO	N-CA	-5.15	1.41	1.47
3	ju	72	ASN	CB-CG	-5.12	1.39	1.52
1	aw	483	PRO	CA-C	-5.11	1.46	1.52
1	cv	323	LEU	CB-CG	-5.10	1.43	1.53
1	ag	93	PRO	N-CA	-5.09	1.43	1.47
1	fr	323	LEU	CB-CG	-5.09	1.43	1.53
3	lq	72	ASN	CB-CG	-5.08	1.39	1.52
3	mm	72	ASN	CB-CG	-5.07	1.39	1.52
1	fr	247	TRP	NE1-CE2	-5.07	1.31	1.37
1	fd	323	LEU	CB-CG	-5.07	1.43	1.53
1	du	145	HIS	CB-CG	-5.05	1.43	1.50
1	df	323	LEU	CB-CG	-5.05	1.43	1.53
1	dl	266	LEU	CB-CG	-5.04	1.43	1.53
1	au	228	MET	SD-CE	-5.02	1.67	1.79
3	mx	72	ASN	CB-CG	-5.02	1.39	1.52
1	gs	323	LEU	CB-CG	-5.02	1.43	1.53

All (7933) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dm	236	GLN	CA-C-N	13.89	146.71	121.70
1	dm	236	GLN	C-N-CA	13.89	146.71	121.70
1	ek	486	GLU	N-CA-C	-13.32	95.45	112.23
1	ba	154	PHE	N-CA-C	-11.27	98.19	113.18
1	gj	96	MET	N-CA-C	10.95	123.22	111.28
1	fn	154	PHE	N-CA-C	-10.43	100.29	113.43
1	em	465	LYS	N-CA-C	-10.25	99.55	113.18
1	el	483	PRO	CA-C-N	10.03	136.41	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	el	483	PRO	C-N-CA	10.03	136.41	122.07
1	ef	154	PHE	N-CA-C	-9.83	100.13	112.72
1	ek	484	PHE	N-CA-C	-9.78	94.51	109.96
2	hf	368	SER	N-CA-C	-9.73	97.98	110.53
1	ce	409	THR	N-CA-C	-9.72	102.21	114.56
1	ha	344	ARG	CA-C-N	9.72	140.10	121.54
1	ha	344	ARG	C-N-CA	9.72	140.10	121.54
2	hn	368	SER	N-CA-C	-9.71	98.00	110.53
1	gl	185	THR	N-CA-C	9.70	124.49	111.30
1	cv	324	THR	N-CA-C	-9.64	97.67	109.72
1	fo	324	THR	N-CA-C	-9.64	97.67	109.72
1	dt	324	THR	N-CA-C	-9.62	97.70	109.72
2	hk	368	SER	N-CA-C	-9.60	98.14	110.53
1	dr	324	THR	N-CA-C	-9.60	97.72	109.72
1	fj	324	THR	N-CA-C	-9.60	97.72	109.72
1	dk	88	VAL	N-CA-C	9.58	121.52	108.11
1	eb	121	THR	N-CA-C	9.55	122.08	110.91
1	ef	324	THR	N-CA-C	-9.54	97.80	109.72
1	bl	88	VAL	N-CA-C	9.54	121.46	108.11
1	ci	446	ALA	N-CA-C	9.51	121.64	111.28
1	er	88	VAL	N-CA-C	9.47	121.37	108.11
1	gv	324	THR	N-CA-C	-9.40	97.97	109.72
2	hm	129	GLN	N-CA-C	-9.29	98.67	110.19
1	cj	88	VAL	N-CA-C	9.22	121.02	108.11
1	br	88	VAL	N-CA-C	9.22	121.02	108.11
2	hh	368	SER	N-CA-C	-9.21	98.38	110.53
1	cn	481	ILE	N-CA-C	9.20	120.90	112.43
1	az	88	VAL	N-CA-C	9.20	120.98	108.11
2	he	368	SER	N-CA-C	-9.18	98.69	110.53
1	fo	88	VAL	N-CA-C	9.18	120.96	108.11
1	fw	409	THR	N-CA-C	-9.13	102.97	114.56
1	fv	88	VAL	N-CA-C	9.12	120.88	108.11
1	fr	324	THR	N-CA-C	-9.10	98.34	109.72
2	hl	368	SER	N-CA-C	-9.10	98.79	110.53
1	ef	88	VAL	N-CA-C	9.08	120.83	108.11
1	aw	88	VAL	N-CA-C	9.06	121.17	108.12
2	hf	36	TYR	N-CA-C	-9.06	104.29	114.62
1	ag	88	VAL	N-CA-C	9.05	120.78	108.11
1	ha	409	THR	N-CA-C	-9.04	103.08	114.56
1	fd	324	THR	N-CA-C	-9.01	98.46	109.72
1	ff	324	THR	N-CA-C	-9.00	98.31	109.65
1	dx	484	PHE	CA-CB-CG	9.00	122.80	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	et	324	THR	N-CA-C	-9.00	98.47	109.72
1	gd	88	VAL	N-CA-C	8.97	120.67	108.11
1	cv	88	VAL	N-CA-C	8.97	121.03	108.12
1	ci	88	VAL	N-CA-C	8.90	120.74	107.75
1	fi	293	ILE	N-CA-C	-8.88	102.17	111.58
1	dy	324	THR	N-CA-C	-8.87	98.64	109.72
1	be	324	THR	N-CA-C	-8.85	98.66	109.72
1	gi	88	VAL	N-CA-C	8.84	120.84	108.12
1	ab	88	VAL	N-CA-C	8.82	120.45	108.11
1	dh	324	THR	N-CA-C	-8.80	98.72	109.72
1	bw	293	ILE	N-CA-C	-8.78	103.29	111.45
1	gd	324	THR	N-CA-C	-8.78	98.75	109.72
1	cx	324	THR	N-CA-C	-8.76	98.78	109.72
1	fk	253	ARG	CA-C-O	-8.75	113.47	119.68
1	hd	88	VAL	N-CA-C	8.74	120.35	108.11
1	br	324	THR	N-CA-C	-8.73	97.10	109.24
1	dx	324	THR	N-CA-C	-8.72	98.82	109.72
1	ed	271	SER	N-CA-C	8.71	123.47	113.02
2	hg	368	SER	N-CA-C	-8.71	98.22	110.50
2	hk	36	TYR	N-CA-C	-8.70	103.79	114.75
2	hm	368	SER	N-CA-C	-8.70	98.81	110.55
1	an	88	VAL	N-CA-C	8.69	120.64	108.12
2	hf	327	VAL	N-CA-C	8.66	120.95	108.48
1	es	154	PHE	N-CA-C	-8.65	102.53	113.43
1	ah	154	PHE	N-CA-C	-8.64	102.55	113.43
1	cy	88	VAL	N-CA-C	8.63	120.55	108.12
1	bm	88	VAL	N-CA-C	8.61	120.29	107.80
1	dm	88	VAL	N-CA-C	8.60	120.27	107.80
1	au	465	LYS	N-CA-C	-8.60	101.75	113.18
3	hy	72	ASN	CA-CB-CG	8.60	121.20	112.60
1	fj	232	ILE	N-CA-C	-8.58	103.52	111.67
1	ee	324	THR	N-CA-C	-8.58	98.99	109.72
1	ez	88	VAL	N-CA-C	8.58	120.12	108.11
1	dz	324	THR	N-CA-C	-8.57	99.00	109.72
1	cm	121	THR	N-CA-C	8.57	123.25	111.17
3	mt	72	ASN	CA-CB-CG	8.57	121.17	112.60
1	el	88	VAL	N-CA-C	8.57	120.11	108.11
1	ha	463	ASP	CA-C-N	8.55	128.29	119.56
1	ha	463	ASP	C-N-CA	8.55	128.29	119.56
1	fl	463	ASP	CA-C-N	8.54	128.28	119.56
1	fl	463	ASP	C-N-CA	8.54	128.28	119.56
1	bt	463	ASP	CA-C-N	8.54	128.27	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bt	463	ASP	C-N-CA	8.54	128.27	119.56
1	ax	88	VAL	N-CA-C	8.54	120.06	108.11
1	df	463	ASP	CA-C-N	8.54	128.27	119.56
1	df	463	ASP	C-N-CA	8.54	128.27	119.56
1	eg	463	ASP	CA-C-N	8.54	128.19	119.82
1	eg	463	ASP	C-N-CA	8.54	128.19	119.82
1	da	88	VAL	N-CA-C	8.53	120.05	108.11
1	bw	463	ASP	CA-C-N	8.53	128.26	119.56
1	bw	463	ASP	C-N-CA	8.53	128.26	119.56
1	cb	483	PRO	CA-C-N	8.53	140.00	124.82
1	cb	483	PRO	C-N-CA	8.53	140.00	124.82
1	ev	287	ASP	N-CA-C	-8.51	101.36	112.68
1	bz	463	ASP	CA-C-N	8.51	128.16	119.82
1	bz	463	ASP	C-N-CA	8.51	128.16	119.82
1	ee	328	LYS	N-CA-C	8.51	123.38	112.92
1	dh	463	ASP	CA-C-N	8.50	128.23	119.56
1	dh	463	ASP	C-N-CA	8.50	128.23	119.56
1	ck	463	ASP	CA-C-N	8.48	128.21	119.56
1	ck	463	ASP	C-N-CA	8.48	128.21	119.56
1	dl	463	ASP	CA-C-N	8.48	128.21	119.56
1	dl	463	ASP	C-N-CA	8.48	128.21	119.56
1	gh	119	SER	N-CA-C	-8.47	100.59	108.22
1	fg	463	ASP	CA-C-N	8.47	128.20	119.56
1	fg	463	ASP	C-N-CA	8.47	128.20	119.56
1	bq	463	ASP	CA-C-N	8.46	128.19	119.56
1	bq	463	ASP	C-N-CA	8.46	128.19	119.56
1	gp	324	THR	N-CA-C	-8.46	99.41	110.07
1	eh	463	ASP	CA-C-N	8.46	128.19	119.56
1	eh	463	ASP	C-N-CA	8.46	128.19	119.56
1	hd	463	ASP	CA-C-N	8.46	128.19	119.56
1	hd	463	ASP	C-N-CA	8.46	128.19	119.56
1	ai	287	ASP	CA-CB-CG	8.46	121.06	112.60
1	bb	463	ASP	CA-C-N	8.46	128.19	119.56
1	bb	463	ASP	C-N-CA	8.46	128.19	119.56
1	dg	88	VAL	N-CA-C	8.46	119.95	108.11
3	hw	37	ASP	CA-CB-CG	8.45	121.05	112.60
1	ev	463	ASP	CA-C-N	8.45	128.18	119.56
1	ev	463	ASP	C-N-CA	8.45	128.18	119.56
3	kw	38	VAL	N-CA-C	8.45	120.50	108.17
1	bj	463	ASP	CA-C-N	8.44	128.17	119.56
1	bj	463	ASP	C-N-CA	8.44	128.17	119.56
1	dp	324	THR	N-CA-C	-8.44	99.17	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fu	463	ASP	CA-C-N	8.44	128.17	119.56
1	fu	463	ASP	C-N-CA	8.44	128.17	119.56
1	gi	463	ASP	CA-C-N	8.44	128.17	119.56
1	gi	463	ASP	C-N-CA	8.44	128.17	119.56
1	aj	463	ASP	CA-C-N	8.43	128.16	119.56
1	aj	463	ASP	C-N-CA	8.43	128.16	119.56
3	kx	46	TYR	N-CA-C	8.43	121.69	109.14
1	dx	463	ASP	CA-C-N	8.42	128.15	119.56
1	dx	463	ASP	C-N-CA	8.42	128.15	119.56
1	fy	463	ASP	CA-C-N	8.42	128.07	119.82
1	fy	463	ASP	C-N-CA	8.42	128.07	119.82
1	gw	88	VAL	N-CA-C	8.42	120.01	107.80
2	ho	47	GLN	CA-C-N	8.41	128.14	119.56
2	ho	47	GLN	C-N-CA	8.41	128.14	119.56
1	gk	186	GLY	N-CA-C	8.41	121.94	111.85
1	bx	88	VAL	N-CA-C	8.40	119.87	108.11
1	cv	463	ASP	CA-C-N	8.40	128.13	119.56
1	cv	463	ASP	C-N-CA	8.40	128.13	119.56
1	cg	463	ASP	CA-C-N	8.40	128.05	119.82
1	cg	463	ASP	C-N-CA	8.40	128.05	119.82
1	fx	406	THR	N-CA-C	-8.40	103.89	114.56
1	ee	88	VAL	N-CA-C	8.40	119.97	107.80
1	de	463	ASP	CA-C-N	8.39	128.12	119.56
1	de	463	ASP	C-N-CA	8.39	128.12	119.56
1	gs	463	ASP	CA-C-N	8.39	128.12	119.56
1	gs	463	ASP	C-N-CA	8.39	128.12	119.56
1	ao	463	ASP	CA-C-N	8.39	128.04	119.82
1	ao	463	ASP	C-N-CA	8.39	128.04	119.82
1	ft	88	VAL	N-CA-C	8.39	120.20	108.12
1	az	324	THR	N-CA-C	-8.39	99.23	109.72
1	ea	88	VAL	N-CA-C	8.39	119.85	108.11
1	gs	88	VAL	N-CA-C	8.39	119.85	108.11
1	ag	324	THR	N-CA-C	-8.38	99.25	109.72
1	ah	463	ASP	CA-C-N	8.38	128.10	119.56
1	ah	463	ASP	C-N-CA	8.38	128.10	119.56
3	le	72	ASN	CA-CB-CG	8.37	120.97	112.60
1	fo	463	ASP	CA-C-N	8.36	128.09	119.56
1	fo	463	ASP	C-N-CA	8.36	128.09	119.56
1	dk	463	ASP	CA-C-N	8.36	128.08	119.56
1	dk	463	ASP	C-N-CA	8.36	128.08	119.56
2	he	36	TYR	N-CA-C	-8.36	104.22	114.75
1	ep	463	ASP	CA-C-N	8.35	128.08	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ep	463	ASP	C-N-CA	8.35	128.08	119.56
1	ap	463	ASP	CA-C-N	8.34	128.07	119.56
1	ap	463	ASP	C-N-CA	8.34	128.07	119.56
1	ex	88	VAL	N-CA-C	8.34	119.78	108.11
1	fp	88	VAL	N-CA-C	8.33	119.88	107.80
1	dy	88	VAL	N-CA-C	8.33	119.88	107.80
1	ar	88	VAL	N-CA-C	8.32	119.87	107.80
1	gd	253	ARG	N-CA-C	8.32	123.92	113.43
3	mv	72	ASN	CA-CB-CG	8.32	120.92	112.60
1	gm	463	ASP	CA-C-N	8.32	128.04	119.56
1	gm	463	ASP	C-N-CA	8.32	128.04	119.56
1	fi	463	ASP	CA-C-N	8.31	128.04	119.56
1	fi	463	ASP	C-N-CA	8.31	128.04	119.56
1	ey	324	THR	N-CA-C	-8.31	99.18	109.65
1	cw	463	ASP	CA-C-N	8.31	128.03	119.56
1	cw	463	ASP	C-N-CA	8.31	128.03	119.56
1	gd	463	ASP	CA-C-N	8.31	128.03	119.56
1	gd	463	ASP	C-N-CA	8.31	128.03	119.56
1	el	440	GLY	CA-C-N	8.30	127.95	119.56
1	el	440	GLY	C-N-CA	8.30	127.95	119.56
1	ca	149	GLY	CA-C-N	8.30	128.24	119.85
1	ca	149	GLY	C-N-CA	8.30	128.24	119.85
1	cd	463	ASP	CA-C-N	8.30	128.02	119.56
1	cd	463	ASP	C-N-CA	8.30	128.02	119.56
1	al	149	GLY	CA-C-N	8.29	128.24	120.03
1	al	149	GLY	C-N-CA	8.29	128.24	120.03
1	fs	88	VAL	N-CA-C	8.29	119.72	108.11
1	ad	463	ASP	CA-C-N	8.29	127.94	119.82
1	ad	463	ASP	C-N-CA	8.29	127.94	119.82
1	gv	463	ASP	CA-C-N	8.29	128.01	119.56
1	gv	463	ASP	C-N-CA	8.29	128.01	119.56
1	ct	463	ASP	CA-C-N	8.28	128.00	119.56
1	ct	463	ASP	C-N-CA	8.28	128.00	119.56
1	bw	88	VAL	N-CA-C	8.27	119.69	108.11
1	by	88	VAL	N-CA-C	8.27	119.69	108.11
1	fe	463	ASP	CA-C-N	8.26	127.99	119.56
1	fe	463	ASP	C-N-CA	8.26	127.99	119.56
1	eu	463	ASP	CA-C-N	8.26	127.99	119.56
1	eu	463	ASP	C-N-CA	8.26	127.99	119.56
1	dj	463	ASP	CA-C-N	8.26	127.98	119.56
1	dj	463	ASP	C-N-CA	8.26	127.98	119.56
2	hj	268	THR	N-CA-C	8.25	123.16	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fn	463	ASP	CA-C-N	8.24	127.97	119.56
1	fn	463	ASP	C-N-CA	8.24	127.97	119.56
1	aw	463	ASP	CA-C-N	8.23	127.96	119.56
1	aw	463	ASP	C-N-CA	8.23	127.96	119.56
1	gl	324	THR	N-CA-C	-8.22	99.44	109.72
1	bb	324	THR	N-CA-C	-8.22	99.71	110.07
1	gv	88	VAL	N-CA-C	8.22	119.72	107.80
1	ek	463	ASP	CA-C-N	8.22	127.94	119.56
1	ek	463	ASP	C-N-CA	8.22	127.94	119.56
1	ci	287	ASP	N-CA-C	-8.22	101.75	112.68
1	fs	72	HIS	N-CA-C	-8.21	97.69	110.42
1	ge	463	ASP	CA-C-N	8.20	127.92	119.56
1	ge	463	ASP	C-N-CA	8.20	127.92	119.56
1	ap	324	THR	N-CA-C	-8.20	99.48	109.72
1	be	463	ASP	CA-C-N	8.19	127.92	119.56
1	be	463	ASP	C-N-CA	8.19	127.92	119.56
1	cz	440	GLY	CA-C-N	8.19	127.83	119.56
1	cz	440	GLY	C-N-CA	8.19	127.83	119.56
1	dk	103	ILE	CA-C-N	8.19	128.21	119.78
1	dk	103	ILE	C-N-CA	8.19	128.21	119.78
1	cm	463	ASP	CA-C-N	8.18	127.91	119.56
1	cm	463	ASP	C-N-CA	8.18	127.91	119.56
1	dt	463	ASP	CA-C-N	8.18	127.91	119.56
1	dt	463	ASP	C-N-CA	8.18	127.91	119.56
1	gw	463	ASP	CA-C-N	8.18	127.91	119.56
1	gw	463	ASP	C-N-CA	8.18	127.91	119.56
1	ad	483	PRO	N-CA-C	-8.18	98.38	111.14
1	dg	463	ASP	CA-C-N	8.18	127.90	119.56
1	dg	463	ASP	C-N-CA	8.18	127.90	119.56
1	bf	463	ASP	CA-C-N	8.17	127.90	119.56
1	bf	463	ASP	C-N-CA	8.17	127.90	119.56
1	bo	88	VAL	N-CA-C	8.17	119.55	108.11
1	fz	463	ASP	CA-C-N	8.17	127.89	119.56
1	fz	463	ASP	C-N-CA	8.17	127.89	119.56
1	gl	149	GLY	CA-C-N	8.17	128.11	120.03
1	gl	149	GLY	C-N-CA	8.17	128.11	120.03
1	ac	463	ASP	CA-C-N	8.16	127.89	119.56
1	ac	463	ASP	C-N-CA	8.16	127.89	119.56
1	fd	463	ASP	CA-C-N	8.16	127.88	119.56
1	fd	463	ASP	C-N-CA	8.16	127.88	119.56
1	aw	149	GLY	CA-C-N	8.15	128.10	120.03
1	aw	149	GLY	C-N-CA	8.15	128.10	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bs	463	ASP	CA-C-N	8.14	127.87	119.56
1	bs	463	ASP	C-N-CA	8.14	127.87	119.56
1	bw	440	GLY	CA-C-N	8.14	127.79	119.56
1	bw	440	GLY	C-N-CA	8.14	127.79	119.56
1	gc	463	ASP	CA-C-N	8.14	127.87	119.56
1	gc	463	ASP	C-N-CA	8.14	127.87	119.56
1	fm	253	ARG	N-CA-C	8.14	123.68	113.43
1	ci	463	ASP	CA-C-N	8.13	127.86	119.56
1	ci	463	ASP	C-N-CA	8.13	127.86	119.56
1	gp	483	PRO	N-CA-C	-8.13	98.45	111.14
1	ch	463	ASP	CA-C-N	8.13	127.86	119.56
1	ch	463	ASP	C-N-CA	8.13	127.86	119.56
1	fb	253	ARG	N-CA-C	8.13	123.74	112.93
1	gi	149	GLY	CA-C-N	8.13	128.06	119.85
1	gi	149	GLY	C-N-CA	8.13	128.06	119.85
1	cb	88	VAL	N-CA-C	8.13	119.83	108.12
1	ez	463	ASP	CA-C-N	8.12	127.84	119.56
1	ez	463	ASP	C-N-CA	8.12	127.84	119.56
1	gp	121	THR	N-CA-C	8.12	121.17	111.02
1	cl	88	VAL	N-CA-C	8.11	119.53	108.17
1	df	324	THR	N-CA-C	-8.12	97.85	109.62
1	gn	463	ASP	CA-C-N	8.10	127.83	119.56
1	gn	463	ASP	C-N-CA	8.10	127.83	119.56
1	dd	253	ARG	N-CA-C	8.10	123.38	111.96
1	ga	293	ILE	N-CA-C	-8.10	102.99	111.58
1	dc	440	GLY	CA-C-N	8.10	127.74	119.56
1	dc	440	GLY	C-N-CA	8.10	127.74	119.56
1	bq	88	VAL	N-CA-C	8.10	119.78	108.12
1	ct	287	ASP	N-CA-C	-8.10	102.16	112.93
1	cs	463	ASP	CA-C-N	8.09	127.81	119.56
1	cs	463	ASP	C-N-CA	8.09	127.81	119.56
1	bh	149	GLY	CA-C-N	8.09	128.03	120.03
1	bh	149	GLY	C-N-CA	8.09	128.03	120.03
1	gx	149	GLY	CA-C-N	8.08	128.01	119.85
1	gx	149	GLY	C-N-CA	8.08	128.01	119.85
1	ca	184	GLU	N-CA-C	-8.07	97.60	108.74
1	al	324	THR	N-CA-C	-8.07	99.64	109.72
1	eb	463	ASP	CA-C-N	8.07	127.73	119.82
1	eb	463	ASP	C-N-CA	8.07	127.73	119.82
1	ci	293	ILE	N-CA-C	-8.06	103.03	111.58
1	fz	154	PHE	N-CA-C	-8.06	102.45	113.18
1	gl	253	ARG	N-CA-C	8.06	123.80	113.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	ml	46	TYR	N-CA-C	8.06	121.16	109.14
1	er	463	ASP	CA-C-N	8.06	127.78	119.56
1	er	463	ASP	C-N-CA	8.06	127.78	119.56
1	eo	463	ASP	CA-C-N	8.05	127.78	119.56
1	eo	463	ASP	C-N-CA	8.05	127.78	119.56
1	ew	463	ASP	CA-C-N	8.06	127.78	119.56
1	ew	463	ASP	C-N-CA	8.06	127.78	119.56
1	gn	88	VAL	N-CA-C	8.05	119.72	108.12
1	hd	253	ARG	N-CA-C	8.05	123.03	112.72
1	br	196	VAL	N-CA-C	8.04	119.70	108.12
1	cz	287	ASP	N-CA-C	-8.04	102.24	112.93
1	db	88	VAL	N-CA-C	8.03	119.45	107.80
1	bf	88	VAL	N-CA-C	8.03	119.68	108.12
1	hc	287	ASP	CA-CB-CG	8.03	120.63	112.60
1	ga	88	VAL	N-CA-C	8.02	119.34	108.11
1	ax	463	ASP	CA-C-N	8.02	127.74	119.56
1	ax	463	ASP	C-N-CA	8.02	127.74	119.56
1	fj	440	GLY	CA-C-N	8.02	127.74	119.56
1	fj	440	GLY	C-N-CA	8.02	127.74	119.56
1	fo	121	THR	N-CA-C	8.02	121.04	111.02
1	hd	287	ASP	N-CA-C	-8.02	102.02	112.68
1	gw	440	GLY	CA-C-N	8.01	127.73	119.56
1	gw	440	GLY	C-N-CA	8.01	127.73	119.56
1	bh	88	VAL	N-CA-C	8.00	119.31	108.11
1	eg	121	THR	N-CA-C	8.00	120.27	110.91
1	az	463	ASP	CA-C-N	8.00	127.72	119.56
1	az	463	ASP	C-N-CA	8.00	127.72	119.56
1	ar	293	ILE	N-CA-C	-8.00	104.01	111.45
1	da	103	ILE	CA-C-N	7.99	128.00	119.78
1	da	103	ILE	C-N-CA	7.99	128.00	119.78
1	dg	253	ARG	N-CA-C	7.98	124.19	113.97
1	gt	149	GLY	CA-C-N	7.98	127.91	119.85
1	gt	149	GLY	C-N-CA	7.98	127.91	119.85
2	hg	327	VAL	N-CA-C	7.98	119.97	108.48
1	du	463	ASP	CA-C-N	7.98	127.70	119.56
1	du	463	ASP	C-N-CA	7.98	127.70	119.56
1	ha	149	GLY	CA-C-N	7.98	127.91	119.85
1	ha	149	GLY	C-N-CA	7.98	127.91	119.85
1	ao	121	THR	N-CA-C	7.97	120.99	111.02
1	cq	440	GLY	CA-C-N	7.97	127.69	119.56
1	cq	440	GLY	C-N-CA	7.97	127.69	119.56
1	ey	463	ASP	CA-C-N	7.97	127.69	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ey	463	ASP	C-N-CA	7.97	127.69	119.56
1	au	324	THR	N-CA-C	-7.96	99.76	109.72
1	bs	324	THR	N-CA-C	-7.96	99.76	109.72
1	ds	287	ASP	N-CA-C	-7.96	102.09	112.68
2	hm	36	TYR	N-CA-C	-7.96	104.72	114.75
1	ay	324	THR	N-CA-C	-7.96	98.08	109.62
1	dp	383	VAL	N-CA-C	-7.96	104.97	111.81
1	gu	463	ASP	CA-C-N	7.96	127.68	119.56
1	gu	463	ASP	C-N-CA	7.96	127.68	119.56
1	dc	149	GLY	CA-C-N	7.94	127.87	119.85
1	dc	149	GLY	C-N-CA	7.94	127.87	119.85
1	gq	463	ASP	CA-C-N	7.93	127.65	119.56
1	gq	463	ASP	C-N-CA	7.93	127.65	119.56
1	ag	253	ARG	N-CA-C	7.93	124.12	113.97
1	ck	253	ARG	N-CA-C	7.93	123.48	112.93
1	dk	324	THR	N-CA-C	-7.92	99.66	109.65
1	ej	287	ASP	N-CA-C	-7.92	102.14	112.68
1	ek	287	ASP	N-CA-C	-7.91	102.16	112.68
1	bv	440	GLY	CA-C-N	7.91	127.55	119.56
1	bv	440	GLY	C-N-CA	7.91	127.55	119.56
1	fe	149	GLY	CA-C-N	7.91	127.83	119.85
1	fe	149	GLY	C-N-CA	7.91	127.83	119.85
1	dz	88	VAL	N-CA-C	7.90	119.29	107.75
3	lj	74	ASP	CA-CB-CG	7.90	120.50	112.60
1	gk	491	ALA	CA-C-N	7.90	128.05	120.31
1	gk	491	ALA	C-N-CA	7.90	128.05	120.31
1	dd	324	THR	N-CA-C	-7.89	99.85	109.72
3	iv	46	TYR	N-CA-C	7.89	120.72	108.96
1	at	440	GLY	CA-C-N	7.89	127.61	119.56
1	at	440	GLY	C-N-CA	7.89	127.61	119.56
1	fu	88	VAL	N-CA-C	7.89	119.24	107.80
1	ev	253	ARG	N-CA-C	7.89	124.49	114.31
1	cd	440	GLY	CA-C-N	7.89	127.61	119.56
1	cd	440	GLY	C-N-CA	7.89	127.61	119.56
1	en	149	GLY	CA-C-N	7.89	127.84	120.03
1	en	149	GLY	C-N-CA	7.89	127.84	120.03
1	dd	154	PHE	N-CA-C	-7.88	103.50	113.43
1	ed	463	ASP	CA-C-N	7.88	127.60	119.56
1	ed	463	ASP	C-N-CA	7.88	127.60	119.56
1	fg	88	VAL	N-CA-C	7.88	119.26	107.75
1	bf	491	ALA	CA-C-N	7.88	128.03	120.31
1	bf	491	ALA	C-N-CA	7.88	128.03	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	go	149	GLY	CA-C-N	7.88	127.81	119.85
1	go	149	GLY	C-N-CA	7.88	127.81	119.85
3	ix	46	TYR	N-CA-C	7.88	120.88	109.14
1	ae	463	ASP	CA-C-N	7.88	127.59	119.56
1	ae	463	ASP	C-N-CA	7.88	127.59	119.56
1	dn	324	THR	N-CA-C	-7.88	99.88	109.72
1	bd	463	ASP	CA-C-N	7.87	127.59	119.56
1	bd	463	ASP	C-N-CA	7.87	127.59	119.56
1	ej	88	VAL	N-CA-C	7.86	119.18	108.17
1	co	115	GLN	CA-C-N	7.86	127.81	120.03
1	co	115	GLN	C-N-CA	7.86	127.81	120.03
1	fa	88	VAL	N-CA-C	7.86	119.18	108.17
1	ad	121	THR	N-CA-C	7.86	122.23	111.39
1	bt	324	THR	N-CA-C	-7.86	98.23	109.62
1	dq	88	VAL	N-CA-C	7.86	119.22	107.75
3	hx	46	TYR	N-CA-C	7.86	120.84	109.14
1	br	440	GLY	CA-C-N	7.85	127.49	119.56
1	br	440	GLY	C-N-CA	7.85	127.49	119.56
1	dm	149	GLY	CA-C-N	7.84	127.77	119.85
1	dm	149	GLY	C-N-CA	7.84	127.77	119.85
1	ek	88	VAL	N-CA-C	7.84	119.17	107.80
3	hy	46	TYR	N-CA-C	7.84	119.92	108.86
1	af	324	THR	N-CA-C	-7.84	99.92	109.72
1	fi	287	ASP	N-CA-C	-7.84	102.50	112.93
2	hj	368	SER	N-CA-C	-7.84	100.42	110.53
1	ek	486	GLU	CA-C-N	7.83	133.24	122.19
1	ek	486	GLU	C-N-CA	7.83	133.24	122.19
1	el	232	ILE	N-CA-C	-7.83	104.23	111.67
1	cq	232	ILE	N-CA-C	-7.83	104.17	111.45
1	bz	324	THR	N-CA-C	-7.83	98.27	109.62
1	cw	149	GLY	CA-C-N	7.82	127.75	119.85
1	cw	149	GLY	C-N-CA	7.82	127.75	119.85
1	dr	253	ARG	N-CA-C	7.82	123.98	113.97
1	ez	324	THR	N-CA-C	-7.82	98.28	109.62
1	fe	406	THR	N-CA-C	-7.82	103.25	114.12
1	gs	121	THR	N-CA-C	7.81	120.78	111.02
1	bq	121	THR	N-CA-C	7.80	120.78	111.02
1	dp	103	ILE	CA-C-N	7.80	127.81	119.78
1	dp	103	ILE	C-N-CA	7.80	127.81	119.78
1	ge	149	GLY	CA-C-N	7.80	127.75	120.03
1	ge	149	GLY	C-N-CA	7.80	127.75	120.03
1	hd	103	ILE	CA-C-N	7.80	127.75	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	hd	103	ILE	C-N-CA	7.80	127.75	120.03
2	hj	331	ILE	N-CA-C	-7.80	104.19	111.45
2	hl	327	VAL	N-CA-C	7.80	120.08	108.46
1	fd	88	VAL	N-CA-C	7.79	119.34	108.12
1	cd	88	VAL	N-CA-C	7.79	119.02	108.11
1	fv	440	GLY	CA-C-N	7.79	127.50	119.56
1	fv	440	GLY	C-N-CA	7.79	127.50	119.56
1	bn	88	VAL	N-CA-C	7.78	119.06	108.17
1	cm	149	GLY	CA-C-N	7.78	127.73	120.03
1	cm	149	GLY	C-N-CA	7.78	127.73	120.03
1	gz	463	ASP	CA-C-N	7.77	127.49	119.56
1	gz	463	ASP	C-N-CA	7.77	127.49	119.56
1	ab	463	ASP	CA-C-N	7.77	127.48	119.56
1	ab	463	ASP	C-N-CA	7.77	127.48	119.56
1	ex	491	ALA	CA-C-N	7.76	127.92	120.31
1	ex	491	ALA	C-N-CA	7.76	127.92	120.31
1	et	88	VAL	N-CA-C	7.76	119.05	107.80
1	bm	149	GLY	CA-C-N	7.75	127.91	120.31
1	bm	149	GLY	C-N-CA	7.75	127.91	120.31
1	gf	88	VAL	N-CA-C	7.75	119.04	107.80
1	bc	463	ASP	CA-C-N	7.75	127.47	119.56
1	bc	463	ASP	C-N-CA	7.75	127.47	119.56
1	ej	463	ASP	CA-C-N	7.75	127.47	119.56
1	ej	463	ASP	C-N-CA	7.75	127.47	119.56
1	ay	287	ASP	N-CA-C	-7.75	102.38	112.68
1	bl	463	ASP	CA-C-N	7.75	127.46	119.56
1	bl	463	ASP	C-N-CA	7.75	127.46	119.56
1	af	463	ASP	CA-C-N	7.74	127.46	119.56
1	af	463	ASP	C-N-CA	7.74	127.46	119.56
3	mh	46	TYR	N-CA-C	7.74	120.67	109.14
1	gg	149	GLY	CA-C-N	7.74	127.66	119.85
1	gg	149	GLY	C-N-CA	7.74	127.66	119.85
1	gj	440	GLY	CA-C-N	7.74	127.45	119.56
1	gj	440	GLY	C-N-CA	7.74	127.45	119.56
1	du	149	GLY	CA-C-N	7.73	127.69	120.03
1	du	149	GLY	C-N-CA	7.73	127.69	120.03
1	ed	88	VAL	N-CA-C	7.73	118.93	108.11
1	av	463	ASP	CA-C-N	7.73	127.44	119.56
1	av	463	ASP	C-N-CA	7.73	127.44	119.56
1	be	145	HIS	CA-C-N	7.73	127.44	119.56
1	be	145	HIS	C-N-CA	7.73	127.44	119.56
1	bo	121	THR	N-CA-C	7.73	120.68	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gh	88	VAL	N-CA-C	7.72	118.99	108.17
1	em	324	THR	N-CA-C	-7.72	98.42	109.62
1	gk	103	ILE	CA-C-N	7.72	127.73	119.78
1	gk	103	ILE	C-N-CA	7.72	127.73	119.78
1	bg	88	VAL	N-CA-C	7.71	118.99	107.80
1	gf	463	ASP	CA-C-N	7.71	127.43	119.56
1	gf	463	ASP	C-N-CA	7.71	127.43	119.56
1	gl	88	VAL	N-CA-C	7.71	118.98	107.80
1	hb	483	PRO	N-CA-C	-7.71	99.12	111.14
1	ds	293	ILE	N-CA-C	-7.70	104.28	111.45
1	bz	121	THR	N-CA-C	7.70	122.02	111.39
1	fh	463	ASP	CA-C-N	7.70	127.41	119.56
1	fh	463	ASP	C-N-CA	7.70	127.41	119.56
3	oe	5	ARG	N-CA-C	-7.69	104.50	114.04
1	df	88	VAL	N-CA-C	7.69	118.98	107.75
1	fu	149	GLY	CA-C-N	7.69	127.62	119.85
1	fu	149	GLY	C-N-CA	7.69	127.62	119.85
1	do	463	ASP	CA-C-N	7.69	127.40	119.56
1	do	463	ASP	C-N-CA	7.69	127.40	119.56
1	bw	253	ARG	CA-C-O	-7.68	114.22	119.68
2	he	353	ASP	CA-C-N	7.68	127.40	119.56
2	he	353	ASP	C-N-CA	7.68	127.40	119.56
1	ba	88	VAL	N-CA-C	7.68	118.94	107.80
1	ed	324	THR	N-CA-C	-7.68	100.12	109.72
1	cw	103	ILE	CA-C-N	7.67	127.68	119.78
1	cw	103	ILE	C-N-CA	7.67	127.68	119.78
1	gm	103	ILE	CA-C-N	7.67	127.68	119.78
1	gm	103	ILE	C-N-CA	7.67	127.68	119.78
1	fk	484	PHE	CA-CB-CG	7.67	121.47	113.80
1	br	232	ILE	N-CA-C	-7.67	104.32	111.45
1	eu	149	GLY	CA-C-N	7.67	127.62	120.03
1	eu	149	GLY	C-N-CA	7.67	127.62	120.03
1	ga	287	ASP	N-CA-C	-7.66	102.49	112.68
1	gc	88	VAL	N-CA-C	7.66	118.84	108.11
1	ag	287	ASP	N-CA-C	-7.66	102.49	112.68
1	ee	253	ARG	N-CA-C	7.66	123.77	113.97
1	ax	440	GLY	CA-C-N	7.66	127.37	119.56
1	ax	440	GLY	C-N-CA	7.66	127.37	119.56
1	cv	149	GLY	CA-C-N	7.65	127.58	119.85
1	cv	149	GLY	C-N-CA	7.65	127.58	119.85
1	fs	149	GLY	CA-C-N	7.65	127.58	119.85
1	fs	149	GLY	C-N-CA	7.65	127.58	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	co	287	ASP	N-CA-C	-7.65	102.75	112.93
1	de	121	THR	N-CA-C	7.65	120.58	111.02
1	au	88	VAL	N-CA-C	7.65	118.88	108.17
3	ji	38	VAL	N-CA-C	7.64	119.33	108.17
3	jv	46	TYR	N-CA-C	7.64	120.53	109.14
1	fa	484	PHE	CA-CB-CG	7.64	121.44	113.80
1	fe	232	ILE	N-CA-C	-7.64	104.41	111.67
1	af	287	ASP	N-CA-C	-7.64	102.77	112.93
1	gl	186	GLY	N-CA-C	7.64	121.22	111.37
1	en	121	THR	N-CA-C	7.64	121.78	111.24
3	nq	46	TYR	N-CA-C	7.64	120.52	109.14
1	ci	468	GLN	CA-C-N	7.63	127.69	119.90
1	ci	468	GLN	C-N-CA	7.63	127.69	119.90
1	gn	149	GLY	CA-C-N	7.63	127.59	120.03
1	gn	149	GLY	C-N-CA	7.63	127.59	120.03
1	at	482	ASN	CA-C-N	7.63	127.69	119.90
1	at	482	ASN	C-N-CA	7.63	127.69	119.90
1	fz	324	THR	N-CA-C	-7.63	100.03	109.65
1	af	328	LYS	N-CA-C	7.63	122.31	112.92
1	dm	463	ASP	CA-C-N	7.63	127.34	119.56
1	dm	463	ASP	C-N-CA	7.63	127.34	119.56
1	al	88	VAL	N-CA-C	7.63	118.86	107.80
1	ep	88	VAL	N-CA-C	7.63	119.11	108.12
3	mx	64	GLN	N-CA-C	-7.63	105.92	114.62
1	fy	121	THR	N-CA-C	7.62	120.55	111.02
1	cx	259	ILE	N-CA-C	7.62	119.81	108.46
1	dw	463	ASP	CA-C-N	7.61	127.32	119.56
1	dw	463	ASP	C-N-CA	7.61	127.32	119.56
1	gs	253	ARG	N-CA-C	7.61	123.13	113.55
1	dh	328	LYS	N-CA-C	7.60	121.86	112.59
1	dj	324	THR	N-CA-C	-7.60	100.22	109.72
1	ej	230	THR	N-CA-C	7.60	119.65	111.36
1	hd	93	PRO	N-CA-CB	-7.60	97.78	102.79
1	ds	285	ASP	N-CA-C	7.60	119.64	111.36
3	jh	46	TYR	N-CA-C	7.59	120.46	109.14
1	ds	406	THR	N-CA-C	-7.59	103.57	114.12
2	hh	268	THR	N-CA-C	7.58	122.12	113.02
1	aa	324	THR	N-CA-C	-7.58	98.35	109.50
1	ap	328	LYS	N-CA-C	7.58	122.25	112.92
1	at	88	VAL	N-CA-C	7.58	118.79	107.80
1	cw	88	VAL	N-CA-C	7.58	119.03	108.12
2	hm	327	VAL	N-CA-C	7.58	119.75	108.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bh	103	ILE	CA-C-N	7.57	127.58	119.78
1	bh	103	ILE	C-N-CA	7.57	127.58	119.78
1	ez	149	GLY	CA-C-N	7.57	127.52	120.03
1	ez	149	GLY	C-N-CA	7.57	127.52	120.03
1	al	463	ASP	CA-C-N	7.57	128.25	119.47
1	al	463	ASP	C-N-CA	7.57	128.25	119.47
1	gw	253	ARG	N-CA-C	7.56	124.07	114.31
1	bh	463	ASP	CA-C-N	7.56	128.24	119.47
1	bh	463	ASP	C-N-CA	7.56	128.24	119.47
1	ef	440	GLY	CA-C-N	7.56	127.27	119.56
1	ef	440	GLY	C-N-CA	7.56	127.27	119.56
1	bc	88	VAL	N-CA-C	7.56	118.76	107.80
1	bz	103	ILE	CA-C-N	7.56	127.56	119.78
1	bz	103	ILE	C-N-CA	7.56	127.56	119.78
1	bj	468	GLN	CA-C-N	7.55	127.47	119.85
1	bj	468	GLN	C-N-CA	7.55	127.47	119.85
1	cj	440	GLY	CA-C-N	7.54	127.26	119.56
1	cj	440	GLY	C-N-CA	7.54	127.26	119.56
1	bk	463	ASP	CA-C-N	7.54	127.25	119.56
1	bk	463	ASP	C-N-CA	7.54	127.25	119.56
1	gg	103	ILE	CA-C-N	7.54	127.55	119.78
1	gg	103	ILE	C-N-CA	7.54	127.55	119.78
1	bq	287	ASP	N-CA-C	-7.54	102.90	112.93
1	di	328	LYS	N-CA-C	7.54	122.60	112.88
3	iz	46	TYR	N-CA-C	7.53	120.35	109.14
1	cy	484	PHE	CA-CB-CG	7.52	121.32	113.80
1	gz	440	GLY	CA-C-N	7.52	127.23	119.56
1	gz	440	GLY	C-N-CA	7.52	127.23	119.56
1	hb	121	THR	N-CA-C	7.52	121.77	111.39
2	hl	59	ASN	CA-C-N	7.52	127.23	119.56
2	hl	59	ASN	C-N-CA	7.52	127.23	119.56
1	af	491	ALA	CA-C-N	7.52	127.68	120.31
1	af	491	ALA	C-N-CA	7.52	127.68	120.31
1	fj	88	VAL	N-CA-C	7.51	118.63	108.11
1	gb	88	VAL	N-CA-C	7.51	118.63	108.11
1	dw	149	GLY	CA-C-N	7.51	127.47	120.03
1	dw	149	GLY	C-N-CA	7.51	127.47	120.03
1	dp	253	ARG	N-CA-C	7.51	122.55	111.96
1	fv	324	THR	N-CA-C	-7.51	100.19	109.65
2	hf	115	PRO	N-CA-C	-7.51	99.44	111.38
1	cm	88	VAL	N-CA-C	7.50	118.62	108.11
1	dg	103	ILE	CA-C-N	7.50	127.50	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dg	103	ILE	C-N-CA	7.50	127.50	119.78
1	dj	491	ALA	CA-C-N	7.50	127.66	120.31
1	dj	491	ALA	C-N-CA	7.50	127.66	120.31
1	fr	440	GLY	CA-C-N	7.49	127.13	119.56
1	fr	440	GLY	C-N-CA	7.49	127.13	119.56
1	gh	149	GLY	CA-C-N	7.49	127.45	120.03
1	gh	149	GLY	C-N-CA	7.49	127.45	120.03
1	cl	324	THR	N-CA-C	-7.49	98.77	109.62
3	jh	37	ASP	CA-CB-CG	7.49	120.09	112.60
1	gr	88	VAL	N-CA-C	7.48	118.59	108.11
1	bi	463	ASP	CA-C-N	7.48	127.19	119.56
1	bi	463	ASP	C-N-CA	7.48	127.19	119.56
1	gx	88	VAL	N-CA-C	7.48	118.64	107.80
1	dp	440	GLY	CA-C-N	7.48	127.19	119.56
1	dp	440	GLY	C-N-CA	7.48	127.19	119.56
1	gc	149	GLY	CA-C-N	7.48	127.43	120.03
1	gc	149	GLY	C-N-CA	7.48	127.43	120.03
1	bc	481	ILE	N-CA-C	7.47	119.27	112.17
2	hi	59	ASN	CA-C-N	7.47	127.18	119.56
2	hi	59	ASN	C-N-CA	7.47	127.18	119.56
3	kf	38	VAL	N-CA-C	7.46	118.87	108.12
1	fb	258	VAL	N-CA-C	7.46	119.58	108.46
1	gy	88	VAL	N-CA-C	7.46	118.64	107.75
1	du	253	ARG	N-CA-C	7.45	123.51	113.97
1	dv	324	THR	N-CA-C	-7.45	98.81	109.62
1	dn	440	GLY	CA-C-N	7.45	127.16	119.56
1	dn	440	GLY	C-N-CA	7.45	127.16	119.56
1	bw	121	THR	N-CA-C	7.45	120.33	111.02
1	co	149	GLY	CA-C-N	7.45	127.37	119.85
1	co	149	GLY	C-N-CA	7.45	127.37	119.85
1	cu	88	VAL	N-CA-C	7.45	118.54	108.11
1	gx	103	ILE	CA-C-N	7.45	127.40	120.03
1	gx	103	ILE	C-N-CA	7.45	127.40	120.03
1	di	149	GLY	CA-C-N	7.45	127.37	119.85
1	di	149	GLY	C-N-CA	7.45	127.37	119.85
1	ee	287	ASP	N-CA-C	-7.45	102.78	112.68
3	lw	72	ASN	CA-CB-CG	7.44	120.04	112.60
1	eg	149	GLY	CA-C-N	7.44	127.36	119.85
1	eg	149	GLY	C-N-CA	7.44	127.36	119.85
1	ab	184	GLU	N-CA-C	-7.44	98.37	108.86
1	bz	440	GLY	CA-C-N	7.44	127.15	119.56
1	bz	440	GLY	C-N-CA	7.44	127.15	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dc	253	ARG	N-CA-C	7.44	123.49	113.97
2	hn	36	TYR	N-CA-C	-7.44	105.38	114.75
1	hb	149	GLY	CA-C-N	7.44	127.39	120.03
1	hb	149	GLY	C-N-CA	7.44	127.39	120.03
1	gp	154	PHE	N-CA-C	-7.43	103.29	113.18
1	eo	88	VAL	N-CA-C	7.43	118.58	108.17
3	mj	46	TYR	N-CA-C	7.43	120.21	109.14
1	cs	88	VAL	N-CA-C	7.42	118.56	108.17
1	dj	88	VAL	N-CA-C	7.42	118.59	107.75
1	cn	484	PHE	CA-CB-CG	7.42	121.22	113.80
1	bd	253	ARG	CA-C-O	-7.42	114.41	119.68
1	ah	88	VAL	N-CA-C	7.42	118.56	107.80
1	cv	87	ALA	N-CA-C	7.42	119.36	111.28
1	dg	406	THR	N-CA-C	-7.42	103.81	114.12
1	ab	149	GLY	CA-C-N	7.42	127.34	119.85
1	ab	149	GLY	C-N-CA	7.42	127.34	119.85
1	gv	185	THR	N-CA-C	7.41	121.66	112.47
1	gx	115	GLN	CA-C-N	7.41	127.37	120.03
1	gx	115	GLN	C-N-CA	7.41	127.37	120.03
1	ct	88	VAL	N-CA-C	7.41	118.55	108.17
1	fb	324	THR	N-CA-C	-7.41	100.46	109.72
1	gq	483	PRO	N-CA-C	-7.41	99.43	111.21
1	ff	483	PRO	N-CA-C	-7.41	99.58	111.14
1	bi	88	VAL	N-CA-C	7.41	118.54	107.80
1	eg	440	GLY	CA-C-N	7.41	127.11	119.56
1	eg	440	GLY	C-N-CA	7.41	127.11	119.56
1	gk	253	ARG	N-CA-C	7.40	122.98	113.88
1	bm	253	ARG	N-CA-C	7.40	123.44	113.97
1	dc	463	ASP	CA-C-N	7.40	127.11	119.56
1	dc	463	ASP	C-N-CA	7.40	127.11	119.56
1	bl	149	GLY	CA-C-N	7.40	127.32	119.85
1	bl	149	GLY	C-N-CA	7.40	127.32	119.85
1	ec	121	THR	N-CA-C	7.40	121.45	111.24
1	el	491	ALA	CA-C-N	7.40	127.56	120.31
1	el	491	ALA	C-N-CA	7.40	127.56	120.31
1	cd	184	GLU	N-CA-C	-7.39	98.43	108.86
1	fd	78	ASN	N-CA-C	-7.39	102.59	111.69
1	fd	440	GLY	CA-C-N	7.39	127.03	119.56
1	fd	440	GLY	C-N-CA	7.39	127.03	119.56
1	ej	149	GLY	CA-C-N	7.39	127.35	120.03
1	ej	149	GLY	C-N-CA	7.39	127.35	120.03
1	ey	481	ILE	N-CA-C	7.39	118.64	108.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cz	463	ASP	CA-C-N	7.39	127.09	119.56
1	cz	463	ASP	C-N-CA	7.39	127.09	119.56
1	dh	440	GLY	CA-C-N	7.39	127.09	119.56
1	dh	440	GLY	C-N-CA	7.39	127.09	119.56
2	hm	391	ASP	CA-CB-CG	7.38	119.98	112.60
3	ng	46	TYR	N-CA-C	7.38	120.14	109.14
1	df	253	ARG	N-CA-C	7.38	122.85	113.55
3	jx	46	TYR	N-CA-C	7.38	120.14	109.14
1	fl	88	VAL	N-CA-C	7.38	118.50	107.80
1	cg	468	GLN	CA-C-N	7.37	127.38	119.78
1	cg	468	GLN	C-N-CA	7.37	127.38	119.78
1	ee	336	ASP	CA-C-N	7.37	127.08	119.56
1	ee	336	ASP	C-N-CA	7.37	127.08	119.56
1	fa	93	PRO	N-CA-CB	-7.37	97.93	102.79
1	fl	324	THR	N-CA-C	-7.37	98.93	109.62
1	ab	336	ASP	CA-C-N	7.37	128.02	119.47
1	ab	336	ASP	C-N-CA	7.37	128.02	119.47
3	lf	46	TYR	N-CA-C	7.37	120.12	109.14
1	dd	483	PRO	N-CA-C	-7.36	99.65	111.14
2	hf	59	ASN	CA-C-N	7.36	127.07	119.56
2	hf	59	ASN	C-N-CA	7.36	127.07	119.56
1	ce	440	GLY	CA-C-N	7.36	126.99	119.56
1	ce	440	GLY	C-N-CA	7.36	126.99	119.56
1	dw	103	ILE	CA-C-N	7.35	127.35	119.78
1	dw	103	ILE	C-N-CA	7.35	127.35	119.78
2	hm	343	ALA	CA-C-N	7.35	127.28	119.85
2	hm	343	ALA	C-N-CA	7.35	127.28	119.85
1	bdl	287	ASP	N-CA-C	-7.35	103.15	112.93
1	eb	324	THR	N-CA-C	-7.35	98.97	109.62
1	ae	287	ASP	N-CA-C	-7.34	102.91	112.68
1	ak	463	ASP	CA-C-N	7.34	127.05	119.56
1	ak	463	ASP	C-N-CA	7.34	127.05	119.56
1	ad	324	THR	N-CA-C	-7.34	98.97	109.62
3	hz	38	VAL	N-CA-C	7.34	119.57	107.24
1	bb	93	PRO	N-CA-CB	-7.34	97.95	102.79
3	mf	46	TYR	N-CA-C	7.34	120.07	109.14
1	di	463	ASP	CA-C-N	7.33	127.04	119.56
1	di	463	ASP	C-N-CA	7.33	127.04	119.56
1	fo	293	ILE	N-CA-C	-7.33	104.63	111.45
1	cd	149	GLY	CA-C-N	7.33	127.29	120.03
1	cd	149	GLY	C-N-CA	7.33	127.29	120.03
1	bn	440	GLY	CA-C-N	7.33	126.96	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bn	440	GLY	C-N-CA	7.33	126.96	119.56
1	dr	88	VAL	N-CA-C	7.33	118.37	108.11
1	fv	149	GLY	CA-C-N	7.33	127.28	120.03
1	fv	149	GLY	C-N-CA	7.33	127.28	120.03
1	bl	336	ASP	CA-C-N	7.32	127.97	119.47
1	bl	336	ASP	C-N-CA	7.32	127.97	119.47
1	cy	483	PRO	N-CA-C	-7.32	99.57	111.21
1	ak	483	PRO	N-CA-C	-7.32	99.57	111.21
1	dl	285	ASP	N-CA-C	7.32	119.34	111.36
3	jn	38	VAL	N-CA-C	7.32	118.60	107.77
1	dr	230	THR	N-CA-C	7.32	119.34	111.36
1	ag	440	GLY	CA-C-N	7.32	126.95	119.56
1	ag	440	GLY	C-N-CA	7.32	126.95	119.56
3	ly	38	VAL	N-CA-C	7.31	118.84	108.17
1	dl	88	VAL	N-CA-C	7.31	118.40	108.17
1	dr	287	ASP	N-CA-C	-7.31	102.96	112.68
1	gt	88	VAL	N-CA-C	7.31	118.34	108.11
1	ax	468	GLN	CA-C-N	7.30	127.35	119.90
1	ax	468	GLN	C-N-CA	7.30	127.35	119.90
2	hn	268	THR	N-CA-C	7.30	122.03	113.20
3	iy	38	VAL	N-CA-C	7.30	118.64	108.12
1	fh	253	ARG	N-CA-C	7.30	122.75	113.55
1	ft	491	ALA	CA-C-N	7.30	127.46	120.31
1	ft	491	ALA	C-N-CA	7.30	127.46	120.31
3	na	46	TYR	N-CA-C	7.30	120.02	109.14
1	as	88	VAL	N-CA-C	7.30	118.38	107.80
1	cr	71	ASP	CA-CB-CG	7.30	119.90	112.60
1	et	121	THR	N-CA-C	7.29	121.31	111.24
1	db	324	THR	N-CA-C	-7.29	99.05	109.62
1	dv	491	ALA	CA-C-N	7.29	127.46	120.31
1	dv	491	ALA	C-N-CA	7.29	127.46	120.31
1	ev	115	GLN	CA-C-N	7.29	127.29	119.78
1	ev	115	GLN	C-N-CA	7.29	127.29	119.78
1	eg	336	ASP	CA-C-N	7.29	127.92	119.47
1	eg	336	ASP	C-N-CA	7.29	127.92	119.47
1	fi	440	GLY	CA-C-N	7.28	126.92	119.56
1	fi	440	GLY	C-N-CA	7.28	126.92	119.56
1	et	253	ARG	N-CA-C	7.28	122.83	113.88
1	da	149	GLY	CA-C-N	7.28	127.23	120.03
1	da	149	GLY	C-N-CA	7.28	127.23	120.03
1	eh	149	GLY	CA-C-N	7.28	127.23	120.03
1	eh	149	GLY	C-N-CA	7.28	127.23	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fc	287	ASP	N-CA-C	-7.27	103.01	112.68
1	gh	328	LYS	N-CA-C	7.27	122.26	112.88
1	dq	463	ASP	CA-C-N	7.27	127.91	119.47
1	dq	463	ASP	C-N-CA	7.27	127.91	119.47
1	ff	88	VAL	N-CA-C	7.27	118.35	108.17
1	gz	149	GLY	CA-C-N	7.27	127.19	119.85
1	gz	149	GLY	C-N-CA	7.27	127.19	119.85
1	bh	253	ARG	N-CA-C	7.27	122.03	112.72
1	ct	103	ILE	CA-C-N	7.27	127.22	120.03
1	ct	103	ILE	C-N-CA	7.27	127.22	120.03
1	cu	149	GLY	CA-C-N	7.27	127.22	120.03
1	cu	149	GLY	C-N-CA	7.27	127.22	120.03
1	dt	88	VAL	N-CA-C	7.27	118.58	108.12
1	es	232	ILE	N-CA-C	-7.26	104.77	111.67
1	fm	149	GLY	CA-C-N	7.26	127.19	119.85
1	fm	149	GLY	C-N-CA	7.26	127.19	119.85
1	eh	491	ALA	CA-C-N	7.26	127.43	120.31
1	eh	491	ALA	C-N-CA	7.26	127.43	120.31
2	hj	59	ASN	CA-C-N	7.26	126.97	119.56
2	hj	59	ASN	C-N-CA	7.26	126.97	119.56
2	hn	370	GLN	CA-C-N	7.26	127.22	120.03
2	hn	370	GLN	C-N-CA	7.26	127.22	120.03
1	dw	119	SER	N-CA-C	-7.26	101.69	108.22
1	fq	336	ASP	CA-C-N	7.26	127.89	119.47
1	fq	336	ASP	C-N-CA	7.26	127.89	119.47
1	eh	324	THR	N-CA-C	-7.25	97.04	109.15
1	by	491	ALA	CA-C-N	7.25	127.42	120.31
1	by	491	ALA	C-N-CA	7.25	127.42	120.31
1	ge	88	VAL	N-CA-C	7.25	118.26	108.11
1	gb	440	GLY	CA-C-N	7.25	126.95	119.56
1	gb	440	GLY	C-N-CA	7.25	126.95	119.56
1	ha	121	THR	N-CA-C	7.25	120.08	111.02
2	ho	36	TYR	N-CA-C	-7.25	105.62	114.75
1	dq	149	GLY	CA-C-N	7.24	127.20	120.03
1	dq	149	GLY	C-N-CA	7.24	127.20	120.03
1	cj	449	TYR	CB-CA-C	-7.24	95.55	109.37
1	cv	232	ILE	N-CA-C	-7.24	104.79	111.67
1	fn	336	ASP	CA-C-N	7.24	126.94	119.56
1	fn	336	ASP	C-N-CA	7.24	126.94	119.56
1	gb	93	PRO	N-CA-CB	-7.24	98.01	102.79
1	gl	103	ILE	CA-C-N	7.24	127.24	119.78
1	gl	103	ILE	C-N-CA	7.24	127.24	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gd	75	ASN	CA-CB-CG	-7.24	105.36	112.60
3	jn	46	TYR	N-CA-C	7.24	119.92	109.14
1	at	491	ALA	CA-C-N	7.23	127.39	120.31
1	at	491	ALA	C-N-CA	7.23	127.39	120.31
1	bs	336	ASP	CA-C-N	7.23	126.94	119.56
1	bs	336	ASP	C-N-CA	7.23	126.94	119.56
1	ch	324	THR	N-CA-C	-7.23	99.19	109.24
3	if	5	ARG	N-CA-C	-7.23	105.38	114.56
1	bx	440	GLY	CA-C-N	7.22	126.93	119.56
1	bx	440	GLY	C-N-CA	7.22	126.93	119.56
1	fg	491	ALA	CA-C-N	7.22	127.14	119.85
1	fg	491	ALA	C-N-CA	7.22	127.14	119.85
1	bu	149	GLY	CA-C-N	7.22	127.18	120.03
1	bu	149	GLY	C-N-CA	7.22	127.18	120.03
1	bq	440	GLY	CA-C-N	7.22	126.85	119.56
1	bq	440	GLY	C-N-CA	7.22	126.85	119.56
1	ei	78	ASN	CA-CB-CG	7.22	119.82	112.60
1	dx	287	ASP	N-CA-C	-7.21	103.33	112.93
1	et	491	ALA	CA-C-N	7.21	127.38	120.31
1	et	491	ALA	C-N-CA	7.21	127.38	120.31
1	fc	463	ASP	CA-C-N	7.21	126.92	119.56
1	fc	463	ASP	C-N-CA	7.21	126.92	119.56
3	ij	46	TYR	N-CA-C	7.21	118.69	108.74
1	gq	88	VAL	N-CA-C	7.21	118.21	108.11
1	cn	406	THR	N-CA-C	-7.21	104.10	114.12
3	le	38	VAL	N-CA-C	7.21	118.69	108.17
1	cu	121	THR	N-CA-C	7.21	120.03	111.02
1	ey	440	GLY	CA-C-N	7.21	126.91	119.56
1	ey	440	GLY	C-N-CA	7.21	126.91	119.56
1	fe	88	VAL	N-CA-C	7.21	118.20	108.11
1	bl	324	THR	N-CA-C	-7.21	99.17	109.62
2	ho	315	ASP	CA-CB-CG	7.21	119.81	112.60
1	ar	103	ILE	CA-C-N	7.20	127.16	120.03
1	ar	103	ILE	C-N-CA	7.20	127.16	120.03
1	dg	149	GLY	CA-C-N	7.20	127.13	119.85
1	dg	149	GLY	C-N-CA	7.20	127.13	119.85
3	ls	64	GLN	N-CA-C	-7.20	106.41	114.62
1	gc	232	ILE	N-CA-C	-7.20	104.75	111.45
3	ob	5	ARG	N-CA-C	-7.20	106.41	114.62
1	df	336	ASP	CA-C-N	7.20	126.90	119.56
1	df	336	ASP	C-N-CA	7.20	126.90	119.56
1	cb	149	GLY	CA-C-N	7.20	127.15	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cb	149	GLY	C-N-CA	7.20	127.15	120.03
1	eu	121	THR	N-CA-C	7.20	121.17	111.24
1	ap	491	ALA	CA-C-N	7.19	127.36	120.31
1	ap	491	ALA	C-N-CA	7.19	127.36	120.31
1	dc	184	GLU	N-CA-C	-7.19	98.72	108.86
1	ec	463	ASP	CA-C-N	7.19	126.90	119.56
1	ec	463	ASP	C-N-CA	7.19	126.90	119.56
1	en	463	ASP	CA-C-N	7.19	126.90	119.56
1	en	463	ASP	C-N-CA	7.19	126.90	119.56
3	mk	38	VAL	N-CA-C	7.19	118.42	107.77
1	fm	440	GLY	CA-C-N	7.19	126.82	119.56
1	fm	440	GLY	C-N-CA	7.19	126.82	119.56
2	he	327	VAL	N-CA-C	7.19	119.17	108.46
1	cn	253	ARG	N-CA-C	7.19	123.17	113.97
1	fm	88	VAL	N-CA-C	7.19	118.22	107.80
1	ce	232	ILE	N-CA-C	-7.18	104.77	111.45
1	bg	336	ASP	CA-C-N	7.18	127.80	119.47
1	bg	336	ASP	C-N-CA	7.18	127.80	119.47
1	ft	119	SER	N-CA-C	-7.18	101.76	108.22
1	gz	121	THR	N-CA-C	7.18	119.99	111.02
1	dy	121	THR	N-CA-C	7.17	121.29	111.17
1	gu	324	THR	N-CA-C	-7.17	98.14	109.04
3	lh	46	TYR	N-CA-C	7.17	119.83	109.14
1	ab	121	THR	N-CA-C	7.17	119.98	111.02
1	ab	245	ASN	CA-C-N	7.17	127.09	119.85
1	ab	245	ASN	C-N-CA	7.17	127.09	119.85
1	dq	483	PRO	N-CA-C	-7.17	99.82	111.21
1	cr	149	GLY	CA-C-N	7.17	127.12	120.03
1	cr	149	GLY	C-N-CA	7.17	127.12	120.03
1	ey	88	VAL	N-CA-C	7.17	118.20	108.17
1	gl	440	GLY	CA-C-N	7.16	126.80	119.56
1	gl	440	GLY	C-N-CA	7.16	126.80	119.56
1	dy	336	ASP	CA-C-N	7.16	127.78	119.47
1	dy	336	ASP	C-N-CA	7.16	127.78	119.47
3	kw	46	TYR	N-CA-C	7.16	118.95	108.86
1	ay	440	GLY	CA-C-N	7.16	126.79	119.56
1	ay	440	GLY	C-N-CA	7.16	126.79	119.56
1	dg	440	GLY	CA-C-N	7.16	126.79	119.56
1	dg	440	GLY	C-N-CA	7.16	126.79	119.56
1	ds	440	GLY	CA-C-N	7.16	126.79	119.56
1	ds	440	GLY	C-N-CA	7.16	126.79	119.56
1	ak	149	GLY	CA-C-N	7.15	127.11	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ak	149	GLY	C-N-CA	7.15	127.11	120.03
2	he	370	GLN	CA-C-N	7.15	127.11	120.03
2	he	370	GLN	C-N-CA	7.15	127.11	120.03
1	aj	149	GLY	CA-C-N	7.15	127.07	119.85
1	aj	149	GLY	C-N-CA	7.15	127.07	119.85
1	bx	324	THR	N-CA-C	-7.15	100.64	109.65
1	fo	103	ILE	CA-C-N	7.15	127.11	120.03
1	fo	103	ILE	C-N-CA	7.15	127.11	120.03
1	an	440	GLY	CA-C-N	7.14	126.78	119.56
1	an	440	GLY	C-N-CA	7.14	126.78	119.56
1	ck	149	GLY	CA-C-N	7.14	127.07	119.85
1	ck	149	GLY	C-N-CA	7.14	127.07	119.85
1	cz	115	GLN	CA-C-N	7.14	127.10	120.03
1	cz	115	GLN	C-N-CA	7.14	127.10	120.03
1	fd	484	PHE	CA-CB-CG	7.14	120.94	113.80
1	ag	336	ASP	CA-C-N	7.14	126.84	119.56
1	ag	336	ASP	C-N-CA	7.14	126.84	119.56
3	ks	72	ASN	CA-CB-CG	7.14	119.74	112.60
1	fp	103	ILE	CA-C-N	7.14	127.10	120.03
1	fp	103	ILE	C-N-CA	7.14	127.10	120.03
1	ad	336	ASP	CA-C-N	7.14	127.75	119.47
1	ad	336	ASP	C-N-CA	7.14	127.75	119.47
1	go	184	GLU	N-CA-C	-7.14	98.89	108.74
1	co	88	VAL	N-CA-C	7.13	118.17	107.75
1	dw	121	THR	N-CA-C	7.13	119.94	111.02
1	fo	440	GLY	CA-C-N	7.13	126.77	119.56
1	fo	440	GLY	C-N-CA	7.13	126.77	119.56
1	fu	293	ILE	N-CA-C	-7.13	104.82	111.45
1	gr	287	ASP	N-CA-C	-7.13	103.45	112.93
3	hr	38	VAL	N-CA-C	7.12	119.21	107.24
1	gk	124	VAL	N-CA-C	7.12	117.75	108.35
3	kl	46	TYR	N-CA-C	7.12	119.75	109.14
1	eq	324	THR	N-CA-C	-7.12	99.30	109.62
1	gm	253	ARG	N-CA-C	7.11	122.39	112.93
1	fq	324	THR	N-CA-C	-7.11	100.83	109.72
1	gr	115	GLN	CA-C-N	7.11	127.07	120.03
1	gr	115	GLN	C-N-CA	7.11	127.07	120.03
1	gd	121	THR	N-CA-C	7.11	119.91	111.02
3	jj	46	TYR	N-CA-C	7.11	119.55	108.96
3	lb	38	VAL	N-CA-C	7.11	118.28	107.77
1	eh	245	ASN	CA-C-N	7.10	127.06	120.03
1	eh	245	ASN	C-N-CA	7.10	127.06	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	db	336	ASP	CA-C-N	7.10	127.71	119.47
1	db	336	ASP	C-N-CA	7.10	127.71	119.47
1	dk	149	GLY	CA-C-N	7.10	127.06	120.03
1	dk	149	GLY	C-N-CA	7.10	127.06	120.03
1	cn	491	ALA	CA-C-N	7.10	127.55	120.52
1	cn	491	ALA	C-N-CA	7.10	127.55	120.52
1	dm	121	THR	N-CA-C	7.10	119.89	111.02
1	hb	440	GLY	CA-C-N	7.10	126.73	119.56
1	hb	440	GLY	C-N-CA	7.10	126.73	119.56
1	ej	293	ILE	N-CA-C	-7.10	104.06	111.58
1	cm	440	GLY	CA-C-N	7.10	126.73	119.56
1	cm	440	GLY	C-N-CA	7.10	126.73	119.56
1	ax	336	ASP	CA-C-N	7.09	127.70	119.47
1	ax	336	ASP	C-N-CA	7.09	127.70	119.47
1	br	193	SER	N-CA-C	-7.09	105.16	114.31
1	ct	336	ASP	CA-C-N	7.09	127.70	119.47
1	ct	336	ASP	C-N-CA	7.09	127.70	119.47
1	dx	440	GLY	CA-C-N	7.09	126.73	119.56
1	dx	440	GLY	C-N-CA	7.09	126.73	119.56
1	fl	121	THR	CB-CA-C	-7.09	101.81	111.89
1	ed	440	GLY	CA-C-N	7.09	126.72	119.56
1	ed	440	GLY	C-N-CA	7.09	126.72	119.56
1	bs	484	PHE	CA-CB-CG	7.09	120.89	113.80
1	ch	440	GLY	CA-C-N	7.09	126.72	119.56
1	ch	440	GLY	C-N-CA	7.09	126.72	119.56
1	gv	118	ASN	N-CA-C	-7.09	104.51	113.72
3	kr	46	TYR	N-CA-C	7.09	119.70	109.14
1	ar	287	ASP	N-CA-C	-7.09	103.25	112.68
1	du	245	ASN	CA-C-N	7.09	127.01	119.85
1	du	245	ASN	C-N-CA	7.09	127.01	119.85
1	ck	88	VAL	N-CA-C	7.08	118.03	108.11
2	hg	115	PRO	N-CA-C	-7.08	100.78	111.41
1	fg	484	PHE	CA-CB-CG	7.08	120.88	113.80
3	lw	38	VAL	N-CA-C	7.08	118.32	108.12
1	gu	336	ASP	CA-C-N	7.08	126.78	119.56
1	gu	336	ASP	C-N-CA	7.08	126.78	119.56
1	cg	336	ASP	CA-C-N	7.08	127.68	119.47
1	cg	336	ASP	C-N-CA	7.08	127.68	119.47
1	aw	440	GLY	CA-C-N	7.08	126.71	119.56
1	aw	440	GLY	C-N-CA	7.08	126.71	119.56
3	ky	72	ASN	CA-CB-CG	7.08	119.68	112.60
1	fc	328	LYS	N-CA-C	7.08	121.61	112.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bg	198	ILE	N-CA-C	7.07	116.90	106.85
1	bt	440	GLY	CA-C-N	7.07	126.70	119.56
1	bt	440	GLY	C-N-CA	7.07	126.70	119.56
1	df	440	GLY	CA-C-N	7.07	126.70	119.56
1	df	440	GLY	C-N-CA	7.07	126.70	119.56
1	di	95	VAL	N-CA-C	7.07	118.05	107.80
1	gs	440	GLY	CA-C-N	7.07	126.70	119.56
1	gs	440	GLY	C-N-CA	7.07	126.70	119.56
1	aj	440	GLY	CA-C-N	7.07	126.70	119.56
1	aj	440	GLY	C-N-CA	7.07	126.70	119.56
1	ch	88	VAL	N-CA-C	7.07	118.46	108.36
1	ds	328	LYS	N-CA-C	7.07	121.61	112.92
1	dy	250	MET	CA-C-N	7.06	127.60	122.16
1	dy	250	MET	C-N-CA	7.06	127.60	122.16
1	cy	103	ILE	CA-C-N	7.06	127.02	120.03
1	cy	103	ILE	C-N-CA	7.06	127.02	120.03
1	da	406	THR	N-CA-C	-7.06	105.21	114.31
1	bd	336	ASP	CA-C-N	7.06	127.66	119.47
1	bd	336	ASP	C-N-CA	7.06	127.66	119.47
1	ay	336	ASP	CA-C-N	7.05	126.76	119.56
1	ay	336	ASP	C-N-CA	7.05	126.76	119.56
1	cj	93	PRO	N-CA-CB	-7.05	98.13	102.79
1	cb	336	ASP	CA-C-N	7.05	127.65	119.47
1	cb	336	ASP	C-N-CA	7.05	127.65	119.47
1	ax	103	ILE	CA-C-N	7.05	127.04	119.78
1	ax	103	ILE	C-N-CA	7.05	127.04	119.78
2	hh	115	PRO	N-CA-C	-7.05	100.83	111.41
1	aa	440	GLY	CA-C-N	7.05	126.68	119.56
1	aa	440	GLY	C-N-CA	7.05	126.68	119.56
1	ay	483	PRO	N-CA-C	-7.05	100.00	111.21
1	bh	245	ASN	CA-C-N	7.05	127.01	120.03
1	bh	245	ASN	C-N-CA	7.05	127.01	120.03
1	bo	328	LYS	N-CA-C	7.05	121.59	112.92
1	au	121	THR	N-CA-C	7.04	119.83	111.02
1	bk	287	ASP	N-CA-C	-7.04	103.56	112.93
1	fp	324	THR	N-CA-C	-7.04	100.92	109.72
1	gg	328	LYS	N-CA-C	7.04	121.97	112.88
1	cc	72	HIS	N-CA-C	-7.04	99.54	110.17
1	fl	93	PRO	N-CA-CB	-7.04	98.14	102.79
1	ck	412	VAL	N-CA-C	-7.04	106.06	111.62
1	dw	446	ALA	N-CA-C	7.04	121.92	113.12
1	cp	324	THR	N-CA-C	-7.04	100.79	109.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ac	336	ASP	CA-C-N	7.03	127.63	119.47
1	ac	336	ASP	C-N-CA	7.03	127.63	119.47
1	cz	72	HIS	N-CA-C	-7.03	99.47	110.36
1	fd	406	THR	N-CA-C	-7.03	105.64	114.56
1	fu	406	THR	N-CA-C	-7.03	105.64	114.56
2	hk	343	ALA	CA-C-N	7.03	126.99	120.03
2	hk	343	ALA	C-N-CA	7.03	126.99	120.03
1	ch	287	ASP	N-CA-C	-7.03	103.58	112.93
1	cs	149	GLY	CA-C-N	7.03	126.98	120.03
1	cs	149	GLY	C-N-CA	7.03	126.98	120.03
2	hg	343	ALA	CA-C-N	7.02	126.94	119.85
2	hg	343	ALA	C-N-CA	7.02	126.94	119.85
2	hk	115	PRO	N-CA-C	-7.02	100.87	111.41
1	cz	293	ILE	N-CA-C	-7.02	104.14	111.58
1	fm	93	PRO	N-CA-CB	-7.02	98.16	102.79
1	gj	491	ALA	CA-C-N	7.02	127.19	120.31
1	gj	491	ALA	C-N-CA	7.02	127.19	120.31
1	go	121	THR	N-CA-C	7.02	120.93	111.24
1	cr	88	VAL	N-CA-C	7.02	117.98	107.80
2	hl	268	THR	N-CA-C	7.02	121.87	113.16
1	ac	88	VAL	N-CA-C	7.02	118.23	108.12
1	bb	88	VAL	N-CA-C	7.02	117.97	107.80
1	fk	88	VAL	N-CA-C	7.02	118.24	107.99
1	cp	484	PHE	CA-CB-CG	7.02	120.82	113.80
3	if	38	VAL	N-CA-C	7.02	118.15	107.77
1	eu	103	ILE	CA-C-N	7.01	126.97	120.03
1	eu	103	ILE	C-N-CA	7.01	126.97	120.03
2	hn	115	PRO	N-CA-C	-7.01	100.89	111.41
3	ku	32	PHE	CA-C-N	7.01	126.71	119.56
3	ku	32	PHE	C-N-CA	7.01	126.71	119.56
1	cl	253	ARG	N-CA-C	7.01	121.70	112.72
1	ga	149	GLY	CA-C-N	7.01	126.93	119.85
1	ga	149	GLY	C-N-CA	7.01	126.93	119.85
3	nn	38	VAL	N-CA-C	7.01	118.15	107.77
1	ah	336	ASP	CA-C-N	7.01	127.60	119.47
1	ah	336	ASP	C-N-CA	7.01	127.60	119.47
1	em	88	VAL	N-CA-C	7.01	117.98	108.17
1	eq	287	ASP	N-CA-C	-7.01	103.36	112.68
1	er	336	ASP	CA-C-N	7.01	127.60	119.47
1	er	336	ASP	C-N-CA	7.01	127.60	119.47
1	hc	440	GLY	CA-C-N	7.01	126.64	119.56
1	hc	440	GLY	C-N-CA	7.01	126.64	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cn	440	GLY	CA-C-N	7.00	126.63	119.56
1	cn	440	GLY	C-N-CA	7.00	126.63	119.56
1	fq	93	PRO	N-CA-CB	-7.00	98.17	102.79
1	gh	440	GLY	CA-C-N	7.00	126.70	119.56
1	gh	440	GLY	C-N-CA	7.00	126.70	119.56
3	ku	64	GLN	N-CA-C	-7.00	106.64	114.62
3	lv	46	TYR	N-CA-C	7.00	119.57	109.14
2	hi	268	THR	N-CA-C	7.00	121.84	113.16
1	de	88	VAL	N-CA-C	7.00	118.20	108.12
1	de	103	ILE	CA-C-N	7.00	126.96	120.03
1	de	103	ILE	C-N-CA	7.00	126.96	120.03
1	el	336	ASP	CA-C-N	7.00	127.59	119.47
1	el	336	ASP	C-N-CA	7.00	127.59	119.47
3	lo	32	PHE	CA-C-N	7.00	126.70	119.56
3	lo	32	PHE	C-N-CA	7.00	126.70	119.56
2	he	172	SER	N-CA-C	7.00	119.56	109.14
3	ni	38	VAL	N-CA-C	7.00	118.99	107.24
1	eq	336	ASP	CA-C-N	6.99	126.69	119.56
1	eq	336	ASP	C-N-CA	6.99	126.69	119.56
1	dk	440	GLY	CA-C-N	6.99	126.62	119.56
1	dk	440	GLY	C-N-CA	6.99	126.62	119.56
1	cr	440	GLY	CA-C-N	6.99	126.62	119.56
1	cr	440	GLY	C-N-CA	6.99	126.62	119.56
1	ar	121	THR	N-CA-C	6.98	120.88	111.24
1	av	121	THR	N-CA-C	6.98	120.88	111.24
1	fy	440	GLY	CA-C-N	6.98	126.61	119.56
1	fy	440	GLY	C-N-CA	6.98	126.61	119.56
1	de	483	PRO	N-CA-C	-6.98	100.25	111.14
2	hk	353	ASP	CA-C-N	6.98	126.68	119.56
2	hk	353	ASP	C-N-CA	6.98	126.68	119.56
2	hn	327	VAL	N-CA-C	6.98	118.86	108.46
1	aj	103	ILE	CA-C-N	6.98	126.94	120.03
1	aj	103	ILE	C-N-CA	6.98	126.94	120.03
1	ek	440	GLY	CA-C-N	6.98	126.61	119.56
1	ek	440	GLY	C-N-CA	6.98	126.61	119.56
1	eu	406	THR	N-CA-C	-6.98	105.31	114.31
1	cp	121	THR	N-CA-C	6.98	120.87	111.24
1	dx	328	LYS	N-CA-C	6.98	121.50	112.92
1	dw	336	ASP	CA-C-N	6.97	127.56	119.47
1	dw	336	ASP	C-N-CA	6.97	127.56	119.47
3	jp	46	TYR	N-CA-C	6.97	119.53	109.14
1	af	149	GLY	CA-C-N	6.97	126.93	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	af	149	GLY	C-N-CA	6.97	126.93	120.03
1	aw	336	ASP	CA-C-N	6.97	127.56	119.47
1	aw	336	ASP	C-N-CA	6.97	127.56	119.47
1	ag	285	ASP	N-CA-C	6.97	118.96	111.36
1	an	328	LYS	N-CA-C	6.97	121.49	112.92
1	ca	88	VAL	N-CA-C	6.97	117.92	107.75
1	dd	121	THR	N-CA-C	6.97	120.86	111.24
1	gj	94	ALA	CB-CA-C	-6.97	108.55	116.63
1	dn	154	PHE	N-CA-C	-6.97	104.65	113.43
1	ck	336	ASP	CA-C-N	6.96	127.55	119.47
1	ck	336	ASP	C-N-CA	6.96	127.55	119.47
1	ab	324	THR	N-CA-C	-6.96	99.52	109.62
1	go	253	ARG	N-CA-C	6.96	122.88	113.97
1	aa	336	ASP	CA-C-N	6.96	127.55	119.47
1	aa	336	ASP	C-N-CA	6.96	127.55	119.47
1	at	336	ASP	CA-C-N	6.96	127.54	119.47
1	at	336	ASP	C-N-CA	6.96	127.54	119.47
1	bg	324	THR	N-CA-C	-6.96	100.88	109.65
1	cs	121	THR	N-CA-C	6.96	120.76	111.30
1	ep	72	HIS	N-CA-C	-6.96	98.86	109.85
1	ee	440	GLY	CA-C-N	6.95	126.58	119.56
1	ee	440	GLY	C-N-CA	6.95	126.58	119.56
1	fo	145	HIS	CA-C-N	6.95	126.65	119.56
1	fo	145	HIS	C-N-CA	6.95	126.65	119.56
1	al	440	GLY	CA-C-N	6.95	126.58	119.56
1	al	440	GLY	C-N-CA	6.95	126.58	119.56
1	bi	271	SER	N-CA-C	6.95	120.31	110.23
1	av	253	ARG	N-CA-C	6.95	122.87	113.97
1	ae	336	ASP	CA-C-N	6.95	126.65	119.56
1	ae	336	ASP	C-N-CA	6.95	126.65	119.56
1	az	336	ASP	CA-C-N	6.95	127.53	119.47
1	az	336	ASP	C-N-CA	6.95	127.53	119.47
3	kq	38	VAL	N-CA-C	6.95	118.05	107.77
1	ac	440	GLY	CA-C-N	6.94	126.64	119.56
1	ac	440	GLY	C-N-CA	6.94	126.64	119.56
3	ib	46	TYR	N-CA-C	6.94	119.49	109.14
1	aq	103	ILE	CA-C-N	6.94	126.90	120.03
1	aq	103	ILE	C-N-CA	6.94	126.90	120.03
1	bf	336	ASP	CA-C-N	6.94	127.52	119.47
1	bf	336	ASP	C-N-CA	6.94	127.52	119.47
3	id	38	VAL	N-CA-C	6.94	118.90	107.24
1	cc	88	VAL	N-CA-C	6.94	118.12	107.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fh	68	ILE	CA-C-N	6.94	127.50	119.94
1	fh	68	ILE	C-N-CA	6.94	127.50	119.94
1	fl	440	GLY	CA-C-N	6.94	126.57	119.56
1	fl	440	GLY	C-N-CA	6.94	126.57	119.56
1	ar	336	ASP	CA-C-N	6.94	127.52	119.47
1	ar	336	ASP	C-N-CA	6.94	127.52	119.47
3	jc	37	ASP	CA-CB-CG	6.94	119.54	112.60
1	bl	440	GLY	CA-C-N	6.93	126.63	119.56
1	bl	440	GLY	C-N-CA	6.93	126.63	119.56
1	bq	446	ALA	N-CA-C	6.93	118.92	111.36
1	ft	440	GLY	CA-C-N	6.93	126.56	119.56
1	ft	440	GLY	C-N-CA	6.93	126.56	119.56
1	fz	440	GLY	CA-C-N	6.93	126.56	119.56
1	fz	440	GLY	C-N-CA	6.93	126.56	119.56
2	hh	343	ALA	CA-C-N	6.93	126.90	120.03
2	hh	343	ALA	C-N-CA	6.93	126.90	120.03
3	kd	46	TYR	N-CA-C	6.93	119.47	109.14
1	gz	245	ASN	CA-C-N	6.93	126.89	120.03
1	gz	245	ASN	C-N-CA	6.93	126.89	120.03
1	bg	440	GLY	CA-C-N	6.93	126.63	119.56
1	bg	440	GLY	C-N-CA	6.93	126.63	119.56
1	ey	336	ASP	CA-C-N	6.93	127.51	119.47
1	ey	336	ASP	C-N-CA	6.93	127.51	119.47
1	el	121	THR	N-CA-C	6.93	119.68	111.02
1	fv	103	ILE	CA-C-N	6.93	126.89	120.03
1	fv	103	ILE	C-N-CA	6.93	126.89	120.03
1	ep	324	THR	N-CA-C	-6.93	101.06	109.72
1	dh	184	GLU	N-CA-C	-6.93	99.98	109.95
1	fb	336	ASP	CA-C-N	6.93	126.62	119.56
1	fb	336	ASP	C-N-CA	6.93	126.62	119.56
1	ft	154	PHE	N-CA-C	-6.93	103.72	112.93
1	gr	253	ARG	N-CA-C	6.93	122.16	113.43
1	dn	149	GLY	CA-C-N	6.92	126.89	120.03
1	dn	149	GLY	C-N-CA	6.92	126.89	120.03
1	fg	336	ASP	CA-C-N	6.92	127.50	119.47
1	fg	336	ASP	C-N-CA	6.92	127.50	119.47
1	fs	184	GLU	N-CA-C	-6.92	98.78	109.24
1	ah	119	SER	N-CA-C	-6.92	101.99	108.22
1	bu	103	ILE	CA-C-N	6.92	126.88	120.03
1	bu	103	ILE	C-N-CA	6.92	126.88	120.03
1	cn	88	VAL	N-CA-C	6.92	117.80	108.11
1	dv	103	ILE	CA-C-N	6.92	126.84	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dv	103	ILE	C-N-CA	6.92	126.84	119.85
1	bx	336	ASP	CA-C-N	6.92	127.49	119.47
1	bx	336	ASP	C-N-CA	6.92	127.49	119.47
1	dl	324	THR	N-CA-C	-6.92	101.08	109.72
1	gu	95	VAL	N-CA-C	6.92	117.83	107.80
1	et	440	GLY	CA-C-N	6.92	126.54	119.56
1	et	440	GLY	C-N-CA	6.92	126.54	119.56
1	ft	287	ASP	N-CA-C	-6.91	103.73	112.93
1	gj	88	VAL	N-CA-C	6.91	118.08	107.99
1	gj	324	THR	N-CA-C	-6.91	101.08	109.72
1	em	121	THR	N-CA-C	6.91	119.66	111.02
1	bx	484	PHE	CA-CB-CG	6.91	120.71	113.80
1	fh	287	ASP	N-CA-C	-6.91	103.49	112.68
1	by	336	ASP	CA-C-N	6.91	127.48	119.47
1	by	336	ASP	C-N-CA	6.91	127.48	119.47
1	bu	440	GLY	CA-C-N	6.91	126.53	119.56
1	bu	440	GLY	C-N-CA	6.91	126.53	119.56
1	cg	440	GLY	CA-C-N	6.91	126.53	119.56
1	cg	440	GLY	C-N-CA	6.91	126.53	119.56
1	ef	336	ASP	CA-C-N	6.91	127.48	119.47
1	ef	336	ASP	C-N-CA	6.91	127.48	119.47
1	am	134	ASP	CA-C-N	6.90	126.60	119.56
1	am	134	ASP	C-N-CA	6.90	126.60	119.56
1	dz	440	GLY	CA-C-N	6.90	126.53	119.56
1	dz	440	GLY	C-N-CA	6.90	126.53	119.56
1	fu	328	LYS	N-CA-C	6.90	121.87	113.17
1	gu	121	THR	N-CA-C	6.90	120.77	111.24
1	bm	336	ASP	CA-C-N	6.90	127.47	119.47
1	bm	336	ASP	C-N-CA	6.90	127.47	119.47
1	fm	121	THR	N-CA-C	6.90	120.91	111.39
2	hi	343	ALA	CA-C-N	6.90	126.86	120.03
2	hi	343	ALA	C-N-CA	6.90	126.86	120.03
1	eu	121	THR	CB-CA-C	-6.90	101.47	112.09
1	eu	440	GLY	CA-C-N	6.90	126.53	119.56
1	eu	440	GLY	C-N-CA	6.90	126.53	119.56
1	fi	406	THR	N-CA-C	-6.90	104.39	114.39
3	kg	38	VAL	N-CA-C	6.90	117.98	107.77
1	gw	93	PRO	N-CA-CB	-6.89	98.24	102.79
2	hl	343	ALA	CA-C-N	6.89	126.86	120.03
2	hl	343	ALA	C-N-CA	6.89	126.86	120.03
1	el	154	PHE	N-CA-C	-6.89	104.74	113.43
1	bh	440	GLY	CA-C-N	6.89	126.52	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bh	440	GLY	C-N-CA	6.89	126.52	119.56
1	cm	324	THR	N-CA-C	-6.89	100.97	109.65
1	er	440	GLY	CA-C-N	6.89	126.52	119.56
1	er	440	GLY	C-N-CA	6.89	126.52	119.56
1	ft	336	ASP	CA-C-N	6.89	126.59	119.56
1	ft	336	ASP	C-N-CA	6.89	126.59	119.56
1	gg	440	GLY	CA-C-N	6.89	126.52	119.56
1	gg	440	GLY	C-N-CA	6.89	126.52	119.56
1	fs	121	THR	N-CA-C	6.89	120.90	111.39
3	mn	46	TYR	N-CA-C	6.89	118.57	108.86
1	cx	103	ILE	CA-C-N	6.89	126.85	120.03
1	cx	103	ILE	C-N-CA	6.89	126.85	120.03
1	fu	103	ILE	CA-C-N	6.89	126.87	119.78
1	fu	103	ILE	C-N-CA	6.89	126.87	119.78
1	bb	440	GLY	CA-C-N	6.88	126.51	119.56
1	bb	440	GLY	C-N-CA	6.88	126.51	119.56
1	dr	440	GLY	CA-C-N	6.88	126.51	119.56
1	dr	440	GLY	C-N-CA	6.88	126.51	119.56
1	al	287	ASP	N-CA-C	-6.88	103.78	112.93
1	ek	121	THR	N-CA-C	6.88	119.62	111.02
3	kl	38	VAL	N-CA-C	6.88	118.03	108.12
1	cz	88	VAL	N-CA-C	6.88	118.03	108.12
3	oe	32	PHE	CA-C-N	6.88	126.58	119.56
3	oe	32	PHE	C-N-CA	6.88	126.58	119.56
1	aa	149	GLY	CA-C-N	6.88	126.84	120.03
1	aa	149	GLY	C-N-CA	6.88	126.84	120.03
1	bx	232	ILE	N-CA-C	-6.88	105.05	111.45
1	da	336	ASP	CA-C-N	6.88	126.57	119.56
1	da	336	ASP	C-N-CA	6.88	126.57	119.56
1	ci	149	GLY	CA-C-N	6.88	126.84	120.03
1	ci	149	GLY	C-N-CA	6.88	126.84	120.03
1	bs	121	THR	N-CA-C	6.87	120.73	111.24
1	gm	440	GLY	CA-C-N	6.87	126.50	119.56
1	gm	440	GLY	C-N-CA	6.87	126.50	119.56
1	dv	118	ASN	N-CA-C	-6.87	104.57	114.12
1	ev	293	ILE	N-CA-C	-6.87	105.06	111.45
1	cf	336	ASP	CA-C-N	6.87	126.57	119.56
1	cf	336	ASP	C-N-CA	6.87	126.57	119.56
2	hj	47	GLN	CA-C-N	6.87	126.56	119.56
2	hj	47	GLN	C-N-CA	6.87	126.56	119.56
1	dm	145	HIS	CA-C-N	6.87	127.43	119.47
1	dm	145	HIS	C-N-CA	6.87	127.43	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eu	88	VAL	N-CA-C	6.87	118.01	108.12
1	ap	440	GLY	CA-C-N	6.86	126.56	119.56
1	ap	440	GLY	C-N-CA	6.86	126.56	119.56
3	hq	46	TYR	N-CA-C	6.86	119.36	109.14
1	ce	103	ILE	CA-C-N	6.86	126.85	119.78
1	ce	103	ILE	C-N-CA	6.86	126.85	119.78
1	dh	253	ARG	N-CA-C	6.86	121.63	111.96
3	mc	46	TYR	N-CA-C	6.86	119.36	109.14
1	al	245	ASN	CA-C-N	6.86	126.82	120.03
1	al	245	ASN	C-N-CA	6.86	126.82	120.03
1	br	406	THR	N-CA-C	-6.86	105.85	114.56
1	ae	103	ILE	CA-C-N	6.86	126.78	119.85
1	ae	103	ILE	C-N-CA	6.86	126.78	119.85
1	bb	232	ILE	N-CA-C	-6.86	105.07	111.45
1	dy	440	GLY	CA-C-N	6.86	126.48	119.56
1	dy	440	GLY	C-N-CA	6.86	126.48	119.56
1	ei	196	VAL	N-CA-C	6.85	118.59	108.45
1	ca	440	GLY	CA-C-N	6.85	126.48	119.56
1	ca	440	GLY	C-N-CA	6.85	126.48	119.56
1	fc	440	GLY	CA-C-N	6.85	126.48	119.56
1	fc	440	GLY	C-N-CA	6.85	126.48	119.56
1	gx	440	GLY	CA-C-N	6.85	126.48	119.56
1	gx	440	GLY	C-N-CA	6.85	126.48	119.56
1	hd	71	ASP	CA-CB-CG	6.85	119.45	112.60
1	fa	149	GLY	CA-C-N	6.85	126.81	120.03
1	fa	149	GLY	C-N-CA	6.85	126.81	120.03
1	fx	440	GLY	CA-C-N	6.85	126.48	119.56
1	fx	440	GLY	C-N-CA	6.85	126.48	119.56
1	gx	287	ASP	N-CA-C	-6.85	103.95	112.72
1	an	336	ASP	CA-C-N	6.85	127.41	119.47
1	an	336	ASP	C-N-CA	6.85	127.41	119.47
1	ec	440	GLY	CA-C-N	6.85	126.48	119.56
1	ec	440	GLY	C-N-CA	6.85	126.48	119.56
1	ej	336	ASP	CA-C-N	6.85	127.41	119.47
1	ej	336	ASP	C-N-CA	6.85	127.41	119.47
1	gv	440	GLY	CA-C-N	6.85	126.48	119.56
1	gv	440	GLY	C-N-CA	6.85	126.48	119.56
2	he	343	ALA	CA-C-N	6.85	126.83	119.78
2	he	343	ALA	C-N-CA	6.85	126.83	119.78
1	gr	336	ASP	CA-C-N	6.85	126.54	119.56
1	gr	336	ASP	C-N-CA	6.85	126.54	119.56
1	eg	468	GLN	CA-C-N	6.84	126.76	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eg	468	GLN	C-N-CA	6.84	126.76	119.85
1	ap	245	ASN	CA-C-N	6.84	126.80	120.03
1	ap	245	ASN	C-N-CA	6.84	126.80	120.03
1	du	336	ASP	CA-C-N	6.84	127.41	119.47
1	du	336	ASP	C-N-CA	6.84	127.41	119.47
1	ea	440	GLY	CA-C-N	6.84	126.47	119.56
1	ea	440	GLY	C-N-CA	6.84	126.47	119.56
1	dl	253	ARG	N-CA-C	6.84	122.52	114.04
3	kv	46	TYR	N-CA-C	6.84	119.33	109.14
1	db	103	ILE	CA-C-N	6.84	126.82	119.78
1	db	103	ILE	C-N-CA	6.84	126.82	119.78
1	di	232	ILE	N-CA-C	-6.84	105.68	111.56
1	de	115	GLN	CB-CA-C	-6.84	105.05	111.00
1	hc	103	ILE	CA-C-N	6.84	126.80	120.03
1	hc	103	ILE	C-N-CA	6.84	126.80	120.03
2	ho	327	VAL	N-CA-C	6.84	118.32	108.48
1	cp	88	VAL	N-CA-C	6.83	117.73	107.75
1	gd	440	GLY	CA-C-N	6.83	126.53	119.56
1	gd	440	GLY	C-N-CA	6.83	126.53	119.56
1	bc	253	ARG	N-CA-C	6.83	122.28	113.88
1	fs	440	GLY	CA-C-N	6.83	126.46	119.56
1	fs	440	GLY	C-N-CA	6.83	126.46	119.56
1	gp	440	GLY	CA-C-N	6.83	126.46	119.56
1	gp	440	GLY	C-N-CA	6.83	126.46	119.56
2	he	268	THR	N-CA-C	6.83	121.47	113.20
2	hh	59	ASN	CA-C-N	6.83	126.53	119.56
2	hh	59	ASN	C-N-CA	6.83	126.53	119.56
1	fc	232	ILE	N-CA-C	-6.83	105.18	111.67
2	hh	327	VAL	N-CA-C	6.83	118.64	108.46
1	cu	93	PRO	N-CA-CB	-6.83	98.28	102.79
1	dz	336	ASP	CA-C-N	6.83	127.39	119.47
1	dz	336	ASP	C-N-CA	6.83	127.39	119.47
1	ck	249	GLU	N-CA-C	6.83	118.48	108.86
1	cs	121	THR	CB-CA-C	-6.83	101.71	111.95
1	do	440	GLY	CA-C-N	6.83	126.45	119.56
1	do	440	GLY	C-N-CA	6.83	126.45	119.56
1	cg	103	ILE	CA-C-N	6.82	126.81	119.78
1	cg	103	ILE	C-N-CA	6.82	126.81	119.78
1	ap	149	GLY	CA-C-N	6.82	126.78	120.03
1	ap	149	GLY	C-N-CA	6.82	126.78	120.03
1	bs	440	GLY	CA-C-N	6.82	126.45	119.56
1	bs	440	GLY	C-N-CA	6.82	126.45	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fp	336	ASP	CA-C-N	6.82	127.38	119.47
1	fp	336	ASP	C-N-CA	6.82	127.38	119.47
1	gx	253	ARG	N-CA-C	6.82	121.48	112.13
1	fd	336	ASP	CA-C-N	6.82	127.38	119.47
1	fd	336	ASP	C-N-CA	6.82	127.38	119.47
3	nz	37	ASP	CA-CB-CG	6.82	119.42	112.60
1	gc	253	ARG	N-CA-C	6.82	121.38	111.02
1	cq	88	VAL	N-CA-C	6.82	117.70	107.75
1	fy	103	ILE	CA-C-N	6.82	126.80	119.78
1	fy	103	ILE	C-N-CA	6.82	126.80	119.78
1	ah	440	GLY	CA-C-N	6.81	126.44	119.56
1	ah	440	GLY	C-N-CA	6.81	126.44	119.56
1	dg	145	HIS	CA-C-N	6.81	127.37	119.47
1	dg	145	HIS	C-N-CA	6.81	127.37	119.47
1	bs	103	ILE	CA-C-N	6.81	126.85	119.90
1	bs	103	ILE	C-N-CA	6.81	126.85	119.90
1	gp	468	GLN	CA-C-N	6.81	126.73	119.85
1	gp	468	GLN	C-N-CA	6.81	126.73	119.85
3	lw	46	TYR	N-CA-C	6.81	119.29	109.14
1	fd	184	GLU	N-CA-C	-6.81	100.14	109.95
1	gb	336	ASP	CA-C-N	6.81	127.37	119.47
1	gb	336	ASP	C-N-CA	6.81	127.37	119.47
1	gg	145	HIS	CA-C-N	6.81	127.37	119.47
1	gg	145	HIS	C-N-CA	6.81	127.37	119.47
2	hl	172	SER	N-CA-C	6.81	120.78	109.95
3	ne	38	VAL	N-CA-C	6.81	117.84	107.77
1	fg	440	GLY	CA-C-N	6.81	126.43	119.56
1	fg	440	GLY	C-N-CA	6.81	126.43	119.56
1	dw	440	GLY	CA-C-N	6.80	126.43	119.56
1	dw	440	GLY	C-N-CA	6.80	126.43	119.56
1	en	440	GLY	CA-C-N	6.80	126.43	119.56
1	en	440	GLY	C-N-CA	6.80	126.43	119.56
1	fw	440	GLY	CA-C-N	6.80	126.43	119.56
1	fw	440	GLY	C-N-CA	6.80	126.43	119.56
1	gw	121	THR	N-CA-C	6.80	120.63	111.24
1	co	336	ASP	CA-C-N	6.80	126.50	119.56
1	co	336	ASP	C-N-CA	6.80	126.50	119.56
1	eh	440	GLY	CA-C-N	6.80	126.50	119.56
1	eh	440	GLY	C-N-CA	6.80	126.50	119.56
1	ch	336	ASP	CA-C-N	6.80	126.50	119.56
1	ch	336	ASP	C-N-CA	6.80	126.50	119.56
1	db	440	GLY	CA-C-N	6.80	126.43	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	db	440	GLY	C-N-CA	6.80	126.43	119.56
1	em	336	ASP	CA-C-N	6.80	126.50	119.56
1	em	336	ASP	C-N-CA	6.80	126.50	119.56
1	ft	324	THR	N-CA-C	-6.80	101.22	109.72
1	gd	103	ILE	CA-C-N	6.80	126.76	120.03
1	gd	103	ILE	C-N-CA	6.80	126.76	120.03
1	at	324	THR	N-CA-C	-6.80	101.22	109.72
1	ba	93	PRO	N-CA-CB	-6.80	98.30	102.79
1	gu	440	GLY	CA-C-N	6.80	126.43	119.56
1	gu	440	GLY	C-N-CA	6.80	126.43	119.56
3	nj	38	VAL	N-CA-C	6.80	117.83	107.77
1	cd	103	ILE	CA-C-N	6.80	126.76	120.03
1	cd	103	ILE	C-N-CA	6.80	126.76	120.03
1	gc	336	ASP	CA-C-N	6.80	127.35	119.47
1	gc	336	ASP	C-N-CA	6.80	127.35	119.47
1	gk	88	VAL	N-CA-C	6.80	117.68	108.17
3	iw	32	PHE	CA-C-N	6.80	126.49	119.56
3	iw	32	PHE	C-N-CA	6.80	126.49	119.56
1	bf	245	ASN	CA-C-N	6.79	126.76	120.03
1	bf	245	ASN	C-N-CA	6.79	126.76	120.03
1	ce	336	ASP	CA-C-N	6.79	126.49	119.56
1	ce	336	ASP	C-N-CA	6.79	126.49	119.56
1	fq	88	VAL	N-CA-C	6.79	117.65	107.80
1	gp	336	ASP	CA-C-N	6.79	126.49	119.56
1	gp	336	ASP	C-N-CA	6.79	126.49	119.56
1	fy	336	ASP	CA-C-N	6.79	127.35	119.47
1	fy	336	ASP	C-N-CA	6.79	127.35	119.47
3	jx	38	VAL	N-CA-C	6.79	117.90	108.12
1	cz	103	ILE	CA-C-N	6.79	126.71	119.85
1	cz	103	ILE	C-N-CA	6.79	126.71	119.85
1	dl	440	GLY	CA-C-N	6.79	126.42	119.56
1	dl	440	GLY	C-N-CA	6.79	126.42	119.56
3	ir	46	TYR	N-CA-C	6.79	119.26	109.14
1	do	149	GLY	CA-C-N	6.79	126.71	119.85
1	do	149	GLY	C-N-CA	6.79	126.71	119.85
1	gd	145	HIS	CA-C-N	6.79	127.35	119.47
1	gd	145	HIS	C-N-CA	6.79	127.35	119.47
3	mf	38	VAL	N-CA-C	6.79	117.89	108.12
1	af	440	GLY	CA-C-N	6.79	126.41	119.56
1	af	440	GLY	C-N-CA	6.79	126.41	119.56
1	bp	149	GLY	CA-C-N	6.79	126.75	120.03
1	bp	149	GLY	C-N-CA	6.79	126.75	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cf	121	THR	CB-CA-C	-6.79	102.25	111.89
1	cf	253	ARG	N-CA-C	6.79	121.95	112.93
1	dm	483	PRO	N-CA-C	-6.79	100.55	111.14
1	en	88	VAL	N-CA-C	6.79	117.64	107.80
1	et	93	PRO	N-CA-CB	-6.79	98.31	102.79
1	ev	336	ASP	CA-C-N	6.79	126.48	119.56
1	ev	336	ASP	C-N-CA	6.79	126.48	119.56
1	cw	198	ILE	N-CA-C	6.78	116.39	106.55
1	ae	88	VAL	N-CA-C	6.78	117.88	108.12
1	dv	440	GLY	CA-C-N	6.78	126.48	119.56
1	dv	440	GLY	C-N-CA	6.78	126.48	119.56
1	et	103	ILE	CA-C-N	6.78	126.74	120.03
1	et	103	ILE	C-N-CA	6.78	126.74	120.03
1	hc	468	GLN	CA-C-N	6.78	126.70	119.85
1	hc	468	GLN	C-N-CA	6.78	126.70	119.85
2	hk	367	GLU	N-CA-C	-6.78	101.24	111.34
3	nk	46	TYR	N-CA-C	6.78	119.24	109.14
1	ao	336	ASP	CA-C-N	6.78	127.33	119.47
1	ao	336	ASP	C-N-CA	6.78	127.33	119.47
1	dx	145	HIS	CA-CB-CG	-6.78	107.02	113.80
1	du	324	THR	N-CA-C	-6.77	99.83	109.24
1	fo	287	ASP	N-CA-C	-6.77	103.67	112.68
1	gq	324	THR	N-CA-C	-6.77	99.40	109.42
3	mx	38	VAL	N-CA-C	6.77	117.87	108.12
1	ce	88	VAL	N-CA-C	6.77	117.64	107.75
1	bu	93	PRO	N-CA-CB	-6.77	98.32	102.79
1	dg	324	THR	N-CA-C	-6.77	99.55	109.50
1	dq	440	GLY	CA-C-N	6.77	126.40	119.56
1	dq	440	GLY	C-N-CA	6.77	126.40	119.56
1	gi	253	ARG	N-CA-C	6.77	122.52	113.72
3	hs	46	TYR	N-CA-C	6.77	119.23	109.14
1	av	440	GLY	CA-C-N	6.77	126.40	119.56
1	av	440	GLY	C-N-CA	6.77	126.40	119.56
1	cx	149	GLY	CA-C-N	6.77	126.75	119.78
1	cx	149	GLY	C-N-CA	6.77	126.75	119.78
2	hn	172	SER	N-CA-C	6.77	120.71	109.95
1	ct	293	ILE	N-CA-C	-6.77	104.41	111.58
1	er	259	ILE	N-CA-C	6.77	117.58	108.11
1	gp	103	ILE	CA-C-N	6.77	126.68	119.85
1	gp	103	ILE	C-N-CA	6.77	126.68	119.85
2	hn	291	LYS	CA-C-N	6.76	128.29	119.84
2	hn	291	LYS	C-N-CA	6.76	128.29	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cw	115	GLN	CA-C-N	6.76	126.72	120.03
1	cw	115	GLN	C-N-CA	6.76	126.72	120.03
1	ee	285	ASP	N-CA-C	6.76	118.73	111.36
1	gc	440	GLY	CA-C-N	6.76	126.39	119.56
1	gc	440	GLY	C-N-CA	6.76	126.39	119.56
1	gv	115	GLN	CA-C-N	6.76	126.75	119.78
1	gv	115	GLN	C-N-CA	6.76	126.75	119.78
1	ed	336	ASP	CA-C-N	6.76	127.31	119.47
1	ed	336	ASP	C-N-CA	6.76	127.31	119.47
1	fh	149	GLY	CA-C-N	6.76	126.72	120.03
1	fh	149	GLY	C-N-CA	6.76	126.72	120.03
1	fp	440	GLY	CA-C-N	6.76	126.46	119.56
1	fp	440	GLY	C-N-CA	6.76	126.46	119.56
1	ge	483	PRO	N-CA-C	-6.76	100.46	111.21
2	hm	115	PRO	N-CA-C	-6.76	101.27	111.41
1	bj	258	VAL	N-CA-C	6.76	118.21	108.48
1	dx	149	GLY	CA-C-N	6.76	126.67	119.85
1	dx	149	GLY	C-N-CA	6.76	126.67	119.85
1	cu	468	GLN	CA-C-N	6.76	126.67	119.85
1	cu	468	GLN	C-N-CA	6.76	126.67	119.85
1	dk	121	THR	N-CA-C	6.76	119.47	111.02
1	gc	103	ILE	CA-C-N	6.75	127.15	119.92
1	gc	103	ILE	C-N-CA	6.75	127.15	119.92
1	gl	480	GLY	N-CA-C	6.75	120.48	110.42
1	gw	149	GLY	CA-C-N	6.75	126.72	120.03
1	gw	149	GLY	C-N-CA	6.75	126.72	120.03
2	ho	172	SER	N-CA-C	6.75	120.52	109.85
1	be	468	GLN	CA-C-N	6.75	126.67	119.85
1	be	468	GLN	C-N-CA	6.75	126.67	119.85
1	dp	463	ASP	CA-C-N	6.75	128.28	119.84
1	dp	463	ASP	C-N-CA	6.75	128.28	119.84
1	gq	440	GLY	CA-C-N	6.75	126.38	119.56
1	gq	440	GLY	C-N-CA	6.75	126.38	119.56
1	am	88	VAL	N-CA-C	6.75	118.58	107.24
1	ar	440	GLY	CA-C-N	6.75	126.38	119.56
1	ar	440	GLY	C-N-CA	6.75	126.38	119.56
1	bj	336	ASP	CA-C-N	6.75	126.45	119.56
1	bj	336	ASP	C-N-CA	6.75	126.45	119.56
1	co	328	LYS	N-CA-C	6.75	121.59	112.88
1	gj	115	GLN	CA-C-N	6.75	126.71	120.03
1	gj	115	GLN	C-N-CA	6.75	126.71	120.03
1	gf	440	GLY	CA-C-N	6.75	126.38	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gf	440	GLY	C-N-CA	6.75	126.38	119.56
1	bd	71	ASP	CA-CB-CG	6.75	119.35	112.60
1	ci	103	ILE	CA-C-N	6.75	126.73	119.78
1	ci	103	ILE	C-N-CA	6.75	126.73	119.78
1	cs	336	ASP	CA-C-N	6.75	127.30	119.47
1	cs	336	ASP	C-N-CA	6.75	127.30	119.47
1	de	440	GLY	CA-C-N	6.75	126.38	119.56
1	de	440	GLY	C-N-CA	6.75	126.38	119.56
1	dl	103	ILE	CA-C-N	6.75	126.73	119.78
1	dl	103	ILE	C-N-CA	6.75	126.73	119.78
1	ey	121	THR	N-CA-C	6.75	120.55	111.24
1	fk	115	GLN	CA-C-N	6.75	126.71	120.03
1	fk	115	GLN	C-N-CA	6.75	126.71	120.03
1	bo	491	ALA	CA-C-N	6.75	126.66	119.85
1	bo	491	ALA	C-N-CA	6.75	126.66	119.85
1	cb	72	HIS	N-CA-C	-6.75	100.24	109.95
1	dy	93	PRO	N-CA-C	6.75	122.68	113.98
1	ef	184	GLU	N-CA-C	-6.75	100.23	109.95
1	el	324	THR	N-CA-C	-6.75	101.15	109.65
1	gd	336	ASP	CA-C-N	6.75	126.44	119.56
1	gd	336	ASP	C-N-CA	6.75	126.44	119.56
1	ca	245	ASN	CA-C-N	6.74	126.71	120.03
1	ca	245	ASN	C-N-CA	6.74	126.71	120.03
1	ex	163	PHE	CA-C-N	6.74	126.92	120.31
1	ex	163	PHE	C-N-CA	6.74	126.92	120.31
1	gl	258	VAL	N-CA-C	6.74	118.51	108.46
1	be	491	ALA	CA-C-N	6.74	127.01	119.32
1	be	491	ALA	C-N-CA	6.74	127.01	119.32
1	eb	491	ALA	CA-C-N	6.74	126.92	120.31
1	eb	491	ALA	C-N-CA	6.74	126.92	120.31
1	cj	154	PHE	N-CA-C	-6.74	104.94	113.43
1	gx	336	ASP	CA-C-N	6.74	126.44	119.56
1	gx	336	ASP	C-N-CA	6.74	126.44	119.56
1	bp	287	ASP	N-CA-C	-6.74	103.97	112.93
1	cq	149	GLY	CA-C-N	6.74	126.66	119.85
1	cq	149	GLY	C-N-CA	6.74	126.66	119.85
1	dp	336	ASP	CA-C-N	6.74	126.43	119.56
1	dp	336	ASP	C-N-CA	6.74	126.43	119.56
1	bj	324	THR	N-CA-C	-6.74	101.30	109.72
1	bx	103	ILE	CA-C-N	6.74	126.70	120.03
1	bx	103	ILE	C-N-CA	6.74	126.70	120.03
1	es	88	VAL	N-CA-C	6.74	117.82	107.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fd	483	PRO	N-CA-C	-6.74	100.50	111.21
1	fi	149	GLY	CA-C-N	6.74	126.65	119.85
1	fi	149	GLY	C-N-CA	6.74	126.65	119.85
1	cl	440	GLY	CA-C-N	6.73	126.36	119.56
1	cl	440	GLY	C-N-CA	6.73	126.36	119.56
1	gr	72	HIS	N-CA-C	-6.73	100.49	110.46
3	lj	46	TYR	N-CA-C	6.73	119.17	109.14
1	aq	245	ASN	CA-C-N	6.73	126.91	120.31
1	aq	245	ASN	C-N-CA	6.73	126.91	120.31
1	bl	253	ARG	N-CA-C	6.73	121.64	112.68
1	cw	232	ILE	N-CA-C	-6.73	105.77	111.56
1	dd	440	GLY	CA-C-N	6.73	126.36	119.56
1	dd	440	GLY	C-N-CA	6.73	126.36	119.56
1	ed	121	THR	N-CA-C	6.73	120.53	111.24
3	jz	46	TYR	N-CA-C	6.73	119.17	109.14
1	be	440	GLY	CA-C-N	6.73	126.36	119.56
1	be	440	GLY	C-N-CA	6.73	126.36	119.56
1	bo	115	GLN	CA-C-N	6.73	126.69	120.03
1	bo	115	GLN	C-N-CA	6.73	126.69	120.03
1	bs	88	VAL	N-CA-C	6.73	117.56	107.80
1	bu	145	HIS	CA-C-N	6.73	127.28	119.47
1	bu	145	HIS	C-N-CA	6.73	127.28	119.47
1	gt	440	GLY	CA-C-N	6.73	126.36	119.56
1	gt	440	GLY	C-N-CA	6.73	126.36	119.56
1	bo	93	PRO	N-CA-CB	-6.73	98.35	102.79
1	cc	121	THR	N-CA-C	6.73	120.68	111.39
1	ez	245	ASN	CA-C-N	6.73	126.69	120.03
1	ez	245	ASN	C-N-CA	6.73	126.69	120.03
1	gm	483	PRO	N-CA-C	-6.73	100.65	111.14
2	hj	353	ASP	CA-C-N	6.73	126.42	119.56
2	hj	353	ASP	C-N-CA	6.73	126.42	119.56
1	go	440	GLY	CA-C-N	6.72	126.35	119.56
1	go	440	GLY	C-N-CA	6.72	126.35	119.56
1	as	287	ASP	N-CA-C	-6.72	102.92	112.13
1	fx	118	ASN	N-CA-C	-6.72	104.78	114.12
1	cz	406	THR	N-CA-C	-6.72	104.78	114.12
1	aq	328	LYS	N-CA-C	6.72	121.64	113.17
1	ez	253	ARG	N-CA-C	6.72	121.32	112.72
1	ai	491	ALA	CA-C-N	6.72	126.89	120.31
1	ai	491	ALA	C-N-CA	6.72	126.89	120.31
1	ck	271	SER	N-CA-C	6.72	119.97	110.50
1	gt	491	ALA	CA-C-N	6.72	126.68	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gt	491	ALA	C-N-CA	6.72	126.68	120.03
1	dx	151	ASP	CA-CB-CG	6.71	119.31	112.60
1	gf	491	ALA	CA-C-N	6.71	126.68	120.03
1	gf	491	ALA	C-N-CA	6.71	126.68	120.03
1	gu	115	GLN	CA-C-N	6.71	126.68	120.03
1	gu	115	GLN	C-N-CA	6.71	126.68	120.03
2	hm	59	ASN	CA-C-N	6.71	126.41	119.56
2	hm	59	ASN	C-N-CA	6.71	126.41	119.56
1	fo	232	ILE	N-CA-C	-6.71	105.21	111.45
1	bi	440	GLY	CA-C-N	6.71	126.34	119.56
1	bi	440	GLY	C-N-CA	6.71	126.34	119.56
1	ef	468	GLN	CA-C-N	6.71	126.63	119.85
1	ef	468	GLN	C-N-CA	6.71	126.63	119.85
1	ft	121	THR	N-CA-C	6.71	119.41	111.02
1	bf	440	GLY	CA-C-N	6.71	126.33	119.56
1	bf	440	GLY	C-N-CA	6.71	126.33	119.56
1	bf	324	THR	N-CA-C	-6.71	101.34	109.72
1	dl	406	THR	N-CA-C	-6.71	104.67	114.39
1	ab	491	ALA	CA-C-N	6.70	126.88	120.31
1	ab	491	ALA	C-N-CA	6.70	126.88	120.31
1	ag	115	GLN	CA-C-N	6.70	126.67	120.03
1	ag	115	GLN	C-N-CA	6.70	126.67	120.03
1	ax	287	ASP	N-CA-C	-6.70	104.02	112.93
1	cp	440	GLY	CA-C-N	6.70	126.33	119.56
1	cp	440	GLY	C-N-CA	6.70	126.33	119.56
1	dg	336	ASP	CA-C-N	6.70	126.40	119.56
1	dg	336	ASP	C-N-CA	6.70	126.40	119.56
1	ej	103	ILE	CA-C-N	6.70	126.67	120.03
1	ej	103	ILE	C-N-CA	6.70	126.67	120.03
1	es	440	GLY	CA-C-N	6.70	126.33	119.56
1	es	440	GLY	C-N-CA	6.70	126.33	119.56
1	gk	256	LYS	N-CA-C	6.70	119.25	109.07
2	hm	172	SER	N-CA-C	6.70	120.60	109.95
1	bn	463	ASP	CA-C-N	6.70	126.39	119.56
1	bn	463	ASP	C-N-CA	6.70	126.39	119.56
1	et	406	THR	N-CA-C	-6.70	105.67	114.31
1	ex	440	GLY	CA-C-N	6.70	126.39	119.56
1	ex	440	GLY	C-N-CA	6.70	126.39	119.56
1	hc	463	ASP	CA-C-N	6.70	128.21	119.84
1	hc	463	ASP	C-N-CA	6.70	128.21	119.84
1	ci	121	THR	N-CA-C	6.70	120.48	111.24
1	du	440	GLY	CA-C-N	6.70	126.39	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	du	440	GLY	C-N-CA	6.70	126.39	119.56
1	er	324	THR	N-CA-C	-6.70	101.21	109.65
1	gk	336	ASP	CA-C-N	6.70	126.39	119.56
1	gk	336	ASP	C-N-CA	6.70	126.39	119.56
3	jr	5	ARG	N-CA-C	-6.69	106.99	114.62
1	ec	103	ILE	CA-C-N	6.69	126.66	120.03
1	ec	103	ILE	C-N-CA	6.69	126.66	120.03
1	er	103	ILE	CA-C-N	6.69	126.66	120.03
1	er	103	ILE	C-N-CA	6.69	126.66	120.03
1	gs	344	ARG	N-CA-C	-6.69	98.86	109.23
2	hi	368	SER	N-CA-C	-6.69	100.58	110.48
1	ct	440	GLY	CA-C-N	6.69	126.32	119.56
1	ct	440	GLY	C-N-CA	6.69	126.32	119.56
1	dm	440	GLY	CA-C-N	6.69	126.31	119.56
1	dm	440	GLY	C-N-CA	6.69	126.31	119.56
1	ed	103	ILE	CA-C-N	6.69	126.65	120.03
1	ed	103	ILE	C-N-CA	6.69	126.65	120.03
1	gt	336	ASP	CA-C-N	6.69	127.23	119.47
1	gt	336	ASP	C-N-CA	6.69	127.23	119.47
3	kc	38	VAL	N-CA-C	6.69	117.93	108.17
1	br	149	GLY	CA-C-N	6.68	126.65	120.03
1	br	149	GLY	C-N-CA	6.68	126.65	120.03
1	cf	406	THR	N-CA-C	-6.68	104.83	114.12
1	dt	468	GLN	CA-C-N	6.68	126.60	119.85
1	dt	468	GLN	C-N-CA	6.68	126.60	119.85
1	eb	440	GLY	CA-C-N	6.68	126.31	119.56
1	eb	440	GLY	C-N-CA	6.68	126.31	119.56
1	gn	440	GLY	CA-C-N	6.68	126.31	119.56
1	gn	440	GLY	C-N-CA	6.68	126.31	119.56
2	ho	59	ASN	CA-C-N	6.68	126.38	119.56
2	ho	59	ASN	C-N-CA	6.68	126.38	119.56
1	av	245	ASN	CA-C-N	6.68	126.64	120.03
1	av	245	ASN	C-N-CA	6.68	126.64	120.03
1	az	468	GLN	CA-C-N	6.68	126.60	119.85
1	az	468	GLN	C-N-CA	6.68	126.60	119.85
1	co	440	GLY	CA-C-N	6.68	126.31	119.56
1	co	440	GLY	C-N-CA	6.68	126.31	119.56
1	dj	440	GLY	CA-C-N	6.68	126.38	119.56
1	dj	440	GLY	C-N-CA	6.68	126.38	119.56
3	kg	46	TYR	N-CA-C	6.68	119.09	109.14
3	nl	72	ASN	CA-CB-CG	6.68	119.28	112.60
1	ad	468	GLN	CA-C-N	6.68	126.59	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ad	468	GLN	C-N-CA	6.68	126.59	119.85
3	of	5	ARG	N-CA-C	-6.68	106.08	114.56
1	af	336	ASP	CA-C-N	6.68	127.22	119.47
1	af	336	ASP	C-N-CA	6.68	127.22	119.47
1	el	134	ASP	CA-C-N	6.68	126.37	119.56
1	el	134	ASP	C-N-CA	6.68	126.37	119.56
1	bn	324	THR	N-CA-C	-6.68	98.89	109.04
1	dt	336	ASP	CA-C-N	6.68	127.22	119.47
1	dt	336	ASP	C-N-CA	6.68	127.22	119.47
2	hm	268	THR	N-CA-C	6.68	121.03	113.02
3	hy	38	VAL	N-CA-C	6.68	117.65	107.77
1	by	468	GLN	CA-C-N	6.67	126.59	119.85
1	by	468	GLN	C-N-CA	6.67	126.59	119.85
1	cd	336	ASP	CA-C-N	6.67	127.21	119.47
1	cd	336	ASP	C-N-CA	6.67	127.21	119.47
1	fh	491	ALA	CA-C-N	6.67	127.13	120.52
1	fh	491	ALA	C-N-CA	6.67	127.13	120.52
1	dm	186	GLY	N-CA-C	6.67	123.43	111.02
1	ey	193	SER	N-CA-C	-6.67	105.77	114.04
1	fq	440	GLY	CA-C-N	6.67	126.30	119.56
1	fq	440	GLY	C-N-CA	6.67	126.30	119.56
1	fv	336	ASP	CA-C-N	6.67	127.21	119.47
1	fv	336	ASP	C-N-CA	6.67	127.21	119.47
1	cj	324	THR	N-CA-C	-6.67	101.25	109.65
1	ei	336	ASP	CA-C-N	6.67	127.20	119.47
1	ei	336	ASP	C-N-CA	6.67	127.20	119.47
1	ft	103	ILE	CA-C-N	6.67	126.65	119.78
1	ft	103	ILE	C-N-CA	6.67	126.65	119.78
1	ec	336	ASP	CA-C-N	6.67	127.20	119.47
1	ec	336	ASP	C-N-CA	6.67	127.20	119.47
1	ei	263	SER	N-CA-C	6.67	119.94	110.14
1	gn	336	ASP	CA-C-N	6.67	127.20	119.47
1	gn	336	ASP	C-N-CA	6.67	127.20	119.47
1	em	440	GLY	CA-C-N	6.67	126.29	119.56
1	em	440	GLY	C-N-CA	6.67	126.29	119.56
1	ac	121	THR	N-CA-C	6.66	120.44	111.24
1	au	184	GLU	N-CA-C	-6.66	100.10	109.69
1	bc	328	LYS	N-CA-C	6.66	120.72	112.59
1	cl	149	GLY	CA-C-N	6.66	126.63	120.03
1	cl	149	GLY	C-N-CA	6.66	126.63	120.03
1	dj	336	ASP	CA-C-N	6.66	126.36	119.56
1	dj	336	ASP	C-N-CA	6.66	126.36	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gl	115	GLN	CA-C-N	6.66	126.64	119.78
1	gl	115	GLN	C-N-CA	6.66	126.64	119.78
1	gr	491	ALA	CA-C-N	6.66	126.84	120.31
1	gr	491	ALA	C-N-CA	6.66	126.84	120.31
1	bc	149	GLY	CA-C-N	6.66	126.84	120.31
1	bc	149	GLY	C-N-CA	6.66	126.84	120.31
1	ha	336	ASP	CA-C-N	6.66	127.20	119.47
1	ha	336	ASP	C-N-CA	6.66	127.20	119.47
3	it	37	ASP	CA-CB-CG	6.66	119.26	112.60
1	ae	285	ASP	N-CA-C	6.66	118.62	111.36
1	aj	491	ALA	CA-C-N	6.66	126.84	120.31
1	aj	491	ALA	C-N-CA	6.66	126.84	120.31
1	dk	336	ASP	CA-C-N	6.66	127.20	119.47
1	dk	336	ASP	C-N-CA	6.66	127.20	119.47
1	fk	263	SER	N-CA-C	6.66	119.54	109.95
1	bx	491	ALA	CA-C-N	6.66	127.20	120.14
1	bx	491	ALA	C-N-CA	6.66	127.20	120.14
1	bz	468	GLN	CA-C-N	6.66	126.58	119.85
1	bz	468	GLN	C-N-CA	6.66	126.58	119.85
1	da	440	GLY	CA-C-N	6.66	126.28	119.56
1	da	440	GLY	C-N-CA	6.66	126.28	119.56
1	fz	88	VAL	N-CA-C	6.66	117.46	107.80
1	an	253	ARG	N-CA-C	6.66	121.24	112.72
1	ci	328	LYS	N-CA-C	6.66	121.11	112.92
1	eo	440	GLY	CA-C-N	6.66	126.28	119.56
1	eo	440	GLY	C-N-CA	6.66	126.28	119.56
1	ff	440	GLY	CA-C-N	6.66	126.28	119.56
1	ff	440	GLY	C-N-CA	6.66	126.28	119.56
1	fi	88	VAL	N-CA-C	6.66	117.70	108.12
1	gx	468	GLN	CA-C-N	6.66	126.57	119.85
1	gx	468	GLN	C-N-CA	6.66	126.57	119.85
1	hc	483	PRO	N-CA-C	-6.66	100.63	111.21
2	ho	368	SER	N-CA-C	-6.66	99.69	110.20
1	gz	336	ASP	CA-C-N	6.65	127.19	119.47
1	gz	336	ASP	C-N-CA	6.65	127.19	119.47
1	gz	468	GLN	CA-C-N	6.65	126.57	119.85
1	gz	468	GLN	C-N-CA	6.65	126.57	119.85
1	bh	121	THR	CB-CA-C	-6.65	102.45	111.89
1	bk	440	GLY	CA-C-N	6.65	126.34	119.56
1	bk	440	GLY	C-N-CA	6.65	126.34	119.56
1	bz	198	ILE	N-CA-C	6.65	113.33	106.21
1	cs	440	GLY	CA-C-N	6.65	126.28	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cs	440	GLY	C-N-CA	6.65	126.28	119.56
1	dw	232	ILE	N-CA-C	-6.65	105.35	111.67
3	jt	37	ASP	CA-CB-CG	6.65	119.25	112.60
1	cj	119	SER	CA-C-N	6.65	126.61	120.03
1	cj	119	SER	C-N-CA	6.65	126.61	120.03
1	ax	258	VAL	N-CA-C	6.65	118.36	108.46
1	bd	324	THR	N-CA-C	-6.65	101.27	109.65
1	bo	440	GLY	CA-C-N	6.65	126.28	119.56
1	bo	440	GLY	C-N-CA	6.65	126.28	119.56
1	dm	336	ASP	CA-C-N	6.65	126.34	119.56
1	dm	336	ASP	C-N-CA	6.65	126.34	119.56
1	ee	484	PHE	CA-CB-CG	6.65	120.45	113.80
1	eh	151	ASP	CA-CB-CG	6.65	119.25	112.60
1	fl	121	THR	N-CA-C	6.65	120.56	111.39
1	bp	336	ASP	CA-C-N	6.64	127.18	119.47
1	bp	336	ASP	C-N-CA	6.64	127.18	119.47
1	eq	285	ASP	N-CA-C	6.64	119.86	111.69
1	db	68	ILE	N-CA-C	6.64	117.47	108.17
1	et	198	ILE	N-CA-C	6.64	113.32	106.21
1	ca	336	ASP	CA-C-N	6.64	127.17	119.47
1	ca	336	ASP	C-N-CA	6.64	127.17	119.47
1	eo	483	PRO	N-CA-C	-6.64	100.65	111.21
1	am	324	THR	N-CA-C	-6.64	101.42	109.72
1	dj	245	ASN	CA-C-N	6.64	126.60	120.03
1	dj	245	ASN	C-N-CA	6.64	126.60	120.03
1	ay	285	ASP	N-CA-C	6.64	118.59	111.36
3	ks	38	VAL	N-CA-C	6.64	117.68	108.12
1	cq	500	MET	N-CA-C	-6.63	101.71	110.40
1	ge	336	ASP	CA-C-N	6.63	127.17	119.47
1	ge	336	ASP	C-N-CA	6.63	127.17	119.47
1	en	253	ARG	N-CA-C	6.63	121.91	113.55
1	ca	201	GLY	N-CA-C	-6.63	104.55	113.24
1	cc	103	ILE	CA-C-N	6.63	126.60	120.03
1	cc	103	ILE	C-N-CA	6.63	126.60	120.03
1	dc	336	ASP	CA-C-N	6.63	127.16	119.47
1	dc	336	ASP	C-N-CA	6.63	127.16	119.47
1	ej	265	GLN	N-CA-C	6.63	119.29	108.55
1	fj	103	ILE	CA-C-N	6.63	126.61	119.78
1	fj	103	ILE	C-N-CA	6.63	126.61	119.78
1	ak	484	PHE	CA-CB-CG	6.63	120.43	113.80
1	av	71	ASP	CA-CB-CG	6.63	119.23	112.60
1	eq	463	ASP	CA-C-N	6.63	128.13	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eq	463	ASP	C-N-CA	6.63	128.13	119.84
1	gw	336	ASP	CA-C-N	6.63	127.16	119.47
1	gw	336	ASP	C-N-CA	6.63	127.16	119.47
1	dm	103	ILE	CA-C-N	6.63	126.59	120.03
1	dm	103	ILE	C-N-CA	6.63	126.59	120.03
1	ee	121	THR	N-CA-C	6.63	120.38	111.24
1	fu	336	ASP	CA-C-N	6.63	126.32	119.56
1	fu	336	ASP	C-N-CA	6.63	126.32	119.56
1	fu	440	GLY	CA-C-N	6.63	126.25	119.56
1	fu	440	GLY	C-N-CA	6.63	126.25	119.56
3	li	72	ASN	CA-CB-CG	6.63	119.23	112.60
1	an	103	ILE	CA-C-N	6.62	126.59	120.03
1	an	103	ILE	C-N-CA	6.62	126.59	120.03
1	cc	145	HIS	CA-C-N	6.62	127.15	119.47
1	cc	145	HIS	C-N-CA	6.62	127.15	119.47
1	cr	271	SER	N-CA-C	6.62	119.83	110.23
1	bt	88	VAL	N-CA-C	6.62	117.65	108.12
1	ev	71	ASP	CA-CB-CG	6.62	119.22	112.60
1	gw	491	ALA	CA-C-N	6.62	126.80	120.31
1	gw	491	ALA	C-N-CA	6.62	126.80	120.31
3	mt	38	VAL	N-CA-C	6.62	117.84	108.17
2	hj	115	PRO	N-CA-C	-6.62	101.48	111.41
1	bm	440	GLY	CA-C-N	6.62	126.24	119.56
1	bm	440	GLY	C-N-CA	6.62	126.24	119.56
1	dc	88	VAL	N-CA-C	6.62	117.41	107.75
1	de	336	ASP	CA-C-N	6.62	127.14	119.47
1	de	336	ASP	C-N-CA	6.62	127.14	119.47
2	hj	327	VAL	N-CA-C	6.62	118.32	108.46
1	ax	324	THR	N-CA-C	-6.61	101.32	109.65
1	cr	336	ASP	CA-C-N	6.61	126.31	119.56
1	cr	336	ASP	C-N-CA	6.61	126.31	119.56
3	lq	67	GLU	N-CA-C	-6.61	104.15	111.36
1	au	440	GLY	CA-C-N	6.61	126.24	119.56
1	au	440	GLY	C-N-CA	6.61	126.24	119.56
1	hd	256	LYS	N-CA-C	6.61	119.12	109.07
1	dj	406	THR	N-CA-C	-6.61	105.78	114.31
1	hc	88	VAL	N-CA-C	6.61	117.36	108.11
1	bv	72	HIS	N-CA-C	-6.61	99.25	109.76
1	cp	149	GLY	CA-C-N	6.61	126.57	120.03
1	cp	149	GLY	C-N-CA	6.61	126.57	120.03
1	dn	121	THR	N-CA-C	6.61	120.49	111.17
1	ei	245	ASN	CA-C-N	6.61	126.78	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ei	245	ASN	C-N-CA	6.61	126.78	120.31
3	jy	72	ASN	CB-CA-C	-6.61	100.50	110.88
1	ai	440	GLY	CA-C-N	6.61	126.23	119.56
1	ai	440	GLY	C-N-CA	6.61	126.23	119.56
1	dn	491	ALA	CA-C-N	6.61	126.78	120.31
1	dn	491	ALA	C-N-CA	6.61	126.78	120.31
1	eq	440	GLY	CA-C-N	6.60	126.23	119.56
1	eq	440	GLY	C-N-CA	6.60	126.23	119.56
1	gw	119	SER	N-CA-C	-6.60	102.28	108.22
1	bz	245	ASN	CA-C-N	6.60	126.57	120.03
1	bz	245	ASN	C-N-CA	6.60	126.57	120.03
3	ob	72	ASN	CA-CB-CG	6.60	119.20	112.60
1	dn	336	ASP	CA-C-N	6.60	127.13	119.47
1	dn	336	ASP	C-N-CA	6.60	127.13	119.47
3	kn	46	TYR	N-CA-C	6.60	118.80	108.96
1	ak	103	ILE	CA-C-N	6.60	126.56	120.03
1	ak	103	ILE	C-N-CA	6.60	126.56	120.03
1	az	245	ASN	CA-C-N	6.60	126.56	120.03
1	az	245	ASN	C-N-CA	6.60	126.56	120.03
1	cy	149	GLY	CA-C-N	6.60	126.52	119.85
1	cy	149	GLY	C-N-CA	6.60	126.52	119.85
1	fa	440	GLY	CA-C-N	6.60	126.23	119.56
1	fa	440	GLY	C-N-CA	6.60	126.23	119.56
3	jm	46	TYR	N-CA-C	6.60	118.97	109.14
1	aj	324	THR	N-CA-C	-6.60	99.35	109.64
1	bz	336	ASP	CA-C-N	6.60	126.29	119.56
1	bz	336	ASP	C-N-CA	6.60	126.29	119.56
1	dt	245	ASN	CA-C-N	6.60	126.56	120.03
1	dt	245	ASN	C-N-CA	6.60	126.56	120.03
1	dq	491	ALA	CA-C-N	6.60	126.77	120.31
1	dq	491	ALA	C-N-CA	6.60	126.77	120.31
1	fn	103	ILE	CA-C-N	6.60	126.57	119.78
1	fn	103	ILE	C-N-CA	6.60	126.57	119.78
1	gz	103	ILE	CA-C-N	6.60	126.62	119.89
1	gz	103	ILE	C-N-CA	6.60	126.62	119.89
2	he	59	ASN	CA-C-N	6.60	126.29	119.56
2	he	59	ASN	C-N-CA	6.60	126.29	119.56
1	bi	149	GLY	CA-C-N	6.59	126.77	120.31
1	bi	149	GLY	C-N-CA	6.59	126.77	120.31
1	ez	440	GLY	CA-C-N	6.59	126.22	119.56
1	ez	440	GLY	C-N-CA	6.59	126.22	119.56
3	iv	38	VAL	N-CA-C	6.59	117.53	107.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	jp	74	ASP	CA-CB-CG	6.59	119.19	112.60
1	bl	245	ASN	CA-C-N	6.59	126.56	120.03
1	bl	245	ASN	C-N-CA	6.59	126.56	120.03
1	el	253	ARG	N-CA-C	6.59	121.74	113.43
3	ke	38	VAL	N-CA-C	6.59	117.53	107.77
1	ao	103	ILE	CA-C-N	6.59	126.51	119.85
1	ao	103	ILE	C-N-CA	6.59	126.51	119.85
1	av	88	VAL	N-CA-C	6.59	117.34	108.11
1	bl	483	PRO	N-CA-C	-6.59	100.73	111.21
1	fe	468	GLN	CA-C-N	6.59	126.51	119.85
1	fe	468	GLN	C-N-CA	6.59	126.51	119.85
1	gf	103	ILE	CA-C-N	6.59	126.57	119.78
1	gf	103	ILE	C-N-CA	6.59	126.57	119.78
1	fk	440	GLY	CA-C-N	6.59	126.22	119.56
1	fk	440	GLY	C-N-CA	6.59	126.22	119.56
1	fp	245	ASN	CA-C-N	6.59	126.55	120.03
1	fp	245	ASN	C-N-CA	6.59	126.55	120.03
1	gh	468	GLN	CA-C-N	6.59	126.50	119.85
1	gh	468	GLN	C-N-CA	6.59	126.50	119.85
1	dx	336	ASP	CA-C-N	6.59	127.11	119.47
1	dx	336	ASP	C-N-CA	6.59	127.11	119.47
1	dy	134	ASP	CA-C-N	6.58	126.28	119.56
1	dy	134	ASP	C-N-CA	6.58	126.28	119.56
2	hg	136	LYS	N-CA-C	-6.58	105.38	113.41
1	bu	468	GLN	CA-C-N	6.58	126.50	119.85
1	bu	468	GLN	C-N-CA	6.58	126.50	119.85
1	ci	440	GLY	CA-C-N	6.58	126.28	119.56
1	ci	440	GLY	C-N-CA	6.58	126.28	119.56
1	cj	114	VAL	N-CA-C	6.58	116.82	111.62
1	gt	324	THR	N-CA-C	-6.58	100.08	109.62
1	du	468	GLN	CA-C-N	6.58	126.50	119.85
1	du	468	GLN	C-N-CA	6.58	126.50	119.85
3	mz	37	ASP	CA-CB-CG	6.58	119.18	112.60
1	ax	72	HIS	N-CA-C	-6.58	99.45	109.85
1	by	440	GLY	CA-C-N	6.58	126.20	119.56
1	by	440	GLY	C-N-CA	6.58	126.20	119.56
1	cw	324	THR	N-CA-C	-6.58	101.36	109.65
3	kf	46	TYR	N-CA-C	6.58	118.94	109.14
1	bl	121	THR	N-CA-C	6.58	120.46	111.39
1	bp	253	ARG	N-CA-C	6.58	121.68	112.93
1	bt	115	GLN	CA-C-N	6.57	126.54	120.03
1	bt	115	GLN	C-N-CA	6.57	126.54	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	df	245	ASN	CA-C-N	6.57	126.54	120.03
1	df	245	ASN	C-N-CA	6.57	126.54	120.03
1	fw	88	VAL	N-CA-C	6.57	117.35	107.75
1	dv	468	GLN	CA-C-N	6.57	126.49	119.85
1	dv	468	GLN	C-N-CA	6.57	126.49	119.85
1	gf	287	ASP	N-CA-C	-6.57	104.19	112.93
1	au	336	ASP	CA-C-N	6.57	126.26	119.56
1	au	336	ASP	C-N-CA	6.57	126.26	119.56
1	go	324	THR	N-CA-C	-6.57	101.37	109.65
1	gr	103	ILE	CA-C-N	6.57	126.55	119.78
1	gr	103	ILE	C-N-CA	6.57	126.55	119.78
1	gv	149	GLY	CA-C-N	6.57	126.53	120.03
1	gv	149	GLY	C-N-CA	6.57	126.53	120.03
1	ba	121	THR	N-CA-C	6.57	120.31	111.24
3	nx	67	GLU	N-CA-C	-6.57	104.20	111.36
1	gr	121	THR	N-CA-C	6.57	120.30	111.24
1	ac	245	ASN	CA-C-N	6.57	126.53	120.03
1	ac	245	ASN	C-N-CA	6.57	126.53	120.03
1	bk	151	ASP	CA-CB-CG	6.57	119.17	112.60
1	gn	103	ILE	CA-C-N	6.57	126.48	119.85
1	gn	103	ILE	C-N-CA	6.57	126.48	119.85
3	my	38	VAL	N-CA-C	6.57	117.75	108.17
3	oa	72	ASN	CA-CB-CG	6.57	119.17	112.60
1	aq	336	ASP	CA-C-N	6.56	127.08	119.47
1	aq	336	ASP	C-N-CA	6.56	127.08	119.47
3	lr	5	ARG	N-CA-C	-6.56	107.14	114.62
3	lv	38	VAL	N-CA-C	6.56	117.57	108.12
1	eh	154	PHE	CA-CB-CG	6.56	120.36	113.80
1	bu	115	GLN	CB-CA-C	-6.56	105.29	111.00
1	dc	406	THR	N-CA-C	-6.56	105.00	114.12
1	ev	440	GLY	CA-C-N	6.56	126.19	119.56
1	ev	440	GLY	C-N-CA	6.56	126.19	119.56
1	fr	468	GLN	CA-C-N	6.56	126.47	119.85
1	fr	468	GLN	C-N-CA	6.56	126.47	119.85
1	ge	103	ILE	CA-C-N	6.56	126.52	120.03
1	ge	103	ILE	C-N-CA	6.56	126.52	120.03
1	gv	336	ASP	CA-C-N	6.56	126.25	119.56
1	gv	336	ASP	C-N-CA	6.56	126.25	119.56
3	nj	72	ASN	CA-CB-CG	6.56	119.16	112.60
1	bd	440	GLY	CA-C-N	6.56	126.18	119.56
1	bd	440	GLY	C-N-CA	6.56	126.18	119.56
1	bo	336	ASP	CA-C-N	6.56	126.25	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bo	336	ASP	C-N-CA	6.56	126.25	119.56
1	cf	440	GLY	CA-C-N	6.56	126.25	119.56
1	cf	440	GLY	C-N-CA	6.56	126.25	119.56
1	fh	336	ASP	CA-C-N	6.56	127.08	119.47
1	fh	336	ASP	C-N-CA	6.56	127.08	119.47
1	gf	115	GLN	CB-CA-C	-6.56	105.29	111.00
3	ip	18	ASP	CA-CB-CG	6.56	119.16	112.60
1	ep	149	GLY	CA-C-N	6.55	126.52	120.03
1	ep	149	GLY	C-N-CA	6.55	126.52	120.03
1	fs	103	ILE	CA-C-N	6.55	126.53	119.78
1	fs	103	ILE	C-N-CA	6.55	126.53	119.78
2	hh	370	GLN	CA-C-N	6.55	126.47	119.85
2	hh	370	GLN	C-N-CA	6.55	126.47	119.85
1	al	468	GLN	CA-C-N	6.55	126.47	119.85
1	al	468	GLN	C-N-CA	6.55	126.47	119.85
3	jd	46	TYR	N-CA-C	6.55	118.90	109.14
1	cu	103	ILE	CA-C-N	6.55	126.53	119.78
1	cu	103	ILE	C-N-CA	6.55	126.53	119.78
1	ev	88	VAL	N-CA-C	6.55	117.31	107.75
1	df	92	GLY	CA-C-N	6.55	128.03	119.84
1	df	92	GLY	C-N-CA	6.55	128.03	119.84
1	gi	121	THR	N-CA-C	6.55	120.28	111.24
1	gm	88	VAL	N-CA-C	6.55	117.29	107.80
1	dd	103	ILE	CA-C-N	6.55	126.46	119.85
1	dd	103	ILE	C-N-CA	6.55	126.46	119.85
1	gk	440	GLY	CA-C-N	6.55	126.17	119.56
1	gk	440	GLY	C-N-CA	6.55	126.17	119.56
1	di	440	GLY	CA-C-N	6.54	126.17	119.56
1	di	440	GLY	C-N-CA	6.54	126.17	119.56
1	ed	287	ASP	N-CA-C	-6.54	104.23	112.93
1	ae	440	GLY	CA-C-N	6.54	126.17	119.56
1	ae	440	GLY	C-N-CA	6.54	126.17	119.56
1	aq	440	GLY	CA-C-N	6.54	126.23	119.56
1	aq	440	GLY	C-N-CA	6.54	126.23	119.56
1	bg	491	ALA	CA-C-N	6.54	126.72	120.31
1	bg	491	ALA	C-N-CA	6.54	126.72	120.31
1	gy	336	ASP	CA-C-N	6.54	126.23	119.56
1	gy	336	ASP	C-N-CA	6.54	126.23	119.56
2	hi	370	GLN	CA-C-N	6.54	126.46	119.85
2	hi	370	GLN	C-N-CA	6.54	126.46	119.85
1	ai	103	ILE	CA-C-N	6.54	126.46	119.85
1	ai	103	ILE	C-N-CA	6.54	126.46	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	al	336	ASP	CA-C-N	6.54	127.06	119.47
1	al	336	ASP	C-N-CA	6.54	127.06	119.47
1	bm	406	THR	N-CA-C	-6.54	105.03	114.12
1	hb	324	THR	N-CA-C	-6.54	101.41	109.65
1	gl	71	ASP	CA-CB-CG	6.54	119.14	112.60
3	ib	67	GLU	N-CA-C	-6.54	103.65	111.69
1	av	232	ILE	N-CA-C	-6.54	105.37	111.45
1	da	256	LYS	N-CA-C	6.54	118.70	108.96
1	dq	103	ILE	CA-C-N	6.54	126.50	120.03
1	dq	103	ILE	C-N-CA	6.54	126.50	120.03
1	ep	440	GLY	CA-C-N	6.54	126.23	119.56
1	ep	440	GLY	C-N-CA	6.54	126.23	119.56
1	eu	336	ASP	CA-C-N	6.53	127.05	119.47
1	eu	336	ASP	C-N-CA	6.53	127.05	119.47
1	ag	468	GLN	CA-C-N	6.53	126.56	119.90
1	ag	468	GLN	C-N-CA	6.53	126.56	119.90
1	dq	336	ASP	CA-C-N	6.53	127.05	119.47
1	dq	336	ASP	C-N-CA	6.53	127.05	119.47
1	ef	103	ILE	CA-C-N	6.53	126.50	120.03
1	ef	103	ILE	C-N-CA	6.53	126.50	120.03
1	ak	440	GLY	CA-C-N	6.53	126.15	119.56
1	ak	440	GLY	C-N-CA	6.53	126.15	119.56
1	cn	324	THR	N-CA-C	-6.53	98.25	109.15
1	de	253	ARG	N-CA-C	6.53	121.61	112.93
1	gq	336	ASP	CA-C-N	6.53	127.04	119.47
1	gq	336	ASP	C-N-CA	6.53	127.04	119.47
1	az	149	GLY	CA-C-N	6.52	126.49	120.03
1	az	149	GLY	C-N-CA	6.52	126.49	120.03
1	dg	121	THR	N-CA-C	6.52	120.37	111.17
1	fg	232	ILE	N-CA-C	-6.52	105.47	111.67
3	mv	38	VAL	N-CA-C	6.52	117.69	108.17
1	gu	103	ILE	CA-C-N	6.52	126.50	119.78
1	gu	103	ILE	C-N-CA	6.52	126.50	119.78
1	am	336	ASP	CA-C-N	6.52	126.21	119.56
1	am	336	ASP	C-N-CA	6.52	126.21	119.56
1	bc	103	ILE	CA-C-N	6.52	126.48	120.03
1	bc	103	ILE	C-N-CA	6.52	126.48	120.03
1	ck	440	GLY	CA-C-N	6.52	126.21	119.56
1	ck	440	GLY	C-N-CA	6.52	126.21	119.56
1	dg	232	ILE	N-CA-C	-6.52	105.39	111.45
1	ek	134	ASP	CA-C-N	6.52	126.14	119.56
1	ek	134	ASP	C-N-CA	6.52	126.14	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dx	468	GLN	CA-C-N	6.52	126.43	119.85
1	dx	468	GLN	C-N-CA	6.52	126.43	119.85
1	cc	328	LYS	N-CA-C	6.52	121.28	112.88
1	ba	336	ASP	CA-C-N	6.51	126.20	119.56
1	ba	336	ASP	C-N-CA	6.51	126.20	119.56
1	dj	119	SER	CA-C-N	6.51	126.46	120.21
1	dj	119	SER	C-N-CA	6.51	126.46	120.21
1	dp	121	THR	CB-CA-C	-6.51	102.06	112.09
1	fr	287	ASP	N-CA-C	-6.51	104.27	112.93
1	cv	491	ALA	CA-C-N	6.51	126.42	119.85
1	cv	491	ALA	C-N-CA	6.51	126.42	119.85
1	hc	336	ASP	CA-C-N	6.51	127.02	119.47
1	hc	336	ASP	C-N-CA	6.51	127.02	119.47
2	hk	268	THR	N-CA-C	6.51	121.06	113.18
3	ju	38	VAL	N-CA-C	6.51	117.40	107.77
1	bv	287	ASP	N-CA-C	-6.51	104.27	112.93
3	kp	38	VAL	N-CA-C	6.51	117.49	108.12
1	fm	245	ASN	CA-C-N	6.51	126.47	120.03
1	fm	245	ASN	C-N-CA	6.51	126.47	120.03
1	gm	245	ASN	CA-C-N	6.51	126.42	119.85
1	gm	245	ASN	C-N-CA	6.51	126.42	119.85
2	hk	59	ASN	CA-C-N	6.51	126.20	119.56
2	hk	59	ASN	C-N-CA	6.51	126.20	119.56
3	ir	38	VAL	N-CA-C	6.51	117.49	108.12
1	fs	336	ASP	CA-C-N	6.50	127.02	119.47
1	fs	336	ASP	C-N-CA	6.50	127.02	119.47
2	hj	136	LYS	N-CA-C	-6.50	105.47	113.41
1	by	324	THR	N-CA-C	-6.50	101.45	109.65
1	cq	121	THR	N-CA-C	6.50	120.21	111.24
1	cy	440	GLY	CA-C-N	6.50	126.13	119.56
1	cy	440	GLY	C-N-CA	6.50	126.13	119.56
1	fk	336	ASP	CA-C-N	6.50	126.19	119.56
1	fk	336	ASP	C-N-CA	6.50	126.19	119.56
1	gh	344	ARG	N-CA-C	-6.50	99.22	109.50
1	gy	440	GLY	CA-C-N	6.50	126.13	119.56
1	gy	440	GLY	C-N-CA	6.50	126.13	119.56
1	ai	336	ASP	CA-C-N	6.50	127.01	119.47
1	ai	336	ASP	C-N-CA	6.50	127.01	119.47
1	ak	245	ASN	CA-C-N	6.50	126.47	120.03
1	ak	245	ASN	C-N-CA	6.50	126.47	120.03
1	cf	468	GLN	CA-C-N	6.50	126.42	119.85
1	cf	468	GLN	C-N-CA	6.50	126.42	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	df	103	ILE	CA-C-N	6.50	126.48	119.78
1	df	103	ILE	C-N-CA	6.50	126.48	119.78
1	ga	72	HIS	N-CA-C	-6.50	99.23	109.50
1	go	406	THR	N-CA-C	-6.50	105.08	114.12
1	bd	412	VAL	N-CA-C	-6.50	106.48	111.62
3	kx	23	ILE	N-CA-C	-6.50	98.28	108.23
1	ep	336	ASP	CA-C-N	6.50	126.19	119.56
1	ep	336	ASP	C-N-CA	6.50	126.19	119.56
1	fj	121	THR	N-CA-C	6.50	120.21	111.24
1	bh	491	ALA	CA-C-N	6.50	126.68	120.31
1	bh	491	ALA	C-N-CA	6.50	126.68	120.31
1	co	72	HIS	N-CA-C	-6.50	100.59	109.95
1	eh	256	LYS	N-CA-C	6.50	118.95	109.07
1	fk	184	GLU	N-CA-C	-6.50	100.59	109.95
1	gs	115	GLN	CA-C-N	6.50	126.46	120.03
1	gs	115	GLN	C-N-CA	6.50	126.46	120.03
1	gu	407	ASP	CA-CB-CG	6.50	119.10	112.60
1	fh	440	GLY	CA-C-N	6.50	126.12	119.56
1	fh	440	GLY	C-N-CA	6.50	126.12	119.56
2	hi	172	SER	N-CA-C	6.50	120.28	109.95
1	ao	440	GLY	CA-C-N	6.49	126.12	119.56
1	ao	440	GLY	C-N-CA	6.49	126.12	119.56
1	ft	253	ARG	N-CA-C	6.49	121.73	113.55
3	nz	5	ARG	N-CA-C	-6.49	106.57	114.75
1	al	121	THR	CB-CA-C	-6.49	102.10	112.09
1	cb	491	ALA	CA-C-N	6.49	126.67	120.31
1	cb	491	ALA	C-N-CA	6.49	126.67	120.31
1	cn	336	ASP	CA-C-N	6.49	126.18	119.56
1	cn	336	ASP	C-N-CA	6.49	126.18	119.56
1	dv	119	SER	CA-C-N	6.49	126.44	120.21
1	dv	119	SER	C-N-CA	6.49	126.44	120.21
1	eb	265	GLN	N-CA-C	6.49	119.06	108.55
1	fl	336	ASP	CA-C-N	6.49	126.18	119.56
1	fl	336	ASP	C-N-CA	6.49	126.18	119.56
1	ah	468	GLN	CA-C-N	6.49	126.40	119.85
1	ah	468	GLN	C-N-CA	6.49	126.40	119.85
1	do	324	THR	N-CA-C	-6.49	101.47	109.65
1	fy	491	ALA	CA-C-N	6.49	126.67	120.31
1	fy	491	ALA	C-N-CA	6.49	126.67	120.31
1	es	336	ASP	CA-C-N	6.49	126.18	119.56
1	es	336	ASP	C-N-CA	6.49	126.18	119.56
1	cn	463	ASP	CA-C-N	6.49	126.18	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cn	463	ASP	C-N-CA	6.49	126.18	119.56
1	ey	93	PRO	N-CA-CB	-6.49	98.51	102.79
1	fx	253	ARG	N-CA-C	6.49	121.56	112.93
1	hb	253	ARG	N-CA-C	6.49	121.56	112.93
1	cr	121	THR	N-CA-C	6.48	120.19	111.24
1	dv	88	VAL	N-CA-C	6.48	117.22	107.75
1	gn	328	LYS	N-CA-C	6.48	121.24	112.88
1	bk	328	LYS	N-CA-C	6.48	120.51	111.56
1	bo	87	ALA	N-CA-C	6.48	118.34	111.28
1	ci	245	ASN	CA-C-N	6.48	126.45	120.03
1	ci	245	ASN	C-N-CA	6.48	126.45	120.03
1	ei	440	GLY	CA-C-N	6.48	126.17	119.56
1	ei	440	GLY	C-N-CA	6.48	126.17	119.56
1	er	245	ASN	CA-C-N	6.48	126.45	120.03
1	er	245	ASN	C-N-CA	6.48	126.45	120.03
1	ak	253	ARG	N-CA-C	6.48	121.55	112.93
1	gp	395	TYR	N-CA-C	6.48	118.03	110.97
3	iu	38	VAL	N-CA-C	6.48	117.36	107.77
1	al	121	THR	N-CA-C	6.48	120.18	111.24
1	ae	201	GLY	N-CA-C	-6.48	104.75	113.24
1	ft	72	HIS	N-CA-C	-6.48	100.32	110.36
1	gv	484	PHE	CA-CB-CG	6.48	120.28	113.80
3	kh	38	VAL	N-CA-C	6.48	117.36	107.77
1	al	92	GLY	CA-C-N	6.48	126.17	119.82
1	al	92	GLY	C-N-CA	6.48	126.17	119.82
1	cm	336	ASP	CA-C-N	6.47	126.98	119.47
1	cm	336	ASP	C-N-CA	6.47	126.98	119.47
1	ha	151	ASP	CA-CB-CG	6.47	119.08	112.60
2	hg	141	SER	N-CA-C	-6.47	100.31	109.96
3	kz	5	ARG	N-CA-C	-6.47	106.59	114.75
1	ab	103	ILE	CA-C-N	6.47	126.49	119.89
1	ab	103	ILE	C-N-CA	6.47	126.49	119.89
1	gu	88	VAL	N-CA-C	6.47	117.20	107.75
1	am	484	PHE	CA-CB-CG	6.47	120.27	113.80
1	fg	328	LYS	N-CA-C	6.47	121.23	112.88
1	as	104	PRO	N-CA-C	6.47	121.22	112.48
1	fg	87	ALA	N-CA-C	6.47	118.33	111.28
2	hh	172	SER	N-CA-C	6.47	120.07	109.85
1	dp	121	THR	N-CA-C	6.47	120.17	111.24
1	fs	121	THR	CB-CA-C	-6.47	102.70	111.89
3	nm	46	TYR	N-CA-C	6.47	118.78	109.14
1	ej	440	GLY	CA-C-N	6.47	126.09	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ej	440	GLY	C-N-CA	6.47	126.09	119.56
3	mq	46	TYR	N-CA-C	6.47	117.98	108.86
1	bv	88	VAL	N-CA-C	6.46	117.16	108.11
1	cz	209	ASP	CA-CB-CG	6.46	119.06	112.60
1	gc	328	LYS	N-CA-C	6.46	121.21	112.88
3	ln	38	VAL	N-CA-C	6.46	117.60	108.17
3	mz	46	TYR	N-CA-C	6.46	117.97	108.86
1	cq	468	GLN	CA-C-N	6.46	126.38	119.85
1	cq	468	GLN	C-N-CA	6.46	126.38	119.85
1	gy	483	PRO	N-CA-C	-6.46	101.06	111.14
1	am	440	GLY	CA-C-N	6.46	126.08	119.56
1	am	440	GLY	C-N-CA	6.46	126.08	119.56
1	ay	88	VAL	N-CA-C	6.46	117.42	108.12
1	ew	483	PRO	N-CA-C	-6.46	100.94	111.21
1	en	103	ILE	CA-C-N	6.46	126.42	120.03
1	en	103	ILE	C-N-CA	6.46	126.42	120.03
3	lc	46	TYR	N-CA-C	6.46	117.96	108.86
1	bh	121	THR	N-CA-C	6.45	120.30	111.39
1	gy	115	GLN	CA-C-N	6.45	126.42	120.03
1	gy	115	GLN	C-N-CA	6.45	126.42	120.03
3	jl	46	TYR	N-CA-C	6.45	118.76	109.14
1	bd	149	GLY	CA-C-N	6.45	126.42	120.03
1	bd	149	GLY	C-N-CA	6.45	126.42	120.03
1	gg	336	ASP	CA-C-N	6.45	126.14	119.56
1	gg	336	ASP	C-N-CA	6.45	126.14	119.56
1	cb	253	ARG	N-CA-C	6.45	121.68	113.55
1	cp	103	ILE	CA-C-N	6.45	126.47	119.89
1	cp	103	ILE	C-N-CA	6.45	126.47	119.89
1	fk	406	THR	N-CA-C	-6.45	105.15	114.12
1	fr	406	THR	N-CA-C	-6.45	105.15	114.12
1	gn	245	ASN	CA-C-N	6.45	126.42	120.03
1	gn	245	ASN	C-N-CA	6.45	126.42	120.03
1	az	406	THR	N-CA-C	-6.45	106.37	114.56
1	ba	440	GLY	CA-C-N	6.45	126.07	119.56
1	ba	440	GLY	C-N-CA	6.45	126.07	119.56
1	ae	115	GLN	CA-C-N	6.45	126.42	119.78
1	ae	115	GLN	C-N-CA	6.45	126.42	119.78
1	gw	103	ILE	CA-C-N	6.45	126.36	119.85
1	gw	103	ILE	C-N-CA	6.45	126.36	119.85
1	cc	245	ASN	CA-C-N	6.45	126.41	120.03
1	cc	245	ASN	C-N-CA	6.45	126.41	120.03
3	hz	32	PHE	CA-C-N	6.45	126.14	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	hz	32	PHE	C-N-CA	6.45	126.14	119.56
1	cv	336	ASP	CA-C-N	6.44	126.13	119.56
1	cv	336	ASP	C-N-CA	6.44	126.13	119.56
1	eg	232	ILE	N-CA-C	-6.44	105.55	111.67
1	ae	328	LYS	N-CA-C	6.44	121.19	112.88
3	mi	46	TYR	N-CA-C	6.44	118.73	109.14
1	cx	440	GLY	CA-C-N	6.44	126.06	119.56
1	cx	440	GLY	C-N-CA	6.44	126.06	119.56
1	dy	115	GLN	CA-C-N	6.44	126.40	120.03
1	dy	115	GLN	C-N-CA	6.44	126.40	120.03
1	fk	245	ASN	CA-C-N	6.44	126.41	120.03
1	fk	245	ASN	C-N-CA	6.44	126.41	120.03
1	bj	440	GLY	CA-C-N	6.44	126.06	119.56
1	bj	440	GLY	C-N-CA	6.44	126.06	119.56
1	dh	103	ILE	CA-C-N	6.44	126.41	119.78
1	dh	103	ILE	C-N-CA	6.44	126.41	119.78
1	fu	145	HIS	CA-C-N	6.44	126.13	119.56
1	fu	145	HIS	C-N-CA	6.44	126.13	119.56
1	ga	245	ASN	CA-C-N	6.44	126.40	120.03
1	ga	245	ASN	C-N-CA	6.44	126.40	120.03
1	gc	412	VAL	N-CA-C	-6.44	106.54	111.62
1	gk	121	THR	N-CA-C	6.43	119.06	111.02
2	he	115	PRO	N-CA-C	-6.43	101.76	111.41
1	da	93	PRO	N-CA-CB	-6.43	98.54	102.79
1	gk	245	ASN	CA-C-N	6.43	126.40	120.03
1	gk	245	ASN	C-N-CA	6.43	126.40	120.03
1	cz	336	ASP	CA-C-N	6.43	126.12	119.56
1	cz	336	ASP	C-N-CA	6.43	126.12	119.56
1	eo	468	GLN	CA-C-N	6.43	126.34	119.85
1	eo	468	GLN	C-N-CA	6.43	126.34	119.85
1	gh	71	ASP	CA-CB-CG	6.43	119.03	112.60
1	dz	103	ILE	CA-C-N	6.43	126.34	119.85
1	dz	103	ILE	C-N-CA	6.43	126.34	119.85
1	bc	440	GLY	CA-C-N	6.43	126.05	119.56
1	bc	440	GLY	C-N-CA	6.43	126.05	119.56
1	eq	232	ILE	N-CA-C	-6.43	105.57	111.67
1	dy	468	GLN	CA-C-N	6.42	126.34	119.85
1	dy	468	GLN	C-N-CA	6.42	126.34	119.85
1	hc	149	GLY	CA-C-N	6.42	126.61	120.31
1	hc	149	GLY	C-N-CA	6.42	126.61	120.31
1	bp	68	ILE	CA-C-N	6.42	126.94	119.94
1	bp	68	ILE	C-N-CA	6.42	126.94	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dh	336	ASP	CA-C-N	6.42	126.92	119.47
1	dh	336	ASP	C-N-CA	6.42	126.92	119.47
1	gf	121	THR	N-CA-C	6.42	120.10	111.24
1	dm	468	GLN	CA-C-N	6.42	126.33	119.85
1	dm	468	GLN	C-N-CA	6.42	126.33	119.85
1	ez	103	ILE	CA-C-N	6.42	126.38	120.03
1	ez	103	ILE	C-N-CA	6.42	126.38	120.03
1	fj	336	ASP	CA-C-N	6.42	126.10	119.56
1	fj	336	ASP	C-N-CA	6.42	126.10	119.56
1	ah	232	ILE	N-CA-C	-6.41	105.58	111.67
1	aq	113	GLY	N-CA-C	-6.41	102.76	112.89
1	ct	92	GLY	CA-C-N	6.41	126.11	119.82
1	ct	92	GLY	C-N-CA	6.41	126.11	119.82
1	dl	198	ILE	N-CA-C	6.41	116.86	107.37
1	dq	92	GLY	CA-C-N	6.41	127.86	119.84
1	dq	92	GLY	C-N-CA	6.41	127.86	119.84
1	ee	71	ASP	CA-CB-CG	6.41	119.01	112.60
3	mq	37	ASP	CA-CB-CG	6.41	119.01	112.60
1	bf	149	GLY	CA-C-N	6.41	126.38	120.03
1	bf	149	GLY	C-N-CA	6.41	126.38	120.03
1	ha	440	GLY	CA-C-N	6.41	126.10	119.56
1	ha	440	GLY	C-N-CA	6.41	126.10	119.56
3	mz	38	VAL	N-CA-C	6.41	117.35	108.12
1	ba	483	PRO	CA-C-N	-6.41	112.89	122.24
1	ba	483	PRO	C-N-CA	-6.41	112.89	122.24
1	fo	68	ILE	CA-C-N	6.41	127.05	119.94
1	fo	68	ILE	C-N-CA	6.41	127.05	119.94
1	al	103	ILE	CA-C-N	6.41	126.37	120.03
1	al	103	ILE	C-N-CA	6.41	126.37	120.03
1	cc	440	GLY	CA-C-N	6.41	126.03	119.56
1	cc	440	GLY	C-N-CA	6.41	126.03	119.56
2	hn	59	ASN	CA-C-N	6.41	126.09	119.56
2	hn	59	ASN	C-N-CA	6.41	126.09	119.56
1	aw	346	ALA	N-CA-C	6.41	118.26	111.28
1	cl	232	ILE	N-CA-C	-6.41	105.58	111.67
1	cq	193	SER	N-CA-C	-6.41	106.10	114.04
1	az	145	HIS	CA-C-N	6.40	126.09	119.56
1	az	145	HIS	C-N-CA	6.40	126.09	119.56
1	bw	113	GLY	N-CA-C	-6.40	102.80	112.60
1	cm	103	ILE	CA-C-N	6.40	126.37	120.03
1	cm	103	ILE	C-N-CA	6.40	126.37	120.03
1	ha	468	GLN	CA-C-N	6.40	126.32	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ha	468	GLN	C-N-CA	6.40	126.32	119.85
3	li	38	VAL	N-CA-C	6.40	117.32	107.78
1	as	440	GLY	CA-C-N	6.40	126.03	119.56
1	as	440	GLY	C-N-CA	6.40	126.03	119.56
1	fm	491	ALA	CA-C-N	6.40	126.32	119.85
1	fm	491	ALA	C-N-CA	6.40	126.32	119.85
1	gj	95	VAL	N-CA-C	6.40	117.07	108.11
2	hk	370	GLN	CA-C-N	6.40	126.37	120.03
2	hk	370	GLN	C-N-CA	6.40	126.37	120.03
1	bi	103	ILE	CA-C-N	6.40	126.36	120.03
1	bi	103	ILE	C-N-CA	6.40	126.36	120.03
1	fh	245	ASN	CA-C-N	6.40	126.36	120.03
1	fh	245	ASN	C-N-CA	6.40	126.36	120.03
1	gl	183	GLN	N-CA-C	-6.40	104.31	111.28
1	bx	468	GLN	CA-C-N	6.40	126.31	119.85
1	bx	468	GLN	C-N-CA	6.40	126.31	119.85
1	fp	184	GLU	N-CA-C	-6.40	100.74	109.95
1	fu	484	PHE	CA-CB-CG	6.40	120.20	113.80
1	gn	484	PHE	CA-CB-CG	6.40	120.20	113.80
1	cb	245	ASN	CA-C-N	6.39	126.36	120.03
1	cb	245	ASN	C-N-CA	6.39	126.36	120.03
1	gm	336	ASP	CA-C-N	6.39	126.08	119.56
1	gm	336	ASP	C-N-CA	6.39	126.08	119.56
2	ho	268	THR	N-CA-C	6.39	121.09	113.16
1	ar	245	ASN	CA-C-N	6.39	126.36	120.03
1	ar	245	ASN	C-N-CA	6.39	126.36	120.03
1	bt	336	ASP	CA-C-N	6.39	126.08	119.56
1	bt	336	ASP	C-N-CA	6.39	126.08	119.56
1	em	184	GLU	N-CA-C	-6.39	100.74	109.95
1	fk	103	ILE	CA-C-N	6.39	126.36	120.03
1	fk	103	ILE	C-N-CA	6.39	126.36	120.03
1	ga	328	LYS	N-CA-C	6.39	120.39	112.59
1	gd	193	SER	N-CA-C	-6.39	106.11	114.04
1	bu	463	ASP	CA-C-N	6.39	126.08	119.56
1	bu	463	ASP	C-N-CA	6.39	126.08	119.56
1	ew	121	THR	N-CA-C	6.39	120.06	111.24
3	lh	38	VAL	N-CA-C	6.39	117.32	108.12
1	bq	119	SER	N-CA-C	-6.39	102.47	108.22
1	co	121	THR	N-CA-C	6.39	120.21	111.39
1	en	336	ASP	CA-C-N	6.39	126.08	119.56
1	en	336	ASP	C-N-CA	6.39	126.08	119.56
1	gj	403	GLY	N-CA-C	6.39	121.77	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lb	5	ARG	N-CA-C	-6.39	106.70	114.75
1	bt	93	PRO	N-CA-CB	-6.39	98.57	102.79
1	fz	287	ASP	N-CA-C	-6.39	104.44	112.93
1	gf	293	ILE	N-CA-C	-6.39	104.81	111.58
1	be	88	VAL	N-CA-C	6.39	117.07	107.75
1	cp	245	ASN	CA-C-N	6.38	126.35	120.03
1	cp	245	ASN	C-N-CA	6.38	126.35	120.03
1	cq	115	GLN	CA-C-N	6.38	126.35	120.03
1	cq	115	GLN	C-N-CA	6.38	126.35	120.03
1	ex	256	LYS	N-CA-C	6.38	118.78	109.07
3	mi	38	VAL	N-CA-C	6.38	116.78	108.35
1	es	245	ASN	CA-C-N	6.38	126.56	120.31
1	es	245	ASN	C-N-CA	6.38	126.56	120.31
1	fu	186	GLY	N-CA-C	6.38	122.89	111.02
1	hd	491	ALA	CA-C-N	6.38	126.56	120.31
1	hd	491	ALA	C-N-CA	6.38	126.56	120.31
3	jr	38	VAL	N-CA-C	6.38	117.22	107.77
2	hn	353	ASP	CA-C-N	6.38	126.07	119.56
2	hn	353	ASP	C-N-CA	6.38	126.07	119.56
1	cb	324	THR	N-CA-C	-6.38	101.75	109.72
1	cf	463	ASP	CA-C-N	6.38	127.81	119.84
1	cf	463	ASP	C-N-CA	6.38	127.81	119.84
1	db	484	PHE	CA-CB-CG	6.38	120.18	113.80
1	fm	71	ASP	CA-CB-CG	6.38	118.98	112.60
1	dd	145	HIS	CA-C-N	6.38	126.87	119.47
1	dd	145	HIS	C-N-CA	6.38	126.87	119.47
1	fh	103	ILE	CA-C-N	6.38	126.35	119.78
1	fh	103	ILE	C-N-CA	6.38	126.35	119.78
1	gs	336	ASP	CA-C-N	6.38	126.06	119.56
1	gs	336	ASP	C-N-CA	6.38	126.06	119.56
1	ff	403	GLY	N-CA-C	6.38	121.48	114.40
1	cw	406	THR	N-CA-C	-6.37	105.26	114.12
1	ea	115	GLN	CA-C-N	6.37	126.34	119.78
1	ea	115	GLN	C-N-CA	6.37	126.34	119.78
1	aj	121	THR	CB-CA-C	-6.37	102.28	112.09
1	az	440	GLY	CA-C-N	6.37	126.00	119.56
1	az	440	GLY	C-N-CA	6.37	126.00	119.56
1	co	145	HIS	CA-C-N	6.37	126.06	119.56
1	co	145	HIS	C-N-CA	6.37	126.06	119.56
1	eq	103	ILE	CA-C-N	6.37	126.29	119.85
1	eq	103	ILE	C-N-CA	6.37	126.29	119.85
1	fa	245	ASN	CA-C-N	6.37	126.34	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fa	245	ASN	C-N-CA	6.37	126.34	120.03
1	fd	103	ILE	CA-C-N	6.37	126.34	120.03
1	fd	103	ILE	C-N-CA	6.37	126.34	120.03
3	jw	37	ASP	CA-CB-CG	6.37	118.97	112.60
3	hw	67	GLU	N-CA-C	-6.37	104.42	111.36
1	cu	324	THR	N-CA-C	-6.37	98.52	109.15
1	be	336	ASP	CA-C-N	6.37	126.86	119.47
1	be	336	ASP	C-N-CA	6.37	126.86	119.47
1	eb	103	ILE	CA-C-N	6.37	126.28	119.85
1	eb	103	ILE	C-N-CA	6.37	126.28	119.85
1	es	483	PRO	N-CA-C	-6.37	101.09	111.21
3	ms	67	GLU	N-CA-C	-6.36	104.42	111.36
1	ag	224	ILE	N-CA-C	6.36	116.66	107.88
1	bm	93	PRO	N-CA-CB	-6.36	98.59	102.79
1	ce	115	GLN	CA-C-N	6.36	126.33	120.03
1	ce	115	GLN	C-N-CA	6.36	126.33	120.03
1	cm	71	ASP	CA-CB-CG	6.36	118.96	112.60
1	cm	468	GLN	CA-C-N	6.36	126.27	119.85
1	cm	468	GLN	C-N-CA	6.36	126.27	119.85
1	dy	121	THR	CB-CA-C	-6.36	102.08	112.06
1	ec	491	ALA	CA-C-N	6.36	126.88	120.14
1	ec	491	ALA	C-N-CA	6.36	126.88	120.14
3	nj	44	ALA	N-CA-C	6.36	121.05	113.16
1	cd	93	PRO	N-CA-CB	-6.36	98.59	102.79
1	fn	440	GLY	CA-C-N	6.36	126.05	119.56
1	fn	440	GLY	C-N-CA	6.36	126.05	119.56
1	bw	484	PHE	CA-CB-CG	6.36	120.16	113.80
1	gw	344	ARG	N-CA-C	-6.36	99.38	109.23
3	ke	44	ALA	N-CA-C	6.36	120.74	112.92
1	do	336	ASP	CA-C-N	6.36	126.04	119.56
1	do	336	ASP	C-N-CA	6.36	126.04	119.56
1	gg	432	ASP	CA-CB-CG	-6.35	106.25	112.60
1	cc	336	ASP	CA-C-N	6.35	126.04	119.56
1	cc	336	ASP	C-N-CA	6.35	126.04	119.56
1	cd	121	THR	N-CA-C	6.35	120.01	111.24
1	ga	121	THR	N-CA-C	6.35	120.13	111.17
3	ia	37	ASP	CA-CB-CG	6.35	118.95	112.60
1	ar	119	SER	N-CA-C	-6.35	102.51	108.22
1	ew	121	THR	CB-CA-C	-6.35	102.31	112.09
1	gb	103	ILE	CA-C-N	6.35	126.37	119.89
1	gb	103	ILE	C-N-CA	6.35	126.37	119.89
3	og	44	ALA	N-CA-C	6.35	121.03	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fo	119	SER	N-CA-C	-6.35	102.51	108.22
1	hb	336	ASP	CA-C-N	6.35	126.03	119.56
1	hb	336	ASP	C-N-CA	6.35	126.03	119.56
1	du	88	VAL	N-CA-C	6.35	117.00	107.80
1	dd	336	ASP	CA-C-N	6.34	126.03	119.56
1	dd	336	ASP	C-N-CA	6.34	126.03	119.56
1	gj	95	VAL	CA-C-N	6.34	128.78	120.28
1	gj	95	VAL	C-N-CA	6.34	128.78	120.28
1	gq	468	GLN	CA-C-N	6.34	126.25	119.85
1	gq	468	GLN	C-N-CA	6.34	126.25	119.85
1	ar	121	THR	CB-CA-C	-6.34	102.33	112.09
1	dp	115	GLN	CA-C-N	6.34	126.30	120.03
1	dp	115	GLN	C-N-CA	6.34	126.30	120.03
1	ef	121	THR	N-CA-C	6.34	120.13	111.39
1	ed	265	GLN	N-CA-C	6.33	118.81	108.55
3	ku	46	TYR	N-CA-C	6.33	118.58	109.14
1	ad	440	GLY	CA-C-N	6.33	125.96	119.56
1	ad	440	GLY	C-N-CA	6.33	125.96	119.56
1	bp	491	ALA	CA-C-N	6.33	127.76	120.98
1	bp	491	ALA	C-N-CA	6.33	127.76	120.98
1	bq	503	ILE	N-CA-C	6.33	116.50	110.42
1	cq	336	ASP	CA-C-N	6.33	126.02	119.56
1	cq	336	ASP	C-N-CA	6.33	126.02	119.56
1	cx	232	ILE	N-CA-C	-6.33	105.65	111.67
1	fm	484	PHE	CA-CB-CG	6.33	120.13	113.80
1	fw	336	ASP	CA-C-N	6.33	126.82	119.47
1	fw	336	ASP	C-N-CA	6.33	126.82	119.47
1	fz	328	LYS	N-CA-C	6.33	120.71	112.92
1	gz	483	PRO	N-CA-C	-6.33	101.26	111.14
3	jo	46	TYR	N-CA-C	6.33	118.58	109.14
1	ah	328	LYS	N-CA-C	6.33	120.71	112.92
1	an	96	MET	N-CA-C	-6.33	104.61	112.90
1	bw	406	THR	N-CA-C	-6.33	105.21	114.39
3	oe	72	ASN	CA-CB-CG	6.33	118.93	112.60
1	fk	198	ILE	N-CA-C	6.33	115.84	106.85
1	hd	440	GLY	CA-C-N	6.33	125.95	119.56
1	hd	440	GLY	C-N-CA	6.33	125.95	119.56
3	iw	72	ASN	CA-CB-CG	6.33	118.93	112.60
1	ao	468	GLN	CA-C-N	6.33	126.24	119.85
1	ao	468	GLN	C-N-CA	6.33	126.24	119.85
1	cw	440	GLY	CA-C-N	6.33	125.95	119.56
1	cw	440	GLY	C-N-CA	6.33	125.95	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fx	186	GLY	N-CA-C	6.33	121.03	112.17
1	by	93	PRO	N-CA-CB	-6.33	98.61	102.79
1	ex	481	ILE	N-CA-C	6.33	117.24	108.89
1	ak	336	ASP	CA-C-N	6.33	126.81	119.47
1	ak	336	ASP	C-N-CA	6.33	126.81	119.47
1	ap	256	LYS	N-CA-C	6.33	118.69	109.07
1	aw	328	LYS	N-CA-C	6.33	121.04	112.88
1	ba	134	ASP	CA-C-N	6.33	126.01	119.56
1	ba	134	ASP	C-N-CA	6.33	126.01	119.56
1	be	121	THR	CB-CA-C	-6.33	102.35	112.09
1	bw	103	ILE	CA-C-N	6.33	126.30	119.78
1	bw	103	ILE	C-N-CA	6.33	126.30	119.78
1	fq	491	ALA	CA-C-N	6.33	126.84	120.14
1	fq	491	ALA	C-N-CA	6.33	126.84	120.14
1	bs	245	ASN	CA-C-N	6.32	126.29	120.03
1	bs	245	ASN	C-N-CA	6.32	126.29	120.03
1	fm	490	GLN	N-CA-C	-6.32	104.26	112.23
1	ei	463	ASP	CA-C-N	6.32	127.74	119.84
1	ei	463	ASP	C-N-CA	6.32	127.74	119.84
1	fa	121	THR	N-CA-C	6.32	119.96	111.24
1	at	245	ASN	CA-C-N	6.32	126.29	120.03
1	at	245	ASN	C-N-CA	6.32	126.29	120.03
1	bn	103	ILE	CA-C-N	6.32	126.29	120.03
1	bn	103	ILE	C-N-CA	6.32	126.29	120.03
1	ct	121	THR	N-CA-C	6.32	119.96	111.24
1	gb	468	GLN	CA-C-N	6.32	126.23	119.85
1	gb	468	GLN	C-N-CA	6.32	126.23	119.85
1	aw	468	GLN	CA-C-N	6.32	126.23	119.85
1	aw	468	GLN	C-N-CA	6.32	126.23	119.85
1	bi	134	ASP	CA-C-N	6.32	125.94	119.56
1	bi	134	ASP	C-N-CA	6.32	125.94	119.56
1	by	487	SER	CA-C-N	6.32	129.38	120.28
1	by	487	SER	C-N-CA	6.32	129.38	120.28
1	ha	245	ASN	CA-C-N	6.32	126.28	120.03
1	ha	245	ASN	C-N-CA	6.32	126.28	120.03
2	hh	21	ARG	CA-C-N	6.32	126.28	120.03
2	hh	21	ARG	C-N-CA	6.32	126.28	120.03
2	hl	302	ALA	CA-C-N	6.32	128.65	120.44
2	hl	302	ALA	C-N-CA	6.32	128.65	120.44
1	gh	491	ALA	CA-C-N	6.31	126.83	120.14
1	gh	491	ALA	C-N-CA	6.31	126.83	120.14
1	dk	245	ASN	CA-C-N	6.31	126.28	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dk	245	ASN	C-N-CA	6.31	126.28	120.03
1	ep	406	THR	N-CA-C	-6.31	105.35	114.12
1	gr	440	GLY	CA-C-N	6.31	125.93	119.56
1	gr	440	GLY	C-N-CA	6.31	125.93	119.56
1	ah	184	GLU	N-CA-C	-6.31	100.87	109.95
1	ah	324	THR	N-CA-C	-6.31	100.23	109.50
1	am	103	ILE	CA-C-N	6.31	126.27	120.03
1	am	103	ILE	C-N-CA	6.31	126.27	120.03
1	dq	245	ASN	CA-C-N	6.31	126.22	119.85
1	dq	245	ASN	C-N-CA	6.31	126.22	119.85
1	gc	468	GLN	CA-C-N	6.31	126.22	119.85
1	gc	468	GLN	C-N-CA	6.31	126.22	119.85
2	hf	21	ARG	CA-C-N	6.31	126.27	120.03
2	hf	21	ARG	C-N-CA	6.31	126.27	120.03
1	dx	245	ASN	CA-C-N	6.30	126.22	119.85
1	dx	245	ASN	C-N-CA	6.30	126.22	119.85
1	eb	484	PHE	N-CA-C	-6.30	102.86	111.56
1	ee	293	ILE	N-CA-C	-6.30	105.59	111.45
1	en	93	PRO	N-CA-CB	-6.30	98.63	102.79
1	dg	328	LYS	N-CA-C	6.30	121.01	112.88
1	fx	103	ILE	CA-C-N	6.30	126.27	120.03
1	fx	103	ILE	C-N-CA	6.30	126.27	120.03
3	nt	46	TYR	N-CA-C	6.30	118.53	109.14
1	bl	103	ILE	CA-C-N	6.30	126.27	120.03
1	bl	103	ILE	C-N-CA	6.30	126.27	120.03
1	eh	468	GLN	CA-C-N	6.30	126.27	120.03
1	eh	468	GLN	C-N-CA	6.30	126.27	120.03
1	fm	115	GLN	CA-C-N	6.30	126.27	120.03
1	fm	115	GLN	C-N-CA	6.30	126.27	120.03
1	af	222	VAL	N-CA-C	6.30	118.81	108.99
1	di	115	GLN	CA-C-N	6.30	126.21	119.85
1	di	115	GLN	C-N-CA	6.30	126.21	119.85
1	gj	196	VAL	N-CA-C	6.30	117.19	108.12
1	co	103	ILE	CA-C-N	6.29	126.26	119.78
1	co	103	ILE	C-N-CA	6.29	126.26	119.78
1	ed	468	GLN	CA-C-N	6.29	126.21	119.85
1	ed	468	GLN	C-N-CA	6.29	126.21	119.85
1	ga	103	ILE	CA-C-N	6.29	126.31	119.89
1	ga	103	ILE	C-N-CA	6.29	126.31	119.89
3	im	46	TYR	N-CA-C	6.29	118.52	109.14
3	is	46	TYR	N-CA-C	6.29	118.52	109.14
1	ca	484	PHE	CA-CB-CG	6.29	120.09	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cn	256	LYS	N-CA-C	6.29	118.33	108.96
1	fx	256	LYS	N-CA-C	6.29	118.98	109.23
1	fv	121	THR	N-CA-C	6.29	119.92	111.24
1	fx	336	ASP	CA-C-N	6.29	125.98	119.56
1	fx	336	ASP	C-N-CA	6.29	125.98	119.56
1	ax	92	GLY	CA-C-N	6.29	125.98	119.82
1	ax	92	GLY	C-N-CA	6.29	125.98	119.82
1	fe	245	ASN	CA-C-N	6.29	126.20	119.85
1	fe	245	ASN	C-N-CA	6.29	126.20	119.85
3	it	46	TYR	N-CA-C	6.29	118.11	109.18
1	bp	103	ILE	CA-C-N	6.29	126.20	119.85
1	bp	103	ILE	C-N-CA	6.29	126.20	119.85
1	ff	151	ASP	CA-CB-CG	6.29	118.89	112.60
1	ai	245	ASN	CA-C-N	6.29	126.25	120.03
1	ai	245	ASN	C-N-CA	6.29	126.25	120.03
1	an	468	GLN	CA-C-N	6.29	126.20	119.85
1	an	468	GLN	C-N-CA	6.29	126.20	119.85
1	fg	121	THR	N-CA-C	6.29	120.06	111.39
1	fz	258	VAL	N-CA-C	6.29	116.91	108.11
1	al	68	ILE	CA-C-N	6.28	126.79	119.94
1	al	68	ILE	C-N-CA	6.28	126.79	119.94
1	bv	336	ASP	CA-C-N	6.28	125.97	119.56
1	bv	336	ASP	C-N-CA	6.28	125.97	119.56
1	hb	463	ASP	CA-C-N	6.28	127.69	119.84
1	hb	463	ASP	C-N-CA	6.28	127.69	119.84
2	hm	370	GLN	CA-C-N	6.28	126.25	120.03
2	hm	370	GLN	C-N-CA	6.28	126.25	120.03
1	cb	440	GLY	CA-C-N	6.28	125.97	119.56
1	cb	440	GLY	C-N-CA	6.28	125.97	119.56
1	ao	491	ALA	CA-C-N	6.28	126.46	120.31
1	ao	491	ALA	C-N-CA	6.28	126.46	120.31
1	cs	115	GLN	CA-C-N	6.28	126.25	120.03
1	cs	115	GLN	C-N-CA	6.28	126.25	120.03
3	mg	37	ASP	CA-CB-CG	6.28	118.88	112.60
1	bp	440	GLY	CA-C-N	6.28	125.90	119.56
1	bp	440	GLY	C-N-CA	6.28	125.90	119.56
1	bi	336	ASP	CA-C-N	6.28	126.75	119.47
1	bi	336	ASP	C-N-CA	6.28	126.75	119.47
1	gt	103	ILE	CA-C-N	6.28	126.19	119.85
1	gt	103	ILE	C-N-CA	6.28	126.19	119.85
3	nu	72	ASN	CA-CB-CG	6.28	118.88	112.60
1	da	468	GLN	CA-C-N	6.28	126.19	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	da	468	GLN	C-N-CA	6.28	126.19	119.85
1	dk	92	GLY	CA-C-N	6.28	127.68	119.84
1	dk	92	GLY	C-N-CA	6.28	127.68	119.84
1	dt	121	THR	N-CA-C	6.28	119.90	111.24
1	dz	463	ASP	CA-C-N	6.28	125.96	119.56
1	dz	463	ASP	C-N-CA	6.28	125.96	119.56
2	hi	36	TYR	N-CA-C	-6.28	107.47	114.62
1	ad	88	VAL	N-CA-C	6.27	116.91	107.75
1	bt	86	GLY	CA-C-N	6.27	128.69	120.28
1	bt	86	GLY	C-N-CA	6.27	128.69	120.28
1	gi	336	ASP	CA-C-N	6.27	125.96	119.56
1	gi	336	ASP	C-N-CA	6.27	125.96	119.56
1	gl	184	GLU	CA-C-N	6.27	131.31	122.46
1	gl	184	GLU	C-N-CA	6.27	131.31	122.46
2	hm	353	ASP	CA-C-N	6.27	127.68	119.84
2	hm	353	ASP	C-N-CA	6.27	127.68	119.84
2	ho	370	GLN	CA-C-N	6.27	126.24	120.03
2	ho	370	GLN	C-N-CA	6.27	126.24	120.03
1	ac	232	ILE	N-CA-C	-6.27	105.62	111.45
1	as	358	ASP	CA-CB-CG	6.27	118.87	112.60
1	bh	68	ILE	CA-C-N	6.27	126.90	119.94
1	bh	68	ILE	C-N-CA	6.27	126.90	119.94
1	bl	110	ASP	CA-CB-CG	6.27	118.87	112.60
1	ci	336	ASP	CA-C-N	6.27	125.95	119.56
1	ci	336	ASP	C-N-CA	6.27	125.95	119.56
1	en	186	GLY	N-CA-C	6.27	119.09	110.56
3	ll	67	GLU	N-CA-C	-6.27	104.53	111.36
1	eb	245	ASN	CA-C-N	6.27	126.23	120.03
1	eb	245	ASN	C-N-CA	6.27	126.23	120.03
1	fq	468	GLN	CA-C-N	6.27	126.18	119.85
1	fq	468	GLN	C-N-CA	6.27	126.18	119.85
3	kc	32	PHE	CA-C-N	6.27	125.95	119.56
3	kc	32	PHE	C-N-CA	6.27	125.95	119.56
1	dr	115	GLN	CA-C-N	6.27	126.23	120.03
1	dr	115	GLN	C-N-CA	6.27	126.23	120.03
1	at	121	THR	N-CA-C	6.26	119.88	111.24
1	bb	103	ILE	CA-C-N	6.26	126.23	120.03
1	bb	103	ILE	C-N-CA	6.26	126.23	120.03
3	np	41	ILE	N-CA-C	6.26	115.75	106.85
1	ee	245	ASN	CA-C-N	6.26	126.23	120.03
1	ee	245	ASN	C-N-CA	6.26	126.23	120.03
1	en	193	SER	N-CA-C	-6.26	106.27	114.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bj	103	ILE	CA-C-N	6.26	126.17	119.85
1	bj	103	ILE	C-N-CA	6.26	126.17	119.85
1	en	328	LYS	N-CA-C	6.26	120.23	112.59
1	gg	468	GLN	CA-C-N	6.26	126.17	119.85
1	gg	468	GLN	C-N-CA	6.26	126.17	119.85
3	ll	46	TYR	N-CA-C	6.26	118.07	109.18
1	an	324	THR	N-CA-C	-6.26	100.30	109.50
1	dk	417	LEU	CB-CA-C	-6.26	101.16	110.67
1	bd	92	GLY	CA-C-N	6.26	125.95	119.82
1	bd	92	GLY	C-N-CA	6.26	125.95	119.82
1	ej	324	THR	N-CA-C	-6.26	100.55	109.62
1	ex	103	ILE	CA-C-N	6.26	126.17	119.85
1	ex	103	ILE	C-N-CA	6.26	126.17	119.85
1	ed	245	ASN	CA-C-N	6.25	126.22	120.03
1	ed	245	ASN	C-N-CA	6.25	126.22	120.03
1	be	245	ASN	CA-C-N	6.25	126.22	120.03
1	be	245	ASN	C-N-CA	6.25	126.22	120.03
1	bi	245	ASN	CA-C-N	6.25	126.22	120.03
1	bi	245	ASN	C-N-CA	6.25	126.22	120.03
1	dg	468	GLN	CA-C-N	6.25	126.17	119.85
1	dg	468	GLN	C-N-CA	6.25	126.17	119.85
1	fk	468	GLN	CA-C-N	6.25	126.17	119.85
1	fk	468	GLN	C-N-CA	6.25	126.17	119.85
1	gn	71	ASP	CA-CB-CG	6.25	118.85	112.60
1	aj	121	THR	N-CA-C	6.25	119.87	111.24
1	ce	93	PRO	N-CA-CB	-6.25	98.66	102.79
1	ct	253	ARG	N-CA-C	6.25	120.99	112.68
1	du	103	ILE	CA-C-N	6.25	126.16	119.85
1	du	103	ILE	C-N-CA	6.25	126.16	119.85
1	eo	336	ASP	CA-C-N	6.25	125.94	119.56
1	eo	336	ASP	C-N-CA	6.25	125.94	119.56
2	ho	208	ASP	CA-CB-CG	6.25	118.85	112.60
3	nd	32	PHE	CA-C-N	6.25	125.94	119.56
3	nd	32	PHE	C-N-CA	6.25	125.94	119.56
1	an	238	GLY	N-CA-C	6.25	123.67	115.36
1	ea	336	ASP	CA-C-N	6.25	125.93	119.56
1	ea	336	ASP	C-N-CA	6.25	125.93	119.56
1	fs	245	ASN	CA-C-N	6.25	126.21	120.03
1	fs	245	ASN	C-N-CA	6.25	126.21	120.03
2	hf	268	THR	N-CA-C	6.25	120.52	113.02
3	ik	32	PHE	CA-C-N	6.25	125.93	119.56
3	ik	32	PHE	C-N-CA	6.25	125.93	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bn	121	THR	N-CA-C	6.25	119.86	111.24
1	fz	245	ASN	CA-C-N	6.25	126.21	120.03
1	fz	245	ASN	C-N-CA	6.25	126.21	120.03
1	ei	328	LYS	N-CA-C	6.24	121.04	113.17
1	as	336	ASP	CA-C-N	6.24	126.71	119.47
1	as	336	ASP	C-N-CA	6.24	126.71	119.47
1	dh	468	GLN	CA-C-N	6.24	126.15	119.85
1	dh	468	GLN	C-N-CA	6.24	126.15	119.85
1	fu	483	PRO	N-CA-C	-6.24	101.28	111.21
3	kk	10	ILE	N-CA-C	6.24	116.85	108.11
1	bb	336	ASP	CA-C-N	6.24	126.71	119.47
1	bb	336	ASP	C-N-CA	6.24	126.71	119.47
1	cj	121	THR	CB-CA-C	-6.24	103.03	111.89
1	dp	149	GLY	CA-C-N	6.24	126.21	120.03
1	dp	149	GLY	C-N-CA	6.24	126.21	120.03
1	eb	336	ASP	CA-C-N	6.24	126.71	119.47
1	eb	336	ASP	C-N-CA	6.24	126.71	119.47
1	eu	93	PRO	N-CA-CB	-6.24	98.67	102.79
1	gs	72	HIS	N-CA-C	-6.24	100.69	110.36
1	bh	232	ILE	N-CA-C	-6.24	105.74	111.67
1	eh	103	ILE	CA-C-N	6.24	126.21	119.78
1	eh	103	ILE	C-N-CA	6.24	126.21	119.78
1	gv	253	ARG	N-CA-C	6.24	121.23	112.93
1	hc	403	GLY	N-CA-C	6.24	121.41	113.24
1	av	103	ILE	CA-C-N	6.24	126.20	120.03
1	av	103	ILE	C-N-CA	6.24	126.20	120.03
1	ds	88	VAL	N-CA-C	6.24	116.85	107.75
3	mb	46	TYR	N-CA-C	6.24	118.43	109.14
1	hd	245	ASN	CA-C-N	6.23	126.20	120.03
1	hd	245	ASN	C-N-CA	6.23	126.20	120.03
1	at	256	LYS	N-CA-C	6.23	118.25	108.96
1	aw	483	PRO	N-CA-C	-6.23	101.42	111.14
1	cr	93	PRO	N-CA-CB	-6.23	98.68	102.79
1	dr	336	ASP	CA-C-N	6.23	125.92	119.56
1	dr	336	ASP	C-N-CA	6.23	125.92	119.56
1	fn	481	ILE	N-CA-C	6.23	117.11	108.89
1	cu	440	GLY	CA-C-N	6.23	125.85	119.56
1	cu	440	GLY	C-N-CA	6.23	125.85	119.56
1	es	121	THR	N-CA-C	6.23	119.84	111.24
1	fi	245	ASN	CA-C-N	6.23	126.20	120.03
1	fi	245	ASN	C-N-CA	6.23	126.20	120.03
1	ge	440	GLY	CA-C-N	6.23	125.85	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ge	440	GLY	C-N-CA	6.23	125.85	119.56
3	nt	44	ALA	N-CA-C	6.23	120.89	113.16
3	od	38	VAL	N-CA-C	6.23	116.99	107.77
1	ec	245	ASN	CA-C-N	6.23	126.19	120.03
1	ec	245	ASN	C-N-CA	6.23	126.19	120.03
1	fv	484	PHE	CA-CB-CG	6.23	120.03	113.80
2	hg	230	ILE	N-CA-C	6.23	119.18	113.20
3	lg	46	TYR	N-CA-C	6.23	117.64	108.86
3	nf	37	ASP	CA-CB-CG	6.23	118.83	112.60
1	bb	483	PRO	N-CA-C	-6.23	101.43	111.14
1	eg	78	ASN	CA-CB-CG	6.23	118.83	112.60
1	bu	88	VAL	N-CA-C	6.22	116.83	107.80
1	ci	406	THR	N-CA-C	-6.22	105.36	114.39
1	cp	336	ASP	CA-C-N	6.22	125.91	119.56
1	cp	336	ASP	C-N-CA	6.22	125.91	119.56
1	dz	287	ASP	N-CA-C	-6.22	104.66	112.93
1	fm	468	GLN	CA-C-N	6.22	126.14	119.85
1	fm	468	GLN	C-N-CA	6.22	126.14	119.85
3	oc	44	ALA	N-CA-C	6.22	120.88	113.16
1	cm	245	ASN	CA-C-N	6.22	126.19	120.03
1	cm	245	ASN	C-N-CA	6.22	126.19	120.03
3	nu	44	ALA	N-CA-C	6.22	120.73	113.20
1	ay	182	PHE	CA-CB-CG	6.22	120.02	113.80
1	ek	115	GLN	CA-C-N	6.22	126.19	120.03
1	ek	115	GLN	C-N-CA	6.22	126.19	120.03
1	fg	121	THR	CB-CA-C	-6.22	103.06	111.89
1	hb	151	ASP	CA-CB-CG	6.22	118.82	112.60
3	na	38	VAL	N-CA-C	6.22	117.25	108.17
1	fi	403	GLY	N-CA-C	6.22	121.39	113.24
1	gl	336	ASP	CA-C-N	6.22	125.90	119.56
1	gl	336	ASP	C-N-CA	6.22	125.90	119.56
1	cw	336	ASP	CA-C-N	6.22	125.90	119.56
1	cw	336	ASP	C-N-CA	6.22	125.90	119.56
1	dc	403	GLY	N-CA-C	6.22	121.38	113.24
1	di	88	VAL	N-CA-C	6.22	116.83	107.75
1	gh	336	ASP	CA-C-N	6.22	125.90	119.56
1	gh	336	ASP	C-N-CA	6.22	125.90	119.56
1	bw	324	THR	N-CA-C	-6.21	101.82	109.65
1	ek	324	THR	N-CA-C	-6.21	99.95	109.64
1	dk	182	PHE	CA-CB-CG	6.21	120.01	113.80
1	en	121	THR	CB-CA-C	-6.21	102.53	112.09
3	nf	46	TYR	N-CA-C	6.21	118.39	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dn	463	ASP	CA-C-N	6.21	127.60	119.84
1	dn	463	ASP	C-N-CA	6.21	127.60	119.84
3	il	46	TYR	N-CA-C	6.21	118.39	109.14
1	ai	328	LYS	N-CA-C	6.21	120.56	112.92
1	cl	209	ASP	CA-CB-CG	6.21	118.81	112.60
1	er	145	HIS	CA-C-N	6.21	126.67	119.47
1	er	145	HIS	C-N-CA	6.21	126.67	119.47
2	ho	353	ASP	CA-C-N	6.21	127.60	119.84
2	ho	353	ASP	C-N-CA	6.21	127.60	119.84
1	bm	468	GLN	CA-C-N	6.21	126.12	119.85
1	bm	468	GLN	C-N-CA	6.21	126.12	119.85
1	do	103	ILE	CA-C-N	6.21	126.56	119.92
1	do	103	ILE	C-N-CA	6.21	126.56	119.92
1	du	121	THR	N-CA-C	6.21	119.81	111.24
1	fl	403	GLY	N-CA-C	6.21	121.37	113.24
1	fo	149	GLY	CA-C-N	6.21	126.39	120.31
1	fo	149	GLY	C-N-CA	6.21	126.39	120.31
2	ho	343	ALA	CA-C-N	6.21	126.12	119.85
2	ho	343	ALA	C-N-CA	6.21	126.12	119.85
3	ht	46	TYR	N-CA-C	6.21	118.39	109.14
2	ho	303	TYR	N-CA-C	-6.20	104.43	111.07
1	aa	88	VAL	N-CA-C	6.20	116.80	107.75
1	cs	103	ILE	CA-C-N	6.20	126.17	120.03
1	cs	103	ILE	C-N-CA	6.20	126.17	120.03
1	fw	103	ILE	CA-C-N	6.20	126.17	120.03
1	fw	103	ILE	C-N-CA	6.20	126.17	120.03
1	fx	468	GLN	CA-C-N	6.20	126.11	119.85
1	fx	468	GLN	C-N-CA	6.20	126.11	119.85
1	fe	121	THR	N-CA-C	6.20	119.79	111.24
1	hd	336	ASP	CA-C-N	6.20	125.88	119.56
1	hd	336	ASP	C-N-CA	6.20	125.88	119.56
1	ac	184	GLU	N-CA-C	-6.20	101.03	109.95
1	ha	115	GLN	CA-C-N	6.20	126.11	119.85
1	ha	115	GLN	C-N-CA	6.20	126.11	119.85
3	im	38	VAL	N-CA-C	6.20	117.22	108.17
1	ar	145	HIS	CA-C-N	6.19	126.66	119.47
1	ar	145	HIS	C-N-CA	6.19	126.66	119.47
1	du	182	PHE	CA-CB-CG	6.19	119.99	113.80
1	gt	196	VAL	N-CA-C	6.19	117.21	108.17
2	hi	327	VAL	N-CA-C	6.19	117.69	108.46
1	aq	484	PHE	CA-CB-CG	6.19	119.99	113.80
1	fe	209	ASP	CA-CB-CG	6.19	118.79	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fr	103	ILE	CA-C-N	6.19	126.16	119.78
1	fr	103	ILE	C-N-CA	6.19	126.16	119.78
1	bh	115	GLN	CA-C-N	6.19	126.16	120.03
1	bh	115	GLN	C-N-CA	6.19	126.16	120.03
1	eq	198	ILE	N-CA-C	6.19	112.83	106.21
1	cp	483	PRO	N-CA-C	-6.19	101.37	111.21
1	dr	121	THR	N-CA-C	6.19	119.78	111.24
1	ab	468	GLN	CA-C-N	6.19	126.10	119.85
1	ab	468	GLN	C-N-CA	6.19	126.10	119.85
1	fx	245	ASN	CA-C-N	6.19	126.16	120.03
1	fx	245	ASN	C-N-CA	6.19	126.16	120.03
3	jk	72	ASN	CA-CB-CG	6.19	118.79	112.60
1	fi	446	ALA	N-CA-C	6.19	118.10	111.36
2	hf	172	SER	N-CA-C	6.19	119.62	109.85
1	ci	270	TYR	N-CA-C	6.18	118.90	110.55
1	fe	186	GLY	N-CA-C	6.18	122.52	111.02
1	aj	336	ASP	CA-C-N	6.18	126.64	119.47
1	aj	336	ASP	C-N-CA	6.18	126.64	119.47
1	cs	483	PRO	N-CA-C	-6.18	101.49	111.14
1	db	281	VAL	N-CA-C	6.18	117.20	111.45
1	fa	336	ASP	CA-C-N	6.18	126.64	119.47
1	fa	336	ASP	C-N-CA	6.18	126.64	119.47
1	go	403	GLY	N-CA-C	6.18	121.34	113.24
1	gp	253	ARG	N-CA-C	6.18	121.15	112.93
3	hs	32	PHE	CA-C-N	6.18	125.87	119.56
3	hs	32	PHE	C-N-CA	6.18	125.87	119.56
1	ag	87	ALA	CA-C-N	-6.18	115.04	123.14
1	ag	87	ALA	C-N-CA	-6.18	115.04	123.14
1	cu	484	PHE	CA-CB-CG	6.18	119.98	113.80
1	ew	440	GLY	CA-C-N	6.18	125.80	119.56
1	ew	440	GLY	C-N-CA	6.18	125.80	119.56
1	fu	72	HIS	N-CA-C	-6.18	100.84	110.42
1	gi	121	THR	CB-CA-C	-6.18	102.57	112.09
1	eh	253	ARG	N-CA-C	6.18	120.59	112.13
1	ba	121	THR	CB-CA-C	-6.18	102.58	112.09
1	bk	103	ILE	CA-C-N	6.18	126.14	119.78
1	bk	103	ILE	C-N-CA	6.18	126.14	119.78
1	bq	336	ASP	CA-C-N	6.18	125.86	119.56
1	bq	336	ASP	C-N-CA	6.18	125.86	119.56
1	ci	285	ASP	N-CA-C	6.18	118.09	111.36
1	dn	184	GLU	N-CA-C	-6.18	101.06	109.95
3	hu	46	TYR	N-CA-C	6.18	118.34	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ff	92	GLY	CA-C-N	6.17	127.56	119.84
1	ff	92	GLY	C-N-CA	6.17	127.56	119.84
1	ga	186	GLY	N-CA-C	6.17	122.50	111.02
3	jg	38	VAL	N-CA-C	6.17	117.01	108.12
1	bu	336	ASP	CA-C-N	6.17	126.63	119.47
1	bu	336	ASP	C-N-CA	6.17	126.63	119.47
1	ga	336	ASP	CA-C-N	6.17	125.85	119.56
1	ga	336	ASP	C-N-CA	6.17	125.85	119.56
1	gn	483	PRO	N-CA-C	-6.17	101.51	111.14
1	aa	121	THR	N-CA-C	6.17	118.73	111.02
1	an	245	ASN	CA-C-N	6.17	126.14	120.03
1	an	245	ASN	C-N-CA	6.17	126.14	120.03
1	bt	258	VAL	N-CA-C	6.17	119.13	108.95
1	cn	481	ILE	CB-CA-C	-6.17	104.12	111.65
1	go	88	VAL	N-CA-C	6.17	116.76	107.75
1	gw	483	PRO	N-CA-C	-6.17	101.40	111.21
1	ar	468	GLN	CA-C-N	6.17	126.08	119.85
1	ar	468	GLN	C-N-CA	6.17	126.08	119.85
1	as	324	THR	N-CA-C	-6.17	100.02	109.64
1	ck	222	VAL	N-CA-C	6.17	119.13	108.95
1	gk	468	GLN	CA-C-N	6.17	126.08	119.85
1	gk	468	GLN	C-N-CA	6.17	126.08	119.85
3	mq	38	VAL	N-CA-C	6.17	117.17	108.17
1	cc	468	GLN	CA-C-N	6.16	126.07	119.85
1	cc	468	GLN	C-N-CA	6.16	126.07	119.85
1	ch	103	ILE	CA-C-N	6.16	126.08	119.85
1	ch	103	ILE	C-N-CA	6.16	126.08	119.85
1	ei	484	PHE	CA-CB-CG	6.16	119.96	113.80
1	ge	115	GLN	CA-C-N	6.16	126.08	119.85
1	ge	115	GLN	C-N-CA	6.16	126.08	119.85
1	gj	463	ASP	CA-C-N	6.16	125.86	119.82
1	gj	463	ASP	C-N-CA	6.16	125.86	119.82
1	gl	121	THR	N-CA-C	6.16	119.90	111.39
2	hg	172	SER	N-CA-C	6.16	119.59	109.85
1	dz	184	GLU	N-CA-C	-6.16	101.08	109.95
1	ba	484	PHE	N-CA-C	6.16	118.41	110.65
1	bq	245	ASN	CA-C-N	6.16	126.13	120.03
1	bq	245	ASN	C-N-CA	6.16	126.13	120.03
1	dc	93	PRO	N-CA-C	6.16	120.80	112.48
1	eq	403	GLY	N-CA-C	6.16	121.31	113.24
1	gi	115	GLN	CA-C-N	6.16	126.13	120.03
1	gi	115	GLN	C-N-CA	6.16	126.13	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gf	187	THR	N-CA-C	6.16	119.28	110.10
1	ae	145	HIS	CA-C-N	6.16	126.34	119.32
1	ae	145	HIS	C-N-CA	6.16	126.34	119.32
1	bt	232	ILE	N-CA-C	-6.16	105.82	111.67
1	cv	93	PRO	N-CA-CB	-6.16	98.73	102.79
1	ds	468	GLN	CA-C-N	6.16	126.07	119.85
1	ds	468	GLN	C-N-CA	6.16	126.07	119.85
1	gl	259	ILE	N-CA-C	6.16	116.73	108.11
1	ch	71	ASP	CA-CB-CG	6.15	118.75	112.60
2	hj	286	GLY	N-CA-C	-6.15	101.05	112.37
1	ai	468	GLN	CA-C-N	6.15	126.06	119.85
1	ai	468	GLN	C-N-CA	6.15	126.06	119.85
1	ap	336	ASP	CA-C-N	6.15	126.61	119.47
1	ap	336	ASP	C-N-CA	6.15	126.61	119.47
1	eg	491	ALA	CA-C-N	6.15	126.12	120.03
1	eg	491	ALA	C-N-CA	6.15	126.12	120.03
3	je	46	TYR	N-CA-C	6.15	118.31	109.14
3	ny	46	TYR	N-CA-C	6.15	118.31	109.14
1	bp	245	ASN	CA-C-N	6.15	126.12	120.03
1	bp	245	ASN	C-N-CA	6.15	126.12	120.03
2	hl	208	ASP	CA-CB-CG	6.15	118.75	112.60
3	lt	17	LEU	N-CA-C	6.15	118.06	111.36
1	fl	265	GLN	N-CA-C	6.15	118.51	108.55
1	bx	209	ASP	CA-CB-CG	6.15	118.75	112.60
1	gb	121	THR	N-CA-C	6.15	119.84	111.17
1	gg	245	ASN	CA-C-N	6.15	126.12	120.03
1	gg	245	ASN	C-N-CA	6.15	126.12	120.03
1	cu	265	GLN	N-CA-C	6.15	118.51	108.55
1	ee	468	GLN	CA-C-N	6.15	126.11	120.03
1	ee	468	GLN	C-N-CA	6.15	126.11	120.03
3	nu	38	VAL	N-CA-C	6.15	117.14	108.17
1	bz	119	SER	N-CA-C	-6.14	102.69	108.22
1	dl	287	ASP	N-CA-C	-6.14	103.30	111.96
1	fl	103	ILE	CA-C-N	6.14	126.06	119.85
1	fl	103	ILE	C-N-CA	6.14	126.06	119.85
1	go	468	GLN	CA-C-N	6.14	126.06	119.85
1	go	468	GLN	C-N-CA	6.14	126.06	119.85
3	lr	38	VAL	N-CA-C	6.14	117.14	108.17
1	al	253	ARG	N-CA-C	6.14	121.10	112.93
1	br	103	ILE	CA-C-N	6.14	126.11	120.03
1	br	103	ILE	C-N-CA	6.14	126.11	120.03
1	bw	149	GLY	CA-C-N	6.14	126.33	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bw	149	GLY	C-N-CA	6.14	126.33	120.31
1	dz	468	GLN	CA-C-N	6.14	126.05	119.85
1	dz	468	GLN	C-N-CA	6.14	126.05	119.85
1	et	463	ASP	CA-C-N	6.14	125.83	119.56
1	et	463	ASP	C-N-CA	6.14	125.83	119.56
1	ew	103	ILE	CA-C-N	6.14	126.05	119.85
1	ew	103	ILE	C-N-CA	6.14	126.05	119.85
1	gr	484	PHE	CA-CB-CG	6.14	119.94	113.80
1	gy	103	ILE	CA-C-N	6.14	126.49	119.92
1	gy	103	ILE	C-N-CA	6.14	126.49	119.92
1	bp	328	LYS	N-CA-C	6.14	120.80	112.88
1	go	121	THR	CB-CA-C	-6.14	102.63	112.09
3	nu	37	ASP	CA-CB-CG	6.14	118.74	112.60
1	ay	115	GLN	CA-C-N	6.14	126.11	120.03
1	ay	115	GLN	C-N-CA	6.14	126.11	120.03
1	bq	468	GLN	CA-C-N	6.14	126.10	119.78
1	bq	468	GLN	C-N-CA	6.14	126.10	119.78
1	cl	103	ILE	CA-C-N	6.14	126.11	120.03
1	cl	103	ILE	C-N-CA	6.14	126.11	120.03
1	fj	468	GLN	CA-C-N	6.14	126.05	119.85
1	fj	468	GLN	C-N-CA	6.14	126.05	119.85
2	hf	353	ASP	CA-C-N	6.14	127.51	119.84
2	hf	353	ASP	C-N-CA	6.14	127.51	119.84
1	ea	134	ASP	CA-C-N	6.14	125.82	119.56
1	ea	134	ASP	C-N-CA	6.14	125.82	119.56
1	ge	245	ASN	CA-C-N	6.14	126.11	120.03
1	ge	245	ASN	C-N-CA	6.14	126.11	120.03
1	dc	265	GLN	N-CA-C	6.14	118.49	108.55
1	go	463	ASP	CA-C-N	6.14	127.51	119.84
1	go	463	ASP	C-N-CA	6.14	127.51	119.84
1	gw	403	GLY	N-CA-C	6.14	121.28	113.24
1	as	468	GLN	CA-C-N	6.13	126.05	119.85
1	as	468	GLN	C-N-CA	6.13	126.05	119.85
1	eb	403	GLY	N-CA-C	6.13	121.27	113.24
1	es	134	ASP	CA-C-N	6.13	125.82	119.56
1	es	134	ASP	C-N-CA	6.13	125.82	119.56
1	au	408	THR	N-CA-C	-6.13	107.02	114.75
1	bd	74	TYR	CA-C-N	6.13	130.92	122.77
1	bd	74	TYR	C-N-CA	6.13	130.92	122.77
1	dw	245	ASN	CA-C-N	6.13	126.10	120.03
1	dw	245	ASN	C-N-CA	6.13	126.10	120.03
1	eg	287	ASP	N-CA-C	-6.13	104.87	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	el	403	GLY	N-CA-C	6.13	121.27	113.24
1	gu	468	GLN	CA-C-N	6.13	126.04	119.85
1	gu	468	GLN	C-N-CA	6.13	126.04	119.85
3	ko	49	PHE	CA-C-N	6.13	126.64	120.14
3	ko	49	PHE	C-N-CA	6.13	126.64	120.14
1	dz	87	ALA	N-CA-C	6.13	117.96	111.28
1	gi	491	ALA	CA-C-N	6.13	126.04	119.85
1	gi	491	ALA	C-N-CA	6.13	126.04	119.85
1	ca	103	ILE	CA-C-N	6.13	126.09	119.78
1	ca	103	ILE	C-N-CA	6.13	126.09	119.78
1	gi	94	ALA	CB-CA-C	-6.13	109.49	116.54
2	hf	286	GLY	N-CA-C	-6.13	101.16	112.62
2	ho	363	VAL	CB-CA-C	-6.13	106.50	111.71
1	ak	259	ILE	N-CA-C	6.13	116.68	107.80
1	bk	245	ASN	CA-C-N	6.13	126.10	120.03
1	bk	245	ASN	C-N-CA	6.13	126.10	120.03
1	do	491	ALA	CA-C-N	6.13	126.04	119.85
1	do	491	ALA	C-N-CA	6.13	126.04	119.85
1	ea	265	GLN	N-CA-C	6.13	119.23	108.75
1	fh	209	ASP	CA-CB-CG	6.13	118.73	112.60
2	hl	136	LYS	N-CA-C	-6.13	105.94	113.41
1	fk	344	ARG	CA-C-N	6.12	133.24	121.54
1	fk	344	ARG	C-N-CA	6.12	133.24	121.54
2	hf	47	GLN	CA-C-N	6.12	125.81	119.56
2	hf	47	GLN	C-N-CA	6.12	125.81	119.56
1	am	92	GLY	CA-C-N	6.12	127.49	119.84
1	am	92	GLY	C-N-CA	6.12	127.49	119.84
1	cq	324	THR	N-CA-C	-6.12	101.94	109.65
1	fo	245	ASN	CA-C-N	6.12	126.03	119.85
1	fo	245	ASN	C-N-CA	6.12	126.03	119.85
1	gc	115	GLN	CA-C-N	6.12	126.09	120.03
1	gc	115	GLN	C-N-CA	6.12	126.09	120.03
3	ll	38	VAL	N-CA-C	6.12	117.11	108.17
1	di	121	THR	N-CA-C	6.12	119.69	111.24
1	cm	115	GLN	CA-C-N	6.12	126.09	120.03
1	cm	115	GLN	C-N-CA	6.12	126.09	120.03
1	ga	271	SER	N-CA-C	6.12	119.10	110.23
1	gw	269	ALA	N-CA-C	6.12	119.86	111.54
1	ba	103	ILE	CA-C-N	6.12	126.08	119.78
1	ba	103	ILE	C-N-CA	6.12	126.08	119.78
1	ba	403	GLY	N-CA-C	6.12	121.40	113.27
1	db	232	ILE	N-CA-C	-6.12	105.76	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	kb	46	TYR	N-CA-C	6.12	117.86	109.18
1	ad	500	MET	N-CA-C	-6.11	102.35	109.93
1	bf	287	ASP	N-CA-C	-6.11	104.89	112.72
3	mw	46	TYR	N-CA-C	6.11	118.25	109.14
1	bt	245	ASN	CA-C-N	6.11	126.08	120.03
1	bt	245	ASN	C-N-CA	6.11	126.08	120.03
1	dz	245	ASN	CA-C-N	6.11	126.08	120.03
1	dz	245	ASN	C-N-CA	6.11	126.08	120.03
1	gf	285	ASP	N-CA-C	6.11	118.02	111.36
1	gf	358	ASP	CA-CB-CG	6.11	118.71	112.60
1	go	336	ASP	CA-C-N	6.11	125.79	119.56
1	go	336	ASP	C-N-CA	6.11	125.79	119.56
1	ha	324	THR	N-CA-C	-6.11	99.75	109.04
1	hb	468	GLN	CA-C-N	6.11	126.02	119.85
1	hb	468	GLN	C-N-CA	6.11	126.02	119.85
1	bl	115	GLN	CB-CA-C	-6.11	105.69	111.00
1	ar	491	ALA	CA-C-N	6.11	126.02	119.85
1	ar	491	ALA	C-N-CA	6.11	126.02	119.85
1	ap	468	GLN	CA-C-N	6.11	126.02	119.85
1	ap	468	GLN	C-N-CA	6.11	126.02	119.85
1	ck	265	GLN	N-CA-C	6.11	118.44	108.55
1	el	468	GLN	CA-C-N	6.11	126.02	119.85
1	el	468	GLN	C-N-CA	6.11	126.02	119.85
1	hb	265	GLN	N-CA-C	6.11	118.44	108.55
2	hk	327	VAL	N-CA-C	6.11	117.56	108.46
2	hk	384	ASN	CA-C-N	6.11	126.07	119.78
2	hk	384	ASN	C-N-CA	6.11	126.07	119.78
1	ev	285	ASP	N-CA-C	6.10	118.85	111.40
2	hl	47	GLN	CA-C-N	6.10	125.79	119.56
2	hl	47	GLN	C-N-CA	6.10	125.79	119.56
1	bg	245	ASN	CA-C-N	6.10	126.07	120.03
1	bg	245	ASN	C-N-CA	6.10	126.07	120.03
1	eb	483	PRO	CB-CA-C	-6.10	103.20	112.11
2	ho	153	ASP	N-CA-C	-6.10	100.47	109.62
3	kl	67	GLU	N-CA-C	-6.10	104.71	111.36
1	aa	285	ASP	N-CA-C	6.10	118.01	111.36
2	hm	295	ASP	CA-CB-CG	6.10	118.70	112.60
1	fp	258	VAL	N-CA-C	6.10	117.26	108.48
1	fs	253	ARG	N-CA-C	6.10	120.56	111.96
1	fx	185	THR	N-CA-C	6.10	119.95	111.90
1	at	463	ASP	CA-C-N	6.10	125.78	119.56
1	at	463	ASP	C-N-CA	6.10	125.78	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dh	232	ILE	N-CA-C	-6.10	105.78	111.45
1	gl	245	ASN	CA-C-N	6.10	126.07	120.03
1	gl	245	ASN	C-N-CA	6.10	126.07	120.03
1	gs	95	VAL	N-CA-C	6.10	116.86	107.78
1	gx	491	ALA	CA-C-N	6.10	126.60	120.14
1	gx	491	ALA	C-N-CA	6.10	126.60	120.14
1	cr	324	THR	N-CA-C	-6.10	99.77	109.04
1	do	121	THR	N-CA-C	6.10	119.65	111.24
1	fo	285	ASP	N-CA-C	6.10	118.00	111.36
1	ci	95	VAL	N-CA-C	6.09	116.86	107.78
1	dn	103	ILE	CA-C-N	6.09	126.06	119.78
1	dn	103	ILE	C-N-CA	6.09	126.06	119.78
1	fj	121	THR	CB-CA-C	-6.09	102.71	112.09
3	in	44	ALA	N-CA-C	6.09	120.72	113.16
1	fj	451	ALA	CA-C-N	6.09	126.03	119.76
1	fj	451	ALA	C-N-CA	6.09	126.03	119.76
3	ko	72	ASN	CA-CB-CG	6.09	118.69	112.60
1	am	463	ASP	CA-C-N	6.09	125.77	119.56
1	am	463	ASP	C-N-CA	6.09	125.77	119.56
1	br	463	ASP	CA-C-N	6.09	125.79	119.82
1	br	463	ASP	C-N-CA	6.09	125.79	119.82
1	cs	468	GLN	CA-C-N	6.09	126.00	119.85
1	cs	468	GLN	C-N-CA	6.09	126.00	119.85
2	hl	21	ARG	CA-C-N	6.09	126.06	120.03
2	hl	21	ARG	C-N-CA	6.09	126.06	120.03
3	hv	25	GLY	N-CA-C	-6.09	104.28	112.14
3	kn	38	VAL	N-CA-C	6.09	116.79	107.77
3	oc	64	GLN	N-CA-C	-6.09	106.49	114.04
1	af	468	GLN	CA-C-N	6.09	126.00	119.85
1	af	468	GLN	C-N-CA	6.09	126.00	119.85
1	cs	72	HIS	N-CA-C	-6.09	100.98	110.42
1	eo	134	ASP	CA-C-N	6.09	125.71	119.56
1	eo	134	ASP	C-N-CA	6.09	125.71	119.56
1	gh	121	THR	N-CA-C	6.09	119.64	111.24
1	gy	245	ASN	CA-C-N	6.09	126.00	119.85
1	gy	245	ASN	C-N-CA	6.09	126.00	119.85
3	le	46	TYR	N-CA-C	6.09	118.21	109.14
3	nh	46	TYR	N-CA-C	6.09	118.21	109.14
1	ev	468	GLN	CA-C-N	6.09	126.00	119.85
1	ev	468	GLN	C-N-CA	6.09	126.00	119.85
1	db	121	THR	CB-CA-C	-6.09	103.25	111.89
1	gp	88	VAL	N-CA-C	6.09	116.64	107.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bb	245	ASN	CA-C-N	6.08	126.05	120.03
1	bb	245	ASN	C-N-CA	6.08	126.05	120.03
1	ci	484	PHE	CA-CB-CG	6.08	119.89	113.80
1	cj	336	ASP	CA-C-N	6.08	126.53	119.47
1	cj	336	ASP	C-N-CA	6.08	126.53	119.47
1	ec	121	THR	CB-CA-C	-6.08	102.72	112.09
3	hv	46	TYR	N-CA-C	6.08	118.21	109.14
1	bg	121	THR	CB-CA-C	-6.08	103.71	111.86
1	ec	184	GLU	N-CA-C	-6.08	100.71	110.14
1	fh	115	GLN	CA-C-N	6.08	126.05	120.03
1	fh	115	GLN	C-N-CA	6.08	126.05	120.03
1	fi	186	GLY	N-CA-C	6.08	122.33	111.02
1	ge	121	THR	N-CA-C	6.08	119.64	111.24
3	ma	37	ASP	CA-CB-CG	6.08	118.68	112.60
1	al	115	GLN	CA-C-N	6.08	126.05	120.03
1	al	115	GLN	C-N-CA	6.08	126.05	120.03
1	ci	119	SER	CA-C-N	6.08	126.05	120.21
1	ci	119	SER	C-N-CA	6.08	126.05	120.21
1	fw	149	GLY	CA-C-N	6.08	125.99	119.85
1	fw	149	GLY	C-N-CA	6.08	125.99	119.85
1	bc	336	ASP	CA-C-N	6.08	125.76	119.56
1	bc	336	ASP	C-N-CA	6.08	125.76	119.56
1	gl	93	PRO	N-CA-C	6.08	120.68	112.48
1	cx	88	VAL	N-CA-C	6.08	116.62	108.11
1	ax	259	ILE	N-CA-C	6.07	117.23	108.48
1	de	491	ALA	CA-C-N	6.07	126.26	120.31
1	de	491	ALA	C-N-CA	6.07	126.26	120.31
1	dh	245	ASN	CA-C-N	6.07	125.98	119.85
1	dh	245	ASN	C-N-CA	6.07	125.98	119.85
1	dt	484	PHE	CA-CB-CG	6.07	119.87	113.80
1	ea	328	LYS	N-CA-C	6.07	120.39	112.92
1	fk	491	ALA	CA-C-N	6.07	126.58	120.14
1	fk	491	ALA	C-N-CA	6.07	126.58	120.14
1	gp	115	GLN	CA-C-N	6.07	126.04	120.03
1	gp	115	GLN	C-N-CA	6.07	126.04	120.03
3	km	49	PHE	CA-C-N	6.07	125.98	119.85
3	km	49	PHE	C-N-CA	6.07	125.98	119.85
3	np	37	ASP	CA-CB-CG	6.07	118.67	112.60
1	bq	403	GLY	N-CA-C	6.07	121.19	113.24
1	fe	336	ASP	CA-C-N	6.07	126.51	119.47
1	fe	336	ASP	C-N-CA	6.07	126.51	119.47
1	fz	92	GLY	CA-C-N	6.07	125.77	119.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fz	92	GLY	C-N-CA	6.07	125.77	119.82
1	gg	88	VAL	N-CA-C	6.07	116.61	107.80
1	bc	412	VAL	N-CA-C	-6.07	106.59	111.81
1	ff	256	LYS	N-CA-C	6.07	118.30	109.07
1	gd	115	GLN	CA-C-N	6.07	126.03	119.78
1	gd	115	GLN	C-N-CA	6.07	126.03	119.78
1	ao	328	LYS	N-CA-C	6.07	120.39	112.92
1	dw	344	ARG	N-CA-C	-6.07	99.82	109.23
1	gl	344	ARG	N-CA-C	-6.07	98.74	109.06
2	hk	286	GLY	N-CA-C	-6.07	101.20	112.37
1	ch	328	LYS	N-CA-C	6.07	120.38	112.92
1	cl	115	GLN	CA-C-N	6.07	126.03	119.78
1	cl	115	GLN	C-N-CA	6.07	126.03	119.78
1	bf	163	PHE	CA-C-N	6.07	125.97	119.85
1	bf	163	PHE	C-N-CA	6.07	125.97	119.85
1	bk	336	ASP	CA-C-N	6.07	125.75	119.56
1	bk	336	ASP	C-N-CA	6.07	125.75	119.56
1	ce	403	GLY	N-CA-C	6.07	121.19	113.24
1	de	201	GLY	N-CA-C	-6.07	105.29	113.24
1	bx	253	ARG	N-CA-C	6.06	122.55	114.12
1	ca	121	THR	N-CA-C	6.06	119.61	111.24
1	di	103	ILE	CA-C-N	6.06	125.97	119.85
1	di	103	ILE	C-N-CA	6.06	125.97	119.85
1	fa	103	ILE	CA-C-N	6.06	125.97	119.85
1	fa	103	ILE	C-N-CA	6.06	125.97	119.85
3	mn	38	VAL	N-CA-C	6.06	117.43	107.24
1	ck	121	THR	N-CA-C	6.06	119.61	111.24
1	cv	121	THR	N-CA-C	6.06	119.61	111.24
1	dc	395	TYR	N-CA-C	6.06	117.56	111.07
1	ek	336	ASP	CA-C-N	6.06	126.50	119.47
1	ek	336	ASP	C-N-CA	6.06	126.50	119.47
1	es	115	GLN	CA-C-N	6.06	125.97	119.85
1	es	115	GLN	C-N-CA	6.06	125.97	119.85
1	fq	245	ASN	CA-C-N	6.06	126.03	120.03
1	fq	245	ASN	C-N-CA	6.06	126.03	120.03
1	aj	232	ILE	N-CA-C	-6.06	106.99	111.90
1	fb	440	GLY	CA-C-N	6.06	125.68	119.56
1	fb	440	GLY	C-N-CA	6.06	125.68	119.56
1	bp	481	ILE	N-CA-C	6.06	116.65	108.17
1	ci	87	ALA	N-CA-C	6.06	117.97	111.36
1	gb	271	SER	N-CA-C	6.06	119.25	110.28
1	ax	482	ASN	CA-CB-CG	6.06	118.66	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dr	71	ASP	CA-CB-CG	6.06	118.66	112.60
1	ax	209	ASP	CA-CB-CG	6.06	118.66	112.60
1	ay	232	ILE	N-CA-C	-6.05	106.35	111.56
1	ex	480	GLY	N-CA-C	6.05	119.62	110.18
1	ey	245	ASN	CA-C-N	6.05	126.02	120.03
1	ey	245	ASN	C-N-CA	6.05	126.02	120.03
1	fc	336	ASP	CA-C-N	6.05	125.73	119.56
1	fc	336	ASP	C-N-CA	6.05	125.73	119.56
1	fk	328	LYS	N-CA-C	6.05	120.37	112.92
1	fe	271	SER	N-CA-C	6.05	119.76	110.20
1	ef	491	ALA	CA-C-N	6.05	126.56	120.14
1	ef	491	ALA	C-N-CA	6.05	126.56	120.14
3	ig	44	ALA	N-CA-C	6.05	120.52	113.20
3	ob	37	ASP	CA-CB-CG	6.05	118.65	112.60
1	ck	256	LYS	N-CA-C	6.05	118.26	109.07
1	cs	151	ASP	CA-CB-CG	6.05	118.65	112.60
1	ct	245	ASN	CA-C-N	6.05	126.02	120.03
1	ct	245	ASN	C-N-CA	6.05	126.02	120.03
1	fx	145	HIS	CA-C-N	6.05	125.73	119.56
1	fx	145	HIS	C-N-CA	6.05	125.73	119.56
1	gp	285	ASP	CA-CB-CG	6.05	118.65	112.60
2	hf	370	GLN	CA-C-N	6.05	126.02	120.03
2	hf	370	GLN	C-N-CA	6.05	126.02	120.03
1	gy	395	TYR	N-CA-C	6.05	117.56	110.97
3	ly	46	TYR	N-CA-C	6.05	118.15	109.14
1	an	182	PHE	CA-CB-CG	6.05	119.85	113.80
1	ep	271	SER	N-CA-C	6.05	118.71	110.55
1	fb	468	GLN	CA-C-N	6.05	125.96	119.85
1	fb	468	GLN	C-N-CA	6.05	125.96	119.85
1	fk	93	PRO	N-CA-CB	-6.05	98.80	102.79
2	hk	47	GLN	CA-C-N	6.05	125.73	119.56
2	hk	47	GLN	C-N-CA	6.05	125.73	119.56
1	am	468	GLN	CA-C-N	6.04	125.96	119.85
1	am	468	GLN	C-N-CA	6.04	125.96	119.85
1	ek	245	ASN	CA-C-N	6.04	126.01	120.03
1	ek	245	ASN	C-N-CA	6.04	126.01	120.03
1	bs	468	GLN	CA-C-N	6.04	125.95	119.85
1	bs	468	GLN	C-N-CA	6.04	125.95	119.85
1	cu	336	ASP	CA-C-N	6.04	125.72	119.56
1	cu	336	ASP	C-N-CA	6.04	125.72	119.56
1	db	209	ASP	CA-CB-CG	6.04	118.64	112.60
1	df	154	PHE	N-CA-C	-6.04	104.98	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gf	336	ASP	CA-C-N	6.04	126.48	119.47
1	gf	336	ASP	C-N-CA	6.04	126.48	119.47
1	ce	463	ASP	CA-C-N	6.04	127.39	119.84
1	ce	463	ASP	C-N-CA	6.04	127.39	119.84
1	ee	93	PRO	N-CA-C	6.04	120.96	114.68
1	fb	329	ALA	N-CA-C	6.04	118.57	111.02
1	fn	209	ASP	CA-CB-CG	6.04	118.64	112.60
1	gu	253	ARG	N-CA-C	6.04	122.10	114.31
1	bs	483	PRO	N-CA-C	-6.04	101.72	111.14
1	gn	93	PRO	N-CA-CB	-6.04	98.80	102.79
2	hm	136	LYS	N-CA-C	-6.04	106.04	113.41
3	io	44	ALA	N-CA-C	6.04	120.51	113.20
1	bo	468	GLN	CA-C-N	6.04	125.95	119.85
1	bo	468	GLN	C-N-CA	6.04	125.95	119.85
1	cs	245	ASN	CA-C-N	6.04	126.01	120.03
1	cs	245	ASN	C-N-CA	6.04	126.01	120.03
2	hk	420	LEU	CA-C-N	6.04	126.00	119.78
2	hk	420	LEU	C-N-CA	6.04	126.00	119.78
1	cl	145	HIS	CA-C-N	6.04	127.39	119.84
1	cl	145	HIS	C-N-CA	6.04	127.39	119.84
3	jy	38	VAL	N-CA-C	6.04	116.98	108.17
1	cs	344	ARG	N-CA-C	-6.04	99.88	109.23
1	cy	256	LYS	N-CA-C	6.04	118.24	109.07
1	ed	92	GLY	CA-C-N	6.04	125.73	119.82
1	ed	92	GLY	C-N-CA	6.04	125.73	119.82
1	fb	151	ASP	CA-CB-CG	6.04	118.64	112.60
1	gj	103	ILE	CA-C-N	6.04	126.06	119.90
1	gj	103	ILE	C-N-CA	6.04	126.06	119.90
3	nm	67	GLU	N-CA-C	-6.04	104.78	111.36
1	ay	484	PHE	CA-CB-CG	6.03	119.83	113.80
1	bu	201	GLY	N-CA-C	-6.03	105.34	113.24
1	dz	209	ASP	CA-CB-CG	6.03	118.63	112.60
1	fa	110	ASP	CA-CB-CG	6.03	118.63	112.60
1	fi	468	GLN	CA-C-N	6.03	125.94	119.85
1	fi	468	GLN	C-N-CA	6.03	125.94	119.85
1	eu	71	ASP	CA-CB-CG	6.03	118.63	112.60
3	le	44	ALA	N-CA-C	6.03	120.50	113.20
1	ew	468	GLN	CA-C-N	6.03	125.94	119.85
1	ew	468	GLN	C-N-CA	6.03	125.94	119.85
1	ez	121	THR	N-CA-C	6.03	119.56	111.24
1	fj	193	SER	N-CA-C	-6.03	106.56	114.04
1	gi	440	GLY	CA-C-N	6.03	125.71	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gi	440	GLY	C-N-CA	6.03	125.71	119.56
1	bx	245	ASN	CA-C-N	6.03	126.00	120.03
1	bx	245	ASN	C-N-CA	6.03	126.00	120.03
1	dh	344	ARG	N-CA-C	-6.03	101.28	110.14
1	ge	198	ILE	N-CA-C	6.03	112.66	106.21
1	ha	103	ILE	CA-C-N	6.03	125.99	119.78
1	ha	103	ILE	C-N-CA	6.03	125.99	119.78
3	ja	37	ASP	CA-CB-CG	6.03	118.63	112.60
3	lj	67	GLU	N-CA-C	-6.03	104.79	111.36
1	dm	250	MET	N-CA-C	6.03	116.51	108.38
1	eb	88	VAL	N-CA-C	6.03	116.55	107.75
1	hb	187	THR	N-CA-C	6.03	119.34	109.76
1	cg	182	PHE	CA-CB-CG	6.02	119.82	113.80
1	cx	256	LYS	N-CA-C	6.02	118.23	109.07
1	gw	324	THR	N-CA-C	-6.02	102.06	109.65
1	ag	403	GLY	N-CA-C	6.02	121.28	113.27
1	at	134	ASP	CA-C-N	6.02	125.70	119.56
1	at	134	ASP	C-N-CA	6.02	125.70	119.56
1	fp	468	GLN	CA-C-N	6.02	125.93	119.85
1	fp	468	GLN	C-N-CA	6.02	125.93	119.85
1	bv	468	GLN	CA-C-N	6.02	125.78	119.76
1	bv	468	GLN	C-N-CA	6.02	125.78	119.76
1	bw	68	ILE	CA-C-N	6.02	126.62	119.94
1	bw	68	ILE	C-N-CA	6.02	126.62	119.94
1	cf	245	ASN	CA-C-N	6.02	125.99	120.03
1	cf	245	ASN	C-N-CA	6.02	125.99	120.03
1	gd	265	GLN	N-CA-C	6.02	118.30	108.55
1	gi	232	ILE	N-CA-C	-6.02	105.95	111.67
1	gz	88	VAL	N-CA-C	6.02	116.53	107.75
1	gz	119	SER	N-CA-C	-6.02	102.81	108.22
1	am	121	THR	N-CA-C	6.02	119.54	111.24
1	cn	468	GLN	CA-C-N	6.02	125.93	119.85
1	cn	468	GLN	C-N-CA	6.02	125.93	119.85
2	hf	136	LYS	N-CA-C	-6.02	106.07	113.41
3	hz	46	TYR	N-CA-C	6.02	117.04	108.74
1	bs	253	ARG	N-CA-C	6.01	120.30	111.34
1	fa	287	ASP	N-CA-C	-6.01	104.06	111.40
3	jn	67	GLU	N-CA-C	-6.01	104.80	111.36
3	lt	67	GLU	N-CA-C	-6.01	104.80	111.36
1	cd	468	GLN	CA-C-N	6.01	125.92	119.85
1	cd	468	GLN	C-N-CA	6.01	125.92	119.85
3	li	46	TYR	N-CA-C	6.01	118.10	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bn	115	GLN	CA-C-N	6.01	125.98	120.03
1	bn	115	GLN	C-N-CA	6.01	125.98	120.03
1	gj	336	ASP	CA-C-N	6.01	125.69	119.56
1	gj	336	ASP	C-N-CA	6.01	125.69	119.56
1	ha	425	ILE	N-CA-C	6.01	116.52	107.80
2	hg	370	GLN	CA-C-N	6.01	125.98	120.03
2	hg	370	GLN	C-N-CA	6.01	125.98	120.03
1	fg	324	THR	N-CA-C	-6.01	100.67	109.50
1	fr	256	LYS	N-CA-C	6.01	118.20	109.07
1	fs	463	ASP	CA-C-N	6.01	125.69	119.56
1	fs	463	ASP	C-N-CA	6.01	125.69	119.56
1	an	463	ASP	CA-C-N	6.01	125.69	119.56
1	an	463	ASP	C-N-CA	6.01	125.69	119.56
1	fi	336	ASP	CA-C-N	6.01	125.69	119.56
1	fi	336	ASP	C-N-CA	6.01	125.69	119.56
1	aq	88	VAL	N-CA-C	6.00	116.52	107.75
1	eh	236	GLN	CA-C-N	6.00	131.19	122.36
1	eh	236	GLN	C-N-CA	6.00	131.19	122.36
3	jl	67	GLU	N-CA-C	-6.00	104.81	111.36
1	ap	103	ILE	CA-C-N	6.00	125.96	119.78
1	ap	103	ILE	C-N-CA	6.00	125.96	119.78
1	az	253	ARG	N-CA-C	6.00	120.92	112.93
1	cm	403	GLY	N-CA-C	6.00	121.25	113.27
1	at	121	THR	CB-CA-C	-6.00	102.85	112.09
1	bm	245	ASN	CA-C-N	6.00	125.97	120.03
1	bm	245	ASN	C-N-CA	6.00	125.97	120.03
1	dj	253	ARG	N-CA-C	6.00	120.35	112.13
1	dw	491	ALA	CA-C-N	6.00	126.50	120.14
1	dw	491	ALA	C-N-CA	6.00	126.50	120.14
1	fk	199	ASP	CA-CB-CG	-6.00	106.60	112.60
1	ga	270	TYR	N-CA-C	6.00	118.65	110.55
2	hn	47	GLN	CA-C-N	6.00	125.68	119.56
2	hn	47	GLN	C-N-CA	6.00	125.68	119.56
1	bg	79	ILE	N-CA-C	-6.00	96.86	109.34
1	bp	392	GLY	CA-C-N	-6.00	116.01	121.65
1	bp	392	GLY	C-N-CA	-6.00	116.01	121.65
1	ch	245	ASN	CA-C-N	6.00	125.97	120.03
1	ch	245	ASN	C-N-CA	6.00	125.97	120.03
1	gy	468	GLN	CA-C-N	6.00	125.91	119.85
1	gy	468	GLN	C-N-CA	6.00	125.91	119.85
1	at	484	PHE	CA-CB-CG	6.00	119.80	113.80
1	cb	103	ILE	CA-C-N	6.00	125.91	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cb	103	ILE	C-N-CA	6.00	125.91	119.85
1	ca	446	ALA	N-CA-C	6.00	120.62	113.12
1	dt	121	THR	CB-CA-C	-6.00	102.86	112.09
1	dy	209	ASP	CA-CB-CG	6.00	118.60	112.60
1	ea	468	GLN	CA-C-N	6.00	125.91	119.85
1	ea	468	GLN	C-N-CA	6.00	125.91	119.85
1	fi	395	TYR	N-CA-C	6.00	117.51	110.97
1	fp	119	SER	CA-C-N	6.00	125.97	120.21
1	fp	119	SER	C-N-CA	6.00	125.97	120.21
1	dj	103	ILE	CA-C-N	5.99	126.00	119.89
1	dj	103	ILE	C-N-CA	5.99	126.00	119.89
3	ng	38	VAL	N-CA-C	5.99	116.75	108.12
1	cq	491	ALA	CA-C-N	5.99	126.49	120.14
1	cq	491	ALA	C-N-CA	5.99	126.49	120.14
1	dy	463	ASP	CA-C-N	5.99	125.67	119.56
1	dy	463	ASP	C-N-CA	5.99	125.67	119.56
1	fs	272	ILE	N-CA-C	5.99	116.16	110.53
1	gn	115	GLN	CA-C-N	5.99	125.90	119.85
1	gn	115	GLN	C-N-CA	5.99	125.90	119.85
1	fe	121	THR	CB-CA-C	-5.99	102.86	112.09
1	fh	468	GLN	CA-C-N	5.99	125.90	119.85
1	fh	468	GLN	C-N-CA	5.99	125.90	119.85
1	fi	484	PHE	CA-CB-CG	5.99	119.79	113.80
1	go	245	ASN	CA-C-N	5.99	125.96	120.03
1	go	245	ASN	C-N-CA	5.99	125.96	120.03
1	ai	130	VAL	N-CA-C	5.99	116.74	108.12
1	am	403	GLY	N-CA-C	5.99	121.23	113.27
1	ds	103	ILE	CA-C-N	5.99	125.90	119.85
1	ds	103	ILE	C-N-CA	5.99	125.90	119.85
1	fn	480	GLY	N-CA-C	5.99	120.37	110.55
1	co	468	GLN	CA-C-N	5.99	125.90	119.85
1	co	468	GLN	C-N-CA	5.99	125.90	119.85
1	af	245	ASN	CA-C-N	5.99	125.89	119.85
1	af	245	ASN	C-N-CA	5.99	125.89	119.85
1	br	119	SER	N-CA-C	-5.99	101.31	108.25
1	gb	324	THR	N-CA-C	-5.99	100.70	109.50
1	gg	324	THR	N-CA-C	-5.99	100.70	109.50
1	hc	328	LYS	N-CA-C	5.98	120.60	112.88
1	aa	287	ASP	N-CA-C	-5.98	103.93	112.13
1	cq	403	GLY	N-CA-C	5.98	121.08	113.24
1	dw	483	PRO	N-CA-C	-5.98	101.70	111.21
1	be	103	ILE	CA-C-N	5.98	125.89	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	be	103	ILE	C-N-CA	5.98	125.89	119.85
1	bn	245	ASN	CA-C-N	5.98	125.95	120.03
1	bn	245	ASN	C-N-CA	5.98	125.95	120.03
1	bs	121	THR	CB-CA-C	-5.98	102.88	112.09
1	fg	93	PRO	N-CA-CB	-5.98	98.84	102.79
3	mp	46	TYR	N-CA-C	5.98	118.05	109.14
1	bo	245	ASN	CA-C-N	5.98	125.95	120.03
1	bo	245	ASN	C-N-CA	5.98	125.95	120.03
1	dh	115	GLN	CB-CA-C	-5.98	105.80	111.00
1	ev	145	HIS	CA-C-N	5.98	125.66	119.56
1	ev	145	HIS	C-N-CA	5.98	125.66	119.56
1	fn	92	GLY	CA-C-N	5.98	125.68	119.82
1	fn	92	GLY	C-N-CA	5.98	125.68	119.82
1	at	71	ASP	CA-CB-CG	5.97	118.57	112.60
1	ep	468	GLN	CA-C-N	5.97	125.89	119.85
1	ep	468	GLN	C-N-CA	5.97	125.89	119.85
1	fh	328	LYS	N-CA-C	5.97	119.88	112.59
3	je	37	ASP	CA-CB-CG	5.97	118.58	112.60
3	oe	44	ALA	N-CA-C	5.97	120.43	113.20
1	az	103	ILE	CA-C-N	5.97	125.98	119.89
1	az	103	ILE	C-N-CA	5.97	125.98	119.89
1	bb	253	ARG	N-CA-C	5.97	120.96	113.43
1	bt	103	ILE	CA-C-N	5.97	126.31	119.92
1	bt	103	ILE	C-N-CA	5.97	126.31	119.92
1	cl	468	GLN	CA-C-N	5.97	125.88	119.85
1	cl	468	GLN	C-N-CA	5.97	125.88	119.85
1	fi	324	THR	N-CA-C	-5.97	102.25	109.72
1	gf	121	THR	CB-CA-C	-5.97	102.89	112.09
2	hh	19	ILE	N-CA-C	5.97	116.53	108.17
1	ak	184	GLU	N-CA-C	-5.97	100.07	109.50
1	au	483	PRO	N-CA-C	-5.97	101.83	111.14
1	ch	271	SER	N-CA-C	5.97	119.12	110.28
1	ej	468	GLN	CA-C-N	5.97	125.88	119.85
1	ej	468	GLN	C-N-CA	5.97	125.88	119.85
1	fa	490	GLN	N-CA-C	-5.97	104.71	112.23
1	gq	344	ARG	N-CA-C	-5.97	99.97	109.23
1	gz	232	ILE	N-CA-C	-5.97	105.90	111.45
1	bo	484	PHE	CA-CB-CG	5.97	119.77	113.80
1	ez	115	GLN	CA-C-N	5.97	125.94	120.03
1	ez	115	GLN	C-N-CA	5.97	125.94	120.03
1	gi	483	PRO	N-CA-C	-5.97	101.83	111.14
2	hm	420	LEU	CA-C-N	5.97	125.93	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hm	420	LEU	C-N-CA	5.97	125.93	119.78
1	as	293	ILE	N-CA-C	-5.97	105.03	110.82
2	hi	47	GLN	CA-C-N	5.97	125.65	119.56
2	hi	47	GLN	C-N-CA	5.97	125.65	119.56
3	kc	37	ASP	CA-CB-CG	5.97	118.57	112.60
1	hc	245	ASN	CA-C-N	5.97	125.94	120.03
1	hc	245	ASN	C-N-CA	5.97	125.94	120.03
1	do	115	GLN	CA-C-N	5.96	125.94	120.03
1	do	115	GLN	C-N-CA	5.96	125.94	120.03
1	es	253	ARG	N-CA-C	5.96	120.23	111.34
1	gx	324	THR	N-CA-C	-5.96	102.26	109.72
1	cj	256	LYS	N-CA-C	5.96	118.13	109.07
1	cy	119	SER	CA-C-N	5.96	126.42	120.52
1	cy	119	SER	C-N-CA	5.96	126.42	120.52
3	me	38	VAL	N-CA-C	5.96	116.59	107.77
1	aa	484	PHE	CA-CB-CG	5.96	119.76	113.80
1	dp	403	GLY	N-CA-C	5.96	121.05	113.24
1	eh	186	GLY	N-CA-C	5.96	122.11	111.02
1	fa	468	GLN	CA-C-N	5.96	125.92	119.78
1	fa	468	GLN	C-N-CA	5.96	125.92	119.78
1	gc	198	ILE	N-CA-C	5.96	116.20	106.72
1	gl	468	GLN	CA-C-N	5.96	125.87	119.85
1	gl	468	GLN	C-N-CA	5.96	125.87	119.85
1	gw	468	GLN	CA-C-N	5.96	125.87	119.85
1	gw	468	GLN	C-N-CA	5.96	125.87	119.85
3	io	72	ASN	CB-CA-C	-5.96	101.48	110.90
1	fy	468	GLN	CA-C-N	5.96	125.87	119.85
1	fy	468	GLN	C-N-CA	5.96	125.87	119.85
1	ck	324	THR	N-CA-C	-5.96	102.14	109.65
1	fa	115	GLN	CA-C-N	5.96	125.93	120.03
1	fa	115	GLN	C-N-CA	5.96	125.93	120.03
3	kv	38	VAL	N-CA-C	5.96	117.25	107.24
1	aw	403	GLY	N-CA-C	5.96	121.04	113.24
1	ba	232	ILE	N-CA-C	-5.96	105.04	110.82
1	eu	115	GLN	CA-C-N	5.96	125.93	120.03
1	eu	115	GLN	C-N-CA	5.96	125.93	120.03
1	go	103	ILE	CA-C-N	5.96	125.87	119.85
1	go	103	ILE	C-N-CA	5.96	125.87	119.85
1	gp	265	GLN	N-CA-C	5.96	118.20	108.55
3	ju	44	ALA	N-CA-C	5.96	120.41	113.20
1	eb	256	LYS	N-CA-C	5.96	118.12	109.07
1	ba	358	ASP	CA-CB-CG	5.95	118.55	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dc	281	VAL	N-CA-C	5.95	116.99	111.45
2	hi	353	ASP	CA-C-N	5.95	127.28	119.84
2	hi	353	ASP	C-N-CA	5.95	127.28	119.84
3	lz	46	TYR	N-CA-C	5.95	117.63	109.18
1	bf	182	PHE	CA-CB-CG	5.95	119.75	113.80
1	ei	468	GLN	CA-C-N	5.95	125.86	119.85
1	ei	468	GLN	C-N-CA	5.95	125.86	119.85
1	gj	402	THR	CA-C-N	5.95	127.63	120.13
1	gj	402	THR	C-N-CA	5.95	127.63	120.13
2	hm	21	ARG	CA-C-N	5.95	125.92	120.03
2	hm	21	ARG	C-N-CA	5.95	125.92	120.03
1	ac	328	LYS	N-CA-C	5.95	121.33	112.94
1	cv	256	LYS	N-CA-C	5.95	118.11	109.07
1	fg	483	PRO	N-CA-C	-5.95	101.75	111.21
1	ge	182	PHE	CA-CB-CG	5.95	119.75	113.80
3	kv	67	GLU	N-CA-C	-5.95	104.88	111.36
1	ac	115	GLN	CA-C-N	5.95	125.92	120.03
1	ac	115	GLN	C-N-CA	5.95	125.92	120.03
1	ax	68	ILE	CA-C-N	5.95	126.42	119.94
1	ax	68	ILE	C-N-CA	5.95	126.42	119.94
1	bv	110	ASP	CA-CB-CG	5.95	118.55	112.60
1	cc	463	ASP	CA-C-N	5.95	125.62	119.56
1	cc	463	ASP	C-N-CA	5.95	125.62	119.56
1	er	468	GLN	CA-C-N	5.95	125.86	119.85
1	er	468	GLN	C-N-CA	5.95	125.86	119.85
1	fa	256	LYS	N-CA-C	5.95	118.11	109.07
1	fr	336	ASP	CA-C-N	5.95	126.37	119.47
1	fr	336	ASP	C-N-CA	5.95	126.37	119.47
1	bw	134	ASP	CA-C-N	5.94	125.62	119.56
1	bw	134	ASP	C-N-CA	5.94	125.62	119.56
1	ct	328	LYS	N-CA-C	5.94	120.53	113.16
1	bw	110	ASP	CA-CB-CG	5.94	118.54	112.60
1	fu	245	ASN	CA-C-N	5.94	125.85	119.85
1	fu	245	ASN	C-N-CA	5.94	125.85	119.85
1	gj	468	GLN	CA-C-N	5.94	125.85	119.85
1	gj	468	GLN	C-N-CA	5.94	125.85	119.85
1	am	121	THR	CB-CA-C	-5.94	102.94	112.09
1	cm	484	PHE	CA-CB-CG	5.94	119.74	113.80
1	ep	245	ASN	CA-C-N	5.94	125.85	119.85
1	ep	245	ASN	C-N-CA	5.94	125.85	119.85
1	fe	484	PHE	CA-CB-CG	5.94	119.74	113.80
1	gm	121	THR	N-CA-C	5.94	119.44	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gx	463	ASP	CA-C-N	5.94	125.62	119.56
1	gx	463	ASP	C-N-CA	5.94	125.62	119.56
1	hd	151	ASP	CA-CB-CG	5.94	118.54	112.60
1	cw	468	GLN	CA-C-N	5.94	125.85	119.85
1	cw	468	GLN	C-N-CA	5.94	125.85	119.85
1	hd	324	THR	N-CA-C	-5.94	102.30	109.72
1	ct	468	GLN	CA-C-N	5.94	125.85	119.85
1	ct	468	GLN	C-N-CA	5.94	125.85	119.85
1	aa	72	HIS	N-CA-C	-5.93	101.16	110.36
1	cj	271	SER	N-CA-C	5.93	118.83	110.23
1	cy	324	THR	N-CA-C	-5.93	102.17	109.65
1	gs	222	VAL	N-CA-C	5.93	118.25	108.99
1	aq	222	VAL	N-CA-C	5.93	118.24	108.99
1	cq	93	PRO	N-CA-CB	-5.93	98.88	102.79
1	fx	119	SER	CA-C-N	5.93	125.90	120.03
1	fx	119	SER	C-N-CA	5.93	125.90	120.03
1	dn	483	PRO	N-CA-C	-5.93	101.78	111.21
2	hh	47	GLN	CA-C-N	5.93	125.61	119.56
2	hh	47	GLN	C-N-CA	5.93	125.61	119.56
1	dd	250	MET	N-CA-C	5.93	117.26	108.60
1	dp	468	GLN	CA-C-N	5.93	125.84	119.85
1	dp	468	GLN	C-N-CA	5.93	125.84	119.85
3	jr	67	GLU	N-CA-C	-5.93	104.90	111.36
1	ag	245	ASN	CA-C-N	5.93	125.84	119.85
1	ag	245	ASN	C-N-CA	5.93	125.84	119.85
1	co	324	THR	N-CA-C	-5.93	100.79	109.50
1	cy	336	ASP	CA-C-N	5.93	126.34	119.47
1	cy	336	ASP	C-N-CA	5.93	126.34	119.47
1	dk	71	ASP	CA-CB-CG	5.93	118.53	112.60
1	gm	468	GLN	CA-C-N	5.93	125.84	119.85
1	gm	468	GLN	C-N-CA	5.93	125.84	119.85
2	hn	343	ALA	CA-C-N	5.93	125.84	119.85
2	hn	343	ALA	C-N-CA	5.93	125.84	119.85
3	ja	44	ALA	N-CA-C	5.93	120.51	113.16
1	bm	121	THR	N-CA-C	5.92	119.41	111.24
1	fc	103	ILE	CA-C-N	5.92	125.88	119.78
1	fc	103	ILE	C-N-CA	5.92	125.88	119.78
1	gf	468	GLN	CA-C-N	5.92	125.83	119.85
1	gf	468	GLN	C-N-CA	5.92	125.83	119.85
1	gm	69	GLY	N-CA-C	-5.92	105.19	112.77
1	fl	468	GLN	CA-C-N	5.92	125.83	119.85
1	fl	468	GLN	C-N-CA	5.92	125.83	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ab	253	ARG	N-CA-C	5.92	120.80	112.93
1	ci	403	GLY	N-CA-C	5.92	121.00	113.24
1	dl	72	HIS	N-CA-C	-5.92	100.96	110.14
1	fn	324	THR	N-CA-C	-5.92	102.32	109.72
3	iq	44	ALA	N-CA-C	5.92	120.50	113.16
3	kq	44	ALA	N-CA-C	5.92	120.50	113.16
2	hg	270	THR	N-CA-C	5.92	120.23	113.19
1	be	134	ASP	CA-C-N	5.92	125.60	119.56
1	be	134	ASP	C-N-CA	5.92	125.60	119.56
1	ca	71	ASP	CA-CB-CG	5.92	118.52	112.60
1	cb	93	PRO	N-CA-CB	-5.92	98.88	102.79
1	dr	468	GLN	CA-C-N	5.92	125.83	119.85
1	dr	468	GLN	C-N-CA	5.92	125.83	119.85
1	ep	93	PRO	N-CA-CB	-5.92	98.89	102.79
3	ny	72	ASN	CA-CB-CG	5.92	118.52	112.60
1	eh	201	GLY	N-CA-C	-5.92	105.49	113.24
1	ex	336	ASP	CA-C-N	5.92	126.33	119.47
1	ex	336	ASP	C-N-CA	5.92	126.33	119.47
1	bq	445	ASP	CA-C-N	5.91	128.69	120.29
1	bq	445	ASP	C-N-CA	5.91	128.69	120.29
1	ga	440	GLY	CA-C-N	5.91	125.59	119.56
1	ga	440	GLY	C-N-CA	5.91	125.59	119.56
3	hx	38	VAL	N-CA-C	5.91	116.59	107.78
1	at	115	GLN	CA-C-N	5.91	125.87	119.78
1	at	115	GLN	C-N-CA	5.91	125.87	119.78
1	dd	88	VAL	N-CA-C	5.91	116.38	107.75
1	du	121	THR	CB-CA-C	-5.91	102.99	112.09
1	fy	115	GLN	CA-C-N	5.91	125.82	119.85
1	fy	115	GLN	C-N-CA	5.91	125.82	119.85
2	hi	21	ARG	CA-C-N	5.91	125.88	120.03
2	hi	21	ARG	C-N-CA	5.91	125.88	120.03
3	my	46	TYR	N-CA-C	5.91	118.39	109.41
1	as	187	THR	N-CA-C	5.91	118.90	110.10
1	dv	121	THR	N-CA-C	5.91	119.54	111.39
1	fv	468	GLN	CA-C-N	5.91	125.82	119.85
1	fv	468	GLN	C-N-CA	5.91	125.82	119.85
1	fx	328	LYS	N-CA-C	5.91	120.35	113.20
1	ga	285	ASP	N-CA-C	5.91	118.96	111.69
2	hj	337	VAL	N-CA-C	5.91	117.27	108.46
1	ba	115	GLN	CA-C-N	5.91	125.86	119.78
1	ba	115	GLN	C-N-CA	5.91	125.86	119.78
1	bf	256	LYS	N-CA-C	5.91	118.26	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bm	115	GLN	CA-C-N	5.91	125.82	119.85
1	bm	115	GLN	C-N-CA	5.91	125.82	119.85
1	bu	253	ARG	N-CA-C	5.91	120.14	111.34
1	cn	103	ILE	CA-C-N	5.91	125.92	119.90
1	cn	103	ILE	C-N-CA	5.91	125.92	119.90
1	eh	336	ASP	CA-C-N	5.91	126.32	119.47
1	eh	336	ASP	C-N-CA	5.91	126.32	119.47
1	eh	480	GLY	CA-C-N	5.91	129.81	121.66
1	eh	480	GLY	C-N-CA	5.91	129.81	121.66
1	fg	103	ILE	CA-C-N	5.91	125.81	119.85
1	fg	103	ILE	C-N-CA	5.91	125.81	119.85
1	ft	451	ALA	CA-C-N	5.91	125.84	119.76
1	ft	451	ALA	C-N-CA	5.91	125.84	119.76
1	go	232	ILE	N-CA-C	-5.91	106.06	111.67
1	ao	483	PRO	N-CA-C	-5.90	101.82	111.21
1	ay	103	ILE	CA-C-N	5.90	125.81	119.85
1	ay	103	ILE	C-N-CA	5.90	125.81	119.85
1	cn	259	ILE	N-CA-C	5.90	116.51	107.77
1	do	88	VAL	N-CA-C	5.90	116.37	107.75
1	fg	119	SER	CA-C-N	5.90	125.87	120.03
1	fg	119	SER	C-N-CA	5.90	125.87	120.03
1	cz	150	PRO	N-CA-C	-5.90	101.83	111.21
1	fb	259	ILE	N-CA-C	5.90	116.36	107.75
1	fn	119	SER	CA-C-N	5.90	125.87	120.21
1	fn	119	SER	C-N-CA	5.90	125.87	120.21
1	fr	88	VAL	N-CA-C	5.90	116.36	107.75
1	gm	121	THR	CB-CA-C	-5.90	103.00	112.09
2	ho	42	THR	N-CA-C	5.90	119.44	109.76
3	ih	17	LEU	N-CA-C	5.90	117.38	111.07
1	ap	186	GLY	N-CA-C	5.90	121.99	111.02
1	cp	121	THR	CB-CA-C	-5.90	103.00	112.09
1	eb	468	GLN	CA-C-N	5.90	125.81	119.85
1	eb	468	GLN	C-N-CA	5.90	125.81	119.85
1	hc	121	THR	N-CA-C	5.90	119.53	111.39
3	ih	38	VAL	N-CA-C	5.90	116.78	108.17
3	ip	46	TYR	N-CA-C	5.90	117.93	109.14
1	ay	403	GLY	N-CA-C	5.90	121.11	113.27
1	df	468	GLN	CA-C-N	5.90	125.81	119.85
1	df	468	GLN	C-N-CA	5.90	125.81	119.85
2	hg	59	ASN	CA-C-N	5.90	125.58	119.56
2	hg	59	ASN	C-N-CA	5.90	125.58	119.56
1	aa	134	ASP	CA-C-N	5.90	125.57	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	aa	134	ASP	C-N-CA	5.90	125.57	119.56
1	cf	491	ALA	CA-C-N	5.90	125.81	119.85
1	cf	491	ALA	C-N-CA	5.90	125.81	119.85
1	ft	468	GLN	CA-C-N	5.90	125.81	119.85
1	ft	468	GLN	C-N-CA	5.90	125.81	119.85
2	hi	286	GLY	N-CA-C	-5.90	101.97	112.58
1	dl	263	SER	N-CA-C	5.89	118.44	109.95
1	eg	103	ILE	CA-C-N	5.89	125.86	120.03
1	eg	103	ILE	C-N-CA	5.89	125.86	120.03
1	fp	294	LEU	CB-CA-C	-5.89	101.63	110.88
2	hg	315	ASP	CA-CB-CG	5.89	118.49	112.60
3	is	44	ALA	N-CA-C	5.89	120.33	113.20
1	ar	323	LEU	N-CA-C	5.89	119.66	110.17
1	cc	403	GLY	N-CA-C	5.89	120.96	113.24
1	dt	93	PRO	N-CA-CB	-5.89	98.90	102.79
1	ae	253	ARG	N-CA-C	5.89	120.26	112.72
1	bb	115	GLN	CB-CA-C	-5.89	105.87	111.00
1	fz	336	ASP	CA-C-N	5.89	126.30	119.47
1	fz	336	ASP	C-N-CA	5.89	126.30	119.47
1	ba	240	ASN	N-CA-C	5.89	119.55	111.54
1	bh	119	SER	CA-C-N	5.89	125.86	120.03
1	bh	119	SER	C-N-CA	5.89	125.86	120.03
1	by	484	PHE	CA-CB-CG	5.89	119.69	113.80
1	cz	468	GLN	CA-C-N	5.89	125.80	119.85
1	cz	468	GLN	C-N-CA	5.89	125.80	119.85
1	fg	426	ASP	CA-CB-CG	-5.89	106.71	112.60
1	gj	124	VAL	N-CA-C	5.89	118.35	108.81
1	gv	103	ILE	CA-C-N	5.89	125.85	119.78
1	gv	103	ILE	C-N-CA	5.89	125.85	119.78
1	ea	245	ASN	CA-C-N	5.89	125.86	120.03
1	ea	245	ASN	C-N-CA	5.89	125.86	120.03
1	ej	245	ASN	CA-C-N	5.89	125.86	120.03
1	ej	245	ASN	C-N-CA	5.89	125.86	120.03
1	ex	232	ILE	N-CA-C	-5.89	106.08	111.67
1	fr	93	PRO	N-CA-CB	-5.89	98.90	102.79
1	fr	149	GLY	CA-C-N	5.89	125.86	120.03
1	fr	149	GLY	C-N-CA	5.89	125.86	120.03
3	nv	72	ASN	CA-CB-CG	5.89	118.49	112.60
1	ak	88	VAL	N-CA-C	5.89	116.35	108.11
1	cq	425	ILE	N-CA-C	5.89	116.41	108.17
1	ff	395	TYR	N-CA-C	5.89	117.39	110.97
2	hh	384	ASN	CA-C-N	5.88	125.84	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hh	384	ASN	C-N-CA	5.88	125.84	119.78
1	dp	281	VAL	N-CA-C	5.88	116.92	111.45
1	en	491	ALA	CA-C-N	5.88	126.38	120.14
1	en	491	ALA	C-N-CA	5.88	126.38	120.14
2	hg	384	ASN	CA-CB-CG	-5.88	106.72	112.60
3	iu	44	ALA	N-CA-C	5.88	120.32	113.20
3	jk	32	PHE	CA-C-N	5.88	125.56	119.56
3	jk	32	PHE	C-N-CA	5.88	125.56	119.56
1	aj	256	LYS	N-CA-C	5.88	118.01	109.07
1	az	154	PHE	N-CA-C	-5.88	105.19	112.72
1	cn	483	PRO	N-CA-C	-5.88	101.86	111.21
1	aj	468	GLN	CA-C-N	5.88	125.79	119.85
1	aj	468	GLN	C-N-CA	5.88	125.79	119.85
1	fy	324	THR	N-CA-C	-5.88	102.24	109.65
1	gv	468	GLN	CA-C-N	5.88	125.79	119.85
1	gv	468	GLN	C-N-CA	5.88	125.79	119.85
3	no	46	TYR	N-CA-C	5.88	117.90	109.14
1	bo	490	GLN	N-CA-C	-5.88	105.00	111.82
1	by	199	ASP	CA-CB-CG	-5.88	106.72	112.60
1	cw	245	ASN	CA-C-N	5.88	125.85	120.03
1	cw	245	ASN	C-N-CA	5.88	125.85	120.03
1	ev	324	THR	N-CA-C	-5.88	102.37	109.72
1	ex	71	ASP	CA-CB-CG	5.88	118.48	112.60
1	fm	336	ASP	CA-C-N	5.88	125.55	119.56
1	fm	336	ASP	C-N-CA	5.88	125.55	119.56
1	bw	468	GLN	CA-C-N	5.88	125.83	119.78
1	bw	468	GLN	C-N-CA	5.88	125.83	119.78
1	dp	92	GLY	CA-C-N	5.87	127.18	119.84
1	dp	92	GLY	C-N-CA	5.87	127.18	119.84
1	ew	358	ASP	CA-CB-CG	5.87	118.47	112.60
1	bu	263	SER	N-CA-C	5.87	118.62	109.52
1	cq	209	ASP	CA-CB-CG	5.87	118.47	112.60
1	gl	198	ILE	N-CA-C	5.87	112.49	106.21
1	gq	491	ALA	CA-C-N	5.87	125.78	119.85
1	gq	491	ALA	C-N-CA	5.87	125.78	119.85
3	ih	16	LYS	CA-C-N	5.87	128.07	120.44
3	ih	16	LYS	C-N-CA	5.87	128.07	120.44
1	ed	149	GLY	CA-C-N	5.87	125.78	119.85
1	ed	149	GLY	C-N-CA	5.87	125.78	119.85
1	fd	209	ASP	CA-CB-CG	5.87	118.47	112.60
1	dc	121	THR	N-CA-C	5.87	119.34	111.24
1	fl	245	ASN	CA-C-N	5.87	125.84	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fl	245	ASN	C-N-CA	5.87	125.84	120.03
1	dd	245	ASN	CA-C-N	5.87	125.84	120.03
1	dd	245	ASN	C-N-CA	5.87	125.84	120.03
1	dy	403	GLY	N-CA-C	5.87	120.92	113.24
1	ad	245	ASN	CA-C-N	5.86	125.83	120.03
1	ad	245	ASN	C-N-CA	5.86	125.83	120.03
1	bb	256	LYS	N-CA-C	5.86	118.32	109.23
1	ca	163	PHE	CA-C-N	5.86	125.77	119.85
1	ca	163	PHE	C-N-CA	5.86	125.77	119.85
1	dc	121	THR	CB-CA-C	-5.86	103.06	112.09
1	es	103	ILE	CA-C-N	5.86	125.82	119.78
1	es	103	ILE	C-N-CA	5.86	125.82	119.78
1	fp	256	LYS	N-CA-C	5.86	117.98	109.07
3	me	44	ALA	N-CA-C	5.86	120.43	113.16
3	mv	46	TYR	N-CA-C	5.86	117.88	109.14
1	bw	336	ASP	CA-C-N	5.86	126.27	119.47
1	bw	336	ASP	C-N-CA	5.86	126.27	119.47
1	cg	245	ASN	CA-C-N	5.86	125.83	120.03
1	cg	245	ASN	C-N-CA	5.86	125.83	120.03
1	do	198	ILE	N-CA-C	5.86	116.60	107.28
1	cj	121	THR	N-CA-C	5.86	119.48	111.39
1	eo	403	GLY	N-CA-C	5.86	120.92	113.24
1	fn	259	ILE	N-CA-C	5.86	116.05	107.37
1	dh	86	GLY	CA-C-N	5.86	128.72	120.28
1	dh	86	GLY	C-N-CA	5.86	128.72	120.28
1	el	506	SER	CA-C-N	-5.86	112.52	121.66
1	el	506	SER	C-N-CA	-5.86	112.52	121.66
1	gu	121	THR	CB-CA-C	-5.86	103.07	112.09
1	aw	92	GLY	CA-C-N	5.86	127.16	119.84
1	aw	92	GLY	C-N-CA	5.86	127.16	119.84
1	dh	265	GLN	N-CA-C	5.86	118.04	108.55
1	eo	253	ARG	N-CA-C	5.86	120.07	111.34
1	ev	103	ILE	CA-C-N	5.86	125.83	120.03
1	ev	103	ILE	C-N-CA	5.86	125.83	120.03
1	ff	121	THR	N-CA-C	5.86	119.32	111.24
1	fv	184	GLU	N-CA-C	-5.86	100.40	109.24
1	br	184	GLU	N-CA-C	-5.86	101.52	109.95
1	dm	115	GLN	CA-C-N	5.86	125.77	119.85
1	dm	115	GLN	C-N-CA	5.86	125.77	119.85
1	fr	245	ASN	CA-C-N	5.86	125.83	120.03
1	fr	245	ASN	C-N-CA	5.86	125.83	120.03
1	ac	403	GLY	N-CA-C	5.85	120.91	113.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eu	253	ARG	N-CA-C	5.85	120.06	111.34
1	cf	103	ILE	CA-C-N	5.85	125.81	119.78
1	cf	103	ILE	C-N-CA	5.85	125.81	119.78
1	fd	93	PRO	N-CA-CB	-5.85	98.93	102.79
1	fy	287	ASP	N-CA-C	-5.85	105.14	112.93
3	ij	67	GLU	N-CA-C	-5.85	104.98	111.36
1	ed	115	GLN	CA-C-N	5.85	125.81	119.78
1	ed	115	GLN	C-N-CA	5.85	125.81	119.78
1	gc	93	PRO	N-CA-CB	-5.85	98.93	102.79
1	gk	486	GLU	CA-C-N	5.85	132.72	121.54
1	gk	486	GLU	C-N-CA	5.85	132.72	121.54
1	eb	115	GLN	CA-C-N	5.85	125.81	119.78
1	eb	115	GLN	C-N-CA	5.85	125.81	119.78
1	fk	480	GLY	N-CA-C	5.85	119.31	110.18
1	hd	258	VAL	N-CA-C	5.85	117.18	108.46
1	de	344	ARG	N-CA-C	-5.85	100.17	109.23
3	jf	38	VAL	N-CA-C	5.85	116.71	108.17
3	nq	72	ASN	CA-CB-CG	5.85	118.45	112.60
1	bb	121	THR	N-CA-C	5.85	119.46	111.39
1	ca	403	GLY	N-CA-C	5.85	121.05	113.27
1	di	426	ASP	CA-CB-CG	-5.85	106.75	112.60
3	ku	38	VAL	N-CA-C	5.85	116.70	108.17
1	ay	92	GLY	CA-C-N	5.84	127.15	119.84
1	ay	92	GLY	C-N-CA	5.84	127.15	119.84
1	eg	253	ARG	N-CA-C	5.84	120.70	112.93
1	gp	403	GLY	N-CA-C	5.84	121.04	113.27
1	gv	259	ILE	N-CA-C	5.84	116.28	107.75
3	in	41	ILE	N-CA-C	5.84	116.28	107.80
1	ba	269	ALA	N-CA-C	5.84	119.45	111.39
1	bt	403	GLY	N-CA-C	5.84	120.89	113.24
1	ep	115	GLN	CA-C-N	5.84	126.17	119.92
1	ep	115	GLN	C-N-CA	5.84	126.17	119.92
1	fi	121	THR	CB-CA-C	-5.84	103.09	112.09
2	hh	420	LEU	CA-C-N	5.84	125.80	119.78
2	hh	420	LEU	C-N-CA	5.84	125.80	119.78
1	bq	110	ASP	CA-CB-CG	5.84	118.44	112.60
1	cg	115	GLN	CA-C-N	5.84	125.80	119.78
1	cg	115	GLN	C-N-CA	5.84	125.80	119.78
1	fh	484	PHE	CA-CB-CG	5.84	119.64	113.80
1	fw	463	ASP	CA-C-N	5.84	127.14	119.84
1	fw	463	ASP	C-N-CA	5.84	127.14	119.84
1	fz	468	GLN	CA-C-N	5.84	125.75	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fz	468	GLN	C-N-CA	5.84	125.75	119.85
1	gn	209	ASP	CA-CB-CG	5.84	118.44	112.60
1	gx	245	ASN	CA-C-N	5.84	125.75	119.85
1	gx	245	ASN	C-N-CA	5.84	125.75	119.85
3	ld	67	GLU	N-CA-C	-5.84	104.51	111.69
1	ad	103	ILE	CA-C-N	5.84	125.75	119.85
1	ad	103	ILE	C-N-CA	5.84	125.75	119.85
1	aq	253	ARG	N-CA-C	5.84	120.19	111.96
1	dl	209	ASP	CA-CB-CG	5.84	118.44	112.60
1	ez	336	ASP	CA-C-N	5.84	126.24	119.47
1	ez	336	ASP	C-N-CA	5.84	126.24	119.47
1	fk	226	GLU	N-CA-C	5.84	117.41	108.42
1	fs	403	GLY	N-CA-C	5.84	120.89	113.24
1	gc	480	GLY	N-CA-C	5.84	119.29	110.18
1	go	115	GLN	CA-C-N	5.84	125.79	119.78
1	go	115	GLN	C-N-CA	5.84	125.79	119.78
1	do	468	GLN	CA-C-N	5.84	125.77	119.76
1	do	468	GLN	C-N-CA	5.84	125.77	119.76
1	ei	324	THR	N-CA-C	-5.84	100.92	109.50
1	er	209	ASP	CA-CB-CG	5.84	118.44	112.60
1	gs	395	TYR	N-CA-C	5.84	117.33	110.97
1	hd	259	ILE	N-CA-C	5.84	116.89	108.48
1	cp	463	ASP	CA-C-N	5.83	125.51	119.56
1	cp	463	ASP	C-N-CA	5.83	125.51	119.56
1	di	250	MET	N-CA-C	5.83	117.94	109.07
1	fh	176	ASP	CA-CB-CG	5.83	118.44	112.60
1	fm	74	TYR	CB-CA-C	5.83	120.87	111.36
1	gc	480	GLY	CA-C-N	5.83	129.71	121.66
1	gc	480	GLY	C-N-CA	5.83	129.71	121.66
2	hn	420	LEU	CA-C-N	5.83	125.79	119.78
2	hn	420	LEU	C-N-CA	5.83	125.79	119.78
1	ek	93	PRO	N-CA-CB	-5.83	98.94	102.79
1	eq	468	GLN	CA-C-N	5.83	125.74	119.85
1	eq	468	GLN	C-N-CA	5.83	125.74	119.85
1	fu	468	GLN	CA-C-N	5.83	125.74	119.85
1	fu	468	GLN	C-N-CA	5.83	125.74	119.85
3	lb	49	PHE	CA-C-N	5.83	126.03	120.31
3	lb	49	PHE	C-N-CA	5.83	126.03	120.31
3	nn	37	ASP	CA-CB-CG	5.83	118.43	112.60
1	by	245	ASN	CA-C-N	5.83	125.80	120.03
1	by	245	ASN	C-N-CA	5.83	125.80	120.03
1	ei	103	ILE	CA-C-N	5.83	125.74	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ei	103	ILE	C-N-CA	5.83	125.74	119.85
1	ex	149	GLY	CA-C-N	5.83	125.74	119.85
1	ex	149	GLY	C-N-CA	5.83	125.74	119.85
3	ip	38	VAL	N-CA-C	5.83	116.68	108.17
1	at	222	VAL	N-CA-C	5.83	118.57	108.95
1	cx	151	ASP	CA-CB-CG	5.83	118.43	112.60
1	ds	403	GLY	N-CA-C	5.83	120.88	113.24
1	br	245	ASN	CA-C-N	5.83	125.80	120.03
1	br	245	ASN	C-N-CA	5.83	125.80	120.03
1	dh	75	ASN	CA-CB-CG	-5.83	106.77	112.60
1	eq	483	PRO	N-CA-C	-5.83	102.05	111.14
3	lt	46	TYR	N-CA-C	5.83	117.82	109.14
1	gb	119	SER	CA-C-N	5.83	125.80	120.03
1	gb	119	SER	C-N-CA	5.83	125.80	120.03
1	gy	145	HIS	CA-C-N	5.83	125.50	119.56
1	gy	145	HIS	C-N-CA	5.83	125.50	119.56
1	bf	232	ILE	N-CA-C	-5.83	106.14	111.67
1	cs	93	PRO	N-CA-CB	-5.83	98.94	102.79
1	cy	93	PRO	N-CA-CB	-5.83	98.95	102.79
1	dt	110	ASP	CA-CB-CG	5.83	118.43	112.60
1	dv	256	LYS	N-CA-C	5.83	117.92	109.07
1	et	149	GLY	CA-C-N	5.83	125.80	120.03
1	et	149	GLY	C-N-CA	5.83	125.80	120.03
1	bi	491	ALA	CA-C-N	5.82	125.73	119.85
1	bi	491	ALA	C-N-CA	5.82	125.73	119.85
1	fo	238	GLY	N-CA-C	5.82	123.39	115.30
1	gy	287	ASP	N-CA-C	-5.82	104.15	112.13
1	az	258	VAL	N-CA-C	5.82	118.56	108.95
1	fs	446	ALA	N-CA-C	5.82	120.40	113.12
1	gi	324	THR	N-CA-C	-5.82	102.31	109.65
1	gy	463	ASP	CA-C-N	5.82	125.50	119.56
1	gy	463	ASP	C-N-CA	5.82	125.50	119.56
1	bq	184	GLU	N-CA-C	-5.82	100.50	109.52
1	cq	285	ASP	CA-C-N	5.82	132.66	121.54
1	cq	285	ASP	C-N-CA	5.82	132.66	121.54
1	ds	484	PHE	CA-CB-CG	5.82	119.62	113.80
1	fh	324	THR	N-CA-C	-5.82	100.94	109.50
3	nl	38	VAL	N-CA-C	5.82	117.06	108.45
1	ad	182	PHE	CA-CB-CG	5.82	119.62	113.80
1	at	232	ILE	N-CA-C	-5.82	106.04	111.45
1	bl	484	PHE	CA-CB-CG	5.82	119.62	113.80
1	cb	263	SER	N-CA-C	5.82	117.06	108.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dj	256	LYS	N-CA-C	5.82	118.03	109.24
1	bj	259	ILE	N-CA-C	5.82	116.24	107.75
1	cb	468	GLN	CA-C-N	5.82	125.73	119.85
1	cb	468	GLN	C-N-CA	5.82	125.73	119.85
1	eh	324	THR	CB-CA-C	5.82	116.84	110.15
1	eu	468	GLN	CA-C-N	5.82	125.73	119.85
1	eu	468	GLN	C-N-CA	5.82	125.73	119.85
1	fg	468	GLN	CA-C-N	5.82	125.73	119.85
1	fg	468	GLN	C-N-CA	5.82	125.73	119.85
1	fn	467	PHE	CA-CB-CG	5.82	119.62	113.80
1	fz	103	ILE	CA-C-N	5.82	125.83	119.90
1	fz	103	ILE	C-N-CA	5.82	125.83	119.90
1	ex	287	ASP	N-CA-C	-5.82	105.19	112.93
1	fh	274	LEU	CB-CA-C	-5.82	101.75	110.88
1	fw	184	GLU	N-CA-C	-5.82	101.58	109.95
1	df	72	HIS	N-CA-C	-5.81	100.66	109.85
1	bc	245	ASN	CA-C-N	5.81	125.78	120.03
1	bc	245	ASN	C-N-CA	5.81	125.78	120.03
1	bs	222	VAL	N-CA-C	5.81	118.54	108.95
1	ee	463	ASP	CA-C-N	5.81	125.49	119.56
1	ee	463	ASP	C-N-CA	5.81	125.49	119.56
1	ey	491	ALA	CA-C-N	5.81	126.30	120.14
1	ey	491	ALA	C-N-CA	5.81	126.30	120.14
1	gi	245	ASN	CA-C-N	5.81	125.72	119.85
1	gi	245	ASN	C-N-CA	5.81	125.72	119.85
3	mo	37	ASP	CA-CB-CG	5.81	118.41	112.60
1	aa	468	GLN	CA-C-N	5.81	125.72	119.85
1	aa	468	GLN	C-N-CA	5.81	125.72	119.85
1	ac	412	VAL	N-CA-C	-5.81	106.81	111.81
1	av	134	ASP	CA-C-N	5.81	125.43	119.56
1	av	134	ASP	C-N-CA	5.81	125.43	119.56
1	bg	463	ASP	CA-C-N	5.81	125.48	119.56
1	bg	463	ASP	C-N-CA	5.81	125.48	119.56
1	gt	463	ASP	CA-C-N	5.81	125.49	119.56
1	gt	463	ASP	C-N-CA	5.81	125.49	119.56
1	bp	463	ASP	CA-C-N	5.81	125.42	119.56
1	bp	463	ASP	C-N-CA	5.81	125.42	119.56
1	ci	186	GLY	N-CA-C	5.81	121.82	111.02
1	co	446	ALA	N-CA-C	5.81	117.61	111.28
1	cw	256	LYS	N-CA-C	5.81	117.90	109.07
1	df	121	THR	N-CA-C	5.81	119.25	111.24
1	fq	154	PHE	CA-CB-CG	5.81	119.61	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ee	110	ASP	CA-CB-CG	5.81	118.41	112.60
1	ag	402	THR	CA-C-N	5.80	127.44	120.13
1	ag	402	THR	C-N-CA	5.80	127.44	120.13
1	ax	245	ASN	CA-C-N	5.80	125.78	120.03
1	ax	245	ASN	C-N-CA	5.80	125.78	120.03
1	cl	483	PRO	N-CA-C	-5.80	102.08	111.14
1	ee	121	THR	CB-CA-C	-5.80	103.15	112.09
1	fi	134	ASP	CA-C-N	5.80	125.42	119.56
1	fi	134	ASP	C-N-CA	5.80	125.42	119.56
1	gf	328	LYS	N-CA-C	5.80	120.22	113.20
1	ag	72	HIS	CA-CB-CG	-5.80	108.00	113.80
1	gc	256	LYS	N-CA-C	5.80	117.89	109.07
3	ms	38	VAL	N-CA-C	5.80	116.64	108.17
1	dc	115	GLN	CA-C-N	5.80	125.76	119.78
1	dc	115	GLN	C-N-CA	5.80	125.76	119.78
1	ev	119	SER	N-CA-C	-5.80	101.52	108.25
3	mg	46	TYR	N-CA-C	5.80	117.78	109.14
1	bu	403	GLY	N-CA-C	5.80	120.98	113.27
2	hl	370	GLN	CA-C-N	5.80	125.71	119.85
2	hl	370	GLN	C-N-CA	5.80	125.71	119.85
1	dg	222	VAL	N-CA-C	5.80	118.52	108.95
1	dh	196	VAL	N-CA-C	5.80	116.64	108.17
1	fk	209	ASP	CA-CB-CG	5.80	118.40	112.60
1	ch	483	PRO	N-CA-C	-5.80	101.99	111.21
1	em	209	ASP	CA-CB-CG	5.80	118.40	112.60
1	ev	245	ASN	CA-C-N	5.80	125.77	120.03
1	ev	245	ASN	C-N-CA	5.80	125.77	120.03
1	ff	115	GLN	CA-C-N	5.80	125.77	120.03
1	ff	115	GLN	C-N-CA	5.80	125.77	120.03
1	em	491	ALA	CA-C-N	5.79	126.28	120.14
1	em	491	ALA	C-N-CA	5.79	126.28	120.14
1	ae	184	GLU	N-CA-C	-5.79	101.16	110.14
1	ak	468	GLN	CA-C-N	5.79	125.70	119.85
1	ak	468	GLN	C-N-CA	5.79	125.70	119.85
1	cy	468	GLN	CA-C-N	5.79	125.70	119.85
1	cy	468	GLN	C-N-CA	5.79	125.70	119.85
1	ey	222	VAL	N-CA-C	5.79	118.03	108.99
1	ff	103	ILE	CA-C-N	5.79	125.75	119.78
1	ff	103	ILE	C-N-CA	5.79	125.75	119.78
2	hf	420	LEU	CA-C-N	5.79	125.70	119.85
2	hf	420	LEU	C-N-CA	5.79	125.70	119.85
3	ky	37	ASP	CA-CB-CG	5.79	118.39	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	ld	38	VAL	N-CA-C	5.79	116.63	108.17
3	mi	44	ALA	N-CA-C	5.79	120.34	113.16
1	ca	115	GLN	CA-C-N	5.79	125.76	120.03
1	ca	115	GLN	C-N-CA	5.79	125.76	120.03
1	dl	451	ALA	CA-C-N	5.79	125.73	119.76
1	dl	451	ALA	C-N-CA	5.79	125.73	119.76
1	eq	182	PHE	CA-CB-CG	5.79	119.59	113.80
2	hn	286	GLY	N-CA-C	-5.79	101.71	112.37
3	ml	67	GLU	N-CA-C	-5.79	105.05	111.36
1	aa	403	GLY	N-CA-C	5.79	120.97	113.27
1	ar	271	SER	N-CA-C	5.79	119.09	110.52
1	de	71	ASP	CA-CB-CG	5.79	118.39	112.60
1	eg	71	ASP	CA-CB-CG	5.79	118.39	112.60
1	gb	182	PHE	CA-CB-CG	5.79	119.59	113.80
1	gl	480	GLY	CA-C-N	5.79	129.65	121.66
1	gl	480	GLY	C-N-CA	5.79	129.65	121.66
1	ai	232	ILE	N-CA-C	-5.79	105.21	110.82
1	ao	88	VAL	N-CA-C	5.79	116.20	107.75
1	at	468	GLN	CA-C-N	5.79	125.69	119.85
1	at	468	GLN	C-N-CA	5.79	125.69	119.85
1	dy	92	GLY	CA-C-N	5.79	125.49	119.82
1	dy	92	GLY	C-N-CA	5.79	125.49	119.82
1	ep	287	ASP	N-CA-C	-5.79	104.20	112.13
1	ah	93	PRO	N-CA-CB	-5.79	98.97	102.79
1	ak	328	LYS	N-CA-C	5.79	120.34	112.88
1	ek	468	GLN	CA-C-N	5.79	125.69	119.85
1	ek	468	GLN	C-N-CA	5.79	125.69	119.85
1	fu	236	GLN	CA-C-N	5.79	130.96	122.63
1	fu	236	GLN	C-N-CA	5.79	130.96	122.63
1	au	358	ASP	CA-CB-CG	5.78	118.38	112.60
1	be	484	PHE	CA-CB-CG	5.78	119.58	113.80
1	bj	491	ALA	CA-C-N	5.78	126.27	120.14
1	bj	491	ALA	C-N-CA	5.78	126.27	120.14
1	cc	287	ASP	N-CA-C	-5.78	104.21	112.13
1	cs	328	LYS	N-CA-C	5.78	120.49	113.38
2	hg	353	ASP	CA-C-N	5.78	127.07	119.84
2	hg	353	ASP	C-N-CA	5.78	127.07	119.84
1	dq	115	GLN	CA-C-N	5.78	125.73	119.78
1	dq	115	GLN	C-N-CA	5.78	125.73	119.78
1	gr	68	ILE	CA-C-N	5.78	126.36	119.94
1	gr	68	ILE	C-N-CA	5.78	126.36	119.94
1	co	87	ALA	N-CA-C	5.78	117.58	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dg	269	ALA	N-CA-C	5.78	117.67	110.91
1	fi	445	ASP	CA-C-N	5.78	128.50	120.29
1	fi	445	ASP	C-N-CA	5.78	128.50	120.29
1	fo	151	ASP	CA-CB-CG	5.78	118.38	112.60
1	fw	263	SER	N-CA-C	5.78	117.01	108.86
1	gf	115	GLN	CA-C-N	5.78	125.75	120.03
1	gf	115	GLN	C-N-CA	5.78	125.75	120.03
1	cn	115	GLN	CA-C-N	5.78	125.73	119.78
1	cn	115	GLN	C-N-CA	5.78	125.73	119.78
1	gp	256	LYS	N-CA-C	5.78	118.19	109.23
1	ae	484	PHE	CA-CB-CG	5.78	119.58	113.80
1	av	468	GLN	CA-C-N	5.78	125.69	119.85
1	av	468	GLN	C-N-CA	5.78	125.69	119.85
1	bg	258	VAL	N-CA-C	5.78	116.44	108.12
1	ce	149	GLY	CA-C-N	5.78	125.69	119.85
1	ce	149	GLY	C-N-CA	5.78	125.69	119.85
1	cn	149	GLY	CA-C-N	5.78	125.69	119.85
1	cn	149	GLY	C-N-CA	5.78	125.69	119.85
1	cw	403	GLY	N-CA-C	5.78	120.95	113.27
1	df	134	ASP	CA-C-N	5.78	125.91	119.32
1	df	134	ASP	C-N-CA	5.78	125.91	119.32
1	gn	91	ILE	N-CA-C	5.78	115.96	110.53
3	mz	44	ALA	N-CA-C	5.78	120.32	113.16
1	eo	259	ILE	N-CA-C	5.78	116.44	108.12
1	gd	119	SER	CA-C-N	5.78	125.75	120.03
1	gd	119	SER	C-N-CA	5.78	125.75	120.03
1	gw	451	ALA	CA-C-N	5.78	125.71	119.76
1	gw	451	ALA	C-N-CA	5.78	125.71	119.76
2	hf	343	ALA	CA-C-N	5.78	125.68	119.85
2	hf	343	ALA	C-N-CA	5.78	125.68	119.85
1	cw	92	GLY	CA-C-N	5.77	127.06	119.84
1	cw	92	GLY	C-N-CA	5.77	127.06	119.84
1	hb	88	VAL	N-CA-C	5.77	116.18	107.75
1	gr	134	ASP	CA-C-N	5.77	125.45	119.56
1	gr	134	ASP	C-N-CA	5.77	125.45	119.56
3	ih	46	TYR	N-CA-C	5.77	117.56	108.96
1	cx	463	ASP	CA-C-N	5.77	125.44	119.56
1	cx	463	ASP	C-N-CA	5.77	125.44	119.56
1	dm	287	ASP	N-CA-C	-5.77	104.23	112.13
1	fc	145	HIS	CA-C-N	5.77	125.44	119.56
1	fc	145	HIS	C-N-CA	5.77	125.44	119.56
1	gc	154	PHE	N-CA-C	-5.77	105.25	112.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gh	451	ALA	CA-C-N	5.77	125.70	119.76
1	gh	451	ALA	C-N-CA	5.77	125.70	119.76
1	gr	209	ASP	CA-CB-CG	5.77	118.37	112.60
1	gu	134	ASP	CA-C-N	5.77	125.44	119.56
1	gu	134	ASP	C-N-CA	5.77	125.44	119.56
1	gx	145	HIS	CA-C-N	5.77	125.39	119.56
1	gx	145	HIS	C-N-CA	5.77	125.39	119.56
2	hh	36	TYR	N-CA-C	-5.77	107.48	114.75
3	ln	17	LEU	N-CA-C	5.77	117.65	111.36
1	bg	265	GLN	N-CA-C	5.77	118.04	108.99
1	bx	271	SER	N-CA-C	5.77	118.33	110.55
1	cl	71	ASP	CA-CB-CG	5.77	118.37	112.60
1	co	134	ASP	CA-C-N	5.77	125.89	119.32
1	co	134	ASP	C-N-CA	5.77	125.89	119.32
1	ew	484	PHE	CA-CB-CG	5.77	119.57	113.80
3	kp	46	TYR	N-CA-C	5.77	117.73	109.14
1	ck	186	GLY	N-CA-C	5.77	121.74	111.02
1	ga	87	ALA	CA-C-N	-5.77	115.59	123.14
1	ga	87	ALA	C-N-CA	-5.77	115.59	123.14
2	hi	136	LYS	N-CA-C	-5.77	106.38	113.41
1	an	483	PRO	N-CA-C	-5.76	102.15	111.14
1	fp	491	ALA	CA-C-N	5.76	126.25	120.14
1	fp	491	ALA	C-N-CA	5.76	126.25	120.14
1	gf	256	LYS	N-CA-C	5.76	117.55	108.96
1	gj	209	ASP	CA-CB-CG	5.76	118.36	112.60
2	hg	420	LEU	CA-C-N	5.76	125.72	119.78
2	hg	420	LEU	C-N-CA	5.76	125.72	119.78
3	kz	41	ILE	N-CA-C	5.76	116.72	107.73
1	ct	72	HIS	N-CA-C	-5.76	101.43	110.36
1	gc	121	THR	N-CA-C	5.76	119.19	111.24
3	kb	67	GLU	N-CA-C	-5.76	105.08	111.36
1	ab	110	ASP	CA-CB-CG	5.76	118.36	112.60
1	cs	412	VAL	N-CA-C	-5.76	106.86	111.81
1	cx	258	VAL	N-CA-C	5.76	117.05	108.46
1	dd	121	THR	CB-CA-C	-5.76	103.22	112.09
1	de	269	ALA	N-CA-C	5.76	119.34	111.39
1	fl	480	GLY	CA-C-N	5.76	129.61	121.66
1	fl	480	GLY	C-N-CA	5.76	129.61	121.66
1	fo	403	GLY	N-CA-C	5.76	120.79	113.24
1	gj	245	ASN	CA-C-N	5.76	125.73	120.03
1	gj	245	ASN	C-N-CA	5.76	125.73	120.03
3	of	46	TYR	N-CA-C	5.76	117.55	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	as	463	ASP	CA-C-N	5.76	125.44	119.56
1	as	463	ASP	C-N-CA	5.76	125.44	119.56
1	bw	245	ASN	CA-C-N	5.76	125.73	120.03
1	bw	245	ASN	C-N-CA	5.76	125.73	120.03
1	ff	484	PHE	CA-CB-CG	5.76	119.56	113.80
1	fs	163	PHE	CA-C-N	5.76	125.67	119.85
1	fs	163	PHE	C-N-CA	5.76	125.67	119.85
3	lk	38	VAL	N-CA-C	5.76	116.29	107.77
1	an	119	SER	CA-C-N	5.76	125.74	120.21
1	an	119	SER	C-N-CA	5.76	125.74	120.21
1	aw	491	ALA	CA-C-N	5.76	126.24	120.14
1	aw	491	ALA	C-N-CA	5.76	126.24	120.14
1	bi	93	PRO	N-CA-CB	-5.76	98.99	102.79
1	ex	468	GLN	CA-C-N	5.76	125.66	119.85
1	ex	468	GLN	C-N-CA	5.76	125.66	119.85
1	fm	463	ASP	CA-C-N	5.76	125.43	119.56
1	fm	463	ASP	C-N-CA	5.76	125.43	119.56
1	fr	463	ASP	CA-C-N	5.76	125.43	119.56
1	fr	463	ASP	C-N-CA	5.76	125.43	119.56
3	jz	38	VAL	N-CA-C	5.76	116.36	107.78
3	mz	67	GLU	N-CA-C	-5.76	105.09	111.36
1	eo	103	ILE	CA-C-N	5.75	125.73	120.03
1	eo	103	ILE	C-N-CA	5.75	125.73	120.03
1	ba	328	LYS	N-CA-C	5.75	120.46	113.38
1	bk	358	ASP	CA-CB-CG	5.75	118.35	112.60
1	dz	269	ALA	N-CA-C	5.75	119.33	111.39
1	em	103	ILE	CA-C-N	5.75	125.66	119.85
1	em	103	ILE	C-N-CA	5.75	125.66	119.85
1	fm	184	GLU	N-CA-C	-5.75	101.50	110.42
1	fu	130	VAL	N-CA-C	5.75	116.17	108.11
1	fv	93	PRO	N-CA-CB	-5.75	98.99	102.79
1	au	491	ALA	CA-C-N	5.75	126.24	120.14
1	au	491	ALA	C-N-CA	5.75	126.24	120.14
1	gx	121	THR	N-CA-C	5.75	119.18	111.24
2	hj	370	GLN	CA-C-N	5.75	125.72	120.03
2	hj	370	GLN	C-N-CA	5.75	125.72	120.03
1	by	481	ILE	N-CA-C	5.75	116.48	108.89
1	fp	484	PHE	CA-CB-CG	5.75	119.55	113.80
1	fv	463	ASP	CA-C-N	5.75	125.42	119.56
1	fv	463	ASP	C-N-CA	5.75	125.42	119.56
1	gg	403	GLY	N-CA-C	5.75	120.77	113.24
1	gm	506	SER	CA-C-N	-5.75	112.69	121.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gm	506	SER	C-N-CA	-5.75	112.69	121.66
1	ai	121	THR	N-CA-C	5.75	119.17	111.24
1	bp	408	THR	N-CA-C	-5.75	107.51	114.75
1	gh	184	GLU	N-CA-C	-5.75	101.67	109.95
3	nw	79	THR	N-CA-C	5.75	115.69	108.45
1	br	256	LYS	N-CA-C	5.75	117.80	109.07
1	ge	484	PHE	CA-CB-CG	5.75	119.55	113.80
2	ho	270	THR	N-CA-C	5.75	120.03	113.19
1	bi	256	LYS	N-CA-C	5.74	117.52	108.96
1	cn	449	TYR	CB-CA-C	-5.74	98.02	109.33
1	cr	265	GLN	N-CA-C	5.74	117.86	108.55
1	dl	115	GLN	CA-C-N	5.74	125.68	119.76
1	dl	115	GLN	C-N-CA	5.74	125.68	119.76
2	he	422	LYS	N-CA-C	5.74	118.60	110.50
1	ar	285	ASP	N-CA-C	5.74	117.62	111.36
1	bd	103	ILE	CA-C-N	5.74	126.06	119.92
1	bd	103	ILE	C-N-CA	5.74	126.06	119.92
1	cs	222	VAL	N-CA-C	5.74	118.42	108.95
1	dd	232	ILE	N-CA-C	-5.74	106.62	111.56
1	fl	263	SER	N-CA-C	5.74	119.02	110.52
2	hl	420	LEU	CA-C-N	5.74	125.65	119.85
2	hl	420	LEU	C-N-CA	5.74	125.65	119.85
3	ki	46	TYR	N-CA-C	5.74	117.70	109.14
3	ms	44	ALA	N-CA-C	5.74	119.98	112.92
1	cf	121	THR	N-CA-C	5.74	119.31	111.39
1	gc	324	THR	N-CA-C	-5.74	101.06	109.50
3	iy	44	ALA	N-CA-C	5.74	120.28	113.16
3	mq	44	ALA	N-CA-C	5.74	120.15	113.20
1	ed	253	ARG	N-CA-C	5.74	120.56	112.93
1	ej	269	ALA	N-CA-C	5.74	119.31	111.39
1	ha	88	VAL	N-CA-C	5.74	116.13	107.75
1	dc	245	ASN	CA-C-N	5.74	125.71	120.03
1	dc	245	ASN	C-N-CA	5.74	125.71	120.03
1	dg	119	SER	CA-C-N	5.74	125.71	120.03
1	dg	119	SER	C-N-CA	5.74	125.71	120.03
3	ig	32	PHE	CA-C-N	5.74	125.41	119.56
3	ig	32	PHE	C-N-CA	5.74	125.41	119.56
1	an	232	ILE	N-CA-C	-5.74	106.12	111.45
1	an	344	ARG	N-CA-C	-5.74	100.34	109.23
1	cx	336	ASP	CA-C-N	5.74	125.41	119.56
1	cx	336	ASP	C-N-CA	5.74	125.41	119.56
1	ds	182	PHE	CA-CB-CG	5.74	119.54	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fw	328	LYS	N-CA-C	5.74	120.44	113.38
1	ai	88	VAL	N-CA-C	5.73	116.36	107.99
1	de	343	ALA	N-CA-C	5.73	118.15	110.35
1	am	110	ASP	CA-CB-CG	5.73	118.33	112.60
1	bn	121	THR	CB-CA-C	-5.73	103.26	112.09
1	br	468	GLN	CA-C-N	5.73	125.64	119.85
1	br	468	GLN	C-N-CA	5.73	125.64	119.85
1	bs	403	GLY	N-CA-C	5.73	120.89	113.27
1	dh	491	ALA	CA-C-N	5.73	126.22	120.14
1	dh	491	ALA	C-N-CA	5.73	126.22	120.14
1	dy	484	PHE	CA-CB-CG	5.73	119.53	113.80
1	eu	245	ASN	CA-C-N	5.73	125.70	120.03
1	eu	245	ASN	C-N-CA	5.73	125.70	120.03
1	ew	88	VAL	N-CA-C	5.73	116.25	107.77
1	fo	468	GLN	CA-C-N	5.73	125.64	119.85
1	fo	468	GLN	C-N-CA	5.73	125.64	119.85
3	ih	67	GLU	N-CA-C	-5.73	105.11	111.36
1	av	336	ASP	CA-C-N	5.73	125.41	119.56
1	av	336	ASP	C-N-CA	5.73	125.41	119.56
1	bu	328	LYS	N-CA-C	5.73	120.27	113.16
1	bv	103	ILE	CA-C-N	5.73	125.75	119.90
1	bv	103	ILE	C-N-CA	5.73	125.75	119.90
1	dg	75	ASN	CA-CB-CG	-5.73	106.87	112.60
1	ds	119	SER	CA-C-N	5.73	125.70	120.03
1	ds	119	SER	C-N-CA	5.73	125.70	120.03
1	dx	483	PRO	N-CA-C	-5.73	102.10	111.21
1	eq	145	HIS	CA-C-N	5.73	125.41	119.56
1	eq	145	HIS	C-N-CA	5.73	125.41	119.56
1	bm	483	PRO	N-CA-C	-5.73	102.10	111.21
1	gh	285	ASP	CA-C-N	5.73	132.48	121.54
1	gh	285	ASP	C-N-CA	5.73	132.48	121.54
1	dr	121	THR	CB-CA-C	-5.73	103.27	112.09
1	fg	490	GLN	N-CA-C	-5.73	105.01	112.23
1	fj	113	GLY	N-CA-C	-5.73	103.84	112.89
1	ga	119	SER	CA-C-N	5.73	125.70	120.03
1	ga	119	SER	C-N-CA	5.73	125.70	120.03
3	jk	67	GLU	N-CA-C	-5.73	104.64	111.69
1	am	151	ASP	CA-CB-CG	5.73	118.33	112.60
1	gb	86	GLY	CA-C-N	5.73	128.53	120.28
1	gb	86	GLY	C-N-CA	5.73	128.53	120.28
1	bn	336	ASP	CA-C-N	5.72	126.11	119.47
1	bn	336	ASP	C-N-CA	5.72	126.11	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cg	253	ARG	N-CA-C	5.72	120.54	112.93
1	cj	103	ILE	CA-C-N	5.72	125.66	119.76
1	cj	103	ILE	C-N-CA	5.72	125.66	119.76
1	cz	93	PRO	N-CA-CB	-5.72	99.01	102.79
1	gi	222	VAL	N-CA-C	5.72	118.39	108.95
3	id	67	GLU	N-CA-C	-5.72	105.12	111.36
1	ab	440	GLY	CA-C-N	5.72	125.40	119.56
1	ab	440	GLY	C-N-CA	5.72	125.40	119.56
1	dw	468	GLN	CA-C-N	5.72	125.67	119.78
1	dw	468	GLN	C-N-CA	5.72	125.67	119.78
1	ei	403	GLY	N-CA-C	5.72	120.74	113.24
1	et	468	GLN	CA-C-N	5.72	125.63	119.85
1	et	468	GLN	C-N-CA	5.72	125.63	119.85
1	cr	463	ASP	CA-C-N	5.72	125.39	119.56
1	cr	463	ASP	C-N-CA	5.72	125.39	119.56
1	ef	232	ILE	N-CA-C	-5.72	106.23	111.67
1	fe	103	ILE	CA-C-N	5.72	125.67	119.78
1	fe	103	ILE	C-N-CA	5.72	125.67	119.78
1	am	198	ILE	N-CA-C	5.72	112.33	106.21
1	cv	440	GLY	CA-C-N	5.72	125.39	119.56
1	cv	440	GLY	C-N-CA	5.72	125.39	119.56
1	ft	463	ASP	CA-C-N	5.72	125.39	119.56
1	ft	463	ASP	C-N-CA	5.72	125.39	119.56
2	hg	268	THR	N-CA-C	5.72	120.10	113.18
3	kh	32	PHE	CA-C-N	5.72	125.39	119.56
3	kh	32	PHE	C-N-CA	5.72	125.39	119.56
1	av	406	THR	N-CA-C	-5.72	106.93	114.31
1	bx	258	VAL	N-CA-C	5.72	116.71	108.48
1	co	484	PHE	CA-CB-CG	5.72	119.52	113.80
1	bb	121	THR	CB-CA-C	-5.72	103.77	111.89
1	cf	256	LYS	N-CA-C	5.72	117.76	109.07
1	dg	186	GLY	N-CA-C	5.72	121.65	111.02
2	he	21	ARG	CA-C-N	5.72	125.91	120.31
2	he	21	ARG	C-N-CA	5.72	125.91	120.31
3	ik	38	VAL	N-CA-C	5.72	116.52	108.17
1	da	121	THR	CB-CA-C	-5.71	103.29	112.09
1	gm	92	GLY	CA-C-N	5.71	125.42	119.82
1	gm	92	GLY	C-N-CA	5.71	125.42	119.82
1	gz	184	GLU	N-CA-C	-5.71	101.72	109.95
1	hc	93	PRO	N-CA-CB	-5.71	99.02	102.79
2	hg	21	ARG	CA-C-N	5.71	125.69	120.03
2	hg	21	ARG	C-N-CA	5.71	125.69	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bk	293	ILE	N-CA-C	-5.71	105.28	110.82
1	fx	93	PRO	N-CA-C	5.71	120.19	112.48
1	ac	121	THR	CB-CA-C	-5.71	103.30	112.09
1	bl	491	ALA	CA-C-N	5.71	126.19	120.14
1	bl	491	ALA	C-N-CA	5.71	126.19	120.14
1	el	245	ASN	CA-C-N	5.71	125.69	120.03
1	el	245	ASN	C-N-CA	5.71	125.69	120.03
1	eo	328	LYS	N-CA-C	5.71	120.41	113.38
1	fj	245	ASN	CA-C-N	5.71	125.62	119.85
1	fj	245	ASN	C-N-CA	5.71	125.62	119.85
1	gy	222	VAL	N-CA-C	5.71	117.90	108.99
1	cn	119	SER	CA-C-N	5.71	126.17	120.52
1	cn	119	SER	C-N-CA	5.71	126.17	120.52
1	gx	480	GLY	N-CA-C	5.71	120.04	110.56
1	am	490	GLN	N-CA-C	-5.71	106.66	113.97
1	br	258	VAL	N-CA-C	5.71	116.70	108.48
1	cf	483	PRO	N-CA-C	-5.71	102.23	111.14
1	cz	480	GLY	N-CA-C	5.71	119.08	110.18
1	gs	103	ILE	CA-C-N	5.71	125.64	119.76
1	gs	103	ILE	C-N-CA	5.71	125.64	119.76
1	gt	468	GLN	CA-C-N	5.71	125.61	119.85
1	gt	468	GLN	C-N-CA	5.71	125.61	119.85
3	kt	46	TYR	N-CA-C	5.71	117.65	109.14
1	df	87	ALA	CA-C-N	-5.71	115.51	123.10
1	df	87	ALA	C-N-CA	-5.71	115.51	123.10
1	dv	265	GLN	N-CA-C	5.71	117.80	108.55
1	ep	121	THR	N-CA-C	5.71	119.12	111.24
1	fe	440	GLY	CA-C-N	5.71	125.38	119.56
1	fe	440	GLY	C-N-CA	5.71	125.38	119.56
1	fo	336	ASP	CA-C-N	5.71	126.09	119.47
1	fo	336	ASP	C-N-CA	5.71	126.09	119.47
2	ho	231	THR	N-CA-C	5.71	118.19	110.88
1	bq	103	ILE	CA-C-N	5.71	125.66	119.78
1	bq	103	ILE	C-N-CA	5.71	125.66	119.78
1	fr	113	GLY	N-CA-C	-5.71	103.67	112.85
1	ao	253	ARG	N-CA-C	5.70	119.69	111.02
1	ba	402	THR	CA-C-N	5.70	127.31	120.13
1	ba	402	THR	C-N-CA	5.70	127.31	120.13
1	bh	256	LYS	N-CA-C	5.70	117.74	109.07
1	bh	336	ASP	CA-C-N	5.70	126.09	119.47
1	bh	336	ASP	C-N-CA	5.70	126.09	119.47
1	bt	468	GLN	CA-C-N	5.70	125.61	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bt	468	GLN	C-N-CA	5.70	125.61	119.85
1	cj	87	ALA	N-CA-C	5.70	117.50	111.28
1	db	483	PRO	N-CA-C	-5.70	102.14	111.21
1	dj	383	VAL	N-CA-C	-5.70	105.53	111.58
1	dx	71	ASP	CA-CB-CG	5.70	118.30	112.60
1	ej	259	ILE	N-CA-C	5.70	116.82	107.24
1	cb	209	ASP	CA-CB-CG	5.70	118.30	112.60
1	cq	463	ASP	CA-C-N	5.70	125.38	119.56
1	cq	463	ASP	C-N-CA	5.70	125.38	119.56
1	dx	88	VAL	N-CA-C	5.70	116.07	107.75
1	eb	449	TYR	CB-CA-C	-5.70	98.48	109.37
1	fg	232	ILE	CB-CA-C	-5.70	105.07	111.80
1	gm	236	GLN	CA-C-N	5.70	130.84	122.63
1	gm	236	GLN	C-N-CA	5.70	130.84	122.63
1	ds	130	VAL	N-CA-C	5.70	116.09	108.11
1	fl	115	GLN	CA-C-N	5.70	125.67	120.03
1	fl	115	GLN	C-N-CA	5.70	125.67	120.03
1	fy	88	VAL	N-CA-C	5.70	116.07	107.75
3	jt	67	GLU	N-CA-C	-5.70	105.15	111.36
3	lz	74	ASP	CA-CB-CG	5.70	118.30	112.60
1	ad	121	THR	CB-CA-C	-5.70	103.80	111.89
1	fy	483	PRO	N-CA-C	-5.70	102.15	111.21
1	gt	115	GLN	CA-C-N	5.70	125.65	119.78
1	gt	115	GLN	C-N-CA	5.70	125.65	119.78
1	dm	93	PRO	N-CA-CB	-5.70	99.03	102.79
1	do	256	LYS	N-CA-C	5.70	117.63	109.14
1	gr	468	GLN	CA-C-N	5.70	125.60	119.85
1	gr	468	GLN	C-N-CA	5.70	125.60	119.85
2	he	384	ASN	CA-C-N	5.70	125.70	119.89
2	he	384	ASN	C-N-CA	5.70	125.70	119.89
3	ip	17	LEU	N-CA-C	5.70	118.43	111.82
1	fa	265	GLN	N-CA-C	5.69	118.49	108.75
3	ka	37	ASP	CA-CB-CG	5.69	118.29	112.60
1	ba	209	ASP	CA-CB-CG	5.69	118.29	112.60
1	cx	115	GLN	CA-C-N	5.69	125.64	119.78
1	cx	115	GLN	C-N-CA	5.69	125.64	119.78
3	im	44	ALA	N-CA-C	5.69	120.22	113.16
3	lo	49	PHE	CA-C-N	5.69	125.89	120.31
3	lo	49	PHE	C-N-CA	5.69	125.89	120.31
1	af	103	ILE	CA-C-N	5.69	125.60	119.85
1	af	103	ILE	C-N-CA	5.69	125.60	119.85
1	ap	151	ASP	CA-CB-CG	5.69	118.29	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bi	115	GLN	CA-C-N	5.69	125.64	119.78
1	bi	115	GLN	C-N-CA	5.69	125.64	119.78
1	bt	87	ALA	N-CA-C	5.69	117.48	111.28
1	fg	403	GLY	N-CA-C	5.69	120.70	113.24
1	fo	474	LYS	N-CA-C	5.69	118.38	108.76
1	gn	468	GLN	CA-C-N	5.69	125.60	119.85
1	gn	468	GLN	C-N-CA	5.69	125.60	119.85
1	bi	468	GLN	CA-C-N	5.69	125.64	119.78
1	bi	468	GLN	C-N-CA	5.69	125.64	119.78
3	iq	46	TYR	N-CA-C	5.69	117.62	109.14
1	av	149	GLY	CA-C-N	5.69	125.59	119.85
1	av	149	GLY	C-N-CA	5.69	125.59	119.85
1	dd	256	LYS	N-CA-C	5.69	117.72	109.07
1	dj	328	LYS	N-CA-C	5.69	120.21	113.16
1	ee	329	ALA	N-CA-C	5.69	117.56	110.91
3	mc	37	ASP	CA-CB-CG	5.69	118.29	112.60
1	ar	72	HIS	N-CA-C	-5.68	100.87	109.85
1	dc	402	THR	CA-C-N	5.68	127.25	120.14
1	dc	402	THR	C-N-CA	5.68	127.25	120.14
1	dz	259	ILE	N-CA-C	5.68	116.32	107.28
1	fi	110	ASP	CA-CB-CG	5.68	118.28	112.60
2	hm	303	TYR	N-CA-C	-5.68	104.99	111.07
1	bl	154	PHE	N-CA-C	-5.68	105.45	112.72
1	br	259	ILE	N-CA-C	5.68	116.31	107.28
1	dt	440	GLY	CA-C-N	5.68	125.35	119.56
1	dt	440	GLY	C-N-CA	5.68	125.35	119.56
1	fp	232	ILE	N-CA-C	-5.68	105.31	110.82
1	cw	486	GLU	CA-C-N	5.68	132.39	121.54
1	cw	486	GLU	C-N-CA	5.68	132.39	121.54
1	ej	115	GLN	CA-C-N	5.68	125.63	119.78
1	ej	115	GLN	C-N-CA	5.68	125.63	119.78
1	fc	151	ASP	CA-CB-CG	5.68	118.28	112.60
1	fc	500	MET	CA-C-N	5.68	126.94	119.84
1	fc	500	MET	C-N-CA	5.68	126.94	119.84
1	gj	406	THR	N-CA-C	-5.68	106.23	114.12
1	gs	263	SER	N-CA-C	5.68	118.04	109.41
3	lf	67	GLU	N-CA-C	-5.68	105.17	111.36
1	at	425	ILE	N-CA-C	5.68	116.28	107.99
1	cx	245	ASN	CA-C-N	5.68	125.65	120.03
1	cx	245	ASN	C-N-CA	5.68	125.65	120.03
1	et	256	LYS	N-CA-C	5.68	118.03	109.23
1	fp	463	ASP	CA-C-N	5.68	125.35	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fp	463	ASP	C-N-CA	5.68	125.35	119.56
1	ga	403	GLY	N-CA-C	5.68	120.68	113.24
1	bp	425	ILE	N-CA-C	5.68	116.03	107.80
1	fh	425	ILE	N-CA-C	5.68	116.28	107.99
1	ac	93	PRO	N-CA-CB	-5.67	99.05	102.79
1	aq	468	GLN	CA-C-N	5.67	125.58	119.85
1	aq	468	GLN	C-N-CA	5.67	125.58	119.85
1	aw	103	ILE	CA-C-N	5.67	125.61	119.76
1	aw	103	ILE	C-N-CA	5.67	125.61	119.76
1	bo	486	GLU	CA-C-N	5.67	132.38	121.54
1	bo	486	GLU	C-N-CA	5.67	132.38	121.54
1	en	468	GLN	CA-C-N	5.67	125.58	119.85
1	en	468	GLN	C-N-CA	5.67	125.58	119.85
1	gq	253	ARG	N-CA-C	5.67	120.48	112.93
1	gr	463	ASP	CA-C-N	5.67	125.35	119.56
1	gr	463	ASP	C-N-CA	5.67	125.35	119.56
2	hl	291	LYS	CA-C-N	5.67	126.93	119.84
2	hl	291	LYS	C-N-CA	5.67	126.93	119.84
3	nl	44	ALA	N-CA-C	5.67	120.06	113.20
1	dn	121	THR	CB-CA-C	-5.67	103.15	112.06
1	dq	253	ARG	N-CA-C	5.67	120.47	112.93
1	du	412	VAL	N-CA-C	-5.67	106.93	111.81
1	bm	402	THR	CA-C-N	5.67	127.28	120.13
1	bm	402	THR	C-N-CA	5.67	127.28	120.13
1	ek	293	ILE	N-CA-C	-5.67	105.32	110.82
1	ff	265	GLN	N-CA-C	5.67	118.45	108.75
1	gj	123	GLN	N-CA-C	5.67	116.03	108.38
1	ay	145	HIS	CA-C-N	5.67	125.34	119.56
1	ay	145	HIS	C-N-CA	5.67	125.34	119.56
1	ca	463	ASP	CA-C-N	5.67	125.34	119.56
1	ca	463	ASP	C-N-CA	5.67	125.34	119.56
1	dp	245	ASN	CA-C-N	5.67	125.64	120.03
1	dp	245	ASN	C-N-CA	5.67	125.64	120.03
1	fs	486	GLU	CA-C-N	5.67	132.37	121.54
1	fs	486	GLU	C-N-CA	5.67	132.37	121.54
1	hd	271	SER	N-CA-C	5.67	118.67	110.28
1	dr	245	ASN	CA-C-N	5.67	125.57	119.85
1	dr	245	ASN	C-N-CA	5.67	125.57	119.85
1	dx	358	ASP	CA-CB-CG	5.67	118.27	112.60
1	ea	149	GLY	CA-C-N	5.67	125.57	119.85
1	ea	149	GLY	C-N-CA	5.67	125.57	119.85
1	gn	232	ILE	N-CA-C	-5.67	106.18	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	nh	38	VAL	N-CA-C	5.67	116.84	108.45
3	od	46	TYR	N-CA-C	5.67	117.58	109.14
1	bv	463	ASP	CA-C-N	5.67	125.34	119.56
1	bv	463	ASP	C-N-CA	5.67	125.34	119.56
1	gf	209	ASP	CA-CB-CG	5.67	118.27	112.60
1	gk	222	VAL	N-CA-C	5.67	118.30	108.95
1	cn	71	ASP	CA-CB-CG	5.67	118.27	112.60
1	bu	245	ASN	CA-C-N	5.66	125.57	119.85
1	bu	245	ASN	C-N-CA	5.66	125.57	119.85
1	dg	266	LEU	N-CA-C	5.66	118.01	109.23
1	dg	484	PHE	CA-CB-CG	5.66	119.46	113.80
1	eb	402	THR	CA-C-N	5.66	127.22	120.14
1	eb	402	THR	C-N-CA	5.66	127.22	120.14
1	gj	71	ASP	CA-CB-CG	5.66	118.26	112.60
1	hb	103	ILE	CA-C-N	5.66	125.61	119.78
1	hb	103	ILE	C-N-CA	5.66	125.61	119.78
3	je	67	GLU	N-CA-C	-5.66	105.19	111.36
1	as	403	GLY	N-CA-C	5.66	120.66	113.24
1	bb	271	SER	N-CA-C	5.66	118.19	110.55
1	by	176	ASP	CA-CB-CG	5.66	118.26	112.60
1	cs	343	ALA	N-CA-C	5.66	118.05	110.35
1	fd	115	GLN	CA-C-N	5.66	125.61	119.78
1	fd	115	GLN	C-N-CA	5.66	125.61	119.78
1	fs	451	ALA	CA-C-N	5.66	126.92	119.84
1	fs	451	ALA	C-N-CA	5.66	126.92	119.84
1	ft	93	PRO	N-CA-CB	-5.66	99.05	102.79
1	gs	403	GLY	N-CA-C	5.66	120.80	113.27
1	as	249	GLU	N-CA-C	5.66	116.84	108.86
1	cn	130	VAL	N-CA-C	5.66	116.27	108.12
1	ea	491	ALA	CA-C-N	5.66	125.57	119.85
1	ea	491	ALA	C-N-CA	5.66	125.57	119.85
1	ex	182	PHE	CA-CB-CG	5.66	119.46	113.80
1	go	93	PRO	N-CA-C	5.66	120.12	112.48
3	jc	10	ILE	N-CA-C	5.66	116.01	107.75
3	lu	67	GLU	N-CA-C	-5.66	105.19	111.36
1	ci	134	ASP	CA-C-N	5.66	125.28	119.56
1	ci	134	ASP	C-N-CA	5.66	125.28	119.56
3	ml	72	ASN	CA-CB-CG	5.66	118.26	112.60
1	ai	121	THR	CB-CA-C	-5.66	103.38	112.09
1	ct	115	GLN	CA-C-N	5.66	125.61	119.78
1	ct	115	GLN	C-N-CA	5.66	125.61	119.78
1	dm	222	VAL	N-CA-C	5.66	117.81	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dq	121	THR	N-CA-C	5.66	119.20	111.39
1	ar	209	ASP	CA-CB-CG	5.66	118.26	112.60
1	el	115	GLN	CA-C-N	5.66	125.61	119.78
1	el	115	GLN	C-N-CA	5.66	125.61	119.78
1	fq	463	ASP	CA-C-N	5.66	125.33	119.56
1	fq	463	ASP	C-N-CA	5.66	125.33	119.56
3	lh	67	GLU	N-CA-C	-5.66	105.19	111.36
3	mu	44	ALA	N-CA-C	5.66	119.76	112.41
1	aw	115	GLN	CA-C-N	5.65	125.60	119.78
1	aw	115	GLN	C-N-CA	5.65	125.60	119.78
1	dv	463	ASP	CA-C-N	5.65	125.33	119.56
1	dv	463	ASP	C-N-CA	5.65	125.33	119.56
1	ef	209	ASP	CA-CB-CG	5.65	118.25	112.60
1	en	426	ASP	CA-CB-CG	-5.65	106.95	112.60
1	fc	324	THR	N-CA-C	-5.65	101.19	109.50
1	fv	256	LYS	N-CA-C	5.65	117.66	109.07
1	gd	245	ASN	CA-C-N	5.65	125.63	120.03
1	gd	245	ASN	C-N-CA	5.65	125.63	120.03
1	bn	256	LYS	N-CA-C	5.65	117.66	109.07
1	cg	483	PRO	N-CA-C	-5.65	102.32	111.14
1	fv	121	THR	CB-CA-C	-5.65	103.38	112.09
1	ag	130	VAL	N-CA-C	5.65	116.02	108.11
1	be	92	GLY	CA-C-N	5.65	125.36	119.82
1	be	92	GLY	C-N-CA	5.65	125.36	119.82
1	br	163	PHE	CA-C-N	5.65	125.56	119.85
1	br	163	PHE	C-N-CA	5.65	125.56	119.85
1	gw	182	PHE	CA-CB-CG	5.65	119.45	113.80
1	at	150	PRO	N-CA-C	-5.65	102.94	111.41
1	cw	87	ALA	CA-C-N	-5.65	115.14	122.99
1	cw	87	ALA	C-N-CA	-5.65	115.14	122.99
1	ar	324	THR	N-CA-C	-5.65	102.53	109.65
1	db	75	ASN	CA-CB-CG	-5.65	106.95	112.60
1	db	406	THR	N-CA-C	-5.65	107.39	114.56
1	em	93	PRO	N-CA-CB	-5.65	99.06	102.79
1	es	237	GLU	N-CA-C	5.65	119.18	111.39
1	fz	149	GLY	CA-C-N	5.65	125.55	119.85
1	fz	149	GLY	C-N-CA	5.65	125.55	119.85
3	iz	38	VAL	N-CA-C	5.65	116.42	108.17
1	ac	468	GLN	CA-C-N	5.64	125.55	119.85
1	ac	468	GLN	C-N-CA	5.64	125.55	119.85
1	ak	119	SER	CA-C-N	5.64	125.62	120.03
1	ak	119	SER	C-N-CA	5.64	125.62	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ar	93	PRO	N-CA-CB	-5.64	99.06	102.79
1	df	265	GLN	N-CA-C	5.64	117.69	108.55
1	el	130	VAL	N-CA-C	5.64	116.01	108.11
1	ey	468	GLN	CA-C-N	5.64	125.55	119.85
1	ey	468	GLN	C-N-CA	5.64	125.55	119.85
1	aj	151	ASP	CA-CB-CG	5.64	118.24	112.60
1	cr	103	ILE	CA-C-N	5.64	125.59	119.78
1	cr	103	ILE	C-N-CA	5.64	125.59	119.78
1	db	119	SER	CA-C-N	5.64	125.62	120.03
1	db	119	SER	C-N-CA	5.64	125.62	120.03
1	dq	403	GLY	N-CA-C	5.64	120.63	113.24
1	gi	103	ILE	CA-C-N	5.64	125.59	119.78
1	gi	103	ILE	C-N-CA	5.64	125.59	119.78
2	hj	172	SER	N-CA-C	5.64	118.75	109.72
3	jt	46	TYR	N-CA-C	5.64	117.55	109.14
1	aw	263	SER	N-CA-C	5.64	118.44	109.81
1	go	402	THR	CA-C-N	5.64	127.19	120.14
1	go	402	THR	C-N-CA	5.64	127.19	120.14
1	bb	451	ALA	CA-C-N	5.64	125.57	119.76
1	bb	451	ALA	C-N-CA	5.64	125.57	119.76
1	bi	287	ASP	N-CA-C	-5.64	105.05	111.14
1	bm	324	THR	N-CA-C	-5.64	101.07	109.42
1	cq	270	TYR	N-CA-C	5.64	118.76	109.85
1	ez	209	ASP	CA-CB-CG	5.64	118.24	112.60
3	kdl	67	GLU	N-CA-C	-5.64	105.13	111.28
1	ah	71	ASP	CA-CB-CG	5.64	118.24	112.60
1	aj	245	ASN	CA-C-N	5.64	125.61	120.03
1	aj	245	ASN	C-N-CA	5.64	125.61	120.03
1	an	87	ALA	N-CA-C	5.64	117.42	111.28
1	as	209	ASP	CA-CB-CG	5.64	118.24	112.60
1	cy	463	ASP	CA-C-N	5.64	125.31	119.56
1	cy	463	ASP	C-N-CA	5.64	125.31	119.56
2	ho	232	ASP	N-CA-C	-5.64	103.20	110.19
1	am	222	VAL	N-CA-C	5.64	117.78	108.99
1	ee	209	ASP	CA-CB-CG	5.64	118.24	112.60
2	hl	115	PRO	N-CA-C	-5.64	102.42	111.38
1	bn	324	THR	CB-CA-C	5.63	116.27	109.85
1	dl	232	ILE	N-CA-C	-5.63	106.32	111.67
1	ej	93	PRO	N-CA-CB	-5.63	99.07	102.79
2	ho	286	GLY	N-CA-C	-5.63	102.08	112.62
1	dg	92	GLY	CA-C-N	5.63	125.34	119.82
1	dg	92	GLY	C-N-CA	5.63	125.34	119.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dw	253	ARG	N-CA-C	5.63	120.42	112.93
2	he	47	GLN	CA-C-N	5.63	125.31	119.56
2	he	47	GLN	C-N-CA	5.63	125.31	119.56
1	da	130	VAL	N-CA-C	5.63	115.99	108.11
1	fd	491	ALA	CA-C-N	5.63	126.11	120.14
1	fd	491	ALA	C-N-CA	5.63	126.11	120.14
1	hd	468	GLN	CA-C-N	5.63	125.54	119.85
1	hd	468	GLN	C-N-CA	5.63	125.54	119.85
3	ht	37	ASP	CA-CB-CG	5.63	118.23	112.60
3	lu	37	ASP	CA-CB-CG	5.63	118.23	112.60
1	ac	71	ASP	CA-CB-CG	5.63	118.23	112.60
1	ag	263	SER	N-CA-C	5.63	118.87	110.14
1	db	468	GLN	CA-C-N	5.63	125.54	119.85
1	db	468	GLN	C-N-CA	5.63	125.54	119.85
1	dn	88	VAL	N-CA-C	5.63	115.97	107.75
1	dy	68	ILE	CA-C-N	5.63	126.19	119.94
1	dy	68	ILE	C-N-CA	5.63	126.19	119.94
1	ez	68	ILE	N-CA-C	5.63	115.97	107.75
1	fx	149	GLY	CA-C-N	5.63	125.54	119.85
1	fx	149	GLY	C-N-CA	5.63	125.54	119.85
1	bg	409	THR	N-CA-C	-5.63	106.41	113.28
1	bl	71	ASP	CA-CB-CG	5.63	118.23	112.60
1	cl	336	ASP	CA-C-N	5.63	125.30	119.56
1	cl	336	ASP	C-N-CA	5.63	125.30	119.56
1	et	245	ASN	CA-C-N	5.63	125.60	120.03
1	et	245	ASN	C-N-CA	5.63	125.60	120.03
2	hi	365	ASP	CA-C-N	5.63	127.70	120.89
2	hi	365	ASP	C-N-CA	5.63	127.70	120.89
3	ms	46	TYR	N-CA-C	5.63	117.53	109.14
1	aa	451	ALA	CA-C-N	5.63	125.57	119.78
1	aa	451	ALA	C-N-CA	5.63	125.57	119.78
1	af	358	ASP	CA-CB-CG	5.63	118.23	112.60
3	mx	41	ILE	N-CA-CB	-5.63	106.60	112.06
1	al	222	VAL	N-CA-C	5.62	118.23	108.95
1	ew	71	ASP	CA-CB-CG	5.62	118.22	112.60
1	gk	93	PRO	N-CA-CB	-5.62	99.08	102.79
2	hf	315	ASP	CA-CB-CG	5.62	118.22	112.60
1	ch	119	SER	CA-C-N	5.62	125.61	120.21
1	ch	119	SER	C-N-CA	5.62	125.61	120.21
1	dk	265	GLN	N-CA-C	5.62	117.65	108.76
1	fs	119	SER	CA-C-N	5.62	125.94	119.92
1	fs	119	SER	C-N-CA	5.62	125.94	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	at	209	ASP	CA-CB-CG	5.62	118.22	112.60
1	av	185	THR	N-CA-C	5.62	119.19	111.54
1	bo	103	ILE	CA-C-N	5.62	125.53	119.85
1	bo	103	ILE	C-N-CA	5.62	125.53	119.85
1	bz	149	GLY	CA-C-N	5.62	125.59	120.03
1	bz	149	GLY	C-N-CA	5.62	125.59	120.03
1	em	71	ASP	CA-CB-CG	5.62	118.22	112.60
1	ep	103	ILE	CA-C-N	5.62	125.64	119.90
1	ep	103	ILE	C-N-CA	5.62	125.64	119.90
1	fm	201	GLY	N-CA-C	-5.62	105.88	113.24
1	fp	110	ASP	CA-CB-CG	5.62	118.22	112.60
3	ik	46	TYR	N-CA-C	5.62	117.52	109.14
3	ka	74	ASP	CA-CB-CG	5.62	118.22	112.60
1	dt	184	GLU	N-CA-C	-5.62	101.86	109.95
1	ei	88	VAL	N-CA-C	5.62	115.95	107.75
1	er	484	PHE	CA-CB-CG	5.62	119.42	113.80
1	eu	324	THR	N-CA-C	-5.62	102.57	109.65
1	gw	245	ASN	CA-C-N	5.62	125.59	120.03
1	gw	245	ASN	C-N-CA	5.62	125.59	120.03
1	bb	119	SER	CA-C-N	5.62	126.40	120.11
1	bb	119	SER	C-N-CA	5.62	126.40	120.11
1	bv	93	PRO	N-CA-CB	-5.62	99.08	102.79
1	er	110	ASP	CA-CB-CG	5.62	118.22	112.60
1	fk	121	THR	CB-CA-C	-5.62	103.44	112.09
1	hc	253	ARG	N-CA-C	5.62	119.88	111.96
1	bk	324	THR	N-CA-C	-5.62	101.24	109.50
1	am	245	ASN	CA-C-N	5.62	125.59	120.03
1	am	245	ASN	C-N-CA	5.62	125.59	120.03
1	aw	256	LYS	N-CA-C	5.62	117.60	109.07
1	em	115	GLN	CA-C-N	5.62	125.56	119.78
1	em	115	GLN	C-N-CA	5.62	125.56	119.78
1	en	395	TYR	N-CA-C	5.62	117.09	110.97
1	fb	483	PRO	N-CA-C	-5.62	102.28	111.21
1	fo	484	PHE	CA-CB-CG	5.62	119.42	113.80
1	gu	483	PRO	N-CA-C	-5.62	102.28	111.21
3	lm	67	GLU	N-CA-C	-5.62	105.24	111.36
1	aq	403	GLY	N-CA-C	5.61	120.59	113.24
1	di	245	ASN	CA-C-N	5.61	125.59	120.03
1	di	245	ASN	C-N-CA	5.61	125.59	120.03
1	eq	88	VAL	N-CA-C	5.61	115.95	107.75
1	gs	468	GLN	CA-C-N	5.61	125.54	119.76
1	gs	468	GLN	C-N-CA	5.61	125.54	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gw	121	THR	CB-CA-C	-5.61	103.44	112.09
1	an	115	GLN	CA-C-N	5.61	125.56	119.78
1	an	115	GLN	C-N-CA	5.61	125.56	119.78
1	cy	252	PHE	CA-CB-CG	5.61	119.41	113.80
1	at	271	SER	N-CA-C	5.61	118.58	110.28
1	ct	232	ILE	N-CA-C	-5.61	106.23	111.45
1	dx	103	ILE	CA-C-N	5.61	125.52	119.85
1	dx	103	ILE	C-N-CA	5.61	125.52	119.85
1	el	71	ASP	CA-CB-CG	5.61	118.21	112.60
1	eo	115	GLN	CA-C-N	5.61	125.56	119.78
1	eo	115	GLN	C-N-CA	5.61	125.56	119.78
1	fw	87	ALA	CA-C-N	-5.61	115.64	123.10
1	fw	87	ALA	C-N-CA	-5.61	115.64	123.10
3	lm	49	PHE	CA-C-N	5.61	125.81	120.31
3	lm	49	PHE	C-N-CA	5.61	125.81	120.31
1	co	196	VAL	N-CA-C	5.61	116.36	108.17
3	lf	38	VAL	N-CA-C	5.61	116.07	107.77
3	lp	38	VAL	N-CA-C	5.61	116.07	107.77
3	nl	41	ILE	N-CA-CB	-5.61	106.67	112.28
1	co	209	ASP	CA-CB-CG	5.61	118.21	112.60
1	cx	92	GLY	CA-C-N	5.61	126.85	119.84
1	cx	92	GLY	C-N-CA	5.61	126.85	119.84
1	dc	491	ALA	CA-C-N	5.61	126.08	120.14
1	dc	491	ALA	C-N-CA	5.61	126.08	120.14
1	dg	500	MET	CA-C-N	5.61	125.51	119.85
1	dg	500	MET	C-N-CA	5.61	125.51	119.85
1	dh	145	HIS	CA-C-N	5.61	125.28	119.56
1	dh	145	HIS	C-N-CA	5.61	125.28	119.56
1	eb	253	ARG	N-CA-C	5.61	119.69	111.34
1	fh	481	ILE	N-CA-C	5.61	121.00	109.34
1	fx	265	GLN	N-CA-C	5.61	117.63	108.55
2	hn	337	VAL	N-CA-C	5.61	116.19	108.12
1	bu	446	ALA	N-CA-C	5.61	119.29	112.23
1	cd	256	LYS	N-CA-C	5.61	117.59	109.07
1	ea	403	GLY	N-CA-C	5.61	120.72	113.27
1	gh	245	ASN	CA-C-N	5.61	125.58	120.03
1	gh	245	ASN	C-N-CA	5.61	125.58	120.03
2	hn	295	ASP	CA-CB-CG	5.61	118.21	112.60
3	nv	38	VAL	N-CA-C	5.61	116.07	107.77
1	bs	69	GLY	N-CA-C	-5.60	105.71	112.49
1	cf	115	GLN	CA-C-N	5.60	125.62	119.90
1	cf	115	GLN	C-N-CA	5.60	125.62	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ac	324	THR	N-CA-C	-5.60	101.27	109.50
1	ax	134	ASP	CA-C-N	5.60	125.71	119.32
1	ax	134	ASP	C-N-CA	5.60	125.71	119.32
1	br	110	ASP	CA-CB-CG	5.60	118.20	112.60
1	cq	271	SER	N-CA-C	5.60	118.57	110.28
1	dl	87	ALA	CA-C-N	-5.60	116.24	123.19
1	dl	87	ALA	C-N-CA	-5.60	116.24	123.19
1	dl	468	GLN	CA-C-N	5.60	125.51	119.85
1	dl	468	GLN	C-N-CA	5.60	125.51	119.85
1	eh	113	GLY	N-CA-C	-5.60	104.04	112.89
1	ey	480	GLY	CA-C-N	5.60	129.39	121.66
1	ey	480	GLY	C-N-CA	5.60	129.39	121.66
1	gx	265	GLN	N-CA-C	5.60	117.62	108.55
1	gz	324	THR	N-CA-C	-5.60	101.26	109.50
3	iw	44	ALA	N-CA-C	5.60	119.98	113.20
3	mh	38	VAL	N-CA-C	5.60	116.35	108.17
1	ch	163	PHE	CA-C-N	5.60	125.51	119.85
1	ch	163	PHE	C-N-CA	5.60	125.51	119.85
1	az	115	GLN	CA-C-N	5.60	125.61	119.90
1	az	115	GLN	C-N-CA	5.60	125.61	119.90
1	cc	121	THR	CB-CA-C	-5.60	103.94	111.89
1	cj	113	GLY	CA-C-N	-5.60	117.22	123.16
1	cj	113	GLY	C-N-CA	-5.60	117.22	123.16
1	du	403	GLY	N-CA-C	5.60	120.72	113.27
1	gs	232	ILE	N-CA-C	-5.60	106.35	111.67
3	li	44	ALA	N-CA-C	5.60	119.97	113.20
3	oa	44	ALA	N-CA-C	5.60	120.10	113.16
3	oc	32	PHE	CA-C-N	5.60	125.27	119.56
3	oc	32	PHE	C-N-CA	5.60	125.27	119.56
1	bk	198	ILE	N-CA-C	5.60	112.20	106.21
1	co	500	MET	CA-C-N	5.60	126.84	119.84
1	co	500	MET	C-N-CA	5.60	126.84	119.84
1	cs	232	ILE	N-CA-C	-5.60	106.35	111.67
1	dd	403	GLY	N-CA-C	5.60	120.57	113.24
1	dx	491	ALA	CA-C-N	5.60	125.58	120.21
1	dx	491	ALA	C-N-CA	5.60	125.58	120.21
1	fc	163	PHE	CA-C-N	5.60	125.50	119.85
1	fc	163	PHE	C-N-CA	5.60	125.50	119.85
1	gl	463	ASP	CA-C-N	5.60	125.27	119.56
1	gl	463	ASP	C-N-CA	5.60	125.27	119.56
1	gq	245	ASN	CA-C-N	5.60	125.57	120.03
1	gq	245	ASN	C-N-CA	5.60	125.57	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	jz	74	ASP	CA-CB-CG	5.60	118.20	112.60
1	bm	103	ILE	CA-C-N	5.59	125.54	119.78
1	bm	103	ILE	C-N-CA	5.59	125.54	119.78
1	bp	113	GLY	CA-C-N	-5.59	117.49	122.97
1	bp	113	GLY	C-N-CA	-5.59	117.49	122.97
1	cp	468	GLN	CA-C-N	5.59	125.50	119.85
1	cp	468	GLN	C-N-CA	5.59	125.50	119.85
1	dd	484	PHE	CA-CB-CG	5.59	119.39	113.80
1	fb	256	LYS	N-CA-C	5.59	117.57	109.07
1	fm	426	ASP	CA-CB-CG	-5.59	107.00	112.60
1	gc	491	ALA	CA-C-N	5.59	126.07	120.14
1	gc	491	ALA	C-N-CA	5.59	126.07	120.14
1	gv	263	SER	N-CA-C	5.59	117.92	109.41
1	bp	468	GLN	CA-C-N	5.59	125.50	119.85
1	bp	468	GLN	C-N-CA	5.59	125.50	119.85
1	fd	154	PHE	N-CA-C	-5.59	105.56	112.72
1	gn	265	GLN	N-CA-C	5.59	117.34	108.79
1	be	483	PRO	N-CA-C	-5.59	102.32	111.21
1	bo	324	THR	N-CA-C	-5.59	101.28	109.50
1	cd	121	THR	CB-CA-C	-5.59	103.48	112.09
1	de	403	GLY	N-CA-C	5.59	120.56	113.24
1	df	121	THR	CB-CA-C	-5.59	103.48	112.09
1	gs	484	PHE	CA-CB-CG	5.59	119.39	113.80
2	ho	365	ASP	CA-C-N	5.59	127.65	120.89
2	ho	365	ASP	C-N-CA	5.59	127.65	120.89
3	mt	46	TYR	N-CA-C	5.59	117.47	109.14
1	bm	484	PHE	CA-CB-CG	5.59	119.39	113.80
1	er	93	PRO	N-CA-CB	-5.59	99.10	102.79
1	gb	245	ASN	CA-C-N	5.59	125.56	120.03
1	gb	245	ASN	C-N-CA	5.59	125.56	120.03
1	cx	87	ALA	CA-C-N	-5.59	115.82	123.14
1	cx	87	ALA	C-N-CA	-5.59	115.82	123.14
1	es	93	PRO	N-CA-CB	-5.59	99.10	102.79
1	ex	253	ARG	N-CA-C	5.59	120.36	112.93
1	gb	484	PHE	CA-CB-CG	5.59	119.39	113.80
1	gj	130	VAL	N-CA-C	5.59	115.93	108.11
3	mc	38	VAL	N-CA-C	5.59	116.72	108.45
3	jw	10	ILE	N-CA-C	5.58	115.93	108.11
1	el	263	SER	N-CA-C	5.58	117.90	109.41
1	gb	463	ASP	CA-C-N	5.58	125.26	119.56
1	gb	463	ASP	C-N-CA	5.58	125.26	119.56
3	mz	72	ASN	CA-CB-CG	5.58	118.18	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cr	232	ILE	N-CA-C	-5.58	106.37	111.67
1	gk	263	SER	N-CA-C	5.58	117.99	109.95
1	gy	293	ILE	N-CA-C	-5.58	105.41	110.82
1	bi	186	GLY	N-CA-C	5.58	121.93	112.22
1	ee	338	ILE	N-CA-C	-5.58	106.26	111.45
1	fp	193	SER	N-CA-C	-5.58	107.12	114.04
1	bg	484	PHE	CA-CB-CG	5.58	119.38	113.80
1	bw	285	ASP	CA-CB-CG	5.58	118.18	112.60
1	cd	151	ASP	CA-CB-CG	5.58	118.18	112.60
1	ck	245	ASN	N-CA-C	5.58	117.61	109.30
1	er	113	GLY	N-CA-C	-5.58	104.08	112.89
1	ap	187	THR	N-CA-C	5.58	119.01	110.20
1	dk	468	GLN	CA-C-N	5.58	125.48	119.85
1	dk	468	GLN	C-N-CA	5.58	125.48	119.85
1	eo	500	MET	CB-CA-C	5.58	116.89	108.86
1	eq	484	PHE	CA-CB-CG	5.58	119.38	113.80
1	ey	329	ALA	N-CA-C	5.58	118.81	111.28
1	bc	403	GLY	N-CA-C	5.58	120.69	113.27
1	bn	468	GLN	CA-C-N	5.58	125.48	119.85
1	bn	468	GLN	C-N-CA	5.58	125.48	119.85
1	ct	491	ALA	CA-C-N	5.58	126.05	120.14
1	ct	491	ALA	C-N-CA	5.58	126.05	120.14
1	dn	245	ASN	CA-C-N	5.58	125.55	120.03
1	dn	245	ASN	C-N-CA	5.58	125.55	120.03
1	et	71	ASP	CA-CB-CG	5.58	118.17	112.60
1	ex	324	THR	N-CA-C	-5.58	101.30	109.50
1	bk	87	ALA	CA-C-N	-5.57	115.69	123.10
1	bk	87	ALA	C-N-CA	-5.57	115.69	123.10
1	bo	263	SER	N-CA-C	5.57	119.06	110.42
1	dk	196	VAL	N-CA-C	5.57	116.70	108.45
1	dl	336	ASP	CA-C-N	5.57	126.81	119.84
1	dl	336	ASP	C-N-CA	5.57	126.81	119.84
1	eq	72	HIS	N-CA-C	-5.57	101.72	110.36
1	ew	110	ASP	CA-CB-CG	5.57	118.17	112.60
1	fk	121	THR	N-CA-C	5.57	118.93	111.24
1	gn	451	ALA	CA-C-N	5.57	125.59	119.90
1	gn	451	ALA	C-N-CA	5.57	125.59	119.90
1	gs	94	ALA	CB-CA-C	-5.57	110.17	116.63
1	hb	256	LYS	N-CA-C	5.57	117.54	109.07
1	au	103	ILE	CA-C-N	5.57	125.48	119.85
1	au	103	ILE	C-N-CA	5.57	125.48	119.85
1	dd	281	VAL	N-CA-C	5.57	116.63	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fa	491	ALA	CA-C-N	5.57	125.48	119.85
1	fa	491	ALA	C-N-CA	5.57	125.48	119.85
1	af	88	VAL	N-CA-C	5.57	115.88	107.75
1	ee	269	ALA	N-CA-C	5.57	119.08	111.39
3	ix	38	VAL	N-CA-C	5.57	116.30	108.17
3	kdl	65	ARG	N-CA-C	5.57	122.67	110.80
1	ar	113	GLY	CA-C-N	-5.57	117.51	122.97
1	ar	113	GLY	C-N-CA	-5.57	117.51	122.97
1	bc	110	ASP	CA-CB-CG	5.57	118.17	112.60
1	ck	323	LEU	N-CA-C	5.57	119.17	110.32
1	cr	468	GLN	CA-C-N	5.57	125.47	119.85
1	cr	468	GLN	C-N-CA	5.57	125.47	119.85
1	cu	115	GLN	CA-C-N	5.57	125.51	119.78
1	cu	115	GLN	C-N-CA	5.57	125.51	119.78
1	da	121	THR	N-CA-C	5.57	118.92	111.24
1	el	93	PRO	N-CA-C	5.57	120.00	112.48
1	gg	265	GLN	N-CA-C	5.57	117.57	108.55
3	ip	37	ASP	CA-CB-CG	5.57	118.17	112.60
3	lt	22	LYS	N-CA-C	5.57	117.31	108.79
1	cd	491	ALA	CA-C-N	5.57	126.04	120.14
1	cd	491	ALA	C-N-CA	5.57	126.04	120.14
1	dj	265	GLN	N-CA-C	5.57	117.56	108.55
1	dr	412	VAL	N-CA-C	-5.57	107.22	111.62
1	em	483	PRO	N-CA-C	-5.57	102.46	111.14
1	gd	149	GLY	CA-C-N	5.57	125.51	119.78
1	gd	149	GLY	C-N-CA	5.57	125.51	119.78
1	gd	163	PHE	CA-C-N	5.57	125.47	119.85
1	gd	163	PHE	C-N-CA	5.57	125.47	119.85
3	lt	49	PHE	CA-C-N	5.57	125.76	120.31
3	lt	49	PHE	C-N-CA	5.57	125.76	120.31
1	cw	265	GLN	N-CA-C	5.56	117.56	108.55
1	dp	151	ASP	CA-CB-CG	5.56	118.16	112.60
1	gg	121	THR	N-CA-C	5.56	118.92	111.24
3	jh	67	GLU	N-CA-C	-5.56	105.30	111.36
1	au	93	PRO	N-CA-C	5.56	119.99	112.48
1	bu	490	GLN	N-CA-C	-5.56	106.33	113.23
1	ct	121	THR	CB-CA-C	-5.56	103.52	112.09
1	dc	328	LYS	N-CA-C	5.56	120.06	112.88
1	dn	130	VAL	N-CA-C	5.56	116.13	108.12
1	fc	403	GLY	N-CA-C	5.56	120.53	113.24
1	fl	174	VAL	N-CA-C	5.56	116.25	109.30
1	gj	285	ASP	N-CA-C	5.56	118.53	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cr	425	ILE	N-CA-C	5.56	116.31	108.36
1	ac	145	HIS	CA-C-N	5.56	125.92	119.47
1	ac	145	HIS	C-N-CA	5.56	125.92	119.47
1	ee	425	ILE	N-CA-C	5.56	116.31	108.36
1	es	403	GLY	N-CA-C	5.56	120.67	113.27
1	fn	88	VAL	N-CA-C	5.56	116.13	108.12
2	hi	384	ASN	CA-C-N	5.56	125.56	119.89
2	hi	384	ASN	C-N-CA	5.56	125.56	119.89
2	hj	365	ASP	CA-C-N	5.56	127.45	121.00
2	hj	365	ASP	C-N-CA	5.56	127.45	121.00
1	ef	119	SER	CA-C-N	5.56	125.53	120.03
1	ef	119	SER	C-N-CA	5.56	125.53	120.03
1	gu	263	SER	N-CA-C	5.56	118.31	110.14
3	nx	16	LYS	CA-C-N	5.56	128.18	120.29
3	nx	16	LYS	C-N-CA	5.56	128.18	120.29
1	ad	136	VAL	N-CA-CB	-5.55	105.90	112.40
1	bd	119	SER	N-CA-C	-5.55	103.22	108.22
1	bk	71	ASP	CA-CB-CG	5.55	118.16	112.60
1	by	480	GLY	N-CA-C	5.55	118.84	110.18
1	co	74	TYR	CA-C-N	5.55	130.16	122.77
1	co	74	TYR	C-N-CA	5.55	130.16	122.77
1	cq	402	THR	CA-C-N	5.55	127.08	120.14
1	cq	402	THR	C-N-CA	5.55	127.08	120.14
1	fd	468	GLN	CA-C-N	5.55	125.46	119.85
1	fd	468	GLN	C-N-CA	5.55	125.46	119.85
1	fy	149	GLY	CA-C-N	5.55	125.46	119.85
1	fy	149	GLY	C-N-CA	5.55	125.46	119.85
1	ha	222	VAL	N-CA-C	5.55	118.11	108.95
3	mj	38	VAL	N-CA-C	5.55	116.12	108.12
1	ds	449	TYR	N-CA-C	5.55	117.48	108.26
1	db	163	PHE	CA-C-N	5.55	125.46	119.85
1	db	163	PHE	C-N-CA	5.55	125.46	119.85
2	hh	353	ASP	CA-C-N	5.55	126.78	119.84
2	hh	353	ASP	C-N-CA	5.55	126.78	119.84
3	hr	67	GLU	N-CA-C	-5.55	105.31	111.36
1	ah	484	PHE	CA-CB-CG	5.55	119.35	113.80
1	bc	263	SER	N-CA-C	5.55	117.84	109.41
1	bj	327	SER	N-CA-C	5.55	117.07	110.19
1	co	256	LYS	N-CA-C	5.55	117.51	109.07
1	el	425	ILE	N-CA-C	5.55	116.30	108.36
1	ep	121	THR	CB-CA-C	-5.55	103.54	112.09
1	es	121	THR	CB-CA-C	-5.55	103.54	112.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ew	130	VAL	N-CA-C	5.55	115.88	108.11
1	fj	115	GLN	CA-C-N	5.55	125.50	119.78
1	fj	115	GLN	C-N-CA	5.55	125.50	119.78
1	gs	425	ILE	N-CA-C	5.55	116.30	108.36
2	hh	114	THR	CA-C-N	5.55	125.53	120.03
2	hh	114	THR	C-N-CA	5.55	125.53	120.03
3	kb	38	VAL	N-CA-C	5.55	116.27	108.17
1	cg	500	MET	CB-CA-C	5.55	117.43	109.11
1	gg	463	ASP	CA-C-N	5.55	125.22	119.56
1	gg	463	ASP	C-N-CA	5.55	125.22	119.56
3	ky	44	ALA	N-CA-C	5.55	120.04	113.16
1	ae	263	SER	N-CA-C	5.55	118.29	110.14
1	bc	481	ILE	CB-CA-C	-5.55	104.81	111.85
1	br	336	ASP	CA-C-N	5.55	125.22	119.56
1	br	336	ASP	C-N-CA	5.55	125.22	119.56
1	bw	271	SER	N-CA-C	5.55	119.02	110.42
1	cu	500	MET	CA-C-N	5.55	125.45	119.85
1	cu	500	MET	C-N-CA	5.55	125.45	119.85
1	di	502	SER	N-CA-C	5.55	115.56	108.24
1	eg	198	ILE	N-CA-C	5.55	116.10	107.28
1	fz	163	PHE	CA-C-N	5.55	125.45	119.85
1	fz	163	PHE	C-N-CA	5.55	125.45	119.85
1	gq	222	VAL	N-CA-C	5.55	118.10	108.95
1	ch	111	ILE	N-CA-C	5.54	116.94	111.67
1	dp	182	PHE	CA-CB-CG	5.54	119.34	113.80
1	eq	110	ASP	CA-CB-CG	5.54	118.14	112.60
1	br	209	ASP	CA-CB-CG	5.54	118.14	112.60
1	dy	491	ALA	CA-C-N	5.54	125.56	119.90
1	dy	491	ALA	C-N-CA	5.54	125.56	119.90
1	fv	245	ASN	CA-C-N	5.54	125.52	120.03
1	fv	245	ASN	C-N-CA	5.54	125.52	120.03
3	kx	72	ASN	CA-CB-CG	5.54	118.14	112.60
1	au	468	GLN	CA-C-N	5.54	125.45	119.85
1	au	468	GLN	C-N-CA	5.54	125.45	119.85
1	ca	353	LEU	N-CA-C	-5.54	104.88	111.69
1	di	93	PRO	N-CA-C	5.54	120.02	111.21
1	eb	483	PRO	N-CA-C	5.54	120.83	113.57
1	fz	71	ASP	CA-CB-CG	5.54	118.14	112.60
1	gy	506	SER	CA-C-N	-5.54	113.01	121.66
1	gy	506	SER	C-N-CA	-5.54	113.01	121.66
1	cc	113	GLY	N-CA-C	-5.54	104.12	112.60
1	hb	491	ALA	CA-C-N	5.54	126.01	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	hb	491	ALA	C-N-CA	5.54	126.01	120.14
3	kt	38	VAL	N-CA-C	5.54	116.26	108.17
3	ni	46	TYR	N-CA-C	5.54	117.39	109.14
1	bg	468	GLN	CA-C-N	5.54	125.44	119.85
1	bg	468	GLN	C-N-CA	5.54	125.44	119.85
1	dx	481	ILE	CA-C-N	-5.54	112.63	120.49
1	dx	481	ILE	C-N-CA	-5.54	112.63	120.49
1	en	222	VAL	N-CA-C	5.54	118.09	108.95
1	ff	336	ASP	CA-C-N	5.54	125.89	119.47
1	ff	336	ASP	C-N-CA	5.54	125.89	119.47
1	fk	481	ILE	N-CA-C	5.54	116.20	108.89
3	lq	32	PHE	CA-C-N	5.54	125.21	119.56
3	lq	32	PHE	C-N-CA	5.54	125.21	119.56
1	bz	88	VAL	N-CA-C	5.54	115.83	107.75
3	jc	44	ALA	N-CA-C	5.54	120.03	113.16
1	bm	403	GLY	N-CA-C	5.54	120.63	113.27
1	cd	344	ARG	N-CA-C	-5.54	100.65	109.23
1	cq	484	PHE	CA-CB-CG	5.54	119.33	113.80
1	ee	483	PRO	N-CA-C	-5.54	102.41	111.21
1	ga	94	ALA	CB-CA-C	-5.54	110.17	116.54
3	jf	46	TYR	N-CA-C	5.54	116.38	108.74
1	cq	121	THR	CB-CA-C	-5.53	103.57	112.09
1	fj	463	ASP	CA-C-N	5.53	125.20	119.56
1	fj	463	ASP	C-N-CA	5.53	125.20	119.56
1	fl	402	THR	CA-C-N	5.53	127.06	120.14
1	fl	402	THR	C-N-CA	5.53	127.06	120.14
2	hg	36	TYR	N-CA-C	-5.53	108.31	114.62
2	ho	115	PRO	N-CA-C	-5.53	102.58	111.38
3	jz	32	PHE	CA-C-N	5.53	125.20	119.56
3	jz	32	PHE	C-N-CA	5.53	125.20	119.56
1	bp	271	SER	N-CA-C	5.53	118.94	110.20
1	bu	110	ASP	CA-CB-CG	5.53	118.13	112.60
1	dc	412	VAL	N-CA-C	-5.53	107.05	111.81
1	df	480	GLY	N-CA-C	5.53	119.62	110.55
1	dz	491	ALA	CA-C-N	5.53	125.44	119.85
1	dz	491	ALA	C-N-CA	5.53	125.44	119.85
1	ag	293	ILE	N-CA-C	-5.53	105.45	110.82
1	cl	258	VAL	N-CA-C	5.53	117.88	108.86
1	fr	163	PHE	CA-C-N	5.53	125.44	119.85
1	fr	163	PHE	C-N-CA	5.53	125.44	119.85
1	gu	265	GLN	N-CA-C	5.53	117.51	108.55
1	bd	88	VAL	N-CA-C	5.53	115.82	107.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	di	145	HIS	CA-C-N	5.53	125.14	119.56
1	di	145	HIS	C-N-CA	5.53	125.14	119.56
1	ar	149	GLY	CA-C-N	5.53	125.43	119.85
1	ar	149	GLY	C-N-CA	5.53	125.43	119.85
1	bc	256	LYS	N-CA-C	5.53	117.47	109.07
1	bf	482	ASN	CA-C-N	5.53	125.54	119.90
1	bf	482	ASN	C-N-CA	5.53	125.54	119.90
1	bk	468	GLN	CA-C-N	5.53	125.43	119.85
1	bk	468	GLN	C-N-CA	5.53	125.43	119.85
1	ff	145	HIS	CA-C-N	5.53	125.20	119.56
1	ff	145	HIS	C-N-CA	5.53	125.20	119.56
3	ns	38	VAL	N-CA-C	5.53	116.24	108.17
1	af	134	ASP	CA-C-N	5.53	125.20	119.56
1	af	134	ASP	C-N-CA	5.53	125.20	119.56
1	dr	93	PRO	N-CA-CB	-5.53	99.14	102.79
1	fu	95	VAL	N-CA-C	5.53	116.24	108.17
3	kq	32	PHE	CA-C-N	5.53	125.19	119.56
3	kq	32	PHE	C-N-CA	5.53	125.19	119.56
3	ll	49	PHE	CA-C-N	5.53	125.72	120.31
3	ll	49	PHE	C-N-CA	5.53	125.72	120.31
1	do	403	GLY	N-CA-C	5.52	120.48	113.24
1	fr	500	MET	CA-C-N	5.52	125.43	119.85
1	fr	500	MET	C-N-CA	5.52	125.43	119.85
1	cv	468	GLN	CA-C-N	5.52	125.43	119.85
1	cv	468	GLN	C-N-CA	5.52	125.43	119.85
1	di	403	GLY	N-CA-C	5.52	120.47	113.24
1	ct	222	VAL	N-CA-C	5.52	118.06	108.95
1	dl	474	LYS	N-CA-C	5.52	118.46	109.24
1	fm	324	THR	N-CA-C	-5.52	102.69	109.65
1	cg	324	THR	N-CA-C	-5.52	101.39	109.50
1	ci	232	ILE	N-CA-C	-5.52	106.43	111.67
1	ez	263	SER	N-CA-C	5.52	118.57	109.85
3	kn	67	GLU	N-CA-C	-5.52	105.34	111.36
1	bb	263	SER	N-CA-C	5.52	118.62	110.46
1	eb	426	ASP	CA-CB-CG	-5.52	107.08	112.60
1	eb	484	PHE	CA-CB-CG	5.52	119.32	113.80
1	fr	259	ILE	N-CA-C	5.52	117.35	108.85
1	cz	253	ARG	N-CA-C	5.52	119.56	111.34
1	da	463	ASP	CA-C-N	5.52	125.19	119.56
1	da	463	ASP	C-N-CA	5.52	125.19	119.56
1	de	468	GLN	CA-C-N	5.52	125.42	119.85
1	de	468	GLN	C-N-CA	5.52	125.42	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ds	72	HIS	N-CA-C	-5.52	101.84	110.17
1	ai	463	ASP	CA-C-N	5.51	125.19	119.56
1	ai	463	ASP	C-N-CA	5.51	125.19	119.56
1	bj	256	LYS	N-CA-C	5.51	117.45	109.07
1	ce	402	THR	CA-C-N	5.51	127.03	120.14
1	ce	402	THR	C-N-CA	5.51	127.03	120.14
1	ck	491	ALA	CA-C-N	5.51	125.98	120.14
1	ck	491	ALA	C-N-CA	5.51	125.98	120.14
1	fq	115	GLN	CA-C-N	5.51	125.46	119.78
1	fq	115	GLN	C-N-CA	5.51	125.46	119.78
1	fq	222	VAL	N-CA-C	5.51	118.05	108.95
1	az	256	LYS	N-CA-C	5.51	117.45	109.07
1	ca	182	PHE	CA-CB-CG	5.51	119.31	113.80
1	dv	245	ASN	CA-C-N	5.51	125.49	120.03
1	dv	245	ASN	C-N-CA	5.51	125.49	120.03
1	fd	253	ARG	N-CA-C	5.51	120.00	111.56
1	gr	149	GLY	CA-C-N	5.51	125.49	120.03
1	gr	149	GLY	C-N-CA	5.51	125.49	120.03
1	af	453	TYR	N-CA-C	-5.51	105.85	113.18
1	aw	245	ASN	CA-C-N	5.51	125.49	120.03
1	aw	245	ASN	C-N-CA	5.51	125.49	120.03
1	fe	491	ALA	CA-C-N	5.51	125.98	120.14
1	fe	491	ALA	C-N-CA	5.51	125.98	120.14
1	ff	245	ASN	CA-C-N	5.51	125.49	120.03
1	ff	245	ASN	C-N-CA	5.51	125.49	120.03
1	fw	403	GLY	N-CA-C	5.51	120.60	113.27
1	bd	329	ALA	N-CA-C	5.51	118.84	111.24
1	bg	403	GLY	N-CA-C	5.51	120.46	113.24
1	cq	256	LYS	N-CA-C	5.51	117.44	109.07
1	cx	209	ASP	CA-CB-CG	5.51	118.11	112.60
1	er	491	ALA	CA-C-N	5.51	125.71	120.31
1	er	491	ALA	C-N-CA	5.51	125.71	120.31
1	fg	134	ASP	CA-C-N	5.51	125.18	119.56
1	fg	134	ASP	C-N-CA	5.51	125.18	119.56
1	ga	134	ASP	CA-C-N	5.51	125.18	119.56
1	ga	134	ASP	C-N-CA	5.51	125.18	119.56
3	la	44	ALA	N-CA-C	5.51	119.86	113.20
1	cu	285	ASP	CA-CB-CG	5.51	118.11	112.60
1	gh	121	THR	CB-CA-C	-5.51	103.61	112.09
1	ah	285	ASP	CA-C-N	5.51	132.06	121.54
1	ah	285	ASP	C-N-CA	5.51	132.06	121.54
1	ao	287	ASP	N-CA-C	-5.51	105.61	112.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cn	482	ASN	N-CA-C	5.51	121.98	109.81
1	el	250	MET	N-CA-C	5.51	117.44	109.07
1	es	402	THR	CA-C-N	5.51	127.07	120.13
1	es	402	THR	C-N-CA	5.51	127.07	120.13
1	ez	121	THR	CB-CA-C	-5.51	103.61	112.09
1	fj	209	ASP	CA-CB-CG	5.51	118.11	112.60
3	nb	72	ASN	CA-CB-CG	5.51	118.11	112.60
3	ny	79	THR	N-CA-C	5.51	116.62	108.86
1	aw	412	VAL	N-CA-C	-5.50	107.08	111.81
1	bo	232	ILE	CB-CA-C	-5.50	105.30	111.80
1	cl	198	ILE	N-CA-C	5.50	115.47	106.72
1	cv	103	ILE	CA-C-N	5.50	125.45	119.78
1	cv	103	ILE	C-N-CA	5.50	125.45	119.78
2	hj	420	LEU	CA-C-N	5.50	125.41	119.85
2	hj	420	LEU	C-N-CA	5.50	125.41	119.85
2	ho	136	LYS	N-CA-C	-5.50	106.69	113.41
3	km	10	ILE	N-CA-C	5.50	115.82	108.11
1	az	119	SER	CA-C-N	5.50	125.48	120.03
1	az	119	SER	C-N-CA	5.50	125.48	120.03
1	cj	491	ALA	CA-C-N	5.50	125.97	120.14
1	cj	491	ALA	C-N-CA	5.50	125.97	120.14
1	co	293	ILE	N-CA-C	-5.50	105.48	110.82
1	ey	71	ASP	CA-CB-CG	5.50	118.10	112.60
1	gv	403	GLY	N-CA-C	5.50	120.59	113.27
1	ax	115	GLN	CA-C-N	5.50	125.45	119.78
1	ax	115	GLN	C-N-CA	5.50	125.45	119.78
1	bc	468	GLN	CA-C-N	5.50	125.41	119.85
1	bc	468	GLN	C-N-CA	5.50	125.41	119.85
1	bd	115	GLN	CA-C-N	5.50	125.48	120.03
1	bd	115	GLN	C-N-CA	5.50	125.48	120.03
1	da	245	ASN	CA-C-N	5.50	125.48	120.03
1	da	245	ASN	C-N-CA	5.50	125.48	120.03
1	db	245	ASN	CA-C-N	5.50	125.48	120.03
1	db	245	ASN	C-N-CA	5.50	125.48	120.03
1	ev	258	VAL	N-CA-C	5.50	116.66	108.46
1	fl	294	LEU	CB-CA-C	-5.50	102.24	110.88
3	ht	38	VAL	N-CA-C	5.50	116.59	108.45
3	in	46	TYR	N-CA-C	5.50	117.34	109.14
3	jn	16	LYS	CA-C-N	5.50	127.92	120.38
3	jn	16	LYS	C-N-CA	5.50	127.92	120.38
3	my	49	PHE	CA-C-N	5.50	125.70	120.31
3	my	49	PHE	C-N-CA	5.50	125.70	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	nt	67	GLU	N-CA-C	-5.50	105.36	111.36
1	db	253	ARG	N-CA-C	5.50	119.53	111.34
1	eq	402	THR	CA-C-N	5.50	127.02	120.14
1	eq	402	THR	C-N-CA	5.50	127.02	120.14
3	ih	5	ARG	N-CA-C	-5.50	106.28	114.64
3	jv	38	VAL	N-CA-C	5.50	115.91	107.77
1	dj	468	GLN	CA-C-N	5.50	125.40	119.85
1	dj	468	GLN	C-N-CA	5.50	125.40	119.85
1	gi	256	LYS	N-CA-C	5.50	117.15	108.96
1	gm	130	VAL	N-CA-C	5.50	115.81	108.11
1	gv	245	ASN	CA-C-N	5.50	125.47	120.03
1	gv	245	ASN	C-N-CA	5.50	125.47	120.03
1	aj	198	ILE	N-CA-C	5.50	112.09	106.21
1	bg	103	ILE	CA-C-N	5.50	125.44	119.78
1	bg	103	ILE	C-N-CA	5.50	125.44	119.78
1	bh	263	SER	N-CA-C	5.50	118.22	109.81
1	cn	222	VAL	N-CA-C	5.50	118.02	108.95
1	dr	491	ALA	CA-C-N	5.50	125.97	120.14
1	dr	491	ALA	C-N-CA	5.50	125.97	120.14
1	ei	193	SER	N-CA-C	-5.50	107.22	114.04
1	fd	236	GLN	CB-CA-C	5.50	118.47	109.90
1	gt	270	TYR	N-CA-C	5.50	117.39	110.24
3	ir	67	GLU	N-CA-C	-5.50	105.37	111.36
1	ck	258	VAL	N-CA-C	5.50	118.02	108.95
1	eb	119	SER	N-CA-C	-5.50	103.28	108.22
1	cy	491	ALA	CA-C-N	5.49	125.25	119.76
1	cy	491	ALA	C-N-CA	5.49	125.25	119.76
1	dw	184	GLU	N-CA-C	-5.49	101.01	109.52
1	eu	182	PHE	CA-CB-CG	5.49	119.29	113.80
1	fc	245	ASN	CA-C-N	5.49	125.47	120.03
1	fc	245	ASN	C-N-CA	5.49	125.47	120.03
1	fc	446	ALA	N-CA-C	5.49	119.99	113.12
1	ha	426	ASP	CA-CB-CG	-5.49	107.11	112.60
2	hm	270	THR	N-CA-C	5.49	119.73	113.19
3	jb	38	VAL	N-CA-C	5.49	116.47	107.24
1	at	184	GLU	N-CA-C	-5.49	102.04	109.95
1	bh	71	ASP	CA-CB-CG	5.49	118.09	112.60
1	cd	245	ASN	CA-C-N	5.49	125.47	120.03
1	cd	245	ASN	C-N-CA	5.49	125.47	120.03
1	en	324	THR	N-CA-C	-5.49	101.43	109.50
1	fx	272	ILE	N-CA-C	5.49	115.69	110.53
1	gj	122	GLY	N-CA-C	-5.49	105.06	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	au	263	SER	N-CA-C	5.49	118.59	110.46
1	bm	491	ALA	CA-C-N	5.49	125.69	120.31
1	bm	491	ALA	C-N-CA	5.49	125.69	120.31
1	ch	236	GLN	CA-C-N	5.49	130.43	122.36
1	ch	236	GLN	C-N-CA	5.49	130.43	122.36
1	do	145	HIS	CA-C-N	5.49	125.11	119.56
1	do	145	HIS	C-N-CA	5.49	125.11	119.56
1	gy	121	THR	N-CA-C	5.49	118.97	111.39
1	hc	491	ALA	CA-C-N	5.49	125.96	120.14
1	hc	491	ALA	C-N-CA	5.49	125.96	120.14
3	lv	25	GLY	N-CA-C	-5.49	104.68	112.37
1	do	197	THR	CA-C-N	-5.49	115.78	123.13
1	do	197	THR	C-N-CA	-5.49	115.78	123.13
1	fn	343	ALA	N-CA-C	5.49	117.81	110.35
1	gs	245	ASN	CA-C-N	5.49	125.46	120.03
1	gs	245	ASN	C-N-CA	5.49	125.46	120.03
3	ky	38	VAL	N-CA-C	5.49	116.46	107.24
1	ac	149	GLY	CA-C-N	5.49	125.69	120.31
1	ac	149	GLY	C-N-CA	5.49	125.69	120.31
1	bo	71	ASP	CA-CB-CG	5.49	118.09	112.60
1	ce	222	VAL	N-CA-C	5.49	118.00	108.95
1	cj	468	GLN	CA-C-N	5.49	125.39	119.85
1	cj	468	GLN	C-N-CA	5.49	125.39	119.85
1	df	115	GLN	CA-C-N	5.49	125.43	119.78
1	df	115	GLN	C-N-CA	5.49	125.43	119.78
1	dn	484	PHE	CA-CB-CG	5.49	119.29	113.80
1	ev	269	ALA	N-CA-C	5.49	117.88	111.02
1	gl	119	SER	CA-C-N	5.49	125.79	119.92
1	gl	119	SER	C-N-CA	5.49	125.79	119.92
1	gz	182	PHE	CA-CB-CG	5.49	119.28	113.80
1	at	103	ILE	CA-C-N	5.48	125.43	119.78
1	at	103	ILE	C-N-CA	5.48	125.43	119.78
1	bv	285	ASP	N-CA-C	5.48	118.44	111.69
1	dw	232	ILE	CB-CA-C	-5.48	105.33	111.80
1	gj	265	GLN	N-CA-C	5.48	118.13	108.75
1	ao	121	THR	CB-CA-C	-5.48	102.21	112.30
1	cq	103	ILE	CA-C-N	5.48	125.43	119.78
1	cq	103	ILE	C-N-CA	5.48	125.43	119.78
1	cv	480	GLY	N-CA-C	5.48	119.54	110.55
1	ee	271	SER	N-CA-C	5.48	117.95	110.55
1	fk	412	VAL	N-CA-C	-5.48	107.29	111.62
1	fq	285	ASP	CA-C-N	5.48	132.01	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fq	285	ASP	C-N-CA	5.48	132.01	121.54
1	gc	451	ALA	CA-C-N	5.48	125.41	119.76
1	gc	451	ALA	C-N-CA	5.48	125.41	119.76
1	gk	125	PHE	CA-CB-CG	5.48	119.28	113.80
1	av	256	LYS	N-CA-C	5.48	117.40	109.07
1	cc	269	ALA	N-CA-C	5.48	117.87	111.02
1	ee	103	ILE	CA-C-N	5.48	125.43	119.78
1	ee	103	ILE	C-N-CA	5.48	125.43	119.78
1	ef	245	ASN	CA-C-N	5.48	125.46	120.03
1	ef	245	ASN	C-N-CA	5.48	125.46	120.03
1	fn	72	HIS	N-CA-C	-5.48	101.19	109.85
1	fx	121	THR	CB-CA-C	-5.48	103.65	112.09
1	ge	403	GLY	N-CA-C	5.48	120.42	113.24
1	gv	93	PRO	N-CA-CB	-5.48	99.17	102.79
3	js	32	PHE	CA-C-N	5.48	125.15	119.56
3	js	32	PHE	C-N-CA	5.48	125.15	119.56
1	at	93	PRO	N-CA-CB	-5.48	99.17	102.79
3	jg	44	ALA	N-CA-C	5.48	119.83	113.20
3	lj	38	VAL	N-CA-C	5.48	116.17	108.17
1	ah	403	GLY	N-CA-C	5.48	120.55	113.27
1	as	149	GLY	CA-C-N	5.48	125.38	119.85
1	as	149	GLY	C-N-CA	5.48	125.38	119.85
1	ea	103	ILE	CA-C-N	5.48	125.42	119.78
1	ea	103	ILE	C-N-CA	5.48	125.42	119.78
1	ev	232	ILE	N-CA-C	-5.48	106.47	111.67
1	fh	121	THR	CB-CA-C	-5.48	103.66	112.09
1	fk	403	GLY	N-CA-C	5.48	120.55	113.27
1	dl	74	TYR	CA-C-N	5.47	129.69	122.30
1	dl	74	TYR	C-N-CA	5.47	129.69	122.30
1	en	245	ASN	CA-C-N	5.47	125.45	120.03
1	en	245	ASN	C-N-CA	5.47	125.45	120.03
1	es	463	ASP	CA-C-N	5.47	125.14	119.56
1	es	463	ASP	C-N-CA	5.47	125.14	119.56
1	et	336	ASP	CA-C-N	5.47	125.82	119.47
1	et	336	ASP	C-N-CA	5.47	125.82	119.47
1	gl	491	ALA	CA-C-N	5.47	125.94	120.14
1	gl	491	ALA	C-N-CA	5.47	125.94	120.14
2	he	270	THR	N-CA-C	5.47	119.70	113.19
3	kj	38	VAL	N-CA-C	5.47	116.16	108.17
1	cx	468	GLN	CA-C-N	5.47	125.38	119.85
1	cx	468	GLN	C-N-CA	5.47	125.38	119.85
1	ef	199	ASP	CA-CB-CG	-5.47	107.13	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eg	328	LYS	N-CA-C	5.47	119.65	112.92
1	gp	484	PHE	CA-CB-CG	5.47	119.27	113.80
1	gu	232	ILE	N-CA-C	-5.47	106.85	111.56
1	gv	145	HIS	CA-C-N	5.47	125.09	119.56
1	gv	145	HIS	C-N-CA	5.47	125.09	119.56
1	ac	103	ILE	CA-C-N	5.47	125.42	119.78
1	ac	103	ILE	C-N-CA	5.47	125.42	119.78
1	ck	468	GLN	CA-C-N	5.47	125.42	119.78
1	ck	468	GLN	C-N-CA	5.47	125.42	119.78
1	db	256	LYS	N-CA-C	5.47	117.39	109.07
1	ab	484	PHE	CA-CB-CG	5.47	119.27	113.80
1	ac	256	LYS	N-CA-C	5.47	117.38	109.07
1	ac	402	THR	CA-C-N	5.47	126.98	120.14
1	ac	402	THR	C-N-CA	5.47	126.98	120.14
1	am	402	THR	CA-C-N	5.47	127.02	120.13
1	am	402	THR	C-N-CA	5.47	127.02	120.13
1	fp	93	PRO	N-CA-CB	-5.47	99.18	102.79
1	fv	182	PHE	CA-CB-CG	5.47	119.27	113.80
1	bx	463	ASP	CA-C-N	5.47	125.14	119.56
1	bx	463	ASP	C-N-CA	5.47	125.14	119.56
1	en	412	VAL	N-CA-C	-5.47	106.47	111.67
1	fr	87	ALA	CA-C-N	-5.47	115.83	123.10
1	fr	87	ALA	C-N-CA	-5.47	115.83	123.10
3	lk	49	PHE	CA-C-N	5.47	125.67	120.31
3	lk	49	PHE	C-N-CA	5.47	125.67	120.31
1	dy	245	ASN	CA-C-N	5.47	125.44	120.03
1	dy	245	ASN	C-N-CA	5.47	125.44	120.03
1	hd	323	LEU	N-CA-C	5.47	118.97	110.17
3	mt	44	ALA	N-CA-C	5.47	119.80	113.18
1	ae	468	GLN	CA-C-N	5.46	125.39	119.76
1	ae	468	GLN	C-N-CA	5.46	125.39	119.76
1	av	449	TYR	CB-CA-C	-5.46	98.56	109.33
1	bx	71	ASP	CA-CB-CG	5.46	118.06	112.60
1	by	271	SER	N-CA-C	5.46	118.61	110.52
1	ds	336	ASP	CA-C-N	5.46	125.81	119.47
1	ds	336	ASP	C-N-CA	5.46	125.81	119.47
1	gk	328	LYS	N-CA-C	5.46	120.82	113.72
1	ar	484	PHE	CA-CB-CG	5.46	119.26	113.80
1	cn	245	ASN	CA-C-N	5.46	125.37	119.85
1	cn	245	ASN	C-N-CA	5.46	125.37	119.85
1	cz	222	VAL	N-CA-C	5.46	117.96	108.95
1	fm	121	THR	CB-CA-C	-5.46	104.14	111.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gc	245	ASN	CA-C-N	5.46	125.37	119.85
1	gc	245	ASN	C-N-CA	5.46	125.37	119.85
1	gl	134	ASP	CA-C-N	5.46	125.13	119.56
1	gl	134	ASP	C-N-CA	5.46	125.13	119.56
2	he	40	VAL	N-CA-C	5.46	115.82	108.17
3	jb	67	GLU	N-CA-C	-5.46	105.41	111.36
3	mp	38	VAL	N-CA-C	5.46	116.14	108.17
1	cs	291	SER	CA-C-N	5.46	126.00	119.94
1	cs	291	SER	C-N-CA	5.46	126.00	119.94
1	dz	149	GLY	CA-C-N	5.46	125.36	119.85
1	dz	149	GLY	C-N-CA	5.46	125.36	119.85
1	fl	149	GLY	CA-C-N	5.46	125.36	119.85
1	fl	149	GLY	C-N-CA	5.46	125.36	119.85
1	ah	113	GLY	N-CA-C	-5.46	104.27	112.89
1	aw	345	TRP	CA-C-N	5.46	127.59	120.28
1	aw	345	TRP	C-N-CA	5.46	127.59	120.28
1	dj	93	PRO	N-CA-CB	-5.46	99.19	102.79
1	ds	402	THR	CA-C-N	5.46	126.96	120.14
1	ds	402	THR	C-N-CA	5.46	126.96	120.14
1	fc	293	ILE	N-CA-C	-5.46	105.53	110.82
1	fg	115	GLN	CA-C-N	5.46	125.40	119.78
1	fg	115	GLN	C-N-CA	5.46	125.40	119.78
1	fp	113	GLY	N-CA-C	-5.46	104.27	112.89
1	gb	396	ALA	N-CA-C	-5.46	100.42	108.99
1	gi	145	HIS	CA-C-N	5.46	125.07	119.56
1	gi	145	HIS	C-N-CA	5.46	125.07	119.56
1	gy	403	GLY	N-CA-C	5.46	120.39	113.24
1	ak	154	PHE	CA-CB-CG	5.46	119.26	113.80
1	cs	271	SER	N-CA-C	5.46	118.56	110.48
1	dd	187	THR	N-CA-C	5.46	118.23	110.10
1	ff	463	ASP	CA-C-N	5.46	125.13	119.56
1	ff	463	ASP	C-N-CA	5.46	125.13	119.56
1	ga	121	THR	CB-CA-C	-5.46	103.50	112.06
2	hk	290	HIS	N-CA-C	-5.46	104.20	111.24
1	gi	343	ALA	N-CA-C	5.46	117.77	110.35
1	gp	491	ALA	CA-C-N	5.46	125.92	120.14
1	gp	491	ALA	C-N-CA	5.46	125.92	120.14
3	ie	32	PHE	CA-C-N	5.46	125.12	119.56
3	ie	32	PHE	C-N-CA	5.46	125.12	119.56
3	kg	67	GLU	N-CA-C	-5.46	105.41	111.36
1	am	149	GLY	CA-C-N	5.45	125.65	120.31
1	am	149	GLY	C-N-CA	5.45	125.65	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ap	253	ARG	N-CA-C	5.45	119.65	111.96
1	bu	71	ASP	CA-CB-CG	5.45	118.05	112.60
1	cj	151	ASP	CA-CB-CG	5.45	118.05	112.60
1	ex	145	HIS	CA-C-N	5.45	125.07	119.56
1	ex	145	HIS	C-N-CA	5.45	125.07	119.56
1	fi	121	THR	N-CA-C	5.45	118.77	111.24
2	hl	286	GLY	N-CA-C	-5.45	102.77	112.58
3	me	67	GLU	N-CA-C	-5.45	105.42	111.36
1	bf	263	SER	N-CA-C	5.45	117.26	109.14
1	bf	468	GLN	CA-C-N	5.45	125.36	119.85
1	bf	468	GLN	C-N-CA	5.45	125.36	119.85
1	fl	119	SER	CA-C-N	5.45	125.43	120.03
1	fl	119	SER	C-N-CA	5.45	125.43	120.03
1	ai	163	PHE	CA-C-N	5.45	125.36	119.85
1	ai	163	PHE	C-N-CA	5.45	125.36	119.85
1	ay	293	ILE	N-CA-C	-5.45	105.53	110.82
1	bd	468	GLN	CA-C-N	5.45	125.36	119.85
1	bd	468	GLN	C-N-CA	5.45	125.36	119.85
1	cj	149	GLY	CA-C-N	5.45	125.43	120.03
1	cj	149	GLY	C-N-CA	5.45	125.43	120.03
1	cp	491	ALA	CA-C-N	5.45	125.92	120.14
1	cp	491	ALA	C-N-CA	5.45	125.92	120.14
1	ff	468	GLN	CA-C-N	5.45	125.36	119.85
1	ff	468	GLN	C-N-CA	5.45	125.36	119.85
1	fk	285	ASP	CA-C-N	5.45	131.95	121.54
1	fk	285	ASP	C-N-CA	5.45	131.95	121.54
1	fl	486	GLU	CA-C-N	5.45	131.95	121.54
1	fl	486	GLU	C-N-CA	5.45	131.95	121.54
2	hl	365	ASP	CA-C-N	5.45	127.49	120.89
2	hl	365	ASP	C-N-CA	5.45	127.49	120.89
3	lu	38	VAL	N-CA-C	5.45	116.13	108.17
3	nf	41	ILE	N-CA-C	5.45	115.17	106.88
3	np	10	ILE	N-CA-C	5.45	115.71	107.75
1	al	154	PHE	N-CA-C	-5.45	105.75	112.72
1	as	121	THR	N-CA-C	5.45	118.76	111.24
1	as	186	GLY	N-CA-C	5.45	120.98	111.50
1	bg	93	PRO	N-CA-CB	-5.45	99.19	102.79
1	ck	115	GLN	CA-C-N	5.45	125.39	119.78
1	ck	115	GLN	C-N-CA	5.45	125.39	119.78
1	di	468	GLN	CA-C-N	5.45	125.35	119.85
1	di	468	GLN	C-N-CA	5.45	125.35	119.85
1	fs	328	LYS	N-CA-C	5.45	119.92	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	hq	67	GLU	N-CA-C	-5.45	105.42	111.36
1	bo	403	GLY	N-CA-C	5.45	120.38	113.24
1	fk	395	TYR	N-CA-C	5.45	116.91	110.97
1	bg	79	ILE	CA-C-O	-5.45	113.97	120.78
1	bm	294	LEU	CB-CA-C	-5.45	102.33	110.88
1	cc	119	SER	CA-C-N	5.45	125.42	120.03
1	cc	119	SER	C-N-CA	5.45	125.42	120.03
1	cv	209	ASP	CA-CB-CG	5.45	118.05	112.60
1	do	500	MET	CA-C-N	5.45	125.45	119.90
1	do	500	MET	C-N-CA	5.45	125.45	119.90
1	er	483	PRO	N-CA-C	-5.45	102.55	111.21
1	ez	71	ASP	CA-CB-CG	5.45	118.05	112.60
1	ez	163	PHE	CA-C-N	5.45	125.35	119.85
1	ez	163	PHE	C-N-CA	5.45	125.35	119.85
1	fr	491	ALA	CA-C-N	5.45	125.35	119.85
1	fr	491	ALA	C-N-CA	5.45	125.35	119.85
1	gq	121	THR	CB-CA-C	-5.45	103.70	112.09
1	gu	324	THR	CB-CA-C	5.45	116.06	109.85
3	lg	72	ASN	CA-CB-CG	5.45	118.05	112.60
3	ne	46	TYR	N-CA-C	5.45	117.25	109.14
1	be	269	ALA	N-CA-C	5.44	118.75	111.24
1	cr	281	VAL	N-CA-C	5.44	116.84	111.67
1	ch	256	LYS	N-CA-C	5.44	117.34	109.07
1	cl	256	LYS	N-CA-C	5.44	117.67	109.23
1	dk	110	ASP	CA-CB-CG	5.44	118.04	112.60
1	dr	245	ASN	N-CA-C	5.44	118.50	109.79
1	eo	256	LYS	N-CA-C	5.44	117.34	109.07
1	fp	259	ILE	N-CA-C	5.44	115.83	107.77
3	mb	38	VAL	N-CA-C	5.44	116.50	108.45
1	eh	480	GLY	N-CA-C	5.44	119.59	110.56
1	gu	491	ALA	CA-C-N	5.44	125.20	119.76
1	gu	491	ALA	C-N-CA	5.44	125.20	119.76
2	hj	114	THR	CA-C-N	5.44	125.42	120.03
2	hj	114	THR	C-N-CA	5.44	125.42	120.03
1	ci	145	HIS	CA-C-N	5.44	125.11	119.56
1	ci	145	HIS	C-N-CA	5.44	125.11	119.56
1	cq	281	VAL	N-CA-C	5.44	116.83	111.67
1	ee	154	PHE	CA-CB-CG	5.44	119.24	113.80
1	ek	250	MET	N-CA-C	5.44	116.54	108.60
1	fe	222	VAL	N-CA-C	5.44	117.92	108.95
1	gv	163	PHE	CA-C-N	5.44	125.34	119.85
1	gv	163	PHE	C-N-CA	5.44	125.34	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	hz	67	GLU	N-CA-C	-5.44	105.35	111.28
1	cr	245	ASN	CA-C-N	5.44	125.34	119.85
1	cr	245	ASN	C-N-CA	5.44	125.34	119.85
2	hg	59	ASN	CA-CB-CG	5.44	118.04	112.60
3	ii	32	PHE	CA-C-N	5.44	125.11	119.56
3	ii	32	PHE	C-N-CA	5.44	125.11	119.56
3	nq	38	VAL	N-CA-C	5.44	115.81	107.77
3	nt	32	PHE	CA-C-N	5.44	125.11	119.56
3	nt	32	PHE	C-N-CA	5.44	125.11	119.56
1	am	483	PRO	N-CA-C	-5.43	102.57	111.21
1	ap	113	GLY	N-CA-C	-5.43	104.30	112.89
1	eg	258	VAL	N-CA-C	5.43	117.47	108.99
1	gl	87	ALA	CA-C-N	-5.43	116.06	123.12
1	gl	87	ALA	C-N-CA	-5.43	116.06	123.12
2	hf	250	LEU	N-CA-C	-5.43	106.33	113.12
3	lc	32	PHE	CA-C-N	5.43	125.10	119.56
3	lc	32	PHE	C-N-CA	5.43	125.10	119.56
1	ao	232	ILE	N-CA-C	-5.43	106.51	111.67
1	bu	74	TYR	CA-C-N	5.43	129.99	122.77
1	bu	74	TYR	C-N-CA	5.43	129.99	122.77
1	ce	285	ASP	CA-C-N	5.43	131.91	121.54
1	ce	285	ASP	C-N-CA	5.43	131.91	121.54
1	da	263	SER	N-CA-C	5.43	118.50	110.46
1	dt	154	PHE	N-CA-C	-5.43	105.77	112.72
1	fu	287	ASP	N-CA-C	-5.43	104.69	112.13
1	gs	145	HIS	CA-C-N	5.43	125.10	119.56
1	gs	145	HIS	C-N-CA	5.43	125.10	119.56
1	gy	163	PHE	CA-C-N	5.43	125.34	119.85
1	gy	163	PHE	C-N-CA	5.43	125.34	119.85
2	hm	47	GLN	CA-C-N	5.43	125.10	119.56
2	hm	47	GLN	C-N-CA	5.43	125.10	119.56
1	ca	344	ARG	N-CA-C	-5.43	99.83	109.06
1	el	480	GLY	N-CA-C	5.43	118.65	110.18
1	gr	121	THR	CB-CA-C	-5.43	103.73	112.09
1	cz	426	ASP	CA-CB-CG	-5.43	107.17	112.60
1	gl	232	ILE	N-CA-C	-5.43	106.40	111.45
3	iw	49	PHE	CA-C-N	5.43	125.63	120.31
3	iw	49	PHE	C-N-CA	5.43	125.63	120.31
3	np	5	ARG	N-CA-C	-5.43	105.31	113.89
1	am	491	ALA	CA-C-N	5.43	125.37	119.78
1	am	491	ALA	C-N-CA	5.43	125.37	119.78
1	bl	87	ALA	N-CA-C	5.43	117.19	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cc	293	ILE	N-CA-C	-5.43	105.56	110.82
1	ea	119	SER	CA-C-N	5.43	125.37	119.78
1	ea	119	SER	C-N-CA	5.43	125.37	119.78
1	eo	145	HIS	CA-C-N	5.43	125.25	119.28
1	eo	145	HIS	C-N-CA	5.43	125.25	119.28
3	kp	32	PHE	CA-C-N	5.43	125.09	119.56
3	kp	32	PHE	C-N-CA	5.43	125.09	119.56
3	nz	49	PHE	CA-C-N	5.43	125.89	120.14
3	nz	49	PHE	C-N-CA	5.43	125.89	120.14
1	bv	222	VAL	N-CA-C	5.42	117.90	108.95
1	ez	426	ASP	CA-CB-CG	-5.42	107.17	112.60
1	gj	125	PHE	CB-CA-C	-5.42	100.75	111.60
1	gu	250	MET	N-CA-C	5.42	117.43	109.24
3	jc	72	ASN	CA-CB-CG	5.42	118.03	112.60
1	ce	121	THR	N-CA-C	5.42	118.60	111.28
1	cz	328	LYS	N-CA-C	5.42	119.88	112.88
1	da	252	PHE	N-CA-C	5.42	117.04	108.96
1	ai	115	GLN	CA-C-N	5.42	125.36	119.78
1	ai	115	GLN	C-N-CA	5.42	125.36	119.78
1	ck	425	ILE	N-CA-C	5.42	116.53	108.23
1	fn	94	ALA	CB-CA-C	-5.42	110.31	116.54
1	gh	103	ILE	CA-C-N	5.42	125.42	119.89
1	gh	103	ILE	C-N-CA	5.42	125.42	119.89
1	gt	256	LYS	N-CA-C	5.42	117.04	108.96
1	bs	509	LYS	N-CA-C	5.42	120.76	114.04
1	cn	324	THR	CB-CA-C	5.42	116.38	110.15
3	ly	67	GLU	N-CA-C	-5.42	105.45	111.36
1	ay	121	THR	CB-CA-C	-5.42	103.75	112.09
1	bm	324	THR	CA-C-N	5.42	125.76	119.47
1	bm	324	THR	C-N-CA	5.42	125.76	119.47
1	ce	468	GLN	CA-C-N	5.42	125.18	119.76
1	ce	468	GLN	C-N-CA	5.42	125.18	119.76
1	ci	121	THR	CB-CA-C	-5.42	103.75	112.09
1	fb	245	ASN	CA-C-N	5.42	125.39	120.03
1	fb	245	ASN	C-N-CA	5.42	125.39	120.03
1	fx	115	GLN	CA-C-N	5.42	125.36	119.78
1	fx	115	GLN	C-N-CA	5.42	125.36	119.78
2	hj	291	LYS	CA-C-N	5.42	126.61	119.84
2	hj	291	LYS	C-N-CA	5.42	126.61	119.84
1	ai	119	SER	CA-C-N	5.42	125.39	120.03
1	ai	119	SER	C-N-CA	5.42	125.39	120.03
1	ao	245	ASN	CA-C-N	5.42	125.32	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ao	245	ASN	C-N-CA	5.42	125.32	119.85
1	bs	71	ASP	CA-CB-CG	5.42	118.02	112.60
1	cr	121	THR	CB-CA-C	-5.42	103.75	112.09
1	eo	209	ASP	CA-CB-CG	5.42	118.02	112.60
1	es	240	ASN	N-CA-C	5.42	119.17	112.24
1	fa	486	GLU	CA-C-N	5.42	131.89	121.54
1	fa	486	GLU	C-N-CA	5.42	131.89	121.54
1	fd	193	SER	N-CA-C	-5.42	107.32	114.04
1	ft	76	ALA	N-CA-C	5.42	117.18	111.28
1	gl	74	TYR	CA-C-N	5.42	129.97	122.77
1	gl	74	TYR	C-N-CA	5.42	129.97	122.77
1	gw	402	THR	CA-C-N	5.42	126.91	120.14
1	gw	402	THR	C-N-CA	5.42	126.91	120.14
3	ma	10	ILE	N-CA-C	5.42	115.66	107.75
1	at	285	ASP	CA-C-N	5.42	131.88	121.54
1	at	285	ASP	C-N-CA	5.42	131.88	121.54
1	au	245	ASN	CA-C-N	5.41	125.32	119.85
1	au	245	ASN	C-N-CA	5.41	125.32	119.85
1	bo	119	SER	CA-C-N	5.41	125.39	120.03
1	bo	119	SER	C-N-CA	5.41	125.39	120.03
1	dm	484	PHE	CA-CB-CG	5.41	119.21	113.80
1	dy	402	THR	CA-C-N	5.41	126.91	120.14
1	dy	402	THR	C-N-CA	5.41	126.91	120.14
1	ek	269	ALA	N-CA-C	5.41	117.79	111.02
1	fd	71	ASP	CA-CB-CG	5.41	118.01	112.60
1	fv	253	ARG	N-CA-C	5.41	119.41	111.34
1	gw	484	PHE	CA-CB-CG	5.41	119.21	113.80
1	aa	87	ALA	N-CA-C	5.41	118.10	111.82
1	ba	115	GLN	CB-CA-C	-5.41	106.29	111.00
1	fp	500	MET	CA-C-N	5.41	125.32	119.85
1	fp	500	MET	C-N-CA	5.41	125.32	119.85
1	go	222	VAL	N-CA-C	5.41	117.88	108.95
1	gs	506	SER	CA-C-N	-5.41	113.93	121.99
1	gs	506	SER	C-N-CA	-5.41	113.93	121.99
3	jz	15	GLN	N-CA-C	5.41	117.62	109.23
3	kt	49	PHE	CA-C-N	5.41	125.88	120.14
3	kt	49	PHE	C-N-CA	5.41	125.88	120.14
1	bn	426	ASP	CA-CB-CG	-5.41	107.19	112.60
1	fs	344	ARG	N-CA-C	-5.41	99.86	109.06
2	hk	172	SER	N-CA-C	5.41	118.55	109.95
3	nk	67	GLU	N-CA-C	-5.41	105.46	111.36
1	dg	115	GLN	CA-C-N	5.41	125.35	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dg	115	GLN	C-N-CA	5.41	125.35	119.78
1	gb	222	VAL	N-CA-C	5.41	117.87	108.95
3	kt	32	PHE	CA-C-N	5.41	125.08	119.56
3	kt	32	PHE	C-N-CA	5.41	125.08	119.56
1	dm	281	VAL	N-CA-C	5.41	116.81	111.67
1	fy	253	ARG	N-CA-C	5.41	119.54	112.13
1	fz	256	LYS	N-CA-C	5.41	117.29	109.07
1	ax	285	ASP	N-CA-C	5.41	118.34	111.69
1	cu	222	VAL	N-CA-C	5.41	117.87	108.95
1	gy	265	GLN	N-CA-C	5.41	117.31	108.55
2	hg	47	GLN	CA-C-N	5.41	125.08	119.56
2	hg	47	GLN	C-N-CA	5.41	125.08	119.56
2	hg	114	THR	CA-C-N	5.41	125.38	120.03
2	hg	114	THR	C-N-CA	5.41	125.38	120.03
2	hh	141	SER	N-CA-C	-5.41	101.91	109.96
3	jq	46	TYR	N-CA-C	5.41	117.19	109.14
3	nf	44	ALA	N-CA-C	5.41	119.74	113.20
1	dr	222	VAL	N-CA-C	5.40	117.87	108.95
1	fo	432	ASP	CA-CB-CG	-5.40	107.20	112.60
1	ge	232	ILE	N-CA-C	-5.40	106.54	111.67
1	cj	182	PHE	CA-CB-CG	5.40	119.20	113.80
1	cn	95	VAL	N-CA-C	5.40	115.83	107.78
1	du	115	GLN	CA-C-N	5.40	125.34	119.78
1	du	115	GLN	C-N-CA	5.40	125.34	119.78
1	eu	328	LYS	N-CA-C	5.40	119.85	112.88
1	gp	245	ASN	CA-C-N	5.40	125.38	120.03
1	gp	245	ASN	C-N-CA	5.40	125.38	120.03
1	gu	145	HIS	CA-C-N	5.40	125.02	119.56
1	gu	145	HIS	C-N-CA	5.40	125.02	119.56
1	at	403	GLY	N-CA-C	5.40	120.31	113.24
1	az	265	GLN	N-CA-C	5.40	117.98	108.75
1	bq	163	PHE	CA-C-N	5.40	125.30	119.85
1	bq	163	PHE	C-N-CA	5.40	125.30	119.85
1	br	113	GLY	N-CA-C	-5.40	104.36	112.89
1	ck	250	MET	N-CA-C	5.40	116.48	108.60
1	ew	245	ASN	CA-C-N	5.40	125.38	120.03
1	ew	245	ASN	C-N-CA	5.40	125.38	120.03
1	ae	119	SER	CA-C-N	5.40	125.39	120.21
1	ae	119	SER	C-N-CA	5.40	125.39	120.21
1	ea	232	ILE	N-CA-C	-5.40	106.43	111.45
1	fa	328	LYS	N-CA-C	5.40	120.02	113.38
1	bm	426	ASP	CA-CB-CG	-5.40	107.20	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	do	490	GLN	N-CA-C	-5.40	105.56	111.82
1	ev	256	LYS	N-CA-C	5.40	117.27	109.07
1	ft	329	ALA	N-CA-C	5.40	118.69	111.24
1	ap	88	VAL	N-CA-C	5.40	115.63	107.75
1	bd	134	ASP	CA-C-N	5.40	125.01	119.56
1	bd	134	ASP	C-N-CA	5.40	125.01	119.56
1	ct	145	HIS	CA-C-N	5.40	125.06	119.56
1	ct	145	HIS	C-N-CA	5.40	125.06	119.56
1	eo	149	GLY	CA-C-N	5.40	125.37	120.03
1	eo	149	GLY	C-N-CA	5.40	125.37	120.03
1	aw	324	THR	N-CA-C	-5.39	101.57	109.50
1	bc	402	THR	CA-C-N	5.39	126.93	120.13
1	bc	402	THR	C-N-CA	5.39	126.93	120.13
1	db	358	ASP	CA-CB-CG	5.39	117.99	112.60
1	fc	468	GLN	CA-C-N	5.39	125.30	119.85
1	fc	468	GLN	C-N-CA	5.39	125.30	119.85
1	fo	163	PHE	CA-C-N	5.39	125.30	119.85
1	fo	163	PHE	C-N-CA	5.39	125.30	119.85
1	gl	481	ILE	N-CA-C	5.39	116.01	108.89
2	hj	250	LEU	N-CA-C	-5.39	104.95	112.45
1	ae	266	LEU	N-CA-C	5.39	117.38	109.24
1	ap	163	PHE	CA-C-N	5.39	125.30	119.85
1	ap	163	PHE	C-N-CA	5.39	125.30	119.85
1	bx	256	LYS	N-CA-C	5.39	117.27	109.07
1	by	463	ASP	CA-C-N	5.39	125.06	119.56
1	by	463	ASP	C-N-CA	5.39	125.06	119.56
1	cg	287	ASP	N-CA-C	-5.39	105.82	112.72
1	cw	474	LYS	N-CA-C	5.39	117.69	108.90
1	ex	463	ASP	CA-C-N	5.39	125.06	119.56
1	ex	463	ASP	C-N-CA	5.39	125.06	119.56
1	gf	134	ASP	CA-C-N	5.39	125.47	119.32
1	gf	134	ASP	C-N-CA	5.39	125.47	119.32
2	hk	365	ASP	CA-C-N	5.39	127.26	121.00
2	hk	365	ASP	C-N-CA	5.39	127.26	121.00
2	hl	353	ASP	CA-C-N	5.39	125.72	119.47
2	hl	353	ASP	C-N-CA	5.39	125.72	119.47
3	mw	49	PHE	CA-C-N	5.39	125.86	120.14
3	mw	49	PHE	C-N-CA	5.39	125.86	120.14
1	al	323	LEU	N-CA-C	5.39	118.89	110.32
1	as	71	ASP	CA-CB-CG	5.39	117.99	112.60
1	bi	500	MET	CA-C-N	5.39	125.40	119.90
1	bi	500	MET	C-N-CA	5.39	125.40	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dc	222	VAL	N-CA-C	5.39	117.84	108.95
1	do	121	THR	CB-CA-C	-5.39	103.79	112.09
1	dq	199	ASP	N-CA-C	5.39	122.28	110.80
1	bi	327	SER	N-CA-C	5.39	116.96	109.31
3	iq	37	ASP	CA-CB-CG	5.39	117.99	112.60
1	bb	412	VAL	N-CA-C	-5.39	106.55	111.67
1	dj	226	GLU	N-CA-C	5.39	116.71	108.52
1	ed	182	PHE	CA-CB-CG	5.39	119.19	113.80
1	ef	256	LYS	N-CA-C	5.39	117.26	109.07
1	ga	484	PHE	CA-CB-CG	5.39	119.19	113.80
1	cf	88	VAL	N-CA-C	5.38	115.61	107.75
1	eb	209	ASP	CA-CB-CG	5.38	117.98	112.60
1	et	222	VAL	N-CA-C	5.38	117.83	108.95
1	fi	103	ILE	CA-C-N	5.38	125.39	119.90
1	fi	103	ILE	C-N-CA	5.38	125.39	119.90
3	kp	67	GLU	N-CA-C	-5.38	105.49	111.36
1	bn	71	ASP	CA-CB-CG	5.38	117.98	112.60
1	cm	182	PHE	CA-CB-CG	5.38	119.18	113.80
2	hi	221	VAL	N-CA-C	-5.38	107.54	111.90
1	ae	395	TYR	N-CA-C	5.38	116.83	110.97
1	bj	119	SER	CA-C-N	5.38	125.36	120.03
1	bj	119	SER	C-N-CA	5.38	125.36	120.03
1	bo	134	ASP	CA-C-N	5.38	125.05	119.56
1	bo	134	ASP	C-N-CA	5.38	125.05	119.56
1	cz	245	ASN	CA-C-N	5.38	125.28	119.85
1	cz	245	ASN	C-N-CA	5.38	125.28	119.85
1	em	468	GLN	CA-C-N	5.38	125.29	119.85
1	em	468	GLN	C-N-CA	5.38	125.29	119.85
1	em	502	SER	N-CA-C	5.38	115.34	108.24
1	ep	358	ASP	CA-CB-CG	5.38	117.98	112.60
1	fb	182	PHE	CA-CB-CG	5.38	119.18	113.80
1	gc	481	ILE	N-CA-C	5.38	115.99	108.89
1	go	285	ASP	CA-C-N	5.38	131.82	121.54
1	go	285	ASP	C-N-CA	5.38	131.82	121.54
2	he	320	LEU	N-CA-C	5.38	120.71	114.04
3	jm	41	ILE	N-CA-C	5.38	115.33	108.12
3	no	38	VAL	N-CA-C	5.38	116.03	108.17
1	ak	256	LYS	N-CA-C	5.38	117.25	109.07
1	bx	110	ASP	CA-CB-CG	5.38	117.98	112.60
1	cb	327	SER	N-CA-C	5.38	116.86	110.19
1	cd	87	ALA	CA-C-N	-5.38	116.09	123.14
1	cd	87	ALA	C-N-CA	-5.38	116.09	123.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cy	115	GLN	CA-C-N	5.38	125.32	119.78
1	cy	115	GLN	C-N-CA	5.38	125.32	119.78
1	eg	199	ASP	CA-CB-CG	-5.38	107.22	112.60
1	eq	293	ILE	N-CA-C	-5.38	105.88	111.58
1	fm	182	PHE	CA-CB-CG	5.38	119.18	113.80
3	ns	44	ALA	N-CA-C	5.38	119.71	113.20
1	am	130	VAL	N-CA-C	5.38	115.64	108.11
1	df	149	GLY	CA-C-N	5.38	125.28	119.85
1	df	149	GLY	C-N-CA	5.38	125.28	119.85
1	fa	74	TYR	CA-C-N	5.38	129.92	122.77
1	fa	74	TYR	C-N-CA	5.38	129.92	122.77
1	gx	113	GLY	CA-C-N	-5.38	117.70	122.97
1	gx	113	GLY	C-N-CA	-5.38	117.70	122.97
3	jz	72	ASN	CA-CB-CG	5.38	117.98	112.60
1	cv	245	ASN	CA-C-N	5.38	125.28	119.85
1	cv	245	ASN	C-N-CA	5.38	125.28	119.85
1	df	271	SER	N-CA-C	5.38	118.44	110.48
1	dh	88	VAL	N-CA-C	5.38	115.60	107.75
1	ey	103	ILE	CA-C-N	5.38	125.32	119.78
1	ey	103	ILE	C-N-CA	5.38	125.32	119.78
1	fa	463	ASP	CA-C-N	5.38	125.04	119.56
1	fa	463	ASP	C-N-CA	5.38	125.04	119.56
1	gm	484	PHE	CA-CB-CG	5.38	119.18	113.80
1	ah	294	LEU	CB-CA-C	-5.38	102.44	110.88
1	au	209	ASP	CA-CB-CG	5.38	117.97	112.60
1	bv	449	TYR	CB-CA-C	-5.38	98.74	109.33
1	ce	256	LYS	N-CA-C	5.38	117.36	109.24
1	cj	134	ASP	CA-C-N	5.38	125.45	119.32
1	cj	134	ASP	C-N-CA	5.38	125.45	119.32
1	fk	134	ASP	CA-C-N	5.38	125.04	119.56
1	fk	134	ASP	C-N-CA	5.38	125.04	119.56
1	fq	258	VAL	N-CA-C	5.38	117.13	108.85
1	ab	266	LEU	N-CA-C	5.37	117.56	109.23
1	ao	187	THR	N-CA-C	5.37	118.11	110.10
1	bq	402	THR	CA-C-N	5.37	126.86	120.14
1	bq	402	THR	C-N-CA	5.37	126.86	120.14
1	bt	480	GLY	CA-C-N	5.37	129.30	122.37
1	bt	480	GLY	C-N-CA	5.37	129.30	122.37
1	dd	130	VAL	N-CA-C	5.37	115.86	108.12
1	dm	500	MET	CB-CA-C	5.37	116.60	108.86
1	eg	113	GLY	N-CA-C	-5.37	104.20	112.85
1	fe	328	LYS	N-CA-C	5.37	119.81	112.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fk	149	GLY	CA-C-N	5.37	125.28	119.85
1	fk	149	GLY	C-N-CA	5.37	125.28	119.85
1	fm	327	SER	N-CA-C	5.37	116.94	109.31
1	gp	209	ASP	CA-CB-CG	5.37	117.97	112.60
2	hh	337	VAL	N-CA-C	5.37	115.86	108.12
2	hn	136	LYS	N-CA-C	-5.37	106.86	113.41
3	jk	49	PHE	CA-C-N	5.37	125.84	120.14
3	jk	49	PHE	C-N-CA	5.37	125.84	120.14
3	mu	38	VAL	N-CA-C	5.37	116.02	108.17
1	bg	222	VAL	N-CA-C	5.37	117.81	108.95
1	bw	232	ILE	N-CA-C	-5.37	106.45	111.45
1	bx	134	ASP	CA-C-N	5.37	125.70	119.47
1	bx	134	ASP	C-N-CA	5.37	125.70	119.47
1	cf	383	VAL	N-CA-C	-5.37	105.89	111.58
1	da	285	ASP	CA-CB-CG	5.37	117.97	112.60
1	dr	149	GLY	CA-C-N	5.37	125.28	119.85
1	dr	149	GLY	C-N-CA	5.37	125.28	119.85
3	is	37	ASP	CA-CB-CG	5.37	117.97	112.60
1	be	110	ASP	CA-CB-CG	5.37	117.97	112.60
1	au	329	ALA	N-CA-C	5.37	118.53	111.28
1	bb	258	VAL	N-CA-C	5.37	117.61	108.86
1	bi	328	LYS	N-CA-C	5.37	119.98	113.38
1	du	491	ALA	CA-C-N	5.37	125.57	120.31
1	du	491	ALA	C-N-CA	5.37	125.57	120.31
1	ej	256	LYS	N-CA-C	5.37	117.23	109.07
1	es	328	LYS	N-CA-C	5.37	119.98	113.38
1	ez	328	LYS	N-CA-C	5.37	119.82	113.16
1	gb	87	ALA	CA-C-N	-5.37	116.11	123.14
1	gb	87	ALA	C-N-CA	-5.37	116.11	123.14
1	gn	454	VAL	CA-C-N	-5.37	114.03	122.73
1	gn	454	VAL	C-N-CA	-5.37	114.03	122.73
3	jn	74	ASP	CA-CB-CG	5.37	117.97	112.60
3	kdl	44	ALA	N-CA-C	5.37	119.82	113.16
3	li	41	ILE	N-CA-CB	-5.37	106.91	112.28
1	do	134	ASP	CA-C-N	5.37	125.03	119.56
1	do	134	ASP	C-N-CA	5.37	125.03	119.56
1	au	285	ASP	CA-C-N	5.37	131.79	121.54
1	au	285	ASP	C-N-CA	5.37	131.79	121.54
1	fv	151	ASP	CA-CB-CG	5.37	117.97	112.60
1	gh	463	ASP	CA-C-N	5.37	125.03	119.56
1	gh	463	ASP	C-N-CA	5.37	125.03	119.56
3	io	49	PHE	CA-C-N	5.37	125.57	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	io	49	PHE	C-N-CA	5.37	125.57	120.31
1	am	263	SER	N-CA-C	5.36	117.67	109.95
1	ay	468	GLN	CA-C-N	5.36	125.27	119.85
1	ay	468	GLN	C-N-CA	5.36	125.27	119.85
1	cj	484	PHE	CA-CB-CG	5.36	119.16	113.80
1	cl	463	ASP	CA-C-N	5.36	125.03	119.56
1	cl	463	ASP	C-N-CA	5.36	125.03	119.56
1	dq	468	GLN	CA-C-N	5.36	125.27	119.85
1	dq	468	GLN	C-N-CA	5.36	125.27	119.85
1	ei	253	ARG	N-CA-C	5.36	120.06	112.93
1	eu	265	GLN	N-CA-C	5.36	117.92	108.75
1	ez	483	PRO	N-CA-C	-5.36	102.77	111.14
3	lx	46	TYR	N-CA-C	5.36	117.13	109.14
1	cl	269	ALA	N-CA-C	5.36	117.72	111.02
1	ds	145	HIS	CA-C-N	5.36	125.69	119.47
1	ds	145	HIS	C-N-CA	5.36	125.69	119.47
1	eo	402	THR	CA-C-N	5.36	126.84	120.14
1	eo	402	THR	C-N-CA	5.36	126.84	120.14
1	gh	329	ALA	N-CA-C	5.36	117.18	110.91
1	dg	256	LYS	N-CA-C	5.36	116.95	108.96
1	dk	506	SER	CA-C-N	-5.36	114.00	121.99
1	dk	506	SER	C-N-CA	-5.36	114.00	121.99
1	ey	425	ILE	N-CA-C	5.36	115.82	107.99
1	fn	468	GLN	CA-C-N	5.36	125.27	119.85
1	fn	468	GLN	C-N-CA	5.36	125.27	119.85
1	gw	256	LYS	N-CA-C	5.36	117.22	109.07
2	ho	145	SER	N-CA-C	-5.36	102.46	110.23
3	jj	38	VAL	N-CA-C	5.36	115.77	107.78
3	nm	38	VAL	N-CA-C	5.36	115.70	107.77
1	cs	491	ALA	CA-C-N	5.36	125.26	119.85
1	cs	491	ALA	C-N-CA	5.36	125.26	119.85
1	dl	222	VAL	N-CA-C	5.36	117.79	108.95
1	dm	245	ASN	CA-C-N	5.36	125.34	120.03
1	dm	245	ASN	C-N-CA	5.36	125.34	120.03
1	gt	480	GLY	N-CA-C	5.36	118.41	110.42
1	an	491	ALA	CA-C-N	5.36	125.82	120.14
1	an	491	ALA	C-N-CA	5.36	125.82	120.14
1	cp	406	THR	N-CA-C	-5.36	106.67	114.12
1	cr	115	GLN	CA-C-N	5.36	125.26	119.85
1	cr	115	GLN	C-N-CA	5.36	125.26	119.85
1	fv	502	SER	CA-C-N	-5.36	113.81	120.56
1	fv	502	SER	C-N-CA	-5.36	113.81	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	hb	395	TYR	N-CA-C	5.36	116.81	110.97
2	hj	230	ILE	N-CA-C	5.36	117.36	112.43
3	ob	25	GLY	N-CA-C	-5.36	104.87	112.37
1	bf	446	ALA	N-CA-C	5.36	119.81	113.12
1	bj	245	ASN	CA-C-N	5.36	125.26	119.85
1	bj	245	ASN	C-N-CA	5.36	125.26	119.85
1	de	245	ASN	CA-C-N	5.36	125.33	120.03
1	de	245	ASN	C-N-CA	5.36	125.33	120.03
1	dk	115	GLN	CA-C-N	5.36	125.30	119.78
1	dk	115	GLN	C-N-CA	5.36	125.30	119.78
1	fd	222	VAL	N-CA-C	5.36	117.79	108.95
2	hn	21	ARG	CA-C-N	5.36	125.56	120.31
2	hn	21	ARG	C-N-CA	5.36	125.56	120.31
3	ip	74	ASP	CA-CB-CG	5.36	117.96	112.60
1	aa	222	VAL	N-CA-C	5.35	117.78	108.95
1	ei	426	ASP	CA-CB-CG	-5.35	107.25	112.60
1	go	256	LYS	N-CA-C	5.35	116.94	108.96
1	hb	403	GLY	N-CA-C	5.35	120.25	113.24
2	hh	315	ASP	CA-CB-CG	5.35	117.95	112.60
3	iy	37	ASP	CA-CB-CG	5.35	117.95	112.60
1	ch	237	GLU	CB-CA-C	-5.35	104.97	111.82
1	cj	396	ALA	N-CA-C	-5.35	100.30	108.76
1	gg	256	LYS	N-CA-C	5.35	117.39	108.99
1	gp	358	ASP	CA-CB-CG	5.35	117.95	112.60
2	hi	420	LEU	CA-C-N	5.35	125.29	119.78
2	hi	420	LEU	C-N-CA	5.35	125.29	119.78
1	cq	509	LYS	N-CA-C	5.35	121.56	114.12
1	dt	426	ASP	CA-CB-CG	-5.35	107.25	112.60
1	ee	265	GLN	N-CA-C	5.35	117.39	108.99
1	ei	491	ALA	CA-C-N	5.35	125.81	120.14
1	ei	491	ALA	C-N-CA	5.35	125.81	120.14
1	fo	265	GLN	N-CA-C	5.35	117.22	108.55
1	gl	267	LYS	N-CA-C	5.35	117.95	109.50
1	gu	71	ASP	CA-CB-CG	5.35	117.95	112.60
1	gu	119	SER	N-CA-C	-5.35	103.40	108.22
1	bb	121	THR	CA-C-N	-5.35	114.85	120.31
1	bb	121	THR	C-N-CA	-5.35	114.85	120.31
1	cj	250	MET	N-CA-C	5.35	116.93	108.96
1	cs	263	SER	N-CA-C	5.35	118.44	110.52
1	ct	265	GLN	N-CA-C	5.35	117.22	108.55
1	dg	87	ALA	N-CA-C	5.35	117.11	111.28
1	dr	103	ILE	CA-C-N	5.35	125.29	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dr	103	ILE	C-N-CA	5.35	125.29	119.78
1	el	426	ASP	CA-CB-CG	-5.35	107.25	112.60
1	ff	358	ASP	CA-CB-CG	5.35	117.95	112.60
1	gd	468	GLN	CA-C-N	5.35	125.25	119.85
1	gd	468	GLN	C-N-CA	5.35	125.25	119.85
1	gq	403	GLY	N-CA-C	5.35	120.25	113.24
3	ny	44	ALA	N-CA-C	5.35	119.67	113.20
1	bl	119	SER	CA-C-N	5.35	125.32	120.03
1	bl	119	SER	C-N-CA	5.35	125.32	120.03
1	dk	258	VAL	N-CA-C	5.35	116.61	108.80
1	ff	71	ASP	CA-CB-CG	5.35	117.95	112.60
1	fw	500	MET	CB-CA-C	5.35	116.56	108.86
3	jb	32	PHE	CA-C-N	5.35	125.02	119.56
3	jb	32	PHE	C-N-CA	5.35	125.02	119.56
3	ml	38	VAL	N-CA-C	5.35	115.82	108.12
1	ea	484	PHE	CA-CB-CG	5.35	119.15	113.80
1	cz	232	ILE	N-CA-C	-5.34	106.48	111.45
1	et	232	ILE	N-CA-C	-5.34	106.59	111.67
1	fx	269	ALA	N-CA-C	5.34	118.61	111.24
1	gd	256	LYS	N-CA-C	5.34	117.52	109.23
3	if	72	ASN	CA-CB-CG	5.34	117.94	112.60
3	ls	32	PHE	CA-C-N	5.34	125.01	119.56
3	ls	32	PHE	C-N-CA	5.34	125.01	119.56
1	cg	88	VAL	N-CA-C	5.34	115.55	107.75
1	cx	72	HIS	CA-CB-CG	-5.34	108.46	113.80
1	hb	484	PHE	CA-CB-CG	5.34	119.14	113.80
1	aq	256	LYS	N-CA-C	5.34	117.19	109.07
1	cc	87	ALA	CA-C-N	-5.34	116.06	122.90
1	cc	87	ALA	C-N-CA	-5.34	116.06	122.90
1	cj	130	VAL	N-CA-C	5.34	115.59	108.11
1	dd	468	GLN	CA-C-N	5.34	125.25	119.85
1	dd	468	GLN	C-N-CA	5.34	125.25	119.85
1	dq	232	ILE	N-CA-C	-5.34	106.48	111.45
1	dz	256	LYS	N-CA-C	5.34	117.19	109.07
1	eg	454	VAL	CA-C-N	-5.34	114.08	122.73
1	eg	454	VAL	C-N-CA	-5.34	114.08	122.73
1	eh	451	ALA	CA-C-N	5.34	126.52	119.84
1	eh	451	ALA	C-N-CA	5.34	126.52	119.84
1	gc	265	GLN	N-CA-C	5.34	117.20	108.55
1	gu	92	GLY	CA-C-N	5.34	125.25	119.85
1	gu	92	GLY	C-N-CA	5.34	125.25	119.85
3	ia	44	ALA	N-CA-C	5.34	119.78	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	iu	32	PHE	CA-C-N	5.34	125.01	119.56
3	iu	32	PHE	C-N-CA	5.34	125.01	119.56
3	my	32	PHE	CA-C-N	5.34	125.01	119.56
3	my	32	PHE	C-N-CA	5.34	125.01	119.56
3	nn	67	GLU	N-CA-C	-5.34	105.54	111.36
1	bs	402	THR	CA-C-N	5.34	126.86	120.13
1	bs	402	THR	C-N-CA	5.34	126.86	120.13
1	bz	115	GLN	CA-C-N	5.34	125.28	119.78
1	bz	115	GLN	C-N-CA	5.34	125.28	119.78
1	cd	222	VAL	N-CA-C	5.34	117.76	108.95
1	ci	71	ASP	CA-CB-CG	5.34	117.94	112.60
1	cx	119	SER	CA-C-N	5.34	125.32	120.03
1	cx	119	SER	C-N-CA	5.34	125.32	120.03
1	da	250	MET	N-CA-C	5.34	117.19	109.07
1	dl	199	ASP	CA-CB-CG	-5.34	107.26	112.60
1	ea	163	PHE	CA-C-N	5.34	125.24	119.85
1	ea	163	PHE	C-N-CA	5.34	125.24	119.85
1	ga	110	ASP	CA-CB-CG	5.34	117.94	112.60
2	hj	41	ALA	N-CA-C	-5.34	102.49	110.23
1	au	115	GLN	CA-C-N	5.34	125.28	119.78
1	au	115	GLN	C-N-CA	5.34	125.28	119.78
1	cy	245	ASN	CA-C-N	5.34	125.31	120.03
1	cy	245	ASN	C-N-CA	5.34	125.31	120.03
1	dl	149	GLY	CA-C-N	5.34	125.24	119.85
1	dl	149	GLY	C-N-CA	5.34	125.24	119.85
1	ek	403	GLY	N-CA-C	5.34	120.23	113.24
1	av	426	ASP	CA-CB-CG	-5.34	107.26	112.60
1	bp	71	ASP	CA-CB-CG	5.34	117.94	112.60
1	ci	87	ALA	CA-C-N	-5.34	116.00	123.10
1	ci	87	ALA	C-N-CA	-5.34	116.00	123.10
1	cj	463	ASP	CA-C-N	5.34	125.00	119.56
1	cj	463	ASP	C-N-CA	5.34	125.00	119.56
1	df	222	VAL	N-CA-C	5.34	117.76	108.95
1	dm	87	ALA	N-CA-C	5.34	117.18	111.36
1	ee	149	GLY	CA-C-N	5.34	125.54	120.31
1	ee	149	GLY	C-N-CA	5.34	125.54	120.31
1	eg	245	ASN	CA-C-N	5.34	125.24	119.85
1	eg	245	ASN	C-N-CA	5.34	125.24	119.85
1	fe	265	GLN	N-CA-C	5.34	117.20	108.55
2	hf	291	LYS	CA-C-N	5.34	126.51	119.84
2	hf	291	LYS	C-N-CA	5.34	126.51	119.84
2	hm	114	THR	CA-C-N	5.34	125.31	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hm	114	THR	C-N-CA	5.34	125.31	120.03
3	md	46	TYR	N-CA-C	5.34	117.09	109.14
1	ah	103	ILE	CA-C-N	5.33	125.28	119.78
1	ah	103	ILE	C-N-CA	5.33	125.28	119.78
1	cx	484	PHE	CA-CB-CG	5.33	119.14	113.80
2	hn	114	THR	CA-C-N	5.33	125.31	120.03
2	hn	114	THR	C-N-CA	5.33	125.31	120.03
3	ks	44	ALA	N-CA-C	5.33	119.66	113.20
1	gf	198	ILE	N-CA-C	5.33	115.20	106.72
1	gq	87	ALA	CA-C-N	-5.33	116.15	123.14
1	gq	87	ALA	C-N-CA	-5.33	116.15	123.14
1	ae	163	PHE	CA-C-N	5.33	125.23	119.85
1	ae	163	PHE	C-N-CA	5.33	125.23	119.85
1	bq	149	GLY	CA-C-N	5.33	125.23	119.85
1	bq	149	GLY	C-N-CA	5.33	125.23	119.85
1	cm	253	ARG	N-CA-C	5.33	119.28	111.34
1	gq	184	GLU	N-CA-C	-5.33	100.62	108.99
1	gx	449	TYR	CB-CA-C	-5.33	98.83	109.33
3	kz	49	PHE	CA-C-N	5.33	125.79	120.14
3	kz	49	PHE	C-N-CA	5.33	125.79	120.14
3	mo	67	GLU	N-CA-C	-5.33	105.55	111.36
3	nn	32	PHE	CA-C-N	5.33	125.00	119.56
3	nn	32	PHE	C-N-CA	5.33	125.00	119.56
1	at	483	PRO	CA-C-O	-5.33	115.34	121.36
1	cu	209	ASP	CA-CB-CG	5.33	117.93	112.60
1	fo	95	VAL	N-CA-C	5.33	115.66	107.77
3	ni	49	PHE	CA-C-N	5.33	125.79	120.14
3	ni	49	PHE	C-N-CA	5.33	125.79	120.14
1	cy	258	VAL	N-CA-C	5.33	117.55	108.86
1	du	402	THR	CA-C-N	5.33	126.84	120.13
1	du	402	THR	C-N-CA	5.33	126.84	120.13
1	dv	483	PRO	N-CA-C	-5.33	102.83	111.14
1	er	426	ASP	CA-CB-CG	-5.33	107.27	112.60
1	fx	491	ALA	CA-C-N	5.33	125.79	120.14
1	fx	491	ALA	C-N-CA	5.33	125.79	120.14
1	gn	500	MET	CA-C-N	5.33	125.23	119.85
1	gn	500	MET	C-N-CA	5.33	125.23	119.85
3	of	49	PHE	CA-C-N	5.33	125.79	120.14
3	of	49	PHE	C-N-CA	5.33	125.79	120.14
1	aa	402	THR	CA-C-N	5.33	126.84	120.13
1	aa	402	THR	C-N-CA	5.33	126.84	120.13
1	br	491	ALA	CA-C-N	5.33	125.79	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	br	491	ALA	C-N-CA	5.33	125.79	120.14
1	fn	265	GLN	N-CA-C	5.33	117.18	108.55
1	aq	491	ALA	CA-C-N	5.33	125.78	120.14
1	aq	491	ALA	C-N-CA	5.33	125.78	120.14
1	bg	486	GLU	CA-C-N	5.33	131.71	121.54
1	bg	486	GLU	C-N-CA	5.33	131.71	121.54
1	ce	324	THR	CA-C-N	5.33	125.65	119.47
1	ce	324	THR	C-N-CA	5.33	125.65	119.47
1	cl	500	MET	N-CA-C	-5.33	103.33	109.93
1	ga	468	GLN	CA-C-N	5.33	125.23	119.85
1	ga	468	GLN	C-N-CA	5.33	125.23	119.85
1	gb	110	ASP	CA-CB-CG	5.33	117.93	112.60
3	kk	38	VAL	N-CA-C	5.33	116.33	108.45
1	az	163	PHE	CA-C-N	5.32	125.23	119.85
1	az	163	PHE	C-N-CA	5.32	125.23	119.85
1	bm	186	GLY	N-CA-C	5.32	122.40	112.77
1	bt	491	ALA	CA-C-N	5.32	125.78	120.14
1	bt	491	ALA	C-N-CA	5.32	125.78	120.14
1	cv	130	VAL	N-CA-C	5.32	115.56	108.11
1	dm	403	GLY	N-CA-C	5.32	120.35	113.27
1	dt	491	ALA	CA-C-N	5.32	125.78	120.14
1	dt	491	ALA	C-N-CA	5.32	125.78	120.14
1	ex	506	SER	CA-C-N	-5.32	113.35	121.66
1	ex	506	SER	C-N-CA	-5.32	113.35	121.66
1	gf	269	ALA	N-CA-C	5.32	118.59	111.24
1	gw	446	ALA	N-CA-C	5.32	120.43	113.88
1	gx	238	GLY	N-CA-C	5.32	122.70	115.30
1	bg	358	ASP	CA-CB-CG	5.32	117.92	112.60
1	bn	93	PRO	N-CA-CB	-5.32	99.28	102.79
1	ci	271	SER	N-CA-C	5.32	117.95	110.23
1	dj	145	HIS	CA-C-N	5.32	124.99	119.56
1	dj	145	HIS	C-N-CA	5.32	124.99	119.56
1	am	426	ASP	CA-CB-CG	-5.32	107.28	112.60
1	cc	149	GLY	CA-C-N	5.32	125.53	120.31
1	cc	149	GLY	C-N-CA	5.32	125.53	120.31
1	dn	115	GLN	CA-C-N	5.32	125.26	119.78
1	dn	115	GLN	C-N-CA	5.32	125.26	119.78
1	er	500	MET	CA-C-N	5.32	126.49	119.84
1	er	500	MET	C-N-CA	5.32	126.49	119.84
1	fh	426	ASP	CA-CB-CG	-5.32	107.28	112.60
1	gy	93	PRO	N-CA-CB	-5.32	99.28	102.79
3	nh	37	ASP	CA-CB-CG	5.32	117.92	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bi	490	GLN	N-CA-C	-5.32	105.53	112.23
1	bj	483	PRO	N-CA-C	-5.32	102.75	111.21
1	bq	293	ILE	N-CA-C	-5.32	105.20	111.00
1	dq	324	THR	CA-C-N	5.32	125.64	119.47
1	dq	324	THR	C-N-CA	5.32	125.64	119.47
1	fc	88	VAL	N-CA-C	5.32	115.52	107.75
1	gd	395	TYR	N-CA-C	5.32	116.77	110.97
1	gq	93	PRO	N-CA-CB	-5.32	99.28	102.79
2	hn	365	ASP	CA-C-N	5.32	127.17	121.00
2	hn	365	ASP	C-N-CA	5.32	127.17	121.00
3	nw	23	ILE	N-CA-C	-5.32	100.09	108.23
1	ay	130	VAL	N-CA-C	5.32	115.56	108.11
1	ci	123	GLN	N-CA-C	5.32	118.07	109.40
1	co	425	ILE	N-CA-C	5.32	115.97	108.36
1	cy	403	GLY	N-CA-C	5.32	120.21	113.24
1	dc	256	LYS	N-CA-C	5.32	117.06	109.14
1	ee	92	GLY	CA-C-N	5.32	126.25	120.83
1	ee	92	GLY	C-N-CA	5.32	126.25	120.83
1	fi	209	ASP	CA-CB-CG	5.32	117.92	112.60
1	gb	209	ASP	CA-CB-CG	5.32	117.92	112.60
1	hd	209	ASP	CA-CB-CG	5.32	117.92	112.60
2	hi	384	ASN	N-CA-C	5.32	117.42	110.08
2	hm	384	ASN	CA-C-N	5.32	125.31	119.89
2	hm	384	ASN	C-N-CA	5.32	125.31	119.89
3	nk	38	VAL	N-CA-C	5.32	115.78	108.12
1	an	94	ALA	CB-CA-C	-5.32	110.43	116.54
1	ek	71	ASP	CA-CB-CG	5.32	117.92	112.60
1	fi	402	THR	CA-C-N	5.32	126.78	120.14
1	fi	402	THR	C-N-CA	5.32	126.78	120.14
1	ge	491	ALA	CA-C-N	5.32	125.22	119.85
1	ge	491	ALA	C-N-CA	5.32	125.22	119.85
1	gi	96	MET	N-CA-C	5.32	119.82	113.23
1	as	134	ASP	CA-C-N	5.31	124.93	119.56
1	as	134	ASP	C-N-CA	5.31	124.93	119.56
1	de	263	SER	N-CA-C	5.31	117.49	109.41
1	bf	110	ASP	CA-CB-CG	5.31	117.91	112.60
1	cq	87	ALA	CA-C-N	-5.31	116.03	123.10
1	cq	87	ALA	C-N-CA	-5.31	116.03	123.10
1	cu	245	ASN	CA-C-N	5.31	125.22	119.85
1	cu	245	ASN	C-N-CA	5.31	125.22	119.85
1	db	185	THR	CA-C-N	5.31	128.66	120.00
1	db	185	THR	C-N-CA	5.31	128.66	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	db	451	ALA	CA-C-N	5.31	126.48	119.84
1	db	451	ALA	C-N-CA	5.31	126.48	119.84
1	eg	87	ALA	CA-C-N	-5.31	116.03	123.10
1	eg	87	ALA	C-N-CA	-5.31	116.03	123.10
1	ey	480	GLY	N-CA-C	5.31	118.47	110.18
1	ez	256	LYS	N-CA-C	5.31	117.26	109.24
1	fc	115	GLN	CA-C-N	5.31	125.25	119.78
1	fc	115	GLN	C-N-CA	5.31	125.25	119.78
1	gg	163	PHE	CA-C-N	5.31	125.22	119.85
1	gg	163	PHE	C-N-CA	5.31	125.22	119.85
1	go	481	ILE	N-CA-C	5.31	115.90	108.89
1	gq	182	PHE	CA-CB-CG	5.31	119.11	113.80
1	hb	245	ASN	CA-C-N	5.31	125.29	120.03
1	hb	245	ASN	C-N-CA	5.31	125.29	120.03
3	mg	49	PHE	CA-C-N	5.31	125.52	120.31
3	mg	49	PHE	C-N-CA	5.31	125.52	120.31
1	eo	265	GLN	N-CA-C	5.31	117.33	108.99
1	ff	199	ASP	CA-CB-CG	-5.31	107.29	112.60
1	bc	115	GLN	CA-C-N	5.31	125.25	119.78
1	bc	115	GLN	C-N-CA	5.31	125.25	119.78
1	dc	145	HIS	CA-C-N	5.31	124.92	119.56
1	dc	145	HIS	C-N-CA	5.31	124.92	119.56
1	dl	256	LYS	N-CA-C	5.31	117.89	109.50
1	gt	269	ALA	N-CA-C	5.31	118.52	111.30
2	hi	115	PRO	N-CA-C	-5.31	103.45	111.41
1	ag	509	LYS	N-CA-C	5.31	119.73	112.88
1	bh	68	ILE	N-CA-C	5.31	115.60	108.17
1	bw	403	GLY	N-CA-C	5.31	120.29	114.40
1	dc	103	ILE	CA-C-N	5.31	125.25	119.78
1	dc	103	ILE	C-N-CA	5.31	125.25	119.78
1	eh	88	VAL	N-CA-C	5.31	115.50	107.75
1	fa	327	SER	N-CA-C	5.31	116.85	109.31
3	jn	49	PHE	CA-C-N	5.31	125.21	119.85
3	jn	49	PHE	C-N-CA	5.31	125.21	119.85
3	ka	46	TYR	N-CA-C	5.31	117.05	109.14
1	dl	145	HIS	CA-C-N	5.31	125.12	119.28
1	dl	145	HIS	C-N-CA	5.31	125.12	119.28
1	fp	115	GLN	CA-C-N	5.31	125.25	119.78
1	fp	115	GLN	C-N-CA	5.31	125.25	119.78
1	fq	263	SER	N-CA-C	5.31	118.31	110.46
1	cg	119	SER	N-CA-C	-5.30	101.27	108.11
1	cj	482	ASN	CA-C-N	5.30	125.31	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	cj	482	ASN	C-N-CA	5.30	125.31	119.90
1	cs	182	PHE	CA-CB-CG	5.30	119.10	113.80
1	db	285	ASP	CA-C-N	5.30	131.67	121.54
1	db	285	ASP	C-N-CA	5.30	131.67	121.54
1	el	199	ASP	CA-CB-CG	-5.30	107.30	112.60
1	fe	480	GLY	CA-C-N	5.30	128.98	121.66
1	fe	480	GLY	C-N-CA	5.30	128.98	121.66
1	fq	69	GLY	N-CA-C	-5.30	106.07	112.49
1	gb	149	GLY	CA-C-N	5.30	125.21	119.85
1	gb	149	GLY	C-N-CA	5.30	125.21	119.85
1	gs	121	THR	CB-CA-C	-5.30	102.54	112.30
1	hc	115	GLN	CA-C-N	5.30	125.59	119.92
1	hc	115	GLN	C-N-CA	5.30	125.59	119.92
2	hf	365	ASP	CA-C-N	5.30	127.31	120.89
2	hf	365	ASP	C-N-CA	5.30	127.31	120.89
3	ip	41	ILE	N-CA-CB	-5.30	106.97	112.28
1	an	68	ILE	CA-C-N	5.30	125.87	119.98
1	an	68	ILE	C-N-CA	5.30	125.87	119.98
1	gp	281	VAL	N-CA-C	5.30	116.38	111.45
1	br	285	ASP	CA-C-N	5.30	131.66	121.54
1	br	285	ASP	C-N-CA	5.30	131.66	121.54
1	cz	269	ALA	N-CA-C	5.30	118.56	111.24
1	el	103	ILE	CA-C-N	5.30	125.24	119.78
1	el	103	ILE	C-N-CA	5.30	125.24	119.78
1	em	245	ASN	CA-C-N	5.30	125.28	120.03
1	em	245	ASN	C-N-CA	5.30	125.28	120.03
1	eo	327	SER	N-CA-C	5.30	116.84	109.31
1	ey	409	THR	N-CA-C	-5.30	106.81	113.28
1	ge	121	THR	CB-CA-C	-5.30	103.92	112.09
3	mj	72	ASN	CA-CB-CG	5.30	117.90	112.60
1	at	402	THR	CA-C-N	5.30	126.76	120.14
1	at	402	THR	C-N-CA	5.30	126.76	120.14
1	bi	71	ASP	CA-CB-CG	5.30	117.90	112.60
1	bp	88	VAL	N-CA-C	5.30	115.49	107.75
1	bq	121	THR	CB-CA-C	-5.30	102.55	112.30
1	bu	209	ASP	CA-CB-CG	5.30	117.90	112.60
3	kc	49	PHE	CA-C-N	5.30	125.50	120.31
3	kc	49	PHE	C-N-CA	5.30	125.50	120.31
3	nj	37	ASP	CA-CB-CG	5.30	117.90	112.60
1	bk	196	VAL	N-CA-C	5.30	114.84	108.06
1	da	201	GLY	N-CA-C	-5.30	106.30	113.24
1	dy	119	SER	CA-C-N	5.30	125.28	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dy	119	SER	C-N-CA	5.30	125.28	120.03
1	af	265	GLN	N-CA-C	5.30	117.31	108.99
1	bm	271	SER	N-CA-C	5.30	117.70	110.55
1	ed	451	ALA	CA-C-N	5.30	125.22	119.76
1	ed	451	ALA	C-N-CA	5.30	125.22	119.76
2	he	291	LYS	CA-C-N	5.30	126.46	119.84
2	he	291	LYS	C-N-CA	5.30	126.46	119.84
3	hp	46	TYR	N-CA-C	5.30	117.03	109.14
3	hu	49	PHE	CA-C-N	5.30	125.50	120.31
3	hu	49	PHE	C-N-CA	5.30	125.50	120.31
1	ad	386	LEU	N-CA-C	-5.29	105.09	112.45
1	cq	245	ASN	CA-C-N	5.29	125.20	119.85
1	cq	245	ASN	C-N-CA	5.29	125.20	119.85
1	gf	245	ASN	CA-C-N	5.29	125.20	119.85
1	gf	245	ASN	C-N-CA	5.29	125.20	119.85
1	gr	269	ALA	N-CA-C	5.29	117.64	111.02
1	bk	281	VAL	N-CA-C	5.29	116.37	111.45
1	br	134	ASP	N-CA-C	5.29	117.75	108.75
1	bz	446	ALA	N-CA-C	5.29	119.74	113.12
1	dz	222	VAL	N-CA-C	5.29	117.49	108.86
1	ej	329	ALA	N-CA-C	5.29	118.55	111.24
1	en	232	ILE	N-CA-C	-5.29	106.53	111.45
1	gb	486	GLU	CA-C-N	5.29	131.65	121.54
1	gb	486	GLU	C-N-CA	5.29	131.65	121.54
1	gf	149	GLY	CA-C-N	5.29	125.20	119.85
1	gf	149	GLY	C-N-CA	5.29	125.20	119.85
2	hh	291	LYS	CA-C-N	5.29	126.46	119.84
2	hh	291	LYS	C-N-CA	5.29	126.46	119.84
1	ay	402	THR	CA-C-N	5.29	126.80	120.13
1	ay	402	THR	C-N-CA	5.29	126.80	120.13
1	bo	483	PRO	N-CA-C	-5.29	102.80	111.21
1	cg	426	ASP	CA-CB-CG	-5.29	107.31	112.60
1	dx	258	VAL	N-CA-C	5.29	116.34	108.46
1	gb	134	ASP	CA-C-N	5.29	125.61	119.47
1	gb	134	ASP	C-N-CA	5.29	125.61	119.47
1	aj	134	ASP	CA-C-N	5.29	125.35	119.32
1	aj	134	ASP	C-N-CA	5.29	125.35	119.32
2	hg	145	SER	N-CA-C	-5.29	103.16	110.35
3	hq	32	PHE	CA-C-N	5.29	124.96	119.56
3	hq	32	PHE	C-N-CA	5.29	124.96	119.56
1	al	256	LYS	N-CA-C	5.29	116.84	108.96
1	bs	425	ILE	N-CA-C	5.29	115.92	108.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ck	245	ASN	CA-C-N	5.29	125.27	120.03
1	ck	245	ASN	C-N-CA	5.29	125.27	120.03
1	ct	182	PHE	CA-CB-CG	5.29	119.09	113.80
1	dl	265	GLN	N-CA-C	5.29	117.79	108.75
1	dv	222	VAL	N-CA-C	5.29	117.67	108.95
1	ew	199	ASP	CA-CB-CG	-5.29	107.31	112.60
1	fu	403	GLY	N-CA-C	5.29	120.27	114.40
3	jm	38	VAL	N-CA-C	5.29	115.60	107.77
1	ch	468	GLN	CA-C-N	5.29	125.23	119.78
1	ch	468	GLN	C-N-CA	5.29	125.23	119.78
1	cj	245	ASN	CA-C-N	5.29	125.19	119.85
1	cj	245	ASN	C-N-CA	5.29	125.19	119.85
1	el	402	THR	CA-C-N	5.29	126.75	120.14
1	el	402	THR	C-N-CA	5.29	126.75	120.14
1	fh	121	THR	N-CA-C	5.29	118.54	111.24
1	fi	163	PHE	CA-C-N	5.29	125.19	119.85
1	fi	163	PHE	C-N-CA	5.29	125.19	119.85
1	gj	484	PHE	CA-CB-CG	5.29	119.09	113.80
1	gy	209	ASP	CA-CB-CG	5.29	117.89	112.60
1	aw	484	PHE	CA-CB-CG	5.29	119.09	113.80
1	bx	121	THR	CB-CA-C	-5.29	104.78	111.86
1	dp	481	ILE	N-CA-C	5.29	115.87	108.89
1	fp	145	HIS	CA-C-N	5.29	124.95	119.56
1	fp	145	HIS	C-N-CA	5.29	124.95	119.56
1	gn	121	THR	N-CA-C	5.29	118.53	111.24
1	am	256	LYS	N-CA-C	5.28	117.10	109.07
1	au	222	VAL	N-CA-C	5.28	117.67	108.95
1	bn	119	SER	N-CA-C	-5.28	103.47	108.22
1	ec	115	GLN	CA-C-N	5.28	125.22	119.78
1	ec	115	GLN	C-N-CA	5.28	125.22	119.78
1	fk	463	ASP	CA-C-N	5.28	124.95	119.56
1	fk	463	ASP	C-N-CA	5.28	124.95	119.56
1	ga	474	LYS	N-CA-C	5.28	118.17	109.72
1	gy	199	ASP	CA-CB-CG	-5.28	107.32	112.60
1	hc	502	SER	CA-C-N	-5.28	113.90	120.56
1	hc	502	SER	C-N-CA	-5.28	113.90	120.56
2	hf	270	THR	N-CA-C	5.28	119.48	113.19
3	lq	44	ALA	N-CA-C	5.28	119.59	113.20
3	nu	46	TYR	N-CA-C	5.28	117.01	109.14
2	hk	145	SER	N-CA-C	-5.28	103.17	110.35
1	ae	245	ASN	CA-C-N	5.28	125.26	120.03
1	ae	245	ASN	C-N-CA	5.28	125.26	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bo	201	GLY	N-CA-C	-5.28	106.32	113.24
1	by	403	GLY	N-CA-C	5.28	120.29	113.27
1	cm	483	PRO	N-CA-C	-5.28	102.81	111.21
1	el	285	ASP	CA-C-N	5.28	131.63	121.54
1	el	285	ASP	C-N-CA	5.28	131.63	121.54
1	ge	324	THR	CA-C-N	5.28	125.60	119.47
1	ge	324	THR	C-N-CA	5.28	125.60	119.47
2	hj	382	SER	N-CA-C	5.28	117.34	110.53
3	no	49	PHE	CA-C-N	5.28	125.74	120.14
3	no	49	PHE	C-N-CA	5.28	125.74	120.14
1	bx	145	HIS	CA-C-N	5.28	124.94	119.56
1	bx	145	HIS	C-N-CA	5.28	124.94	119.56
1	by	130	VAL	N-CA-C	5.28	115.50	108.11
1	dv	506	SER	CA-C-N	-5.28	114.12	121.99
1	dv	506	SER	C-N-CA	-5.28	114.12	121.99
1	cc	402	THR	CA-C-N	5.28	126.74	120.14
1	cc	402	THR	C-N-CA	5.28	126.74	120.14
1	ci	236	GLN	CA-C-N	5.28	130.23	122.63
1	ci	236	GLN	C-N-CA	5.28	130.23	122.63
1	cu	463	ASP	CA-C-N	5.28	124.94	119.56
1	cu	463	ASP	C-N-CA	5.28	124.94	119.56
1	do	245	ASN	CA-C-N	5.28	125.18	119.85
1	do	245	ASN	C-N-CA	5.28	125.18	119.85
2	hm	286	GLY	N-CA-C	-5.28	103.08	112.58
3	jt	49	PHE	CA-C-N	5.28	125.48	120.31
3	jt	49	PHE	C-N-CA	5.28	125.48	120.31
1	cx	115	GLN	CB-CA-C	-5.28	106.41	111.00
1	de	87	ALA	CA-C-N	-5.28	115.66	122.99
1	de	87	ALA	C-N-CA	-5.28	115.66	122.99
1	fk	402	THR	CA-C-N	5.28	126.78	120.13
1	fk	402	THR	C-N-CA	5.28	126.78	120.13
1	bb	87	ALA	N-CA-C	5.27	117.03	111.28
1	bi	110	ASP	CA-CB-CG	5.27	117.87	112.60
1	dt	232	ILE	N-CA-C	-5.27	106.66	111.67
1	fc	121	THR	N-CA-C	5.27	117.08	110.91
1	af	110	ASP	CA-CB-CG	5.27	117.87	112.60
1	ar	134	ASP	CA-C-N	5.27	125.33	119.32
1	ar	134	ASP	C-N-CA	5.27	125.33	119.32
1	bz	491	ALA	CA-C-N	5.27	125.73	120.14
1	bz	491	ALA	C-N-CA	5.27	125.73	120.14
1	eg	446	ALA	N-CA-C	5.27	119.71	113.12
1	el	256	LYS	N-CA-C	5.27	117.08	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gg	258	VAL	N-CA-C	5.27	117.65	108.95
3	nl	10	ILE	N-CA-C	5.27	115.45	107.75
3	kz	46	TYR	N-CA-C	5.27	116.99	109.14
1	ap	93	PRO	N-CA-CB	-5.27	99.31	102.79
1	ax	425	ILE	N-CA-C	5.27	115.90	108.36
1	bp	121	THR	CB-CA-C	-5.27	103.98	112.09
1	ds	222	VAL	N-CA-C	5.27	117.65	108.95
1	eo	245	ASN	CA-C-N	5.27	125.25	120.03
1	eo	245	ASN	C-N-CA	5.27	125.25	120.03
1	fb	252	PHE	N-CA-C	5.27	116.81	108.96
1	fo	426	ASP	CA-CB-CG	-5.27	107.33	112.60
1	fp	285	ASP	CA-C-N	5.27	131.60	121.54
1	fp	285	ASP	C-N-CA	5.27	131.60	121.54
1	gd	491	ALA	CA-C-N	5.27	125.73	120.14
1	gd	491	ALA	C-N-CA	5.27	125.73	120.14
1	gg	121	THR	CB-CA-C	-5.27	103.97	112.09
2	hk	114	THR	CA-C-N	5.27	125.25	120.03
2	hk	114	THR	C-N-CA	5.27	125.25	120.03
3	mo	49	PHE	CA-C-N	5.27	125.47	120.31
3	mo	49	PHE	C-N-CA	5.27	125.47	120.31
1	aq	402	THR	CA-C-N	5.27	126.72	120.14
1	aq	402	THR	C-N-CA	5.27	126.72	120.14
1	cz	256	LYS	N-CA-C	5.27	117.08	109.07
1	eg	197	THR	CA-C-N	-5.27	116.07	123.13
1	eg	197	THR	C-N-CA	-5.27	116.07	123.13
1	fn	491	ALA	CA-C-N	5.27	125.72	120.14
1	fn	491	ALA	C-N-CA	5.27	125.72	120.14
3	ld	74	ASP	CA-CB-CG	5.27	117.87	112.60
1	ea	463	ASP	CA-C-N	5.27	124.93	119.56
1	ea	463	ASP	C-N-CA	5.27	124.93	119.56
1	fo	68	ILE	N-CA-C	5.27	115.54	108.17
1	fy	245	ASN	CA-C-N	5.27	125.24	120.03
1	fy	245	ASN	C-N-CA	5.27	125.24	120.03
2	hj	40	VAL	N-CA-C	5.27	116.16	108.58
2	hl	367	GLU	N-CA-C	-5.27	103.49	111.34
1	ae	87	ALA	CA-C-N	-5.26	115.67	122.99
1	ae	87	ALA	C-N-CA	-5.26	115.67	122.99
1	am	285	ASP	N-CA-C	5.26	118.17	111.69
1	bk	446	ALA	N-CA-C	5.26	120.36	113.88
1	dl	245	ASN	CA-C-N	5.26	125.24	120.03
1	dl	245	ASN	C-N-CA	5.26	125.24	120.03
1	es	491	ALA	CA-C-N	5.26	125.72	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	es	491	ALA	C-N-CA	5.26	125.72	120.14
2	hh	367	GLU	N-CA-C	-5.26	103.50	111.34
3	iw	38	VAL	N-CA-C	5.26	115.86	108.17
1	ba	463	ASP	CA-C-N	5.26	124.93	119.56
1	ba	463	ASP	C-N-CA	5.26	124.93	119.56
1	dz	451	ALA	CA-C-N	5.26	126.42	119.84
1	dz	451	ALA	C-N-CA	5.26	126.42	119.84
1	gw	287	ASP	N-CA-C	-5.26	105.98	112.72
2	hn	270	THR	N-CA-C	5.26	119.45	113.19
3	lm	32	PHE	CA-C-N	5.26	124.93	119.56
3	lm	32	PHE	C-N-CA	5.26	124.93	119.56
1	dr	250	MET	N-CA-C	5.26	116.80	108.96
1	ew	336	ASP	CA-C-N	5.26	125.57	119.47
1	ew	336	ASP	C-N-CA	5.26	125.57	119.47
1	ex	134	ASP	CA-C-N	5.26	125.57	119.47
1	ex	134	ASP	C-N-CA	5.26	125.57	119.47
1	fa	69	GLY	N-CA-C	-5.26	106.40	112.50
1	fw	115	GLN	CA-C-N	5.26	125.20	119.78
1	fw	115	GLN	C-N-CA	5.26	125.20	119.78
1	fy	484	PHE	CA-CB-CG	5.26	119.06	113.80
1	gd	425	ILE	N-CA-C	5.26	115.88	108.36
1	gz	484	PHE	CA-CB-CG	5.26	119.06	113.80
2	hm	363	VAL	N-CA-C	5.26	116.42	111.48
3	kv	40	LYS	CA-C-N	-5.26	116.70	121.65
3	kv	40	LYS	C-N-CA	-5.26	116.70	121.65
1	ct	134	ASP	CA-C-N	5.26	124.87	119.56
1	ct	134	ASP	C-N-CA	5.26	124.87	119.56
1	dg	110	ASP	CA-CB-CG	5.26	117.86	112.60
1	ex	480	GLY	CA-C-N	5.26	128.92	121.66
1	ex	480	GLY	C-N-CA	5.26	128.92	121.66
1	ez	468	GLN	CA-C-N	5.26	125.16	119.85
1	ez	468	GLN	C-N-CA	5.26	125.16	119.85
1	fm	119	SER	CA-C-N	5.26	125.26	120.21
1	fm	119	SER	C-N-CA	5.26	125.26	120.21
3	mu	46	TYR	N-CA-C	5.26	116.98	109.14
3	nn	46	TYR	N-CA-C	5.26	116.98	109.14
1	af	209	ASP	CA-CB-CG	5.26	117.86	112.60
1	ey	134	ASP	CA-C-N	5.26	124.87	119.56
1	ey	134	ASP	C-N-CA	5.26	124.87	119.56
1	hd	221	LEU	N-CA-CB	-5.26	102.67	110.71
1	ay	344	ARG	CA-C-O	-5.26	114.61	120.66
1	ba	256	LYS	N-CA-C	5.26	116.79	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bx	250	MET	N-CA-C	5.26	117.38	109.23
1	gk	483	PRO	N-CA-C	-5.26	102.85	111.21
1	gn	490	GLN	N-CA-C	-5.26	105.61	112.23
1	ap	232	ILE	N-CA-C	-5.25	106.68	111.67
1	eg	222	VAL	N-CA-C	5.25	117.62	108.95
1	er	324	THR	CA-C-N	5.25	125.57	119.47
1	er	324	THR	C-N-CA	5.25	125.57	119.47
1	fj	222	VAL	N-CA-C	5.25	117.62	108.95
1	ap	236	GLN	CA-C-N	5.25	129.60	122.19
1	ap	236	GLN	C-N-CA	5.25	129.60	122.19
1	bj	238	GLY	N-CA-C	5.25	122.60	115.30
1	bl	468	GLN	CA-C-N	5.25	125.16	119.85
1	bl	468	GLN	C-N-CA	5.25	125.16	119.85
1	by	402	THR	CA-C-N	5.25	126.75	120.13
1	by	402	THR	C-N-CA	5.25	126.75	120.13
1	gm	455	ALA	N-CA-C	5.25	117.74	109.39
2	hm	365	ASP	CA-C-N	5.25	127.09	121.00
2	hm	365	ASP	C-N-CA	5.25	127.09	121.00
3	ir	44	ALA	N-CA-C	5.25	119.67	113.16
3	jd	32	PHE	CA-C-N	5.25	124.92	119.56
3	jd	32	PHE	C-N-CA	5.25	124.92	119.56
3	oc	46	TYR	N-CA-C	5.25	116.97	109.14
1	aa	245	ASN	CA-C-N	5.25	125.23	120.03
1	aa	245	ASN	C-N-CA	5.25	125.23	120.03
1	bu	324	THR	N-CA-C	-5.25	101.78	109.50
1	df	75	ASN	CA-CB-CG	-5.25	107.35	112.60
1	dh	329	ALA	N-CA-C	5.25	117.05	110.91
1	eq	245	ASN	CA-C-N	5.25	125.23	120.03
1	eq	245	ASN	C-N-CA	5.25	125.23	120.03
1	fw	509	LYS	N-CA-C	5.25	121.42	114.12
1	gp	402	THR	CA-C-N	5.25	126.75	120.13
1	gp	402	THR	C-N-CA	5.25	126.75	120.13
3	io	38	VAL	N-CA-C	5.25	115.84	108.17
3	ku	67	GLU	N-CA-C	-5.25	105.64	111.36
3	lg	38	VAL	N-CA-C	5.25	115.84	108.17
1	cn	74	TYR	CA-C-N	5.25	129.96	122.72
1	cn	74	TYR	C-N-CA	5.25	129.96	122.72
1	eb	328	LYS	N-CA-C	5.25	119.67	113.16
1	eg	265	GLN	N-CA-C	5.25	117.23	108.99
1	eu	87	ALA	CA-C-N	-5.25	115.69	122.99
1	eu	87	ALA	C-N-CA	-5.25	115.69	122.99
1	fs	256	LYS	N-CA-C	5.25	117.05	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	ij	38	VAL	N-CA-C	5.25	115.60	107.78
1	be	209	ASP	CA-CB-CG	5.25	117.85	112.60
1	co	253	ARG	N-CA-C	5.25	119.00	111.02
1	eh	163	PHE	CA-C-N	5.25	125.15	119.85
1	eh	163	PHE	C-N-CA	5.25	125.15	119.85
1	ej	209	ASP	CA-CB-CG	5.25	117.85	112.60
1	ey	266	LEU	N-CA-C	5.25	117.36	109.23
1	bn	143	ALA	N-CA-C	5.25	117.08	111.36
1	bx	115	GLN	CA-C-N	5.25	125.16	119.76
1	bx	115	GLN	C-N-CA	5.25	125.16	119.76
1	by	258	VAL	N-CA-C	5.25	116.04	108.48
1	ft	121	THR	CB-CA-C	-5.25	102.65	112.30
2	hh	53	TYR	N-CA-C	5.25	117.79	109.24
3	ni	67	GLU	N-CA-C	-5.25	105.64	111.36
1	dh	115	GLN	CA-C-N	5.25	125.16	119.76
1	dh	115	GLN	C-N-CA	5.25	125.16	119.76
1	ej	131	TYR	N-CA-C	5.25	118.14	109.85
1	ek	402	THR	CA-C-N	5.25	126.70	120.14
1	ek	402	THR	C-N-CA	5.25	126.70	120.14
1	fj	256	LYS	N-CA-C	5.25	117.04	109.07
1	gj	68	ILE	CA-C-N	5.25	125.66	119.94
1	gj	68	ILE	C-N-CA	5.25	125.66	119.94
1	gk	131	TYR	N-CA-C	5.25	118.14	109.85
1	cd	134	ASP	CA-C-N	5.24	124.91	119.56
1	cd	134	ASP	C-N-CA	5.24	124.91	119.56
1	dr	256	LYS	N-CA-C	5.24	117.16	109.24
1	ei	74	TYR	CA-C-N	5.24	129.38	122.30
1	ei	74	TYR	C-N-CA	5.24	129.38	122.30
1	fc	134	ASP	CA-C-N	5.24	125.05	119.28
1	fc	134	ASP	C-N-CA	5.24	125.05	119.28
2	hk	19	ILE	N-CA-C	5.24	115.86	108.36
1	bo	145	HIS	CA-C-N	5.24	124.91	119.56
1	bo	145	HIS	C-N-CA	5.24	124.91	119.56
1	cr	324	THR	CB-CA-C	5.24	115.83	109.85
1	do	187	THR	N-CA-C	5.24	117.91	110.10
1	gm	491	ALA	CA-C-N	5.24	125.70	120.14
1	gm	491	ALA	C-N-CA	5.24	125.70	120.14
2	hk	136	LYS	N-CA-C	-5.24	107.02	113.41
3	nb	46	TYR	N-CA-C	5.24	116.95	109.14
1	bh	258	VAL	N-CA-C	5.24	116.27	108.46
1	cw	222	VAL	N-CA-C	5.24	117.59	108.95
1	fn	134	ASP	CA-CB-CG	-5.24	107.36	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gp	149	GLY	CA-C-N	5.24	125.22	120.03
1	gp	149	GLY	C-N-CA	5.24	125.22	120.03
1	gw	145	HIS	CA-C-N	5.24	124.91	119.56
1	gw	145	HIS	C-N-CA	5.24	124.91	119.56
2	hl	114	THR	CA-C-N	5.24	125.14	119.85
2	hl	114	THR	C-N-CA	5.24	125.14	119.85
1	ax	95	VAL	N-CA-C	5.24	115.59	107.78
1	fu	266	LEU	N-CA-C	5.24	117.35	109.23
3	jo	32	PHE	CA-C-N	5.24	124.90	119.56
3	jo	32	PHE	C-N-CA	5.24	124.90	119.56
3	jw	49	PHE	CA-C-N	5.24	125.44	120.31
3	jw	49	PHE	C-N-CA	5.24	125.44	120.31
1	bp	480	GLY	N-CA-C	5.24	118.22	110.42
1	er	163	PHE	CA-C-N	5.24	125.14	119.85
1	er	163	PHE	C-N-CA	5.24	125.14	119.85
1	aa	266	LEU	N-CA-C	5.24	117.14	109.24
1	fl	269	ALA	N-CA-C	5.24	117.56	111.02
1	fm	328	LYS	N-CA-C	5.24	120.53	113.72
1	fo	113	GLY	N-CA-C	-5.24	104.62	112.89
1	gh	484	PHE	CA-CB-CG	5.24	119.03	113.80
1	gl	245	ASN	N-CA-C	5.24	117.10	109.30
1	am	186	GLY	N-CA-C	5.23	120.75	111.02
1	br	87	ALA	N-CA-C	5.23	116.99	111.28
1	ca	184	GLU	CA-C-O	-5.23	115.81	121.36
1	cs	324	THR	N-CA-C	-5.23	101.81	109.50
1	ey	121	THR	CB-CA-C	-5.23	104.03	112.09
1	ge	256	LYS	N-CA-C	5.23	117.21	108.99
1	gk	115	GLN	CA-C-N	5.23	125.17	119.78
1	gk	115	GLN	C-N-CA	5.23	125.17	119.78
1	ay	338	ILE	N-CA-C	-5.23	105.75	110.82
1	bp	121	THR	N-CA-C	5.23	118.46	111.24
1	co	500	MET	CB-CA-C	5.23	116.95	109.26
1	dr	263	SER	N-CA-C	5.23	116.94	109.14
1	du	285	ASP	CA-C-N	5.23	131.53	121.54
1	du	285	ASP	C-N-CA	5.23	131.53	121.54
1	dz	285	ASP	N-CA-C	5.23	118.13	111.69
1	ep	209	ASP	CA-CB-CG	5.23	117.83	112.60
1	fy	263	SER	N-CA-C	5.23	117.82	109.81
1	fz	245	ASN	N-CA-C	5.23	117.10	109.30
1	gs	209	ASP	CA-CB-CG	5.23	117.83	112.60
1	ha	484	PHE	CA-CB-CG	5.23	119.03	113.80
2	hi	369	LEU	CA-C-N	-5.23	114.55	122.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hi	369	LEU	C-N-CA	-5.23	114.55	122.29
2	hj	145	SER	N-CA-C	-5.23	103.23	110.35
1	au	258	VAL	N-CA-C	5.23	117.58	108.95
1	aw	84	THR	N-CA-C	5.23	117.20	108.99
1	ay	121	THR	N-CA-C	5.23	118.46	111.24
1	by	285	ASP	CA-C-N	5.23	131.53	121.54
1	by	285	ASP	C-N-CA	5.23	131.53	121.54
1	do	480	GLY	N-CA-C	5.23	119.24	110.56
1	fs	324	THR	N-CA-C	-5.23	101.81	109.50
1	ge	119	SER	N-CA-C	-5.23	103.51	108.22
1	gz	115	GLN	CA-C-N	5.23	125.17	119.78
1	gz	115	GLN	C-N-CA	5.23	125.17	119.78
1	hb	115	GLN	CA-C-N	5.23	125.17	119.78
1	hb	115	GLN	C-N-CA	5.23	125.17	119.78
1	bt	263	SER	N-CA-C	5.23	118.20	110.46
1	dv	145	HIS	CA-C-N	5.23	124.89	119.56
1	dv	145	HIS	C-N-CA	5.23	124.89	119.56
1	er	451	ALA	CA-C-N	5.23	125.17	119.78
1	er	451	ALA	C-N-CA	5.23	125.17	119.78
1	bn	136	VAL	N-CA-CB	-5.23	107.42	112.65
1	fu	115	GLN	CA-C-N	5.23	125.17	119.78
1	fu	115	GLN	C-N-CA	5.23	125.17	119.78
3	mj	25	GLY	N-CA-C	-5.23	105.05	112.37
1	aa	193	SER	N-CA-C	-5.23	107.45	113.88
1	cp	110	ASP	CA-CB-CG	5.23	117.83	112.60
1	ag	463	ASP	CA-C-N	5.22	124.89	119.56
1	ag	463	ASP	C-N-CA	5.22	124.89	119.56
1	ai	403	GLY	N-CA-C	5.22	120.22	113.27
1	dy	95	VAL	N-CA-C	5.22	115.56	107.78
1	ge	468	GLN	CA-C-N	5.22	125.13	119.85
1	ge	468	GLN	C-N-CA	5.22	125.13	119.85
1	gy	119	SER	N-CA-C	-5.22	103.52	108.22
2	hf	303	TYR	N-CA-C	-5.22	105.48	111.07
2	ho	21	ARG	CA-C-N	5.22	125.43	120.31
2	ho	21	ARG	C-N-CA	5.22	125.43	120.31
3	il	65	ARG	N-CA-C	5.22	121.93	110.80
3	is	38	VAL	N-CA-C	5.22	116.18	108.45
1	al	110	ASP	CA-CB-CG	5.22	117.82	112.60
1	cc	266	LEU	N-CA-C	5.22	117.33	109.23
1	cg	491	ALA	CA-C-N	5.22	125.67	120.14
1	cg	491	ALA	C-N-CA	5.22	125.67	120.14
2	hk	302	ALA	CA-C-N	5.22	127.23	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hk	302	ALA	C-N-CA	5.22	127.23	120.44
3	ka	32	PHE	CA-C-N	5.22	124.89	119.56
3	ka	32	PHE	C-N-CA	5.22	124.89	119.56
3	lb	67	GLU	N-CA-C	-5.22	105.59	111.28
1	di	253	ARG	N-CA-C	5.22	121.05	114.31
1	du	87	ALA	CA-C-N	-5.22	116.33	123.12
1	du	87	ALA	C-N-CA	-5.22	116.33	123.12
1	fe	93	PRO	N-CA-CB	-5.22	99.34	102.79
1	cb	281	VAL	N-CA-C	5.22	116.63	111.67
1	en	115	GLN	CA-C-N	5.22	125.16	119.78
1	en	115	GLN	C-N-CA	5.22	125.16	119.78
1	ep	449	TYR	CB-CA-C	-5.22	99.05	109.33
1	gg	93	PRO	N-CA-C	5.22	119.53	112.48
1	gg	115	GLN	CA-C-N	5.22	125.16	119.78
1	gg	115	GLN	C-N-CA	5.22	125.16	119.78
1	gz	265	GLN	N-CA-C	5.22	117.01	108.76
3	ld	46	TYR	N-CA-C	5.22	116.92	109.14
1	ad	454	VAL	CA-C-N	-5.22	114.28	122.73
1	ad	454	VAL	C-N-CA	-5.22	114.28	122.73
1	cv	75	ASN	CA-CB-CG	-5.22	107.38	112.60
1	dl	480	GLY	CA-C-N	5.22	129.50	122.93
1	dl	480	GLY	C-N-CA	5.22	129.50	122.93
1	es	149	GLY	CA-C-N	5.22	125.20	120.03
1	es	149	GLY	C-N-CA	5.22	125.20	120.03
1	eu	119	SER	CA-C-N	5.22	125.20	120.03
1	eu	119	SER	C-N-CA	5.22	125.20	120.03
1	fm	395	TYR	CA-C-N	5.22	130.10	121.86
1	fm	395	TYR	C-N-CA	5.22	130.10	121.86
1	gu	87	ALA	CA-C-N	-5.22	116.16	123.10
1	gu	87	ALA	C-N-CA	-5.22	116.16	123.10
1	gz	143	ALA	N-CA-C	5.22	117.05	111.36
1	hd	115	GLN	CA-C-N	5.22	125.15	119.78
1	hd	115	GLN	C-N-CA	5.22	125.15	119.78
3	kr	67	GLU	N-CA-C	-5.22	105.67	111.36
1	aj	358	ASP	CA-CB-CG	5.22	117.82	112.60
1	as	193	SER	N-CA-C	-5.22	107.46	113.88
1	at	483	PRO	N-CA-CB	5.22	107.84	103.25
1	bb	149	GLY	CA-C-N	5.22	125.67	120.14
1	bb	149	GLY	C-N-CA	5.22	125.67	120.14
1	bt	402	THR	CA-C-N	5.22	126.66	120.14
1	bt	402	THR	C-N-CA	5.22	126.66	120.14
1	cm	222	VAL	N-CA-C	5.22	117.56	108.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dm	121	THR	CB-CA-C	-5.22	102.70	112.30
1	fm	256	LYS	N-CA-C	5.22	117.00	109.07
1	ca	392	GLY	CA-C-N	-5.21	115.86	122.43
1	ca	392	GLY	C-N-CA	-5.21	115.86	122.43
1	ct	95	VAL	N-CA-C	5.21	115.55	107.78
1	cu	483	PRO	N-CA-C	-5.21	102.92	111.21
1	de	324	THR	CA-C-N	5.21	125.52	119.47
1	de	324	THR	C-N-CA	5.21	125.52	119.47
1	dm	293	ILE	N-CA-C	-5.21	105.76	110.82
1	dr	500	MET	CA-C-N	5.21	125.13	119.76
1	dr	500	MET	C-N-CA	5.21	125.13	119.76
1	ej	258	VAL	N-CA-C	5.21	115.99	108.48
1	ff	149	GLY	CA-C-N	5.21	125.42	120.31
1	ff	149	GLY	C-N-CA	5.21	125.42	120.31
1	gu	245	ASN	CA-C-N	5.21	125.12	119.85
1	gu	245	ASN	C-N-CA	5.21	125.12	119.85
1	gy	232	ILE	N-CA-C	-5.21	106.60	111.45
3	ia	67	GLU	N-CA-C	-5.21	105.67	111.36
3	ih	49	PHE	CA-C-N	5.21	125.67	120.14
3	ih	49	PHE	C-N-CA	5.21	125.67	120.14
3	iu	67	GLU	N-CA-C	-5.21	105.68	111.36
1	bt	68	ILE	N-CA-C	5.21	115.47	108.17
1	da	484	PHE	CA-CB-CG	5.21	119.01	113.80
1	fm	285	ASP	CA-C-N	5.21	131.50	121.54
1	fm	285	ASP	C-N-CA	5.21	131.50	121.54
1	hd	149	GLY	CA-C-N	5.21	125.19	120.03
1	hd	149	GLY	C-N-CA	5.21	125.19	120.03
3	km	37	ASP	CA-CB-CG	5.21	117.81	112.60
3	kw	67	GLU	N-CA-C	-5.21	105.68	111.36
3	la	49	PHE	CA-C-N	5.21	125.42	120.31
3	la	49	PHE	C-N-CA	5.21	125.42	120.31
1	av	115	GLN	CA-C-N	5.21	125.15	119.78
1	av	115	GLN	C-N-CA	5.21	125.15	119.78
1	bd	222	VAL	N-CA-C	5.21	117.55	108.95
1	dy	69	GLY	N-CA-C	-5.21	106.45	112.50
1	et	115	GLN	CA-C-N	5.21	125.15	119.78
1	et	115	GLN	C-N-CA	5.21	125.15	119.78
1	fh	110	ASP	CA-CB-CG	5.21	117.81	112.60
1	hc	182	PHE	CA-CB-CG	5.21	119.01	113.80
3	la	32	PHE	CA-C-N	5.21	124.88	119.56
3	la	32	PHE	C-N-CA	5.21	124.88	119.56
1	af	199	ASP	CA-CB-CG	-5.21	107.39	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ft	131	TYR	N-CA-C	5.21	118.08	109.85
1	gu	222	VAL	N-CA-C	5.21	117.55	108.95
1	ag	87	ALA	N-CA-C	5.21	117.70	111.71
1	au	71	ASP	CA-CB-CG	5.21	117.81	112.60
1	dm	464	PRO	CA-C-N	-5.21	112.39	120.31
1	dm	464	PRO	C-N-CA	-5.21	112.39	120.31
1	gb	256	LYS	N-CA-C	5.21	116.99	109.07
1	gt	186	GLY	N-CA-C	5.21	117.78	110.38
2	hi	230	ILE	N-CA-C	5.21	120.17	109.34
1	cc	491	ALA	CA-C-N	5.21	125.66	120.14
1	cc	491	ALA	C-N-CA	5.21	125.66	120.14
1	eo	394	SER	N-CA-C	5.21	116.86	108.32
1	fb	238	GLY	N-CA-C	5.21	123.10	115.08
1	fk	193	SER	N-CA-C	-5.21	107.58	114.04
1	fv	115	GLN	CA-C-N	5.21	125.14	119.78
1	fv	115	GLN	C-N-CA	5.21	125.14	119.78
1	hb	154	PHE	CA-CB-CG	5.21	119.01	113.80
1	hc	129	ALA	N-CA-C	-5.21	101.97	110.20
2	hi	291	LYS	CA-C-N	5.21	126.35	119.84
2	hi	291	LYS	C-N-CA	5.21	126.35	119.84
1	ae	131	TYR	N-CA-C	5.21	116.98	109.07
1	dk	253	ARG	N-CA-C	5.21	118.93	111.02
1	fg	486	GLU	CA-C-N	5.21	131.48	121.54
1	fg	486	GLU	C-N-CA	5.21	131.48	121.54
2	hh	320	LEU	N-CA-C	5.21	120.49	114.04
1	er	269	ALA	N-CA-C	5.20	118.42	111.24
1	ga	115	GLN	CA-C-N	5.20	125.14	119.78
1	ga	115	GLN	C-N-CA	5.20	125.14	119.78
1	hb	186	GLY	N-CA-C	5.20	120.70	111.02
3	ju	67	GLU	N-CA-C	-5.20	105.69	111.36
3	mm	10	ILE	N-CA-C	5.20	115.35	107.75
1	av	222	VAL	N-CA-C	5.20	117.53	108.95
1	bt	426	ASP	CA-CB-CG	-5.20	107.40	112.60
1	ch	113	GLY	N-CA-C	-5.20	104.67	112.89
1	ea	209	ASP	CA-CB-CG	5.20	117.80	112.60
1	go	281	VAL	N-CA-C	5.20	116.61	111.67
3	ic	74	ASP	CA-CB-CG	5.20	117.80	112.60
3	mm	44	ALA	N-CA-C	5.20	119.59	112.88
1	bd	245	ASN	CA-C-N	5.20	125.18	120.03
1	bd	245	ASN	C-N-CA	5.20	125.18	120.03
1	bq	71	ASP	CA-CB-CG	5.20	117.80	112.60
1	cu	184	GLU	N-CA-C	-5.20	101.28	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dc	285	ASP	CA-C-N	5.20	131.47	121.54
1	dc	285	ASP	C-N-CA	5.20	131.47	121.54
1	em	329	ALA	N-CA-C	5.20	118.30	111.28
1	et	134	ASP	CA-C-N	5.20	125.50	119.47
1	et	134	ASP	C-N-CA	5.20	125.50	119.47
1	ex	243	THR	N-CA-C	5.20	116.19	108.86
1	fd	93	PRO	N-CA-C	5.20	122.85	113.70
1	gd	209	ASP	CA-CB-CG	5.20	117.80	112.60
1	gu	259	ILE	N-CA-C	5.20	115.16	108.82
1	gw	486	GLU	CA-C-N	5.20	131.47	121.54
1	gw	486	GLU	C-N-CA	5.20	131.47	121.54
1	as	222	VAL	N-CA-C	5.20	117.53	108.95
1	bm	118	ASN	N-CA-C	-5.20	105.68	113.89
1	bq	256	LYS	N-CA-C	5.20	117.15	108.99
1	cw	402	THR	CA-C-N	5.20	126.68	120.13
1	cw	402	THR	C-N-CA	5.20	126.68	120.13
1	fi	256	LYS	N-CA-C	5.20	117.15	108.99
1	ad	93	PRO	N-CA-CB	-5.20	99.36	102.79
1	bl	446	ALA	N-CA-C	5.20	120.27	113.88
1	de	451	ALA	CA-C-N	5.20	125.11	119.76
1	de	451	ALA	C-N-CA	5.20	125.11	119.76
1	es	281	VAL	N-CA-C	5.20	116.61	111.67
1	ga	269	ALA	N-CA-C	5.20	118.50	111.17
1	gn	271	SER	N-CA-C	5.20	117.84	110.10
2	hf	213	ASP	CA-CB-CG	5.20	117.80	112.60
3	jz	67	GLU	N-CA-C	-5.20	105.69	111.36
1	ab	265	GLN	N-CA-C	5.20	116.97	108.76
1	ba	324	THR	N-CA-C	-5.20	101.86	109.50
1	ba	327	SER	N-CA-C	5.20	116.69	109.31
1	bw	87	ALA	N-CA-C	5.20	117.02	111.36
1	cp	324	THR	CA-C-N	5.20	125.50	119.47
1	cp	324	THR	C-N-CA	5.20	125.50	119.47
1	ej	134	ASP	CA-C-N	5.20	125.24	119.32
1	ej	134	ASP	C-N-CA	5.20	125.24	119.32
1	es	119	SER	CA-C-N	5.20	125.66	120.52
1	es	119	SER	C-N-CA	5.20	125.66	120.52
1	fx	88	VAL	N-CA-C	5.20	115.34	107.75
1	gb	198	ILE	N-CA-C	5.20	111.77	106.21
1	gg	74	TYR	CB-CA-C	5.20	119.83	111.36
3	kj	49	PHE	CA-C-N	5.20	125.40	120.31
3	kj	49	PHE	C-N-CA	5.20	125.40	120.31
3	kq	37	ASP	CA-CB-CG	5.20	117.80	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bq	500	MET	CA-C-N	5.19	126.33	119.84
1	bq	500	MET	C-N-CA	5.19	126.33	119.84
1	bu	265	GLN	N-CA-C	5.19	116.96	108.55
1	ce	134	ASP	CA-C-N	5.19	124.81	119.56
1	ce	134	ASP	C-N-CA	5.19	124.81	119.56
1	cw	134	ASP	CA-C-N	5.19	125.49	119.47
1	cw	134	ASP	C-N-CA	5.19	125.49	119.47
1	ey	182	PHE	CA-CB-CG	5.19	118.99	113.80
1	fh	256	LYS	N-CA-C	5.19	116.96	109.07
3	nb	32	PHE	CA-C-N	5.19	124.86	119.56
3	nb	32	PHE	C-N-CA	5.19	124.86	119.56
1	at	145	HIS	CA-C-N	5.19	124.86	119.56
1	at	145	HIS	C-N-CA	5.19	124.86	119.56
1	by	222	VAL	N-CA-C	5.19	117.52	108.95
1	bz	265	GLN	N-CA-C	5.19	116.73	108.79
1	ci	284	MET	N-CA-C	-5.19	102.80	110.48
1	fo	111	ILE	N-CA-CB	-5.19	105.38	112.28
1	fv	500	MET	CA-C-N	5.19	125.09	119.85
1	fv	500	MET	C-N-CA	5.19	125.09	119.85
1	gl	119	SER	N-CA-C	-5.19	103.55	108.22
1	hb	93	PRO	N-CA-CB	-5.19	99.36	102.79
2	hg	303	TYR	N-CA-C	-5.19	105.52	111.07
1	ah	199	ASP	CA-CB-CG	-5.19	107.41	112.60
1	bt	119	SER	CA-C-N	5.19	125.17	120.03
1	bt	119	SER	C-N-CA	5.19	125.17	120.03
1	gu	268	ALA	N-CA-C	5.19	117.73	111.40
1	bo	324	THR	CA-C-N	5.19	125.49	119.47
1	bo	324	THR	C-N-CA	5.19	125.49	119.47
1	cv	110	ASP	CA-CB-CG	5.19	117.79	112.60
1	ft	245	ASN	CA-C-N	5.19	125.09	119.85
1	ft	245	ASN	C-N-CA	5.19	125.09	119.85
1	gz	130	VAL	N-CA-C	5.19	115.59	108.12
2	he	286	GLY	N-CA-C	-5.19	103.24	112.58
1	cb	187	THR	N-CA-C	5.19	118.00	109.76
1	fo	115	GLN	CA-C-N	5.19	125.12	119.78
1	fo	115	GLN	C-N-CA	5.19	125.12	119.78
3	jg	49	PHE	CA-C-N	5.19	125.39	120.31
3	jg	49	PHE	C-N-CA	5.19	125.39	120.31
1	ae	265	GLN	N-CA-C	5.18	116.95	108.76
1	de	182	PHE	CA-CB-CG	5.18	118.98	113.80
1	es	451	ALA	CA-C-N	5.18	125.12	119.78
1	es	451	ALA	C-N-CA	5.18	125.12	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	jw	67	GLU	N-CA-C	-5.18	105.71	111.36
3	ky	46	TYR	N-CA-C	5.18	116.54	109.18
3	mq	49	PHE	CA-C-N	5.18	125.39	120.31
3	mq	49	PHE	C-N-CA	5.18	125.39	120.31
1	al	271	SER	N-CA-C	5.18	117.55	110.55
1	ax	454	VAL	CA-C-N	-5.18	113.46	122.37
1	ax	454	VAL	C-N-CA	-5.18	113.46	122.37
1	cf	151	ASP	CA-CB-CG	5.18	117.78	112.60
1	cn	474	LYS	N-CA-C	5.18	117.87	109.06
1	ee	119	SER	N-CA-C	-5.18	103.56	108.22
1	ez	454	VAL	CA-C-N	-5.18	114.76	122.74
1	ez	454	VAL	C-N-CA	-5.18	114.76	122.74
1	fq	119	SER	CA-C-N	5.18	125.16	120.03
1	fq	119	SER	C-N-CA	5.18	125.16	120.03
3	ib	49	PHE	CA-C-N	5.18	125.63	120.14
3	ib	49	PHE	C-N-CA	5.18	125.63	120.14
3	jg	72	ASN	CB-CA-C	-5.18	102.74	110.88
1	ar	451	ALA	CA-C-N	5.18	125.10	119.76
1	ar	451	ALA	C-N-CA	5.18	125.10	119.76
1	bj	93	PRO	N-CA-C	5.18	119.47	112.48
1	cs	119	SER	CA-C-N	5.18	125.16	120.03
1	cs	119	SER	C-N-CA	5.18	125.16	120.03
1	dw	324	THR	CA-C-N	5.18	125.48	119.47
1	dw	324	THR	C-N-CA	5.18	125.48	119.47
3	kz	37	ASP	CA-CB-CG	5.18	117.78	112.60
1	ao	149	GLY	CA-C-N	5.18	125.39	120.31
1	ao	149	GLY	C-N-CA	5.18	125.39	120.31
1	ap	119	SER	CA-C-N	5.18	126.31	119.84
1	ap	119	SER	C-N-CA	5.18	126.31	119.84
1	bf	113	GLY	N-CA-C	-5.18	104.79	113.02
1	ej	145	HIS	CA-C-N	5.18	124.84	119.56
1	ej	145	HIS	C-N-CA	5.18	124.84	119.56
1	fg	245	ASN	CA-C-N	5.18	125.16	120.03
1	fg	245	ASN	C-N-CA	5.18	125.16	120.03
1	gq	426	ASP	CA-CB-CG	-5.18	107.42	112.60
1	af	486	GLU	CA-C-N	5.18	131.43	121.54
1	af	486	GLU	C-N-CA	5.18	131.43	121.54
1	db	491	ALA	CA-C-N	5.18	125.63	120.14
1	db	491	ALA	C-N-CA	5.18	125.63	120.14
1	ej	323	LEU	N-CA-C	5.18	118.55	110.32
1	er	222	VAL	N-CA-C	5.18	117.49	108.95
1	fr	198	ILE	N-CA-C	5.18	114.06	106.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	hd	222	VAL	N-CA-C	5.18	117.49	108.95
1	ad	483	PRO	CA-C-O	-5.17	115.44	121.34
1	ae	506	SER	CA-C-N	-5.17	113.59	121.66
1	ae	506	SER	C-N-CA	-5.17	113.59	121.66
1	ax	491	ALA	CA-C-N	5.17	125.62	120.14
1	ax	491	ALA	C-N-CA	5.17	125.62	120.14
1	be	115	GLN	CA-C-N	5.17	125.18	119.90
1	be	115	GLN	C-N-CA	5.17	125.18	119.90
1	cd	451	ALA	CA-C-N	5.17	125.11	119.78
1	cd	451	ALA	C-N-CA	5.17	125.11	119.78
1	ch	480	GLY	CA-C-N	5.17	129.04	122.37
1	ch	480	GLY	C-N-CA	5.17	129.04	122.37
1	cu	196	VAL	N-CA-C	5.17	114.68	108.06
1	de	149	GLY	CA-C-N	5.17	125.38	120.31
1	de	149	GLY	C-N-CA	5.17	125.38	120.31
1	do	327	SER	N-CA-C	5.17	116.66	109.31
1	dv	131	TYR	N-CA-C	5.17	117.06	109.24
1	fw	324	THR	N-CA-C	-5.17	101.89	109.50
1	gh	110	ASP	CA-CB-CG	5.17	117.77	112.60
1	gu	509	LYS	N-CA-C	5.17	121.31	114.12
2	hk	337	VAL	N-CA-C	5.17	115.57	108.12
1	aa	130	VAL	N-CA-C	5.17	115.35	108.11
1	ck	317	GLY	N-CA-C	-5.17	104.69	112.60
1	fn	115	GLN	CA-C-N	5.17	125.11	119.78
1	fn	115	GLN	C-N-CA	5.17	125.11	119.78
1	gd	95	VAL	N-CA-C	5.17	115.49	107.78
1	gl	222	VAL	N-CA-C	5.17	117.48	108.95
3	hr	49	PHE	CA-C-N	5.17	125.62	120.14
3	hr	49	PHE	C-N-CA	5.17	125.62	120.14
3	nz	67	GLU	N-CA-C	-5.17	105.33	111.69
3	oe	41	ILE	N-CA-C	5.17	115.54	107.99
1	cg	113	GLY	N-CA-C	-5.17	104.80	113.02
1	ci	402	THR	CA-C-N	5.17	126.61	120.14
1	ci	402	THR	C-N-CA	5.17	126.61	120.14
1	dq	93	PRO	N-CA-CB	-5.17	97.82	103.25
1	ef	285	ASP	CA-C-N	5.17	131.42	121.54
1	ef	285	ASP	C-N-CA	5.17	131.42	121.54
1	gj	232	ILE	N-CA-C	-5.17	106.64	111.45
1	gr	245	ASN	CA-C-N	5.17	125.07	119.85
1	gr	245	ASN	C-N-CA	5.17	125.07	119.85
2	hk	352	ASP	N-CA-C	-5.17	102.83	110.48
3	ig	49	PHE	CA-C-N	5.17	125.38	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	ig	49	PHE	C-N-CA	5.17	125.38	120.31
3	jx	67	GLU	N-CA-C	-5.17	105.72	111.36
3	kc	72	ASN	CA-CB-CG	5.17	117.77	112.60
3	kk	46	TYR	N-CA-C	5.17	116.85	109.14
1	ab	269	ALA	N-CA-C	5.17	117.48	111.02
1	co	222	VAL	N-CA-C	5.17	117.48	108.95
1	cw	249	GLU	N-CA-C	5.17	117.05	109.24
1	cy	500	MET	CB-CA-C	5.17	116.86	109.26
1	fs	500	MET	CA-C-N	5.17	126.30	119.84
1	fs	500	MET	C-N-CA	5.17	126.30	119.84
1	gn	358	ASP	CA-CB-CG	5.17	117.77	112.60
3	ie	49	PHE	CA-C-N	5.17	125.62	120.14
3	ie	49	PHE	C-N-CA	5.17	125.62	120.14
1	aa	450	TYR	CA-C-N	-5.17	116.48	123.46
1	aa	450	TYR	C-N-CA	-5.17	116.48	123.46
1	bo	426	ASP	CA-CB-CG	-5.17	107.43	112.60
1	bt	392	GLY	CA-C-N	-5.17	116.79	121.65
1	bt	392	GLY	C-N-CA	-5.17	116.79	121.65
1	cx	425	ILE	N-CA-C	5.17	115.53	107.99
1	da	285	ASP	N-CA-C	5.17	118.05	111.69
1	ev	134	ASP	CA-C-N	5.17	125.21	119.32
1	ev	134	ASP	C-N-CA	5.17	125.21	119.32
3	lg	44	ALA	N-CA-C	5.17	119.57	113.16
3	ma	32	PHE	CA-C-N	5.17	124.83	119.56
3	ma	32	PHE	C-N-CA	5.17	124.83	119.56
3	mu	49	PHE	CA-C-N	5.17	125.38	120.31
3	mu	49	PHE	C-N-CA	5.17	125.38	120.31
1	ak	451	ALA	CA-C-N	5.17	126.30	119.84
1	ak	451	ALA	C-N-CA	5.17	126.30	119.84
1	ao	110	ASP	CA-CB-CG	5.17	117.77	112.60
1	bl	285	ASP	CA-C-N	5.17	131.41	121.54
1	bl	285	ASP	C-N-CA	5.17	131.41	121.54
1	df	256	LYS	N-CA-C	5.17	117.04	109.24
1	er	265	GLN	N-CA-C	5.17	116.92	108.76
1	fh	186	GLY	N-CA-C	5.17	120.63	111.02
3	ia	46	TYR	N-CA-C	5.17	116.84	109.14
1	by	115	GLN	CA-C-N	5.17	125.10	119.78
1	by	115	GLN	C-N-CA	5.17	125.10	119.78
1	er	131	TYR	N-CA-C	5.17	116.66	108.96
1	ey	249	GLU	N-CA-C	5.17	116.92	109.07
1	bb	143	ALA	N-CA-C	5.16	116.99	111.36
1	br	358	ASP	CA-CB-CG	5.16	117.76	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dd	402	THR	CA-C-N	5.16	126.59	120.14
1	dd	402	THR	C-N-CA	5.16	126.59	120.14
1	gn	491	ALA	CA-C-N	5.16	125.06	119.85
1	gn	491	ALA	C-N-CA	5.16	125.06	119.85
3	hu	44	ALA	N-CA-C	5.16	119.56	113.16
3	iv	67	GLU	N-CA-C	-5.16	105.73	111.36
3	ko	38	VAL	N-CA-C	5.16	115.71	108.17
1	ah	392	GLY	CA-C-N	-5.16	116.80	121.65
1	ah	392	GLY	C-N-CA	-5.16	116.80	121.65
1	fk	232	ILE	N-CA-C	-5.16	106.63	111.48
1	ga	199	ASP	CA-CB-CG	-5.16	107.44	112.60
1	bd	256	LYS	N-CA-C	5.16	116.92	109.07
1	bn	393	ILE	N-CA-C	5.16	111.73	106.21
1	en	256	LYS	N-CA-C	5.16	116.91	109.07
1	ey	455	ALA	N-CA-C	5.16	117.35	107.75
1	fq	454	VAL	CA-C-N	-5.16	113.49	122.37
1	fq	454	VAL	C-N-CA	-5.16	113.49	122.37
1	gs	92	GLY	CA-C-N	5.16	124.82	119.56
1	gs	92	GLY	C-N-CA	5.16	124.82	119.56
1	gs	149	GLY	CA-C-N	5.16	125.06	119.85
1	gs	149	GLY	C-N-CA	5.16	125.06	119.85
3	na	49	PHE	CA-C-N	5.16	125.61	120.14
3	na	49	PHE	C-N-CA	5.16	125.61	120.14
1	cl	92	GLY	CA-C-N	5.16	124.82	119.56
1	cl	92	GLY	C-N-CA	5.16	124.82	119.56
1	cw	327	SER	N-CA-C	5.16	116.64	109.31
1	dn	119	SER	CA-C-N	5.16	125.14	120.03
1	dn	119	SER	C-N-CA	5.16	125.14	120.03
1	eb	425	ILE	N-CA-C	5.16	115.73	108.36
1	ej	324	THR	CA-C-N	5.16	125.45	119.47
1	ej	324	THR	C-N-CA	5.16	125.45	119.47
1	ey	245	ASN	N-CA-C	5.16	116.98	109.30
1	fc	95	VAL	N-CA-C	5.16	115.47	107.78
1	gi	468	GLN	CA-C-N	5.16	125.06	119.85
1	gi	468	GLN	C-N-CA	5.16	125.06	119.85
1	gj	149	GLY	CA-C-N	5.16	125.14	120.03
1	gj	149	GLY	C-N-CA	5.16	125.14	120.03
3	hs	67	GLU	N-CA-C	-5.16	105.74	111.36
3	ix	49	PHE	CA-C-N	5.16	125.61	120.14
3	ix	49	PHE	C-N-CA	5.16	125.61	120.14
3	kn	49	PHE	CA-C-N	5.16	125.61	120.14
3	kn	49	PHE	C-N-CA	5.16	125.61	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bg	490	GLN	N-CA-C	-5.16	105.73	112.23
1	fm	103	ILE	CA-C-N	5.16	125.09	119.78
1	fm	103	ILE	C-N-CA	5.16	125.09	119.78
1	am	115	GLN	CA-C-N	5.16	125.09	119.78
1	am	115	GLN	C-N-CA	5.16	125.09	119.78
1	as	245	ASN	CA-C-N	5.16	125.06	119.85
1	as	245	ASN	C-N-CA	5.16	125.06	119.85
1	az	110	ASP	CA-CB-CG	5.16	117.76	112.60
1	dr	145	HIS	CA-C-N	5.16	124.77	119.56
1	dr	145	HIS	C-N-CA	5.16	124.77	119.56
1	gl	163	PHE	CA-C-N	5.16	125.06	119.85
1	gl	163	PHE	C-N-CA	5.16	125.06	119.85
2	ho	420	LEU	CA-C-N	5.16	125.09	119.78
2	ho	420	LEU	C-N-CA	5.16	125.09	119.78
3	hw	38	VAL	N-CA-C	5.16	115.70	108.17
3	iq	72	ASN	CA-CB-CG	5.16	117.75	112.60
3	ko	44	ALA	N-CA-C	5.16	119.44	113.20
1	bq	501	PRO	CA-C-N	5.15	131.38	121.54
1	bq	501	PRO	C-N-CA	5.15	131.38	121.54
1	ca	328	LYS	N-CA-C	5.15	119.55	113.16
1	bg	232	ILE	N-CA-C	-5.15	106.77	111.67
1	cg	256	LYS	N-CA-C	5.15	116.90	109.07
1	el	149	GLY	CA-C-N	5.15	125.05	119.85
1	el	149	GLY	C-N-CA	5.15	125.05	119.85
1	ga	113	GLY	N-CA-C	-5.15	104.75	112.89
1	af	154	PHE	CA-CB-CG	5.15	118.95	113.80
1	cb	186	GLY	N-CA-C	5.15	120.60	111.02
1	dt	87	ALA	CA-C-N	-5.15	115.83	122.99
1	dt	87	ALA	C-N-CA	-5.15	115.83	122.99
3	je	44	ALA	N-CA-C	5.15	119.55	113.16
3	ji	37	ASP	CA-CB-CG	5.15	117.75	112.60
3	jr	48	THR	N-CA-C	5.15	116.12	108.86
3	na	74	ASP	CA-CB-CG	5.15	117.75	112.60
3	nq	32	PHE	CA-C-N	5.15	124.81	119.56
3	nq	32	PHE	C-N-CA	5.15	124.81	119.56
1	aw	402	THR	CA-C-N	5.15	126.58	120.14
1	aw	402	THR	C-N-CA	5.15	126.58	120.14
1	cq	252	PHE	CA-CB-CG	5.15	118.95	113.80
1	fq	121	THR	N-CA-C	5.15	118.34	111.24
3	ju	10	ILE	N-CA-C	5.15	115.27	107.75
1	aq	237	GLU	N-CA-C	5.15	118.92	111.56
1	bc	451	ALA	CA-C-N	5.15	125.08	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bc	451	ALA	C-N-CA	5.15	125.08	119.78
1	ce	446	ALA	N-CA-C	5.15	120.21	113.88
1	cv	263	SER	N-CA-C	5.15	117.71	110.14
1	di	402	THR	CA-C-N	5.15	126.57	120.14
1	di	402	THR	C-N-CA	5.15	126.57	120.14
1	dj	269	ALA	N-CA-C	5.15	117.45	111.02
1	ek	145	HIS	CA-C-N	5.15	124.81	119.56
1	ek	145	HIS	C-N-CA	5.15	124.81	119.56
1	eq	74	TYR	CA-C-N	5.15	130.03	122.77
1	eq	74	TYR	C-N-CA	5.15	130.03	122.77
1	fm	324	THR	CA-C-N	5.15	125.44	119.47
1	fm	324	THR	C-N-CA	5.15	125.44	119.47
3	il	38	VAL	N-CA-C	5.15	115.69	108.17
1	as	105	ASN	N-CA-C	5.15	121.76	110.80
1	cr	123	GLN	N-CA-C	5.15	116.78	108.34
1	ex	259	ILE	N-CA-C	5.15	114.90	106.72
1	ey	119	SER	N-CA-C	-5.15	103.59	108.22
1	gq	265	GLN	N-CA-C	5.15	116.89	108.55
2	hi	208	ASP	CA-CB-CG	5.15	117.75	112.60
1	bm	119	SER	CA-C-N	5.14	125.12	120.03
1	bm	119	SER	C-N-CA	5.14	125.12	120.03
1	ce	454	VAL	CA-C-N	-5.14	113.52	122.37
1	ce	454	VAL	C-N-CA	-5.14	113.52	122.37
1	dj	490	GLN	N-CA-C	5.14	119.41	113.18
1	dl	258	VAL	N-CA-C	5.14	117.24	108.86
3	ic	49	PHE	CA-C-N	5.14	125.35	120.31
3	ic	49	PHE	C-N-CA	5.14	125.35	120.31
3	iy	46	TYR	N-CA-C	5.14	116.81	109.14
3	ms	32	PHE	CA-C-N	5.14	124.81	119.56
3	ms	32	PHE	C-N-CA	5.14	124.81	119.56
1	ak	71	ASP	CA-CB-CG	5.14	117.74	112.60
1	as	199	ASP	CA-CB-CG	-5.14	107.46	112.60
1	bk	370	ARG	CA-C-N	-5.14	115.60	122.54
1	bk	370	ARG	C-N-CA	-5.14	115.60	122.54
1	bu	151	ASP	CA-CB-CG	5.14	117.74	112.60
1	ca	324	THR	CA-C-N	5.14	125.44	119.47
1	ca	324	THR	C-N-CA	5.14	125.44	119.47
1	cc	92	GLY	CA-C-N	5.14	126.27	119.84
1	cc	92	GLY	C-N-CA	5.14	126.27	119.84
1	el	209	ASP	CA-CB-CG	5.14	117.74	112.60
1	ga	263	SER	N-CA-C	5.14	118.07	110.46
1	gc	197	THR	CA-C-N	-5.14	116.11	123.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gc	197	THR	C-N-CA	-5.14	116.11	123.10
1	az	232	ILE	N-CA-C	-5.14	106.79	111.67
1	eb	93	PRO	N-CA-CB	-5.14	99.40	102.79
1	eo	285	ASP	CA-C-N	5.14	131.36	121.54
1	eo	285	ASP	C-N-CA	5.14	131.36	121.54
1	bg	250	MET	N-CA-C	5.14	116.10	108.60
1	cc	134	ASP	CA-C-N	5.14	124.80	119.56
1	cc	134	ASP	C-N-CA	5.14	124.80	119.56
1	ck	285	ASP	CA-C-N	5.14	131.36	121.54
1	ck	285	ASP	C-N-CA	5.14	131.36	121.54
1	et	72	HIS	N-CA-C	-5.14	103.14	110.59
1	fw	121	THR	N-CA-C	5.14	118.33	111.24
1	fx	182	PHE	CA-CB-CG	5.14	118.94	113.80
1	gu	490	GLN	N-CA-C	-5.14	105.75	112.23
1	gx	256	LYS	N-CA-C	5.14	116.62	108.96
2	hm	291	LYS	CA-C-N	5.14	126.26	119.84
2	hm	291	LYS	C-N-CA	5.14	126.26	119.84
3	js	67	GLU	N-CA-C	-5.14	105.76	111.36
3	mi	67	GLU	N-CA-C	-5.14	105.76	111.36
3	ob	67	GLU	N-CA-C	-5.14	105.76	111.36
1	ci	503	ILE	CB-CA-C	-5.14	105.20	112.14
1	fj	425	ILE	N-CA-C	5.14	115.71	108.36
1	ai	149	GLY	CA-C-N	5.14	125.11	120.03
1	ai	149	GLY	C-N-CA	5.14	125.11	120.03
1	bx	78	ASN	CA-C-O	-5.14	113.17	120.51
1	dm	503	ILE	CB-CA-C	-5.14	105.40	111.97
1	dz	134	ASP	CA-C-N	5.14	125.43	119.47
1	dz	134	ASP	C-N-CA	5.14	125.43	119.47
1	fi	115	GLN	CA-C-N	5.14	125.07	119.78
1	fi	115	GLN	C-N-CA	5.14	125.07	119.78
1	fs	209	ASP	CA-CB-CG	5.14	117.74	112.60
1	ft	116	PRO	CA-C-N	-5.14	113.58	120.87
1	ft	116	PRO	C-N-CA	-5.14	113.58	120.87
3	no	67	GLU	N-CA-C	-5.14	105.76	111.36
1	af	484	PHE	CA-CB-CG	5.13	118.93	113.80
1	as	402	THR	CA-C-N	5.13	126.56	120.14
1	as	402	THR	C-N-CA	5.13	126.56	120.14
1	az	500	MET	CB-CA-C	5.13	116.25	108.86
1	bf	480	GLY	N-CA-C	5.13	118.97	110.55
1	bp	209	ASP	CA-CB-CG	5.13	117.73	112.60
1	br	484	PHE	CA-CB-CG	5.13	118.93	113.80
1	ce	481	ILE	N-CA-C	5.13	115.67	108.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	de	324	THR	N-CA-C	-5.13	103.18	109.65
1	fd	266	LEU	N-CA-C	5.13	117.19	109.23
1	ff	491	ALA	CA-C-N	5.13	127.46	120.79
1	ff	491	ALA	C-N-CA	5.13	127.46	120.79
1	hb	324	THR	CA-C-N	5.13	125.42	119.47
1	hb	324	THR	C-N-CA	5.13	125.42	119.47
1	cp	269	ALA	N-CA-C	5.13	117.44	111.02
1	cr	189	TYR	N-CA-C	-5.13	99.92	108.34
1	eg	121	THR	CB-CA-C	-5.13	103.29	112.27
1	ep	263	SER	N-CA-C	5.13	116.47	109.18
3	ij	49	PHE	CA-C-N	5.13	125.58	120.14
3	ij	49	PHE	C-N-CA	5.13	125.58	120.14
1	aj	93	PRO	N-CA-CB	-5.13	99.40	102.79
1	ao	265	GLN	N-CA-C	5.13	116.87	108.76
1	ca	324	THR	N-CA-C	-5.13	101.96	109.50
1	cx	358	ASP	CA-CB-CG	5.13	117.73	112.60
1	dk	256	LYS	N-CA-C	5.13	116.87	109.07
1	fb	88	VAL	N-CA-C	5.13	115.24	107.75
1	ed	71	ASP	CA-CB-CG	5.13	117.73	112.60
1	fs	324	THR	CA-C-N	5.13	125.42	119.47
1	fs	324	THR	C-N-CA	5.13	125.42	119.47
2	hj	334	LYS	N-CA-C	-5.13	108.05	114.56
2	hl	145	SER	N-CA-C	-5.13	102.79	110.23
3	ib	38	VAL	N-CA-C	5.13	115.66	108.17
3	lg	49	PHE	CA-C-N	5.13	125.34	120.31
3	lg	49	PHE	C-N-CA	5.13	125.34	120.31
1	ce	87	ALA	CA-C-N	-5.13	116.28	123.10
1	ce	87	ALA	C-N-CA	-5.13	116.28	123.10
1	cs	265	GLN	N-CA-C	5.13	116.86	108.55
1	dt	483	PRO	N-CA-C	-5.13	103.06	111.21
1	fo	199	ASP	CA-CB-CG	-5.13	107.47	112.60
1	fz	259	ILE	N-CA-C	5.13	115.44	107.28
3	iu	10	ILE	N-CA-C	5.13	115.23	107.80
3	jc	46	TYR	N-CA-C	5.13	116.78	109.14
3	lz	49	PHE	CA-C-N	5.13	125.58	120.14
3	lz	49	PHE	C-N-CA	5.13	125.58	120.14
1	ah	120	PRO	N-CA-C	-5.13	102.15	110.40
1	bg	329	ALA	N-CA-C	5.13	118.31	111.24
1	cz	131	TYR	N-CA-C	5.13	117.95	109.85
1	da	115	GLN	CB-CA-C	-5.13	106.54	111.00
1	dq	119	SER	CA-C-N	5.13	125.11	120.03
1	dq	119	SER	C-N-CA	5.13	125.11	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ef	134	ASP	CA-C-N	5.13	125.42	119.47
1	ef	134	ASP	C-N-CA	5.13	125.42	119.47
1	gk	71	ASP	CA-CB-CG	5.13	117.73	112.60
1	gw	324	THR	CA-C-N	5.13	125.42	119.47
1	gw	324	THR	C-N-CA	5.13	125.42	119.47
1	ca	232	ILE	N-CA-C	-5.12	106.80	111.67
1	de	151	ASP	CA-CB-CG	5.12	117.72	112.60
1	df	93	PRO	N-CA-CB	-5.12	97.87	103.25
1	ek	199	ASP	CA-CB-CG	-5.12	107.47	112.60
1	gu	285	ASP	CA-C-N	5.12	131.33	121.54
1	gu	285	ASP	C-N-CA	5.12	131.33	121.54
3	ln	49	PHE	CA-C-N	5.12	125.57	120.14
3	ln	49	PHE	C-N-CA	5.12	125.57	120.14
1	ad	154	PHE	CA-CB-CG	5.12	118.92	113.80
1	ap	154	PHE	CA-CB-CG	5.12	118.92	113.80
1	aw	485	ALA	N-CA-C	5.12	117.53	111.33
1	bk	88	VAL	N-CA-C	5.12	115.23	107.75
1	bp	484	PHE	N-CA-C	-5.12	106.85	114.64
1	cs	350	PHE	CA-CB-CG	5.12	118.92	113.80
1	ct	209	ASP	CA-CB-CG	5.12	117.72	112.60
1	ei	486	GLU	CA-C-N	5.12	131.33	121.54
1	ei	486	GLU	C-N-CA	5.12	131.33	121.54
1	gc	285	ASP	CA-C-N	5.12	131.33	121.54
1	gc	285	ASP	C-N-CA	5.12	131.33	121.54
1	gv	402	THR	CA-C-N	5.12	126.59	120.13
1	gv	402	THR	C-N-CA	5.12	126.59	120.13
3	ip	49	PHE	CA-C-N	5.12	125.57	120.14
3	ip	49	PHE	C-N-CA	5.12	125.57	120.14
3	mt	67	GLU	N-CA-C	-5.12	105.78	111.36
3	nn	44	ALA	N-CA-C	5.12	119.51	113.16
1	ad	256	LYS	N-CA-C	5.12	116.85	109.07
1	em	403	GLY	N-CA-C	5.12	119.95	113.24
1	ew	145	HIS	CA-C-N	5.12	124.73	119.56
1	ew	145	HIS	C-N-CA	5.12	124.73	119.56
2	he	365	ASP	CA-C-N	5.12	127.09	120.89
2	he	365	ASP	C-N-CA	5.12	127.09	120.89
1	cz	324	THR	N-CA-C	-5.12	103.20	109.65
1	dt	71	ASP	CA-CB-CG	5.12	117.72	112.60
1	fv	222	VAL	N-CA-C	5.12	117.40	108.95
3	lk	67	GLU	N-CA-C	-5.12	105.78	111.36
1	bi	451	ALA	CA-C-N	5.12	125.05	119.78
1	bi	451	ALA	C-N-CA	5.12	125.05	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	by	267	LYS	N-CA-C	5.12	117.59	109.50
1	cf	134	ASP	CA-C-N	5.12	125.16	119.32
1	cf	134	ASP	C-N-CA	5.12	125.16	119.32
1	cg	238	GLY	N-CA-C	5.12	122.96	115.08
1	dj	121	THR	CB-CA-C	-5.12	104.46	111.73
1	et	454	VAL	CA-C-N	-5.12	114.44	122.73
1	et	454	VAL	C-N-CA	-5.12	114.44	122.73
1	ey	285	ASP	CA-C-N	5.12	131.32	121.54
1	ey	285	ASP	C-N-CA	5.12	131.32	121.54
1	fo	145	HIS	CA-CB-CG	5.12	118.92	113.80
1	gg	344	ARG	N-CA-C	-5.12	101.30	109.23
3	kx	32	PHE	CA-C-N	5.12	124.78	119.56
3	kx	32	PHE	C-N-CA	5.12	124.78	119.56
1	bk	484	PHE	CA-CB-CG	5.12	118.92	113.80
1	cg	149	GLY	CA-C-N	5.12	125.02	119.85
1	cg	149	GLY	C-N-CA	5.12	125.02	119.85
1	df	237	GLU	N-CA-C	5.12	116.90	110.91
1	dl	238	GLY	N-CA-C	5.12	122.96	115.08
3	ke	46	TYR	N-CA-C	5.12	116.77	109.14
1	bg	500	MET	CB-CA-C	5.12	117.70	109.41
1	cg	484	PHE	CA-CB-CG	5.12	118.92	113.80
1	du	134	ASP	CA-C-N	5.12	124.73	119.56
1	du	134	ASP	C-N-CA	5.12	124.73	119.56
1	eg	324	THR	CA-C-N	5.12	125.41	119.47
1	eg	324	THR	C-N-CA	5.12	125.41	119.47
1	ex	328	LYS	N-CA-C	5.12	119.21	112.92
3	ob	72	ASN	CB-CG-ND2	-5.12	108.73	116.40
1	ap	222	VAL	N-CA-C	5.11	117.39	108.95
1	cv	134	ASP	CA-C-N	5.11	124.78	119.56
1	cv	134	ASP	C-N-CA	5.11	124.78	119.56
1	ea	324	THR	CA-C-N	5.11	125.40	119.47
1	ea	324	THR	C-N-CA	5.11	125.40	119.47
1	eq	338	ILE	N-CA-C	-5.11	105.86	110.82
1	fs	402	THR	CA-C-N	5.11	126.53	120.14
1	fs	402	THR	C-N-CA	5.11	126.53	120.14
3	iw	67	GLU	N-CA-C	-5.11	105.79	111.36
3	nj	74	ASP	CA-CB-CG	5.11	117.71	112.60
3	nw	46	TYR	N-CA-C	5.11	116.76	109.14
1	an	222	VAL	N-CA-C	5.11	117.39	108.95
1	dq	263	SER	N-CA-C	5.11	118.06	110.14
1	dq	324	THR	N-CA-C	-5.11	101.85	109.42
1	fk	67	GLU	N-CA-C	-5.11	101.63	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gy	324	THR	CA-C-N	5.11	125.40	119.47
1	gy	324	THR	C-N-CA	5.11	125.40	119.47
3	ji	49	PHE	CA-C-N	5.11	125.32	120.31
3	ji	49	PHE	C-N-CA	5.11	125.32	120.31
3	nb	38	VAL	N-CA-C	5.11	115.73	108.42
1	bd	209	ASP	CA-CB-CG	5.11	117.71	112.60
1	bu	402	THR	CA-C-N	5.11	126.57	120.13
1	bu	402	THR	C-N-CA	5.11	126.57	120.13
1	cg	72	HIS	N-CA-C	-5.11	102.59	109.95
1	dg	250	MET	N-CA-C	5.11	116.96	109.24
1	dn	468	GLN	CA-C-N	5.11	125.01	119.85
1	dn	468	GLN	C-N-CA	5.11	125.01	119.85
1	dv	336	ASP	CA-C-N	5.11	125.40	119.47
1	dv	336	ASP	C-N-CA	5.11	125.40	119.47
1	fo	134	ASP	CA-C-N	5.11	125.15	119.32
1	fo	134	ASP	C-N-CA	5.11	125.15	119.32
3	ji	32	PHE	CA-C-N	5.11	124.77	119.56
3	ji	32	PHE	C-N-CA	5.11	124.77	119.56
3	lo	74	ASP	CA-CB-CG	5.11	117.71	112.60
3	mz	49	PHE	CA-C-N	5.11	125.32	120.31
3	mz	49	PHE	C-N-CA	5.11	125.32	120.31
3	nv	49	PHE	CA-C-N	5.11	125.56	120.14
3	nv	49	PHE	C-N-CA	5.11	125.56	120.14
1	bv	145	HIS	CA-C-N	5.11	124.77	119.56
1	bv	145	HIS	C-N-CA	5.11	124.77	119.56
1	cx	263	SER	N-CA-C	5.11	118.02	110.46
1	fc	253	ARG	N-CA-C	5.11	119.16	111.96
3	mx	49	PHE	CA-C-N	5.11	125.32	120.31
3	mx	49	PHE	C-N-CA	5.11	125.32	120.31
1	aj	127	LEU	N-CA-C	5.11	117.23	108.90
1	au	451	ALA	CA-C-N	5.11	125.02	119.76
1	au	451	ALA	C-N-CA	5.11	125.02	119.76
1	bd	199	ASP	CA-CB-CG	-5.11	107.49	112.60
1	ce	184	GLU	N-CA-C	-5.11	102.60	109.95
1	dd	491	ALA	CA-C-N	5.11	125.55	120.14
1	dd	491	ALA	C-N-CA	5.11	125.55	120.14
1	dr	463	ASP	CA-C-N	5.11	124.77	119.56
1	dr	463	ASP	C-N-CA	5.11	124.77	119.56
1	ed	110	ASP	CA-CB-CG	5.11	117.71	112.60
1	fr	456	LEU	N-CA-C	5.11	118.37	111.17
1	fv	232	ILE	N-CA-C	-5.11	106.82	111.67
1	ge	327	SER	N-CA-C	5.11	116.56	109.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	gm	324	THR	CA-C-N	5.11	124.77	119.56
1	gm	324	THR	C-N-CA	5.11	124.77	119.56
2	hl	320	LEU	N-CA-C	5.11	120.37	114.04
1	ax	68	ILE	N-CA-C	5.11	116.95	108.99
1	ax	199	ASP	CA-CB-CG	-5.11	107.50	112.60
1	bb	486	GLU	CA-C-N	5.11	131.29	121.54
1	bb	486	GLU	C-N-CA	5.11	131.29	121.54
1	bn	174	VAL	N-CA-C	5.11	115.93	108.58
1	cu	324	THR	CB-CA-C	5.11	116.02	110.15
1	da	87	ALA	CA-C-N	-5.11	116.45	123.14
1	da	87	ALA	C-N-CA	-5.11	116.45	123.14
3	ob	49	PHE	CA-C-N	5.11	125.55	120.14
3	ob	49	PHE	C-N-CA	5.11	125.55	120.14
1	bj	454	VAL	CA-C-N	-5.10	113.59	122.37
1	bj	454	VAL	C-N-CA	-5.10	113.59	122.37
1	ct	263	SER	N-CA-C	5.10	117.64	110.14
1	dd	134	ASP	CA-C-N	5.10	125.39	119.47
1	dd	134	ASP	C-N-CA	5.10	125.39	119.47
1	gs	406	THR	N-CA-C	-5.10	106.90	113.23
1	as	474	LYS	N-CA-C	5.10	117.14	109.23
1	dc	209	ASP	CA-CB-CG	5.10	117.70	112.60
1	ef	463	ASP	CA-C-N	5.10	124.77	119.56
1	ef	463	ASP	C-N-CA	5.10	124.77	119.56
1	ez	258	VAL	N-CA-C	5.10	117.37	108.95
1	ha	266	LEU	N-CA-C	5.10	116.94	109.24
2	hi	320	LEU	N-CA-C	5.10	119.97	113.18
3	ki	67	GLU	N-CA-C	-5.10	105.80	111.36
3	kq	67	GLU	N-CA-C	-5.10	105.80	111.36
3	kv	49	PHE	CA-C-N	5.10	125.55	120.14
3	kv	49	PHE	C-N-CA	5.10	125.55	120.14
3	nv	46	TYR	N-CA-C	5.10	116.56	108.96
1	am	113	GLY	N-CA-C	-5.10	104.52	112.58
1	dd	149	GLY	CA-C-N	5.10	125.08	120.03
1	dd	149	GLY	C-N-CA	5.10	125.08	120.03
1	fv	451	ALA	CA-C-N	5.10	125.03	119.78
1	fv	451	ALA	C-N-CA	5.10	125.03	119.78
1	gi	344	ARG	CA-C-N	5.10	131.28	121.54
1	gi	344	ARG	C-N-CA	5.10	131.28	121.54
3	id	15	GLN	N-CA-C	5.10	117.14	109.23
1	av	328	LYS	N-CA-C	5.10	119.19	112.92
1	bb	163	PHE	CA-C-N	5.10	125.00	119.85
1	bb	163	PHE	C-N-CA	5.10	125.00	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bi	232	ILE	N-CA-C	-5.10	106.83	111.67
1	bz	456	LEU	N-CA-C	5.10	118.28	111.24
1	ck	93	PRO	N-CA-C	5.10	122.97	112.47
1	gx	209	ASP	CA-CB-CG	5.10	117.70	112.60
2	he	420	LEU	CA-C-N	5.10	125.03	119.78
2	he	420	LEU	C-N-CA	5.10	125.03	119.78
3	km	44	ALA	N-CA-C	5.10	119.48	113.16
3	kq	74	ASP	CA-CB-CG	5.10	117.70	112.60
3	mb	44	ALA	N-CA-C	5.10	119.48	113.16
1	ce	245	ASN	CA-C-N	5.10	125.00	119.85
1	ce	245	ASN	C-N-CA	5.10	125.00	119.85
1	da	209	ASP	CA-CB-CG	5.10	117.70	112.60
1	fc	130	VAL	N-CA-C	5.10	115.25	108.11
1	fn	258	VAL	N-CA-C	5.10	116.06	108.46
1	fs	426	ASP	CA-CB-CG	-5.10	107.50	112.60
1	gm	500	MET	N-CA-C	-5.10	103.65	110.07
1	gs	402	THR	CA-C-N	5.10	126.55	120.13
1	gs	402	THR	C-N-CA	5.10	126.55	120.13
1	bc	484	PHE	CA-CB-CG	5.10	118.90	113.80
1	bm	209	ASP	CA-CB-CG	5.10	117.70	112.60
1	bo	463	ASP	CA-C-N	5.10	124.76	119.56
1	bo	463	ASP	C-N-CA	5.10	124.76	119.56
1	eg	110	ASP	CA-CB-CG	5.10	117.70	112.60
1	gb	490	GLN	N-CA-C	-5.10	105.81	112.23
1	ae	483	PRO	N-CA-C	-5.09	103.11	111.21
1	ai	209	ASP	CA-CB-CG	5.09	117.69	112.60
1	ch	258	VAL	N-CA-C	5.09	115.82	108.48
1	cj	397	ALA	N-CA-C	5.09	116.27	108.42
1	dg	245	ASN	CA-C-N	5.09	125.07	120.03
1	dg	245	ASN	C-N-CA	5.09	125.07	120.03
1	ey	69	GLY	N-CA-C	-5.09	106.59	112.50
1	fl	258	VAL	N-CA-C	5.09	117.36	108.95
1	ge	134	ASP	CA-C-N	5.09	124.76	119.56
1	ge	134	ASP	C-N-CA	5.09	124.76	119.56
1	gn	500	MET	CB-CA-C	5.09	116.20	108.86
3	lk	46	TYR	N-CA-C	5.09	116.73	109.14
1	fo	121	THR	CB-CA-C	-5.09	102.93	112.30
2	hm	384	ASN	N-CA-C	5.09	117.11	110.08
1	ac	285	ASP	CA-C-N	5.09	131.27	121.54
1	ac	285	ASP	C-N-CA	5.09	131.27	121.54
1	ah	209	ASP	CA-CB-CG	5.09	117.69	112.60
1	be	149	GLY	CA-C-N	5.09	125.30	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	be	149	GLY	C-N-CA	5.09	125.30	120.31
1	bs	238	GLY	N-CA-C	5.09	122.92	115.08
1	gv	256	LYS	N-CA-C	5.09	116.81	109.07
3	ka	49	PHE	CA-C-N	5.09	125.54	120.14
3	ka	49	PHE	C-N-CA	5.09	125.54	120.14
3	lp	67	GLU	N-CA-C	-5.09	105.81	111.36
1	ag	103	ILE	CA-C-N	5.09	125.02	119.78
1	ag	103	ILE	C-N-CA	5.09	125.02	119.78
1	an	285	ASP	CA-C-N	5.09	131.26	121.54
1	an	285	ASP	C-N-CA	5.09	131.26	121.54
1	bp	134	ASP	CA-C-N	5.09	124.75	119.56
1	bp	134	ASP	C-N-CA	5.09	124.75	119.56
1	bx	249	GLU	N-CA-C	5.09	117.41	109.52
1	cw	93	PRO	N-CA-CB	-5.09	97.91	103.25
1	cz	263	SER	N-CA-C	5.09	117.15	109.41
1	ek	265	GLN	N-CA-C	5.09	116.80	108.76
1	em	263	SER	N-CA-C	5.09	118.31	110.42
1	fb	134	ASP	CA-C-N	5.09	124.70	119.56
1	fb	134	ASP	C-N-CA	5.09	124.70	119.56
1	fg	71	ASP	CA-CB-CG	5.09	117.69	112.60
1	fh	134	ASP	CA-CB-CG	-5.09	107.51	112.60
1	fx	463	ASP	CA-C-N	5.09	126.20	119.84
1	fx	463	ASP	C-N-CA	5.09	126.20	119.84
1	gy	258	VAL	N-CA-C	5.09	117.35	108.95
3	lz	48	THR	N-CA-C	5.09	116.72	109.14
3	mh	74	ASP	CA-CB-CG	5.09	117.69	112.60
3	nd	49	PHE	CA-C-N	5.09	125.30	120.31
3	nd	49	PHE	C-N-CA	5.09	125.30	120.31
3	nx	49	PHE	CA-C-N	5.09	125.54	120.14
3	nx	49	PHE	C-N-CA	5.09	125.54	120.14
1	bd	130	VAL	N-CA-C	5.09	115.45	108.12
1	ew	79	ILE	CB-CA-C	-5.09	105.36	112.02
3	hu	32	PHE	CA-C-N	5.09	124.75	119.56
3	hu	32	PHE	C-N-CA	5.09	124.75	119.56
1	ay	245	ASN	CA-C-N	5.09	125.07	120.03
1	ay	245	ASN	C-N-CA	5.09	125.07	120.03
1	br	328	LYS	N-CA-C	5.09	119.47	113.16
1	cg	328	LYS	N-CA-C	5.09	119.35	113.20
1	cj	378	ALA	N-CA-C	5.09	116.80	109.07
1	dd	115	GLN	CA-C-N	5.09	125.02	119.78
1	dd	115	GLN	C-N-CA	5.09	125.02	119.78
1	fb	149	GLY	CA-C-N	5.09	124.99	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fb	149	GLY	C-N-CA	5.09	124.99	119.85
1	fh	134	ASP	CA-C-N	5.09	124.70	119.56
1	fh	134	ASP	C-N-CA	5.09	124.70	119.56
1	hc	324	THR	CA-C-N	5.09	125.37	119.47
1	hc	324	THR	C-N-CA	5.09	125.37	119.47
1	as	115	GLN	CA-C-N	5.08	125.02	119.78
1	as	115	GLN	C-N-CA	5.08	125.02	119.78
1	bd	227	GLY	N-CA-C	-5.08	104.42	112.66
1	er	256	LYS	N-CA-C	5.08	116.80	109.07
1	fw	468	GLN	CA-C-N	5.08	124.84	119.76
1	fw	468	GLN	C-N-CA	5.08	124.84	119.76
1	gc	145	HIS	CA-C-N	5.08	124.75	119.56
1	gc	145	HIS	C-N-CA	5.08	124.75	119.56
1	hc	119	SER	CA-C-N	5.08	125.06	120.03
1	hc	119	SER	C-N-CA	5.08	125.06	120.03
1	al	346	ALA	N-CA-C	5.08	116.82	111.28
1	cs	324	THR	CA-C-N	5.08	125.37	119.47
1	cs	324	THR	C-N-CA	5.08	125.37	119.47
1	dd	463	ASP	CA-C-N	5.08	126.19	119.84
1	dd	463	ASP	C-N-CA	5.08	126.19	119.84
1	dz	110	ASP	CA-CB-CG	5.08	117.68	112.60
1	en	285	ASP	N-CA-C	5.08	117.94	111.69
1	ff	230	THR	N-CA-C	-5.08	105.74	111.28
1	fi	199	ASP	CA-CB-CG	-5.08	107.52	112.60
1	ga	182	PHE	CA-CB-CG	5.08	118.88	113.80
1	gu	163	PHE	CA-C-N	5.08	124.98	119.85
1	gu	163	PHE	C-N-CA	5.08	124.98	119.85
2	he	136	LYS	N-CA-C	-5.08	106.77	113.12
1	ad	149	GLY	CA-C-N	5.08	125.29	120.31
1	ad	149	GLY	C-N-CA	5.08	125.29	120.31
1	bj	236	GLN	CA-C-N	5.08	130.60	122.93
1	bj	236	GLN	C-N-CA	5.08	130.60	122.93
1	br	121	THR	N-CA-C	5.08	116.86	110.91
1	ci	209	ASP	CA-CB-CG	5.08	117.68	112.60
1	co	269	ALA	N-CA-C	5.08	117.37	111.02
1	ei	93	PRO	N-CA-CB	-5.08	99.44	102.79
1	ej	121	THR	N-CA-C	5.08	116.86	110.91
1	et	143	ALA	N-CA-C	5.08	116.90	111.36
1	ey	119	SER	CA-C-N	5.08	125.09	120.21
1	ey	119	SER	C-N-CA	5.08	125.09	120.21
1	fn	245	ASN	CA-C-N	5.08	124.98	119.85
1	fn	245	ASN	C-N-CA	5.08	124.98	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fv	344	ARG	N-CA-C	-5.08	101.57	109.24
1	gj	94	ALA	N-CA-C	5.08	116.67	108.08
1	gp	151	ASP	CA-CB-CG	5.08	117.68	112.60
1	gq	115	GLN	CA-C-N	5.08	125.01	119.78
1	gq	115	GLN	C-N-CA	5.08	125.01	119.78
1	gy	236	GLN	CA-C-N	5.08	129.95	122.63
1	gy	236	GLN	C-N-CA	5.08	129.95	122.63
1	hb	209	ASP	CA-CB-CG	5.08	117.68	112.60
3	in	74	ASP	CA-CB-CG	5.08	117.68	112.60
3	nl	49	PHE	CA-C-N	5.08	125.53	120.14
3	nl	49	PHE	C-N-CA	5.08	125.53	120.14
1	bs	68	ILE	CA-C-N	5.08	125.48	119.94
1	bs	68	ILE	C-N-CA	5.08	125.48	119.94
1	fh	88	VAL	N-CA-C	5.08	115.17	107.75
1	fy	256	LYS	N-CA-C	5.08	116.79	109.07
1	fz	451	ALA	CA-C-N	5.08	124.99	119.76
1	fz	451	ALA	C-N-CA	5.08	124.99	119.76
3	lq	46	TYR	N-CA-C	5.08	116.71	109.14
3	no	32	PHE	CA-C-N	5.08	124.74	119.56
3	no	32	PHE	C-N-CA	5.08	124.74	119.56
1	bp	266	LEU	N-CA-C	5.08	117.10	109.23
1	bq	199	ASP	CA-CB-CG	-5.08	107.52	112.60
1	ca	486	GLU	CA-C-N	5.08	131.24	121.54
1	ca	486	GLU	C-N-CA	5.08	131.24	121.54
1	cl	245	ASN	CA-C-N	5.08	125.06	120.03
1	cl	245	ASN	C-N-CA	5.08	125.06	120.03
1	cx	163	PHE	CA-C-N	5.08	124.98	119.85
1	cx	163	PHE	C-N-CA	5.08	124.98	119.85
1	ds	249	GLU	N-CA-C	5.08	117.13	109.41
1	en	163	PHE	CA-C-N	5.08	124.98	119.85
1	en	163	PHE	C-N-CA	5.08	124.98	119.85
1	fj	184	GLU	N-CA-C	-5.08	102.64	109.95
1	fk	324	THR	CA-C-N	5.08	125.36	119.47
1	fk	324	THR	C-N-CA	5.08	125.36	119.47
1	ft	256	LYS	N-CA-C	5.08	116.79	109.07
1	gv	186	GLY	N-CA-C	5.08	123.14	112.17
1	cb	463	ASP	CA-C-N	5.08	124.74	119.56
1	cb	463	ASP	C-N-CA	5.08	124.74	119.56
1	cv	71	ASP	CA-CB-CG	5.08	117.68	112.60
1	ew	113	GLY	N-CA-C	-5.08	104.68	112.85
1	ga	250	MET	N-CA-C	5.08	116.53	108.96
1	hc	451	ALA	CA-C-N	5.08	124.99	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	hc	451	ALA	C-N-CA	5.08	124.99	119.76
1	ad	425	ILE	N-CA-C	5.08	115.62	108.36
1	bp	265	GLN	N-CA-C	5.08	116.78	108.76
1	ca	402	THR	CA-C-N	5.08	126.53	120.13
1	ca	402	THR	C-N-CA	5.08	126.53	120.13
1	fy	324	THR	CA-C-N	5.08	125.36	119.47
1	fy	324	THR	C-N-CA	5.08	125.36	119.47
1	gj	455	ALA	N-CA-C	5.08	117.46	109.39
2	hn	219	ILE	CB-CA-C	-5.08	105.47	111.97
3	ko	32	PHE	CA-C-N	5.08	124.74	119.56
3	ko	32	PHE	C-N-CA	5.08	124.74	119.56
3	mx	44	ALA	N-CA-C	5.08	119.34	113.20
1	bf	103	ILE	CA-C-N	5.07	124.98	119.76
1	bf	103	ILE	C-N-CA	5.07	124.98	119.76
1	by	68	ILE	N-CA-C	-5.07	101.27	108.58
1	dw	266	LEU	N-CA-C	5.07	116.90	109.24
1	dx	403	GLY	N-CA-C	5.07	118.82	112.73
1	gg	263	SER	N-CA-C	5.07	117.97	110.46
1	gh	500	MET	CA-C-N	5.07	124.97	119.85
1	gh	500	MET	C-N-CA	5.07	124.97	119.85
2	hh	145	SER	N-CA-C	-5.07	103.45	110.35
1	ca	294	LEU	CB-CA-C	-5.07	102.92	110.88
1	cf	150	PRO	N-CA-C	-5.07	103.14	111.21
1	gs	236	GLN	CA-C-N	5.07	129.93	122.63
1	gs	236	GLN	C-N-CA	5.07	129.93	122.63
3	nn	49	PHE	CA-C-N	5.07	125.28	120.31
3	nn	49	PHE	C-N-CA	5.07	125.28	120.31
1	bj	151	ASP	CA-CB-CG	5.07	117.67	112.60
1	bu	256	LYS	N-CA-C	5.07	116.78	109.07
1	cm	402	THR	CA-C-N	5.07	126.52	120.13
1	cm	402	THR	C-N-CA	5.07	126.52	120.13
1	di	454	VAL	CA-C-N	-5.07	113.65	122.37
1	di	454	VAL	C-N-CA	-5.07	113.65	122.37
1	dq	163	PHE	CA-C-N	5.07	124.97	119.85
1	dq	163	PHE	C-N-CA	5.07	124.97	119.85
1	dw	113	GLY	N-CA-C	-5.07	105.82	112.82
1	dz	93	PRO	N-CA-CB	-5.07	99.44	102.79
1	dz	120	PRO	N-CA-C	-5.07	104.12	111.22
1	ej	344	ARG	CA-C-N	5.07	131.22	121.54
1	ej	344	ARG	C-N-CA	5.07	131.22	121.54
1	et	209	ASP	CA-CB-CG	5.07	117.67	112.60
1	fe	87	ALA	CA-C-N	-5.07	116.50	123.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	fe	87	ALA	C-N-CA	-5.07	116.50	123.14
1	fz	68	ILE	CA-C-N	5.07	125.47	119.94
1	fz	68	ILE	C-N-CA	5.07	125.47	119.94
1	gl	263	SER	N-CA-C	5.07	117.59	110.14
3	jl	38	VAL	N-CA-C	5.07	115.34	107.78
3	jp	38	VAL	N-CA-C	5.07	115.42	108.12
3	lc	22	LYS	N-CA-C	5.07	116.55	108.79
3	mv	44	ALA	N-CA-C	5.07	119.33	113.20
1	ce	502	SER	N-CA-C	5.07	115.03	107.88
1	cz	199	ASP	CA-CB-CG	-5.07	107.53	112.60
1	ej	222	VAL	N-CA-C	5.07	117.31	108.95
1	fo	71	ASP	CA-CB-CG	5.07	117.67	112.60
1	hd	119	SER	N-CA-C	-5.07	103.66	108.22
2	hf	151	SER	CA-C-N	5.07	131.22	121.54
2	hf	151	SER	C-N-CA	5.07	131.22	121.54
1	cd	269	ALA	N-CA-C	5.07	118.62	111.52
1	fm	483	PRO	N-CA-C	-5.07	103.15	111.21
1	ge	324	THR	N-CA-C	-5.07	102.05	109.50
2	hh	302	ALA	CA-C-N	5.07	127.03	120.44
2	hh	302	ALA	C-N-CA	5.07	127.03	120.44
2	hi	267	TYR	CB-CA-C	5.07	118.70	109.83
3	la	72	ASN	CA-CB-CG	5.07	117.67	112.60
1	ah	491	ALA	CA-C-N	5.07	125.51	120.14
1	ah	491	ALA	C-N-CA	5.07	125.51	120.14
1	bd	121	THR	N-CA-C	5.07	118.12	111.28
1	bk	329	ALA	N-CA-C	5.07	117.35	111.02
1	de	121	THR	CB-CA-C	-5.07	102.98	112.30
1	dm	209	ASP	CA-CB-CG	5.07	117.67	112.60
1	eg	115	GLN	CA-C-N	5.07	125.00	119.78
1	eg	115	GLN	C-N-CA	5.07	125.00	119.78
1	ff	93	PRO	N-CA-CB	-5.07	97.93	103.25
1	gd	71	ASP	CA-CB-CG	5.07	117.67	112.60
1	hc	402	THR	CA-C-N	5.07	126.47	120.14
1	hc	402	THR	C-N-CA	5.07	126.47	120.14
1	hc	484	PHE	CA-CB-CG	5.07	118.86	113.80
2	hi	302	ALA	CA-C-N	5.07	127.03	120.44
2	hi	302	ALA	C-N-CA	5.07	127.03	120.44
3	iy	49	PHE	CA-C-N	5.07	125.51	120.14
3	iy	49	PHE	C-N-CA	5.07	125.51	120.14
1	bp	426	ASP	CA-CB-CG	-5.06	107.54	112.60
1	bt	393	ILE	N-CA-C	5.06	111.63	106.21
1	dx	199	ASP	CA-CB-CG	-5.06	107.54	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ek	115	GLN	CB-CA-C	-5.06	106.59	111.00
1	fn	110	ASP	CA-CB-CG	5.06	117.66	112.60
3	ji	44	ALA	N-CA-C	5.06	119.33	113.20
1	ag	199	ASP	CA-CB-CG	-5.06	107.54	112.60
1	cc	187	THR	N-CA-C	5.06	117.64	110.10
1	ck	232	ILE	N-CA-C	-5.06	106.86	111.67
1	cm	291	SER	CA-C-N	5.06	125.56	119.94
1	cm	291	SER	C-N-CA	5.06	125.56	119.94
1	cu	451	ALA	CA-C-N	5.06	125.00	119.78
1	cu	451	ALA	C-N-CA	5.06	125.00	119.78
1	ey	130	VAL	N-CA-C	5.06	115.20	108.11
1	fo	209	ASP	CA-CB-CG	5.06	117.66	112.60
1	fs	287	ASP	N-CA-C	-5.06	107.17	113.55
2	hk	316	THR	CB-CA-C	-5.06	103.71	111.66
3	jb	46	TYR	N-CA-C	5.06	115.73	108.74
1	an	151	ASP	CA-CB-CG	5.06	117.66	112.60
1	co	136	VAL	N-CA-CB	-5.06	107.59	112.65
1	cx	93	PRO	N-CA-C	5.06	122.90	112.47
1	dh	269	ALA	N-CA-C	5.06	117.35	111.02
1	ds	227	GLY	N-CA-C	-5.06	104.46	112.66
1	ed	263	SER	N-CA-C	5.06	117.58	110.14
1	ef	150	PRO	N-CA-C	-5.06	103.33	111.38
1	fu	209	ASP	CA-CB-CG	5.06	117.66	112.60
1	gp	232	ILE	N-CA-C	-5.06	106.86	111.67
2	hi	314	CYS	N-CA-C	5.06	116.95	107.99
3	kp	72	ASN	CA-CB-CG	5.06	117.66	112.60
3	kv	72	ASN	CA-CB-CG	5.06	117.66	112.60
1	ag	209	ASP	CA-CB-CG	5.06	117.66	112.60
1	an	490	GLN	N-CA-C	-5.06	106.27	112.90
1	ap	287	ASP	N-CA-C	-5.06	105.23	111.40
1	aq	110	ASP	CA-CB-CG	5.06	117.66	112.60
1	at	199	ASP	CA-CB-CG	-5.06	107.54	112.60
1	bx	451	ALA	CA-C-N	5.06	124.99	119.78
1	bx	451	ALA	C-N-CA	5.06	124.99	119.78
1	cc	451	ALA	CA-C-N	5.06	124.99	119.78
1	cc	451	ALA	C-N-CA	5.06	124.99	119.78
1	cy	454	VAL	CA-C-N	-5.06	113.67	122.37
1	cy	454	VAL	C-N-CA	-5.06	113.67	122.37
1	df	484	PHE	CA-CB-CG	5.06	118.86	113.80
1	dw	120	PRO	N-CA-C	-5.06	104.14	111.22
1	ea	402	THR	CA-C-N	5.06	126.50	120.13
1	ea	402	THR	C-N-CA	5.06	126.50	120.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	ea	500	MET	CA-C-N	5.06	125.06	119.90
1	ea	500	MET	C-N-CA	5.06	125.06	119.90
1	fd	454	VAL	CA-C-N	-5.06	114.53	122.73
1	fd	454	VAL	C-N-CA	-5.06	114.53	122.73
1	fq	221	LEU	N-CA-CB	-5.06	103.01	110.90
1	gr	480	GLY	N-CA-C	5.06	118.85	110.55
1	gv	271	SER	N-CA-C	5.06	117.38	110.55
1	gx	480	GLY	CA-C-N	5.06	128.90	122.37
1	gx	480	GLY	C-N-CA	5.06	128.90	122.37
3	nh	32	PHE	CA-C-N	5.06	124.72	119.56
3	nh	32	PHE	C-N-CA	5.06	124.72	119.56
1	be	260	GLU	CB-CG-CD	5.06	121.20	112.60
1	bj	88	VAL	N-CA-C	5.06	115.13	107.75
1	ck	134	ASP	CA-C-N	5.06	124.72	119.56
1	ck	134	ASP	C-N-CA	5.06	124.72	119.56
1	cy	324	THR	CA-C-N	5.06	125.34	119.47
1	cy	324	THR	C-N-CA	5.06	125.34	119.47
1	dp	328	LYS	N-CA-C	5.06	119.43	113.16
1	fn	145	HIS	CA-C-N	5.06	124.72	119.56
1	fn	145	HIS	C-N-CA	5.06	124.72	119.56
1	fn	324	THR	CA-C-N	5.06	125.34	119.47
1	fn	324	THR	C-N-CA	5.06	125.34	119.47
1	gm	115	GLN	CA-C-N	5.06	124.99	119.78
1	gm	115	GLN	C-N-CA	5.06	124.99	119.78
1	gs	243	THR	N-CA-C	5.06	116.68	109.14
3	ir	49	PHE	CA-C-N	5.06	125.50	120.14
3	ir	49	PHE	C-N-CA	5.06	125.50	120.14
3	jg	46	TYR	N-CA-C	5.06	116.67	109.14
1	bx	78	ASN	N-CA-C	-5.06	100.03	110.80
1	dx	115	GLN	CA-C-N	5.06	124.99	119.78
1	dx	115	GLN	C-N-CA	5.06	124.99	119.78
1	el	271	SER	N-CA-C	5.06	117.76	110.28
3	ij	37	ASP	CA-CB-CG	5.06	117.66	112.60
3	ik	67	GLU	N-CA-C	-5.06	105.85	111.36
1	ah	454	VAL	CA-C-N	-5.05	114.54	122.73
1	ah	454	VAL	C-N-CA	-5.05	114.54	122.73
1	ce	480	GLY	N-CA-C	5.05	118.95	110.56
1	cr	328	LYS	N-CA-C	5.05	119.09	113.02
1	cx	93	PRO	N-CA-CB	-5.05	97.94	103.25
1	dd	406	THR	N-CA-C	-5.05	107.11	113.28
1	ef	328	LYS	N-CA-C	5.05	119.43	113.16
1	eu	112	CYS	CA-C-N	-5.05	117.09	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eu	112	CYS	C-N-CA	-5.05	117.09	122.30
1	go	454	VAL	CA-C-N	-5.05	113.68	122.37
1	go	454	VAL	C-N-CA	-5.05	113.68	122.37
1	gt	145	HIS	CA-C-N	5.05	124.72	119.56
1	gt	145	HIS	C-N-CA	5.05	124.72	119.56
3	jj	49	PHE	CA-C-N	5.05	125.50	120.14
3	jj	49	PHE	C-N-CA	5.05	125.50	120.14
3	jq	37	ASP	CA-CB-CG	5.05	117.65	112.60
3	nq	74	ASP	CA-CB-CG	5.05	117.66	112.60
3	of	38	VAL	N-CA-C	5.05	115.93	108.45
1	dm	75	ASN	CA-CB-CG	-5.05	107.55	112.60
1	ds	199	ASP	CA-CB-CG	-5.05	107.55	112.60
1	gd	87	ALA	N-CA-C	5.05	116.79	111.28
1	gj	324	THR	CA-C-N	5.05	125.33	119.47
1	gj	324	THR	C-N-CA	5.05	125.33	119.47
1	gs	285	ASP	CA-CB-CG	5.05	117.65	112.60
1	ac	198	ILE	N-CA-C	5.05	119.85	109.34
1	bm	463	ASP	CA-C-N	5.05	124.71	119.56
1	bm	463	ASP	C-N-CA	5.05	124.71	119.56
1	bp	243	THR	N-CA-C	5.05	116.49	108.96
1	br	119	SER	CA-C-N	5.05	125.03	120.03
1	br	119	SER	C-N-CA	5.05	125.03	120.03
1	bv	209	ASP	CA-CB-CG	5.05	117.65	112.60
1	cu	256	LYS	N-CA-C	5.05	116.75	109.07
1	cw	119	SER	CA-C-N	5.05	125.03	120.03
1	cw	119	SER	C-N-CA	5.05	125.03	120.03
1	en	119	SER	CA-C-N	5.05	125.03	120.03
1	en	119	SER	C-N-CA	5.05	125.03	120.03
1	fe	281	VAL	N-CA-C	5.05	116.47	111.67
1	fm	154	PHE	CA-CB-CG	5.05	118.85	113.80
1	gi	249	GLU	N-CA-C	5.05	115.71	108.74
1	hb	328	LYS	N-CA-C	5.05	119.13	112.92
3	jy	44	ALA	N-CA-C	5.05	119.42	113.16
3	nh	72	ASN	CA-CB-CG	5.05	117.65	112.60
1	ch	281	VAL	N-CA-C	5.05	116.47	111.67
1	dn	121	THR	CA-C-O	-5.05	116.41	122.27
1	dq	484	PHE	CA-CB-CG	5.05	118.85	113.80
1	ed	209	ASP	CA-CB-CG	5.05	117.65	112.60
1	gg	402	THR	CA-C-N	5.05	126.45	120.14
1	gg	402	THR	C-N-CA	5.05	126.45	120.14
1	gm	134	ASP	CA-C-N	5.05	124.66	119.56
1	gm	134	ASP	C-N-CA	5.05	124.66	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	hb	425	ILE	N-CA-C	5.05	115.58	108.36
3	md	49	PHE	CA-C-N	5.05	125.49	120.14
3	md	49	PHE	C-N-CA	5.05	125.49	120.14
1	al	209	ASP	CA-CB-CG	5.05	117.65	112.60
1	ao	86	GLY	CA-C-N	5.05	127.55	120.28
1	ao	86	GLY	C-N-CA	5.05	127.55	120.28
1	ex	263	SER	N-CA-C	5.05	116.66	109.14
1	gn	90	GLN	CA-C-N	5.05	127.02	120.56
1	gn	90	GLN	C-N-CA	5.05	127.02	120.56
1	ai	68	ILE	N-CA-C	5.05	115.18	108.11
1	bh	209	ASP	CA-CB-CG	5.05	117.65	112.60
1	cz	324	THR	CA-C-N	5.05	125.32	119.47
1	cz	324	THR	C-N-CA	5.05	125.32	119.47
1	fw	245	ASN	CA-C-N	5.05	124.95	119.85
1	fw	245	ASN	C-N-CA	5.05	124.95	119.85
1	gr	163	PHE	CA-C-N	5.05	124.95	119.85
1	gr	163	PHE	C-N-CA	5.05	124.95	119.85
2	hf	363	VAL	N-CA-C	5.05	116.22	111.48
2	ho	320	LEU	N-CA-C	5.05	120.30	114.04
3	lm	38	VAL	N-CA-C	5.05	115.54	108.17
3	of	30	VAL	N-CA-CB	-5.05	105.08	111.64
1	am	209	ASP	CA-CB-CG	5.04	117.64	112.60
1	ff	186	GLY	N-CA-C	5.04	120.40	111.02
1	fg	402	THR	CA-C-N	5.04	126.45	120.14
1	fg	402	THR	C-N-CA	5.04	126.45	120.14
3	kx	67	GLU	N-CA-C	-5.04	105.86	111.36
1	at	149	GLY	CA-C-N	5.04	125.02	120.03
1	at	149	GLY	C-N-CA	5.04	125.02	120.03
1	aw	201	GLY	N-CA-C	-5.04	106.63	113.24
1	bw	163	PHE	CA-C-N	5.04	124.94	119.85
1	bw	163	PHE	C-N-CA	5.04	124.94	119.85
1	by	209	ASP	CA-CB-CG	5.04	117.64	112.60
1	cr	133	LYS	CB-CA-C	-5.04	103.54	111.51
1	do	265	GLN	N-CA-C	5.04	116.73	108.76
1	fa	324	THR	CA-C-N	5.04	125.32	119.47
1	fa	324	THR	C-N-CA	5.04	125.32	119.47
3	nt	49	PHE	CA-C-N	5.04	125.49	120.14
3	nt	49	PHE	C-N-CA	5.04	125.49	120.14
1	al	95	VAL	N-CA-C	5.04	115.29	107.78
1	aw	451	ALA	CA-C-N	5.04	124.97	119.78
1	aw	451	ALA	C-N-CA	5.04	124.97	119.78
1	bz	403	GLY	N-CA-C	5.04	119.98	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	dr	119	SER	N-CA-C	-5.04	103.68	108.22
1	ft	327	SER	N-CA-C	5.04	117.31	110.35
1	gb	127	LEU	N-CA-C	5.04	116.74	108.52
1	gh	115	GLN	CA-C-N	5.04	124.97	119.78
1	gh	115	GLN	C-N-CA	5.04	124.97	119.78
1	gi	209	ASP	CA-CB-CG	5.04	117.64	112.60
3	kh	49	PHE	CA-C-N	5.04	125.48	120.14
3	kh	49	PHE	C-N-CA	5.04	125.48	120.14
1	aq	258	VAL	N-CA-C	5.04	115.38	108.12
1	bh	163	PHE	CA-C-N	5.04	124.94	119.85
1	bh	163	PHE	C-N-CA	5.04	124.94	119.85
1	do	446	ALA	N-CA-C	5.04	119.50	112.90
1	ed	236	GLN	CA-C-N	5.04	131.16	121.54
1	ed	236	GLN	C-N-CA	5.04	131.16	121.54
1	fv	358	ASP	CA-CB-CG	5.04	117.64	112.60
3	jz	49	PHE	CA-C-N	5.04	125.48	120.14
3	jz	49	PHE	C-N-CA	5.04	125.48	120.14
3	lv	49	PHE	CA-C-N	5.04	125.48	120.14
3	lv	49	PHE	C-N-CA	5.04	125.48	120.14
1	ak	285	ASP	N-CA-C	5.04	117.89	111.69
1	bd	87	ALA	CA-C-N	-5.04	116.40	123.10
1	bd	87	ALA	C-N-CA	-5.04	116.40	123.10
1	bw	395	TYR	N-CA-C	5.04	116.46	111.07
1	dg	265	GLN	N-CA-C	5.04	116.72	108.76
1	dv	149	GLY	CA-C-N	5.04	124.94	119.85
1	dv	149	GLY	C-N-CA	5.04	124.94	119.85
1	gj	123	GLN	CA-C-N	5.04	130.04	122.58
1	gj	123	GLN	C-N-CA	5.04	130.04	122.58
1	gs	281	VAL	N-CA-C	5.04	116.46	111.67
1	ba	426	ASP	CA-CB-CG	-5.04	107.56	112.60
1	bg	402	THR	CA-C-N	5.04	126.44	120.14
1	bg	402	THR	C-N-CA	5.04	126.44	120.14
1	bl	87	ALA	CA-C-N	-5.04	116.54	123.14
1	bl	87	ALA	C-N-CA	-5.04	116.54	123.14
1	dr	193	SER	N-CA-C	-5.04	107.80	114.04
1	ec	328	LYS	N-CA-C	5.04	119.52	113.17
1	em	87	ALA	N-CA-C	5.04	116.77	111.28
1	en	265	GLN	N-CA-C	5.04	116.18	108.52
1	ab	143	ALA	N-CA-C	5.04	116.85	111.36
1	aj	328	LYS	N-CA-C	5.04	119.11	112.92
1	bg	285	ASP	CA-C-N	5.04	131.16	121.54
1	bg	285	ASP	C-N-CA	5.04	131.16	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	bw	281	VAL	N-CA-C	5.04	116.45	111.67
1	cy	71	ASP	CA-CB-CG	5.04	117.64	112.60
1	dx	256	LYS	N-CA-C	5.04	117.78	109.72
1	el	483	PRO	CA-N-CD	-5.04	104.95	112.00
1	eo	269	ALA	N-CA-C	5.04	117.31	111.02
1	eq	491	ALA	CA-C-N	5.04	125.48	120.14
1	eq	491	ALA	C-N-CA	5.04	125.48	120.14
1	et	483	PRO	N-CA-C	-5.04	103.19	111.15
1	ga	409	THR	N-CA-C	-5.04	105.50	111.69
1	gm	265	GLN	N-CA-C	5.04	116.72	108.76
3	jg	67	GLU	N-CA-C	-5.04	105.87	111.36
1	af	115	GLN	CB-CA-C	-5.03	106.62	111.00
1	aj	145	HIS	CA-C-N	5.03	124.69	119.56
1	aj	145	HIS	C-N-CA	5.03	124.69	119.56
1	at	480	GLY	N-CA-C	5.03	118.03	110.18
1	bj	287	ASP	N-CA-C	-5.03	106.28	112.72
1	bl	425	ILE	N-CA-C	5.03	115.56	108.36
1	co	451	ALA	CA-C-N	5.03	124.97	119.78
1	co	451	ALA	C-N-CA	5.03	124.97	119.78
1	dk	486	GLU	CA-C-N	5.03	131.15	121.54
1	dk	486	GLU	C-N-CA	5.03	131.15	121.54
1	el	145	HIS	CA-C-N	5.03	124.69	119.56
1	el	145	HIS	C-N-CA	5.03	124.69	119.56
1	gh	182	PHE	CA-CB-CG	5.03	118.83	113.80
2	hh	40	VAL	N-CA-C	5.03	115.10	107.80
3	jh	38	VAL	N-CA-C	5.03	115.52	108.17
3	nk	49	PHE	CA-C-N	5.03	125.47	120.14
3	nk	49	PHE	C-N-CA	5.03	125.47	120.14
3	oe	10	ILE	N-CA-C	5.03	115.10	107.75
1	cv	269	ALA	N-CA-C	5.03	117.31	111.02
1	du	245	ASN	N-CA-C	5.03	117.84	109.79
2	hm	422	LYS	N-CA-C	5.03	117.59	110.50
3	ij	25	GLY	N-CA-C	-5.03	105.33	112.37
3	js	46	TYR	N-CA-C	5.03	116.64	109.14
1	ab	184	GLU	CA-C-O	-5.03	115.81	121.40
1	bg	252	PHE	N-CA-C	5.03	116.45	108.96
1	bw	199	ASP	CA-CB-CG	-5.03	107.57	112.60
1	dt	265	GLN	N-CA-C	5.03	116.70	108.55
1	eh	232	ILE	N-CA-C	-5.03	106.89	111.67
1	eu	256	LYS	N-CA-C	5.03	116.72	109.07
1	gm	281	VAL	N-CA-C	5.03	116.45	111.67
1	gr	425	ILE	N-CA-C	5.03	115.33	107.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	ky	41	ILE	N-CA-C	5.03	115.09	107.80
1	ac	163	PHE	CA-C-N	5.03	124.93	119.85
1	ac	163	PHE	C-N-CA	5.03	124.93	119.85
1	cb	253	ARG	N-CA-CB	-5.03	103.11	110.40
1	ac	509	LYS	N-CA-C	5.03	121.11	114.12
1	bj	149	GLY	CA-C-N	5.03	124.93	119.85
1	bj	149	GLY	C-N-CA	5.03	124.93	119.85
1	bo	402	THR	CA-C-N	5.03	126.42	120.14
1	bo	402	THR	C-N-CA	5.03	126.42	120.14
1	br	176	ASP	CA-CB-CG	5.03	117.63	112.60
1	cj	115	GLN	CA-C-N	5.03	124.96	119.78
1	cj	115	GLN	C-N-CA	5.03	124.96	119.78
1	dw	328	LYS	N-CA-C	5.03	119.10	112.92
1	dz	425	ILE	N-CA-C	5.03	115.33	107.99
1	eo	392	GLY	CA-C-N	-5.03	116.92	121.65
1	eo	392	GLY	C-N-CA	-5.03	116.92	121.65
1	gd	199	ASP	CA-CB-CG	-5.03	107.57	112.60
2	hk	303	TYR	N-CA-C	-5.03	105.69	111.07
3	mj	67	GLU	N-CA-C	-5.03	105.88	111.36
1	ap	193	SER	N-CA-C	-5.03	107.81	114.04
1	bv	115	GLN	CA-C-N	5.03	124.96	119.78
1	bv	115	GLN	C-N-CA	5.03	124.96	119.78
1	cd	184	GLU	CA-C-O	-5.03	115.82	121.40
1	fh	93	PRO	N-CA-C	5.03	119.27	112.48
1	fq	74	TYR	CA-C-N	5.03	129.45	122.77
1	fq	74	TYR	C-N-CA	5.03	129.45	122.77
1	fy	113	GLY	N-CA-C	-5.03	104.76	112.85
1	ga	145	HIS	CA-C-N	5.03	124.69	119.56
1	ga	145	HIS	C-N-CA	5.03	124.69	119.56
1	gt	245	ASN	CA-C-N	5.03	125.00	120.03
1	gt	245	ASN	C-N-CA	5.03	125.00	120.03
1	at	451	ALA	CA-C-N	5.02	124.95	119.78
1	at	451	ALA	C-N-CA	5.02	124.95	119.78
1	bh	222	VAL	N-CA-C	5.02	117.24	108.95
1	dn	232	ILE	N-CA-C	-5.02	106.90	111.67
1	fl	163	PHE	CA-C-N	5.02	124.92	119.85
1	fl	163	PHE	C-N-CA	5.02	124.92	119.85
1	fx	209	ASP	CA-CB-CG	5.02	117.62	112.60
1	ha	209	ASP	CA-CB-CG	5.02	117.62	112.60
2	hk	21	ARG	CA-C-N	5.02	125.00	120.03
2	hk	21	ARG	C-N-CA	5.02	125.00	120.03
2	hm	145	SER	N-CA-C	-5.02	103.52	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	ia	49	PHE	CA-C-N	5.02	125.47	120.14
3	ia	49	PHE	C-N-CA	5.02	125.47	120.14
3	lp	25	GLY	N-CA-C	-5.02	105.66	112.14
1	bg	209	ASP	CA-CB-CG	5.02	117.62	112.60
1	bo	329	ALA	N-CA-C	5.02	117.30	111.02
1	bw	115	GLN	CA-C-N	5.02	124.95	119.78
1	bw	115	GLN	C-N-CA	5.02	124.95	119.78
1	ce	480	GLY	CA-C-N	5.02	128.59	121.66
1	ce	480	GLY	C-N-CA	5.02	128.59	121.66
1	cr	243	THR	N-CA-C	5.02	116.44	108.96
1	dk	121	THR	CB-CA-C	-5.02	103.06	112.30
1	ea	75	ASN	CA-CB-CG	-5.02	107.58	112.60
1	gj	222	VAL	N-CA-C	5.02	115.14	108.11
1	gk	463	ASP	CA-C-N	5.02	124.68	119.56
1	gk	463	ASP	C-N-CA	5.02	124.68	119.56
3	ji	10	ILE	N-CA-C	5.02	115.14	108.11
3	ju	46	TYR	N-CA-C	5.02	116.62	109.14
3	oa	32	PHE	CA-C-N	5.02	124.68	119.56
3	oa	32	PHE	C-N-CA	5.02	124.68	119.56
1	ag	110	ASP	CA-CB-CG	5.02	117.62	112.60
1	dc	480	GLY	N-CA-C	5.02	118.89	110.56
1	dt	149	GLY	CA-C-N	5.02	125.23	120.31
1	dt	149	GLY	C-N-CA	5.02	125.23	120.31
1	et	198	ILE	CB-CA-C	-5.02	107.60	113.22
1	fo	222	VAL	N-CA-C	5.02	115.14	108.11
1	fu	506	SER	CA-C-N	-5.02	114.51	121.99
1	fu	506	SER	C-N-CA	-5.02	114.51	121.99
1	gx	474	LYS	N-CA-C	5.02	117.62	109.24
1	ad	407	ASP	CA-CB-CG	5.02	117.62	112.60
1	ad	426	ASP	CA-CB-CG	-5.02	107.58	112.60
1	af	509	LYS	N-CA-C	5.02	120.78	114.31
1	aj	88	VAL	N-CA-C	5.02	115.08	107.75
1	az	500	MET	CA-C-N	5.02	126.12	119.84
1	az	500	MET	C-N-CA	5.02	126.12	119.84
1	ei	113	GLY	N-CA-C	-5.02	104.96	112.89
1	eo	344	ARG	CA-C-N	5.02	131.13	121.54
1	eo	344	ARG	C-N-CA	5.02	131.13	121.54
1	fc	121	THR	CB-CA-C	-5.02	103.49	112.27
1	ga	265	GLN	N-CA-C	5.02	116.68	108.55
1	gl	266	LEU	N-CA-C	5.02	116.82	109.24
2	hj	302	ALA	CA-C-N	5.02	126.97	120.44
2	hj	302	ALA	C-N-CA	5.02	126.97	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hj	343	ALA	CA-C-N	5.02	124.95	119.78
2	hj	343	ALA	C-N-CA	5.02	124.95	119.78
1	ec	285	ASP	CA-C-N	5.02	131.12	121.54
1	ec	285	ASP	C-N-CA	5.02	131.12	121.54
1	gd	269	ALA	N-CA-C	5.02	117.29	111.02
1	ae	259	ILE	N-CA-C	5.02	115.07	107.80
1	ag	186	GLY	N-CA-C	5.02	120.35	111.02
1	bi	412	VAL	N-CA-C	-5.02	107.50	111.81
1	es	426	ASP	CA-CB-CG	-5.02	107.58	112.60
1	gi	186	GLY	N-CA-C	5.02	117.50	110.38
1	gm	256	LYS	N-CA-C	5.02	116.69	109.07
1	go	480	GLY	N-CA-C	5.02	118.89	110.56
2	hi	270	THR	N-CA-C	5.02	119.16	113.19
1	ab	163	PHE	CA-C-N	5.01	124.92	119.85
1	ab	163	PHE	C-N-CA	5.01	124.92	119.85
1	cb	329	ALA	N-CA-C	5.01	118.16	111.24
1	cw	281	VAL	N-CA-C	5.01	116.43	111.67
1	dc	324	THR	CA-C-N	5.01	125.29	119.47
1	dc	324	THR	C-N-CA	5.01	125.29	119.47
1	es	209	ASP	CA-CB-CG	5.01	117.61	112.60
1	fs	87	ALA	CA-C-N	-5.01	116.57	123.14
1	fs	87	ALA	C-N-CA	-5.01	116.57	123.14
1	gb	121	THR	CB-CA-C	-5.01	104.19	112.06
1	ae	256	LYS	N-CA-C	5.01	116.69	109.07
1	bp	163	PHE	CA-C-N	5.01	124.91	119.85
1	bp	163	PHE	C-N-CA	5.01	124.91	119.85
1	bp	324	THR	CA-C-N	5.01	125.28	119.47
1	bp	324	THR	C-N-CA	5.01	125.28	119.47
1	dh	358	ASP	CA-CB-CG	5.01	117.61	112.60
1	dv	474	LYS	N-CA-C	5.01	117.61	109.24
1	fb	491	ALA	CA-C-N	5.01	125.45	120.14
1	fb	491	ALA	C-N-CA	5.01	125.45	120.14
1	gv	490	GLN	N-CA-C	-5.01	107.01	113.23
3	mv	10	ILE	N-CA-C	5.01	115.07	107.75
3	ne	37	ASP	CA-CB-CG	5.01	117.61	112.60
1	au	486	GLU	CA-C-N	5.01	131.11	121.54
1	au	486	GLU	C-N-CA	5.01	131.11	121.54
1	ci	409	THR	N-CA-C	-5.01	107.02	113.23
1	cn	209	ASP	CA-CB-CG	5.01	117.61	112.60
1	cy	232	ILE	N-CA-C	-5.01	106.79	111.45
1	db	71	ASP	CA-CB-CG	5.01	117.61	112.60
1	dv	500	MET	N-CA-C	-5.01	103.75	110.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	eg	134	ASP	CA-C-N	5.01	125.28	119.47
1	eg	134	ASP	C-N-CA	5.01	125.28	119.47
1	ep	134	ASP	CA-C-N	5.01	124.67	119.56
1	ep	134	ASP	C-N-CA	5.01	124.67	119.56
2	hk	291	LYS	CA-C-N	5.01	126.11	119.84
2	hk	291	LYS	C-N-CA	5.01	126.11	119.84
3	in	67	GLU	N-CA-C	-5.01	105.90	111.36
1	bj	222	VAL	N-CA-C	5.01	117.22	108.95
1	bs	491	ALA	CA-C-N	5.01	125.45	120.14
1	bs	491	ALA	C-N-CA	5.01	125.45	120.14
1	bw	328	LYS	N-CA-C	5.01	119.34	112.88
1	ed	258	VAL	N-CA-C	5.01	117.03	108.86
1	fd	285	ASP	CA-C-N	5.01	131.11	121.54
1	fd	285	ASP	C-N-CA	5.01	131.11	121.54
1	fj	130	VAL	N-CA-C	5.01	115.12	108.11
3	lt	25	GLY	N-CA-C	-5.01	105.68	112.14
3	kt	15	GLN	N-CA-C	5.01	117.57	109.06
1	bd	127	LEU	N-CA-C	5.01	116.57	108.41
1	cy	87	ALA	N-CA-C	5.01	116.74	111.28
1	fr	328	LYS	N-CA-C	5.01	119.37	113.16
3	kk	37	ASP	CA-CB-CG	5.01	117.61	112.60
1	bi	269	ALA	N-CA-C	5.00	117.28	111.02
1	bk	222	VAL	N-CA-C	5.00	115.12	108.11
1	ci	92	GLY	CA-C-N	5.00	126.10	119.84
1	ci	92	GLY	C-N-CA	5.00	126.10	119.84
1	dk	416	VAL	N-CA-C	5.00	115.18	107.77
1	ez	491	ALA	CA-C-N	5.00	125.44	120.14
1	ez	491	ALA	C-N-CA	5.00	125.44	120.14
1	ap	263	SER	N-CA-C	5.00	117.86	110.46
1	ba	486	GLU	N-CA-C	-5.00	105.83	111.28
1	bv	366	ARG	CB-CA-C	-5.00	103.03	110.88
1	dj	149	GLY	CA-C-N	5.00	124.93	119.78
1	dj	149	GLY	C-N-CA	5.00	124.93	119.78
1	dp	480	GLY	CA-C-N	5.00	128.57	121.66
1	dp	480	GLY	C-N-CA	5.00	128.57	121.66
1	fe	480	GLY	N-CA-C	5.00	118.87	110.56
1	fl	71	ASP	CA-CB-CG	5.00	117.60	112.60
1	fo	451	ALA	CA-C-N	5.00	124.93	119.78
1	fo	451	ALA	C-N-CA	5.00	124.93	119.78
1	fv	71	ASP	CA-CB-CG	5.00	117.60	112.60
1	gy	193	SER	N-CA-C	-5.00	107.73	113.88
1	hd	121	THR	N-CA-C	5.00	118.30	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	hj	232	ASP	N-CA-C	-5.00	103.98	110.19
3	ke	49	PHE	CA-C-N	5.00	125.21	120.31
3	ke	49	PHE	C-N-CA	5.00	125.21	120.31
3	nm	37	ASP	CA-CB-CG	5.00	117.60	112.60
1	an	150	PRO	N-CA-C	-5.00	103.91	111.41
1	av	480	GLY	N-CA-C	5.00	117.98	110.18
1	bk	145	HIS	CA-C-N	5.00	124.66	119.56
1	bk	145	HIS	C-N-CA	5.00	124.66	119.56
1	ck	324	THR	CA-C-N	5.00	125.27	119.47
1	ck	324	THR	C-N-CA	5.00	125.27	119.47
1	cm	324	THR	CA-C-N	5.00	125.27	119.47
1	cm	324	THR	C-N-CA	5.00	125.27	119.47
1	ct	252	PHE	N-CA-C	5.00	116.41	108.96
1	cv	115	GLN	CA-C-N	5.00	124.93	119.78
1	cv	115	GLN	C-N-CA	5.00	124.93	119.78
1	fc	209	ASP	CA-CB-CG	5.00	117.60	112.60
1	fr	258	VAL	N-CA-C	5.00	115.91	108.46
1	ga	87	ALA	N-CA-C	5.00	116.73	111.28
1	ga	324	THR	CA-C-N	5.00	125.27	119.47
1	ga	324	THR	C-N-CA	5.00	125.27	119.47
1	gp	425	ILE	N-CA-C	5.00	115.51	108.36
2	ho	151	SER	CA-C-N	5.00	131.09	121.54
2	ho	151	SER	C-N-CA	5.00	131.09	121.54
3	jv	32	PHE	CA-C-N	5.00	124.66	119.56
3	jv	32	PHE	C-N-CA	5.00	124.66	119.56
3	lw	32	PHE	CA-C-N	5.00	124.66	119.56
3	lw	32	PHE	C-N-CA	5.00	124.66	119.56
3	ns	32	PHE	CA-C-N	5.00	124.66	119.56
3	ns	32	PHE	C-N-CA	5.00	124.66	119.56

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	aq	480	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	aa	3425	0	3371	9	0
1	ab	3425	0	3371	8	0
1	ac	3425	0	3371	8	0
1	ad	3425	0	3371	7	0
1	ae	3425	0	3371	14	0
1	af	3425	0	3371	13	0
1	ag	3425	0	3371	11	0
1	ah	3425	0	3371	10	0
1	ai	3425	0	3371	13	0
1	aj	3425	0	3371	8	0
1	ak	3425	0	3371	8	0
1	al	3425	0	3371	13	0
1	am	3425	0	3371	15	0
1	an	3425	0	3371	9	0
1	ao	3425	0	3371	13	0
1	ap	3425	0	3371	4	0
1	aq	3425	0	3371	16	0
1	ar	3425	0	3371	13	0
1	as	3425	0	3371	8	0
1	at	3425	0	3371	9	0
1	au	3425	0	3371	15	0
1	av	3425	0	3371	8	0
1	aw	3425	0	3371	17	0
1	ax	3425	0	3371	12	0
1	ay	3425	0	3371	16	0
1	az	3425	0	3371	12	0
1	ba	3425	0	3371	13	0
1	bb	3425	0	3371	8	0
1	bc	3425	0	3371	13	0
1	bd	3425	0	3371	11	0
1	be	3425	0	3371	12	0
1	bf	3425	0	3371	8	0
1	bg	3425	0	3371	11	0
1	bh	3425	0	3371	9	0
1	bi	3425	0	3371	12	0
1	bj	3425	0	3371	10	0
1	bk	3425	0	3371	5	0
1	bl	3425	0	3371	12	0
1	bm	3425	0	3371	9	0
1	bn	3425	0	3371	12	0
1	bo	3425	0	3371	14	0
1	bp	3425	0	3371	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	bq	3425	0	3371	6	0
1	br	3425	0	3371	10	0
1	bs	3425	0	3371	11	0
1	bt	3425	0	3371	9	0
1	bu	3425	0	3371	12	0
1	bv	3425	0	3371	6	0
1	bw	3425	0	3371	12	0
1	bx	3425	0	3371	12	0
1	by	3425	0	3371	11	0
1	bz	3425	0	3371	9	0
1	ca	3425	0	3371	16	0
1	cb	3425	0	3371	14	0
1	cc	3425	0	3371	8	0
1	cd	3425	0	3371	10	0
1	ce	3425	0	3371	13	0
1	cf	3425	0	3371	10	0
1	cg	3425	0	3371	12	0
1	ch	3425	0	3371	11	0
1	ci	3425	0	3371	6	0
1	cj	3425	0	3371	8	0
1	ck	3425	0	3371	8	0
1	cl	3425	0	3371	8	0
1	cm	3425	0	3371	8	0
1	cn	3425	0	3371	5	0
1	co	3425	0	3371	6	0
1	cp	3425	0	3371	12	0
1	cq	3425	0	3371	9	0
1	cr	3425	0	3371	11	0
1	cs	3425	0	3371	8	0
1	ct	3425	0	3371	9	0
1	cu	3425	0	3371	8	0
1	cv	3425	0	3371	7	0
1	cw	3425	0	3371	13	0
1	cx	3425	0	3371	10	0
1	cy	3425	0	3371	12	0
1	cz	3425	0	3371	8	0
1	da	3425	0	3371	10	0
1	db	3425	0	3371	12	0
1	dc	3425	0	3371	10	0
1	dd	3425	0	3371	7	0
1	de	3425	0	3371	13	0
1	df	3425	0	3371	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	dg	3425	0	3371	9	0
1	dh	3425	0	3371	14	0
1	di	3425	0	3371	7	0
1	dj	3425	0	3371	9	0
1	dk	3425	0	3371	5	0
1	dl	3425	0	3371	12	0
1	dm	3425	0	3371	6	0
1	dn	3425	0	3371	7	0
1	do	3425	0	3371	10	0
1	dp	3425	0	3371	8	0
1	dq	3425	0	3371	11	0
1	dr	3425	0	3371	7	0
1	ds	3425	0	3371	7	0
1	dt	3425	0	3371	9	0
1	du	3425	0	3371	15	0
1	dv	3425	0	3371	11	0
1	dw	3249	0	3209	14	0
1	dx	3425	0	3371	10	0
1	dy	3425	0	3371	10	0
1	dz	3425	0	3371	8	0
1	ea	3425	0	3371	10	0
1	eb	3425	0	3371	17	0
1	ec	3425	0	3371	15	0
1	ed	3425	0	3371	20	0
1	ee	3425	0	3371	15	0
1	ef	3425	0	3371	11	0
1	eg	3425	0	3371	11	0
1	eh	3425	0	3371	4	0
1	ei	3425	0	3371	8	0
1	ej	3425	0	3371	8	0
1	ek	3425	0	3371	13	0
1	el	3425	0	3371	8	0
1	em	3425	0	3371	10	0
1	en	3425	0	3371	11	0
1	eo	3425	0	3371	15	0
1	ep	3425	0	3371	14	0
1	eq	3425	0	3371	6	0
1	er	3425	0	3371	12	0
1	es	3425	0	3371	11	0
1	et	3425	0	3371	9	0
1	eu	3425	0	3371	9	0
1	ev	3425	0	3371	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	ew	3425	0	3371	8	0
1	ex	3425	0	3371	8	0
1	ey	3425	0	3371	8	0
1	ez	3425	0	3371	11	0
1	fa	3425	0	3371	10	0
1	fb	3425	0	3371	7	0
1	fc	3425	0	3371	8	0
1	fd	3425	0	3371	6	0
1	fe	3425	0	3371	10	0
1	ff	3425	0	3371	8	0
1	fg	3425	0	3371	10	0
1	fh	3425	0	3371	11	0
1	fi	3425	0	3371	8	0
1	fj	3425	0	3371	19	0
1	fk	3425	0	3371	10	0
1	fl	3425	0	3371	7	0
1	fm	3425	0	3371	14	0
1	fn	3425	0	3371	9	0
1	fo	3425	0	3371	8	0
1	fp	3425	0	3371	10	0
1	fq	3425	0	3371	9	0
1	fr	3425	0	3371	8	0
1	fs	3425	0	3371	9	0
1	ft	3425	0	3371	12	0
1	fu	3425	0	3371	8	0
1	fv	3425	0	3371	9	0
1	fw	3425	0	3371	16	0
1	fx	3425	0	3371	7	0
1	fy	3425	0	3371	14	0
1	fz	3425	0	3371	11	0
1	ga	3425	0	3371	11	0
1	gb	3425	0	3371	11	0
1	gc	3425	0	3371	17	0
1	gd	3425	0	3371	6	0
1	ge	3425	0	3371	15	0
1	gf	3425	0	3371	4	0
1	gg	3425	0	3371	12	0
1	gh	3425	0	3371	9	0
1	gi	3425	0	3371	10	0
1	gj	3425	0	3371	12	0
1	gk	3425	0	3371	8	0
1	gl	3425	0	3371	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	gm	3425	0	3371	12	0
1	gn	3425	0	3371	8	0
1	go	3425	0	3371	12	0
1	gp	3425	0	3371	11	0
1	gq	3425	0	3371	14	0
1	gr	3425	0	3371	12	0
1	gs	3425	0	3371	11	0
1	gt	3425	0	3371	9	0
1	gu	3425	0	3371	11	0
1	gv	3425	0	3371	6	0
1	gw	3425	0	3371	8	0
1	gx	3425	0	3371	9	0
1	gy	3425	0	3371	10	0
1	gz	3425	0	3371	12	0
1	ha	3425	0	3371	9	0
1	hb	3425	0	3371	7	0
1	hc	3425	0	3371	8	0
1	hd	3425	0	3371	13	0
2	he	3208	0	3205	14	0
2	hf	3208	0	3205	7	0
2	hg	3208	0	3205	9	0
2	hh	3208	0	3205	6	0
2	hi	3208	0	3205	10	0
2	hj	3208	0	3205	7	0
2	hk	3208	0	3205	11	0
2	hl	3208	0	3205	6	0
2	hm	3208	0	3205	10	0
2	hn	3208	0	3205	10	0
2	ho	3208	0	3205	7	0
3	hp	633	0	608	4	0
3	hq	633	0	608	4	0
3	hr	633	0	608	2	0
3	hs	633	0	608	4	0
3	ht	633	0	608	3	0
3	hu	633	0	608	5	0
3	hv	633	0	608	5	0
3	hw	633	0	608	3	0
3	hx	633	0	608	2	0
3	hy	633	0	608	2	0
3	hz	633	0	608	5	0
3	ia	633	0	608	2	0
3	ib	633	0	608	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	ic	633	0	608	4	0
3	id	633	0	608	2	0
3	ie	633	0	608	4	0
3	if	633	0	608	1	0
3	ig	633	0	608	3	0
3	ih	633	0	608	2	0
3	ii	633	0	608	5	0
3	ij	633	0	608	4	0
3	ik	633	0	608	6	0
3	il	633	0	608	3	0
3	im	633	0	608	5	0
3	in	633	0	608	2	0
3	io	633	0	608	3	0
3	ip	633	0	608	1	0
3	iq	633	0	608	4	0
3	ir	633	0	608	4	0
3	is	633	0	608	2	0
3	it	633	0	608	4	0
3	iu	633	0	608	6	0
3	iv	633	0	608	3	0
3	iw	633	0	608	4	0
3	ix	633	0	608	3	0
3	iy	633	0	608	3	0
3	iz	633	0	608	5	0
3	ja	633	0	608	3	0
3	jb	633	0	608	4	0
3	jc	633	0	608	6	0
3	jd	633	0	608	3	0
3	je	633	0	608	4	0
3	jf	633	0	608	6	0
3	jg	633	0	608	5	0
3	jh	633	0	608	4	0
3	ji	633	0	608	4	0
3	jj	633	0	608	1	0
3	jk	633	0	608	1	0
3	jl	633	0	608	4	0
3	jm	633	0	608	2	0
3	jn	633	0	608	3	0
3	jo	633	0	608	4	0
3	jp	633	0	608	2	0
3	jq	633	0	608	3	0
3	jr	633	0	608	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	js	633	0	608	2	0
3	jt	633	0	608	3	0
3	ju	633	0	608	3	0
3	jv	633	0	608	1	0
3	jw	633	0	608	4	0
3	jx	633	0	608	3	0
3	jy	633	0	608	3	0
3	jz	633	0	608	3	0
3	ka	633	0	608	6	0
3	kb	633	0	608	5	0
3	kc	633	0	608	3	0
3	kd	633	0	608	2	0
3	ke	633	0	608	5	0
3	kf	633	0	608	3	0
3	kg	633	0	608	6	0
3	kh	633	0	608	2	0
3	ki	633	0	608	2	0
3	kj	633	0	608	2	0
3	kk	633	0	608	5	0
3	kl	633	0	608	5	0
3	km	633	0	608	2	0
3	kn	633	0	608	4	0
3	ko	633	0	608	4	0
3	kp	633	0	608	5	0
3	kq	633	0	608	4	0
3	kr	633	0	608	4	0
3	ks	633	0	608	3	0
3	kt	633	0	608	3	0
3	ku	633	0	608	3	0
3	633	0	608	3	0	
3	kw	633	0	608	2	0
3	kx	633	0	608	2	0
3	ky	633	0	608	4	0
3	kz	633	0	608	1	0
3	la	633	0	608	5	0
3	lb	633	0	608	4	0
3	lc	633	0	608	3	0
3	ld	633	0	608	2	0
3	le	633	0	608	5	0
3	lf	633	0	608	4	0
3	lg	633	0	608	5	0
3	lh	633	0	608	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	li	633	0	608	3	0
3	lj	633	0	608	5	0
3	lk	633	0	608	3	0
3	ll	633	0	608	1	0
3	lm	633	0	608	5	0
3	ln	633	0	608	2	0
3	lo	633	0	608	4	0
3	lp	633	0	608	6	0
3	lq	633	0	608	3	0
3	lr	633	0	608	1	0
3	ls	633	0	608	4	0
3	lt	633	0	608	5	0
3	lu	633	0	608	5	0
3	lv	633	0	608	4	0
3	lw	633	0	608	3	0
3	lx	633	0	608	4	0
3	ly	633	0	608	3	0
3	lz	633	0	608	5	0
3	ma	633	0	608	3	0
3	mb	633	0	608	3	0
3	mc	633	0	608	1	0
3	md	633	0	608	2	0
3	me	633	0	608	4	0
3	mf	633	0	608	5	0
3	mg	633	0	608	2	0
3	mh	633	0	608	4	0
3	mi	633	0	608	3	0
3	mj	633	0	608	5	0
3	mk	633	0	608	5	0
3	ml	633	0	608	1	0
3	mm	633	0	608	4	0
3	mn	633	0	608	5	0
3	mo	633	0	608	5	0
3	mp	633	0	608	4	0
3	mq	633	0	608	3	0
3	ms	633	0	608	4	0
3	mt	633	0	608	4	0
3	mu	633	0	608	3	0
3	mv	633	0	608	2	0
3	mw	633	0	608	1	0
3	mx	633	0	608	3	0
3	my	633	0	608	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	mz	633	0	608	4	0
3	na	633	0	608	2	0
3	nb	633	0	608	3	0
3	nc	633	0	608	4	0
3	nd	633	0	608	4	0
3	ne	633	0	608	3	0
3	nf	633	0	608	3	0
3	ng	633	0	608	3	0
3	nh	633	0	608	4	0
3	ni	633	0	608	2	0
3	nj	633	0	608	3	0
3	nk	633	0	608	5	0
3	nl	633	0	608	1	0
3	nm	633	0	608	2	0
3	nn	633	0	608	4	0
3	no	633	0	608	3	0
3	np	633	0	608	3	0
3	nq	633	0	608	4	0
3	ns	633	0	608	3	0
3	nt	633	0	608	3	0
3	nu	633	0	608	7	0
3	nv	633	0	608	4	0
3	nw	633	0	608	6	0
3	nx	633	0	608	2	0
3	ny	633	0	608	6	0
3	nz	633	0	608	1	0
3	oa	633	0	608	2	0
3	ob	633	0	608	3	0
3	oc	633	0	608	1	0
3	od	633	0	608	3	0
3	oe	633	0	608	4	0
3	of	633	0	608	2	0
3	og	633	0	608	2	0
All	All	781038	0	766675	2284	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (2284) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ea:99:VAL:HG21	1:eb:483:PRO:HG3	1.35	1.09
1:ca:99:VAL:HG21	1:cb:483:PRO:HB2	1.67	0.76
1:fq:121:THR:HG22	1:fq:260:GLU:HG2	1.74	0.69
3:hv:9:ASN:ND2	3:hv:51:SER:OG	2.26	0.69
1:an:74:TYR:CE2	1:ao:260:GLU:HG2	2.28	0.69
1:ee:266:LEU:HG	1:ef:155:SER:HB3	1.75	0.69
1:am:71:ASP:HB2	1:ao:231:SER:HB3	1.77	0.67
3:kb:9:ASN:ND2	3:kb:51:SER:OG	2.27	0.67
1:bn:121:THR:HG22	1:bn:260:GLU:HG2	1.78	0.65
1:ga:128:ARG:HD2	1:ga:253:ARG:HH12	1.61	0.65
1:au:404:PHE:HZ	1:au:417:LEU:HA	1.61	0.64
1:du:67:GLU:HB3	1:ed:274:LEU:HD22	1.80	0.64
1:ag:481:ILE:HD11	1:ag:501:PRO:HB3	1.79	0.64
1:az:83:GLN:NE2	3:ic:36:SER:OG	2.30	0.64
3:ne:9:ASN:ND2	3:ne:51:SER:OG	2.31	0.64
1:ab:67:GLU:HG3	1:bd:251:GLY:HA3	1.80	0.63
1:dz:274:LEU:HD22	1:eo:67:GLU:HB3	1.79	0.63
1:bc:121:THR:HG22	1:bc:260:GLU:HG2	1.82	0.62
1:ai:67:GLU:HB3	1:ar:274:LEU:HD22	1.81	0.62
1:ey:266:LEU:HG	1:ez:155:SER:HB3	1.81	0.62
1:ca:99:VAL:CG2	1:cb:483:PRO:HB2	2.29	0.62
1:bw:112:CYS:HB3	1:bw:448:ILE:HG23	1.82	0.61
3:mb:9:ASN:ND2	3:mb:51:SER:OG	2.34	0.61
1:bh:264:ARG:HH22	1:bi:153:MET:HA	1.65	0.61
1:gh:345:TRP:HE1	1:gi:344:ARG:H	1.49	0.61
1:ef:83:GLN:NE2	3:mj:36:SER:OG	2.34	0.61
1:ep:274:LEU:HD22	1:es:67:GLU:HB3	1.82	0.61
1:bo:136:VAL:HG22	1:bo:253:ARG:HD2	1.82	0.60
1:ek:492:PRO:HG2	1:ek:495:ARG:HA	1.83	0.60
2:hn:208:ASP:OD2	2:hn:212:LYS:NZ	2.34	0.60
1:fg:136:VAL:HG22	1:fg:253:ARG:HD2	1.83	0.60
2:hm:208:ASP:OD2	2:hm:212:LYS:NZ	2.34	0.60
1:ea:476:ARG:NH2	1:eb:230:THR:OG1	2.34	0.60
3:it:9:ASN:ND2	3:it:51:SER:OG	2.35	0.59
1:bi:74:TYR:CE2	1:bj:260:GLU:HG2	2.37	0.59
1:bu:133:LYS:HG2	1:bu:249:GLU:HG2	1.85	0.59
1:fw:121:THR:HG22	1:fw:260:GLU:HG2	1.83	0.59
3:lr:9:ASN:ND2	3:lr:51:SER:OG	2.36	0.59
1:dl:121:THR:HG22	1:dl:260:GLU:HG2	1.85	0.59
1:hd:317:GLY:HA2	1:hd:514:ARG:HE	1.68	0.59
1:gt:297:GLU:HG2	1:gu:250:MET:HE1	1.84	0.59
1:ce:345:TRP:CD2	1:cf:348:GLU:HG2	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fl:234:GLU:HG2	1:fl:235:LEU:HD12	1.85	0.59
1:aj:160:ALA:HB2	1:aj:228:MET:HG3	1.85	0.58
1:bk:74:TYR:CE1	1:bl:260:GLU:HG2	2.37	0.58
3:lj:9:ASN:ND2	3:lj:51:SER:OG	2.36	0.58
1:gm:131:TYR:HB3	1:gm:250:MET:HE2	1.85	0.58
1:cj:251:GLY:HA3	1:cr:67:GLU:CD	2.28	0.58
1:ba:126:ALA:HB2	1:ba:483:PRO:HB3	1.86	0.58
1:fx:121:THR:HG22	1:fx:260:GLU:HG2	1.85	0.58
1:ga:184:GLU:HB3	1:ga:366:ARG:HH22	1.69	0.58
1:be:74:TYR:CE2	1:bf:260:GLU:HG2	2.38	0.58
1:bh:264:ARG:HG3	1:bh:477:TYR:HE1	1.68	0.58
1:el:83:GLN:NE2	3:ma:36:SER:OG	2.37	0.58
1:ge:83:GLN:NE2	3:mo:36:SER:OG	2.36	0.58
1:ez:142:GLU:HG2	1:ez:145:HIS:HB2	1.86	0.57
1:ew:231:SER:HB3	1:fa:71:ASP:HB2	1.85	0.57
3:nc:9:ASN:ND2	3:nc:51:SER:OG	2.36	0.57
2:hn:289:LYS:NZ	2:hn:294:ASP:OD2	2.37	0.57
1:bg:79:ILE:O	1:bg:81:ALA:N	2.38	0.57
1:ep:257:GLN:HG3	1:ep:497:GLN:HG3	1.86	0.57
1:fm:344:ARG:O	1:fm:345:TRP:HB2	2.02	0.57
1:fs:297:GLU:HG2	1:ft:250:MET:HE1	1.87	0.57
1:cb:351:LYS:NZ	1:cb:395:TYR:O	2.37	0.57
1:ch:117:MET:HB2	1:ch:453:TYR:HB2	1.87	0.57
3:hp:40:LYS:H	3:hp:72:ASN:HD21	1.53	0.57
3:iq:26:LYS:NZ	3:iq:74:ASP:OD2	2.37	0.57
2:hg:208:ASP:OD2	2:hg:212:LYS:NZ	2.37	0.57
1:bg:404:PHE:HZ	1:bg:417:LEU:HA	1.69	0.57
2:hj:208:ASP:OD2	2:hj:212:LYS:NZ	2.38	0.56
1:cg:297:GLU:HG2	1:ch:250:MET:HE1	1.86	0.56
2:hg:341:PHE:O	2:hg:343:ALA:N	2.38	0.56
3:iz:9:ASN:ND2	3:iz:51:SER:OG	2.38	0.56
1:ca:72:HIS:HB2	1:cb:260:GLU:CD	2.31	0.56
1:fa:344:ARG:O	1:fa:345:TRP:HB2	2.05	0.56
2:ho:341:PHE:O	2:ho:343:ALA:N	2.38	0.56
3:kg:26:LYS:NZ	3:kg:74:ASP:OD2	2.39	0.56
1:ax:120:PRO:O	1:ax:121:THR:OG1	2.19	0.56
1:ds:114:VAL:O	1:ds:115:GLN:C	2.49	0.56
1:ey:83:GLN:NE2	3:lv:36:SER:OG	2.39	0.56
1:gv:120:PRO:O	1:gv:121:THR:OG1	2.22	0.56
3:ko:14:GLU:OE2	3:nu:16:LYS:NZ	2.38	0.56
1:ck:328:LYS:NZ	1:ck:336:ASP:OD2	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:dn:297:GLU:HG2	1:do:250:MET:HE1	1.87	0.56
1:dp:444:MET:O	1:dp:449:TYR:OH	2.24	0.56
3:nk:9:ASN:ND2	3:nk:51:SER:OG	2.38	0.56
3:nw:26:LYS:NZ	3:nw:74:ASP:OD2	2.39	0.56
2:hh:289:LYS:NZ	2:hh:294:ASP:OD2	2.38	0.56
1:cz:67:GLU:HB2	1:gr:270:TYR:HA	1.88	0.56
1:fw:74:TYR:OH	1:fy:229:ALA:HA	2.06	0.55
1:fm:345:TRP:CE3	1:fn:348:GLU:HB2	2.41	0.55
1:da:260:GLU:HG2	1:df:74:TYR:CE1	2.42	0.55
1:fs:351:LYS:NZ	1:fs:394:SER:O	2.39	0.55
2:hf:208:ASP:OD2	2:hf:212:LYS:NZ	2.39	0.55
1:ai:328:LYS:NZ	1:ai:336:ASP:OD2	2.39	0.55
1:dx:145:HIS:CD2	1:dx:490:GLN:HG2	2.41	0.55
1:ec:266:LEU:HG	1:ed:155:SER:HB3	1.88	0.55
1:bs:328:LYS:NZ	1:bs:336:ASP:OD2	2.39	0.55
3:iu:26:LYS:NZ	3:iu:74:ASP:OD2	2.40	0.55
3:jw:16:LYS:NZ	3:kg:14:GLU:OE2	2.39	0.55
3:ib:26:LYS:NZ	3:ib:74:ASP:OD2	2.39	0.55
1:db:273:GLU:OE2	1:fe:474:LYS:NZ	2.38	0.55
1:eb:266:LEU:HG	1:ec:155:SER:HB3	1.89	0.55
1:gu:328:LYS:NZ	1:gu:336:ASP:OD2	2.40	0.55
3:jx:9:ASN:ND2	3:jx:51:SER:OG	2.38	0.55
3:mf:9:ASN:ND2	3:mf:51:SER:OG	2.39	0.55
1:ee:155:SER:HB3	1:ej:266:LEU:HG	1.88	0.55
3:nj:26:LYS:NZ	3:nj:74:ASP:OD2	2.39	0.55
1:am:260:GLU:HG2	1:ar:74:TYR:CE1	2.42	0.55
1:cd:463:ASP:OD2	1:cl:465:LYS:NZ	2.40	0.55
1:ag:155:SER:HB3	1:al:266:LEU:HG	1.89	0.55
1:bx:273:GLU:OE2	1:cn:474:LYS:NZ	2.40	0.55
1:du:327:SER:OG	1:du:328:LYS:N	2.39	0.55
1:ei:344:ARG:O	1:ei:345:TRP:HB2	2.08	0.55
1:fc:142:GLU:HB3	1:fc:145:HIS:HB2	1.87	0.55
1:fr:344:ARG:O	1:fr:345:TRP:HB2	2.07	0.55
1:er:83:GLN:NE2	3:lm:36:SER:OG	2.40	0.54
2:hk:341:PHE:O	2:hk:343:ALA:N	2.39	0.54
3:lx:9:ASN:ND2	3:lx:51:SER:OG	2.39	0.54
1:dr:328:LYS:NZ	1:dr:336:ASP:OD2	2.40	0.54
1:fz:328:LYS:NZ	1:fz:336:ASP:OD2	2.41	0.54
2:hf:239:SER:OG	2:hf:240:TYR:N	2.41	0.54
2:hh:208:ASP:OD2	2:hh:212:LYS:NZ	2.40	0.54
1:ba:328:LYS:NZ	1:ba:336:ASP:OD2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:es:328:LYS:NZ	1:es:336:ASP:OD2	2.41	0.54
1:fg:344:ARG:O	1:fg:345:TRP:HB2	2.08	0.54
1:ez:351:LYS:NZ	1:ez:395:TYR:O	2.41	0.54
1:gv:344:ARG:O	1:gv:345:TRP:HB2	2.08	0.54
2:hh:341:PHE:O	2:hh:343:ALA:N	2.40	0.54
3:ih:26:LYS:NZ	3:ih:74:ASP:OD2	2.41	0.54
1:bi:297:GLU:HG2	1:bj:250:MET:HE1	1.90	0.54
1:cy:120:PRO:O	1:cy:121:THR:OG1	2.21	0.54
1:fj:112:CYS:HB3	1:fj:448:ILE:HG23	1.89	0.54
1:fn:328:LYS:NZ	1:fn:336:ASP:OD2	2.41	0.54
1:fe:328:LYS:NZ	1:fe:336:ASP:OD2	2.41	0.54
1:gk:328:LYS:NZ	1:gk:336:ASP:OD2	2.39	0.54
1:aq:456:LEU:H	1:aq:475:THR:HG22	1.72	0.54
1:aw:345:TRP:CG	1:aw:346:ALA:H	2.26	0.54
1:gv:328:LYS:NZ	1:gv:336:ASP:OD2	2.41	0.54
2:he:23:ASN:HD22	2:hi:46:ASN:H	1.56	0.54
3:lz:9:ASN:ND2	3:lz:51:SER:OG	2.40	0.54
1:dd:344:ARG:O	1:dd:345:TRP:HB2	2.09	0.53
1:fv:344:ARG:O	1:fv:345:TRP:HB2	2.07	0.53
2:hj:23:ASN:HD22	2:hm:46:ASN:H	1.56	0.53
1:en:328:LYS:NZ	1:en:336:ASP:OD2	2.41	0.53
1:fs:344:ARG:O	1:fs:345:TRP:HB2	2.08	0.53
2:hm:128:LEU:C	2:hm:129:GLN:O	2.47	0.53
1:ge:327:SER:OG	1:ge:328:LYS:N	2.42	0.53
3:mn:26:LYS:NZ	3:mn:74:ASP:OD2	2.40	0.53
1:ak:328:LYS:NZ	1:ak:336:ASP:OD2	2.41	0.53
1:dv:266:LEU:HG	1:dw:155:SER:HB3	1.90	0.53
1:dz:120:PRO:O	1:dz:121:THR:OG1	2.24	0.53
3:ly:26:LYS:NZ	3:ly:74:ASP:OD2	2.42	0.53
1:bc:72:HIS:HB2	1:bd:260:GLU:CD	2.34	0.53
1:gs:297:GLU:HG2	1:gt:250:MET:HE1	1.89	0.53
2:hl:239:SER:OG	2:hl:240:TYR:N	2.42	0.53
1:cg:114:VAL:O	1:cg:115:GLN:C	2.52	0.53
1:ee:328:LYS:NZ	1:ee:336:ASP:OD2	2.42	0.53
1:fw:328:LYS:NZ	1:fw:336:ASP:OD2	2.41	0.53
2:he:208:ASP:OD2	2:he:212:LYS:NZ	2.42	0.53
1:aa:521:ILE:O	1:ab:359:LYS:NZ	2.42	0.53
1:ar:319:SER:N	1:ar:322:THR:OG1	2.41	0.53
1:bh:395:TYR:CG	1:bh:396:ALA:N	2.76	0.53
1:ce:328:LYS:NZ	1:ce:336:ASP:OD2	2.42	0.53
1:ep:328:LYS:NZ	1:ep:336:ASP:OD2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:es:327:SER:OG	1:es:328:LYS:N	2.42	0.53
1:gb:86:GLY:O	1:gx:495:ARG:NH1	2.41	0.53
3:nd:26:LYS:NZ	3:nd:74:ASP:OD2	2.42	0.53
1:gi:328:LYS:NZ	1:gi:336:ASP:OD2	2.42	0.53
1:cz:328:LYS:NZ	1:cz:336:ASP:OD2	2.42	0.53
1:dv:266:LEU:CD2	1:dw:155:SER:HB3	2.39	0.53
1:eb:328:LYS:NZ	1:eb:336:ASP:OD2	2.41	0.53
1:fa:328:LYS:NZ	1:fa:336:ASP:OD2	2.42	0.53
3:lp:40:LYS:H	3:lp:72:ASN:HD21	1.57	0.53
1:ci:123:GLN:HB2	1:cn:93:PRO:HB2	1.91	0.52
1:ct:83:GLN:NE2	3:jn:36:SER:OG	2.42	0.52
1:go:327:SER:OG	1:go:328:LYS:N	2.42	0.52
1:gz:344:ARG:O	1:gz:345:TRP:HB2	2.09	0.52
1:bu:297:GLU:HG2	1:bv:250:MET:HE1	1.91	0.52
1:by:297:GLU:HG2	1:bz:250:MET:HE1	1.91	0.52
1:al:83:GLN:NE2	3:hv:36:SER:OG	2.43	0.52
1:cv:474:LYS:NZ	1:gs:273:GLU:OE2	2.42	0.52
1:el:486:GLU:HG3	1:el:509:LYS:HB3	1.90	0.52
1:eo:327:SER:OG	1:eo:328:LYS:N	2.42	0.52
1:fh:131:TYR:HB3	1:fh:250:MET:HE2	1.90	0.52
2:hm:28:THR:OG1	2:hm:29:ARG:N	2.42	0.52
1:bp:351:LYS:NZ	1:bp:395:TYR:O	2.41	0.52
1:bt:67:GLU:HB3	1:bw:274:LEU:CD2	2.40	0.52
1:go:328:LYS:NZ	1:go:336:ASP:OD2	2.42	0.52
1:gs:131:TYR:HB3	1:gs:250:MET:HB3	1.91	0.52
1:bc:328:LYS:NZ	1:bc:336:ASP:OD2	2.43	0.52
1:ep:274:LEU:CD2	1:es:67:GLU:HB3	2.39	0.52
1:gw:344:ARG:O	1:gw:345:TRP:HB2	2.10	0.52
1:bi:328:LYS:NZ	1:bi:336:ASP:OD2	2.42	0.52
1:bp:328:LYS:NZ	1:bp:336:ASP:OD2	2.43	0.52
1:de:394:SER:O	1:de:395:TYR:C	2.53	0.52
1:di:328:LYS:NZ	1:di:336:ASP:OD2	2.42	0.52
1:eb:266:LEU:CD2	1:ec:155:SER:HB3	2.40	0.52
1:ec:327:SER:OG	1:ec:328:LYS:N	2.42	0.52
3:jh:40:LYS:H	3:jh:72:ASN:HD21	1.56	0.52
3:jr:26:LYS:NZ	3:jr:74:ASP:OD2	2.43	0.52
3:na:79:THR:O	3:na:80:GLY:C	2.53	0.52
1:bm:328:LYS:NZ	1:bm:336:ASP:OD2	2.43	0.52
1:bq:502:SER:OG	1:bq:503:ILE:N	2.43	0.52
1:bw:83:GLN:NE2	3:jb:36:SER:OG	2.43	0.52
1:dd:131:TYR:HE1	1:dd:141:LYS:HE3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fv:72:HIS:HB2	1:fw:260:GLU:CD	2.35	0.52
1:ea:328:LYS:NZ	1:ea:336:ASP:OD2	2.42	0.52
1:fc:328:LYS:NZ	1:fc:336:ASP:OD2	2.43	0.52
1:ga:454:VAL:HB	1:ga:476:ARG:HB2	1.91	0.52
2:hg:239:SER:OG	2:hg:240:TYR:N	2.42	0.52
1:bp:327:SER:OG	1:bp:328:LYS:N	2.43	0.52
1:cy:344:ARG:O	1:cy:345:TRP:HB2	2.10	0.52
1:ea:266:LEU:HG	1:eb:155:SER:HB3	1.90	0.52
2:hh:239:SER:OG	2:hh:240:TYR:N	2.43	0.52
3:hz:26:LYS:NZ	3:hz:74:ASP:OD2	2.43	0.52
1:ay:398:GLN:OE1	1:ay:398:GLN:N	2.43	0.52
1:ba:327:SER:OG	1:ba:328:LYS:N	2.43	0.52
1:bl:344:ARG:O	1:bl:345:TRP:HB2	2.10	0.52
3:io:26:LYS:NZ	3:io:74:ASP:OD2	2.43	0.52
1:ce:327:SER:OG	1:ce:328:LYS:N	2.43	0.51
1:cq:474:LYS:NZ	1:cy:273:GLU:OE2	2.40	0.51
1:de:328:LYS:NZ	1:de:336:ASP:OD2	2.43	0.51
1:fb:328:LYS:NZ	1:fb:336:ASP:OD2	2.43	0.51
1:fw:327:SER:OG	1:fw:328:LYS:N	2.43	0.51
2:hi:239:SER:OG	2:hi:240:TYR:N	2.43	0.51
3:mm:26:LYS:NZ	3:mm:74:ASP:OD2	2.43	0.51
1:an:344:ARG:O	1:an:345:TRP:HB2	2.09	0.51
1:ax:328:LYS:NZ	1:ax:336:ASP:OD2	2.43	0.51
3:kk:26:LYS:NZ	3:kk:74:ASP:OD2	2.42	0.51
3:mf:35:TYR:HE1	3:mf:41:ILE:HD12	1.74	0.51
1:fj:345:TRP:HE1	1:fk:344:ARG:HB2	1.75	0.51
1:ge:121:THR:HG22	1:ge:260:GLU:HG2	1.91	0.51
1:ae:297:GLU:HG2	1:af:250:MET:HE1	1.91	0.51
1:bh:328:LYS:NZ	1:bh:336:ASP:OD2	2.43	0.51
1:br:120:PRO:O	1:br:121:THR:OG1	2.28	0.51
1:du:328:LYS:NZ	1:du:336:ASP:OD2	2.43	0.51
1:fw:73:GLY:C	1:fw:75:ASN:H	2.18	0.51
1:gh:344:ARG:O	1:gh:345:TRP:HB2	2.11	0.51
1:gs:344:ARG:O	1:gs:345:TRP:HB2	2.10	0.51
3:ji:26:LYS:NZ	3:ji:74:ASP:OD2	2.43	0.51
3:jj:26:LYS:NZ	3:jj:74:ASP:OD2	2.43	0.51
3:ka:16:LYS:NZ	3:ny:14:GLU:OE2	2.43	0.51
3:mx:26:LYS:NZ	3:mx:74:ASP:OD2	2.44	0.51
1:af:131:TYR:HB3	1:af:250:MET:HB3	1.91	0.51
1:dg:351:LYS:NZ	1:dg:394:SER:O	2.44	0.51
1:er:474:LYS:NZ	1:es:234:GLU:OE2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:go:74:TYR:CE1	1:gp:260:GLU:HG2	2.45	0.51
1:cs:344:ARG:O	1:cs:345:TRP:HB2	2.09	0.51
1:eu:328:LYS:NZ	1:eu:336:ASP:OD2	2.43	0.51
3:mj:26:LYS:NZ	3:mj:74:ASP:OD2	2.43	0.51
3:ng:26:LYS:NZ	3:ng:74:ASP:OD2	2.44	0.51
1:aw:327:SER:OG	1:aw:328:LYS:N	2.44	0.51
1:bg:502:SER:OG	1:bg:503:ILE:N	2.43	0.51
1:da:74:TYR:CE2	1:db:260:GLU:HG2	2.46	0.51
1:dh:257:GLN:HG3	1:dh:497:GLN:HG3	1.93	0.51
1:fm:328:LYS:NZ	1:fm:336:ASP:OD2	2.44	0.51
1:gp:72:HIS:HB2	1:gq:260:GLU:CD	2.35	0.51
1:hb:327:SER:OG	1:hb:328:LYS:N	2.44	0.51
2:he:239:SER:OG	2:he:240:TYR:N	2.43	0.51
1:ae:327:SER:OG	1:ae:328:LYS:N	2.42	0.51
1:ak:327:SER:OG	1:ak:328:LYS:N	2.43	0.51
1:cf:328:LYS:NZ	1:cf:336:ASP:OD2	2.36	0.51
1:cw:328:LYS:NZ	1:cw:336:ASP:OD2	2.44	0.51
1:gq:328:LYS:NZ	1:gq:336:ASP:OD2	2.44	0.51
2:ho:239:SER:OG	2:ho:240:TYR:N	2.43	0.51
3:jq:26:LYS:NZ	3:jq:74:ASP:OD2	2.44	0.51
3:kr:26:LYS:NZ	3:kr:74:ASP:OD2	2.44	0.51
1:aw:345:TRP:CG	1:aw:346:ALA:N	2.79	0.51
1:cq:67:GLU:HB3	1:dl:274:LEU:HD13	1.93	0.51
3:ht:9:ASN:ND2	3:ht:51:SER:OG	2.43	0.51
3:kb:79:THR:O	3:kb:80:GLY:C	2.53	0.51
3:lm:26:LYS:NZ	3:lm:74:ASP:OD2	2.44	0.51
1:ax:344:ARG:O	1:ax:345:TRP:HB2	2.11	0.51
1:gj:142:GLU:HB3	1:gj:145:HIS:HB2	1.92	0.51
3:ix:40:LYS:H	3:ix:72:ASN:HD21	1.58	0.51
1:ae:114:VAL:O	1:ae:115:GLN:C	2.53	0.50
1:aq:344:ARG:O	1:aq:345:TRP:HB2	2.11	0.50
1:cr:134:ASP:OD1	1:cr:134:ASP:N	2.41	0.50
1:cx:134:ASP:OD1	1:cx:134:ASP:N	2.43	0.50
1:hc:328:LYS:NZ	1:hc:336:ASP:OD2	2.44	0.50
1:hd:83:GLN:NE2	3:no:36:SER:OG	2.44	0.50
3:hq:26:LYS:NZ	3:hq:74:ASP:OD2	2.43	0.50
3:iy:26:LYS:NZ	3:iy:74:ASP:OD2	2.44	0.50
3:ke:26:LYS:NZ	3:ke:74:ASP:OD2	2.45	0.50
1:ac:328:LYS:NZ	1:ac:336:ASP:OD2	2.44	0.50
1:cq:351:LYS:NZ	1:cq:390:ASP:O	2.44	0.50
1:eg:327:SER:OG	1:eg:328:LYS:N	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:gu:121:THR:HG22	1:gu:260:GLU:HG3	1.93	0.50
3:kq:26:LYS:NZ	3:kq:74:ASP:OD2	2.45	0.50
1:ae:521:ILE:O	1:af:359:LYS:NZ	2.42	0.50
1:ba:345:TRP:CD2	1:bb:348:GLU:HG2	2.46	0.50
1:ca:267:LYS:NZ	1:cb:237:GLU:OE1	2.45	0.50
1:cr:398:GLN:N	1:cr:398:GLN:OE1	2.44	0.50
1:dc:328:LYS:NZ	1:dc:336:ASP:OD2	2.43	0.50
1:de:344:ARG:O	1:de:345:TRP:HB2	2.11	0.50
1:dq:521:ILE:O	1:dr:359:LYS:NZ	2.41	0.50
1:fh:327:SER:OG	1:fh:328:LYS:N	2.43	0.50
1:fi:297:GLU:HB3	1:fj:250:MET:HE1	1.92	0.50
1:fy:454:VAL:HB	1:fy:476:ARG:HB2	1.94	0.50
2:hm:129:GLN:O	2:hm:131:ALA:N	2.42	0.50
3:li:26:LYS:NZ	3:li:74:ASP:OD2	2.44	0.50
3:mt:26:LYS:NZ	3:mt:74:ASP:OD2	2.45	0.50
1:aq:327:SER:OG	1:aq:328:LYS:N	2.44	0.50
1:bx:126:ALA:HB2	1:bx:483:PRO:HB3	1.94	0.50
1:cc:234:GLU:OE2	1:ch:474:LYS:NZ	2.44	0.50
1:cc:346:ALA:HB2	1:cd:341:ARG:HD3	1.93	0.50
1:dy:155:SER:HB3	1:ed:266:LEU:CD2	2.42	0.50
1:fe:83:GLN:NE2	3:mz:36:SER:OG	2.44	0.50
1:fu:327:SER:OG	1:fu:328:LYS:N	2.43	0.50
1:fx:266:LEU:HG	1:fy:155:SER:HB3	1.93	0.50
3:mw:26:LYS:NZ	3:mw:74:ASP:OD2	2.45	0.50
1:ad:145:HIS:CD2	1:ad:490:GLN:HG2	2.46	0.50
1:dh:409:THR:OG1	1:dh:410:LYS:N	2.45	0.50
1:ep:351:LYS:NZ	1:ep:390:ASP:O	2.39	0.50
1:fg:72:HIS:HB2	1:fh:260:GLU:OE2	2.12	0.50
1:gx:328:LYS:NZ	1:gx:336:ASP:OD2	2.44	0.50
1:al:317:GLY:O	1:al:318:LYS:C	2.53	0.50
1:bc:345:TRP:CG	1:bc:346:ALA:H	2.30	0.50
1:bn:96:MET:HE3	1:bo:115:GLN:HG2	1.92	0.50
1:eg:328:LYS:NZ	1:eg:336:ASP:OD2	2.44	0.50
1:fv:297:GLU:HB3	1:fw:250:MET:HE1	1.94	0.50
2:hl:341:PHE:O	2:hl:343:ALA:N	2.44	0.50
3:hu:26:LYS:NZ	3:hu:74:ASP:OD2	2.45	0.50
3:kt:26:LYS:NZ	3:kt:74:ASP:OD2	2.44	0.50
3:lp:26:LYS:NZ	3:lp:74:ASP:OD2	2.45	0.50
1:av:142:GLU:HG2	1:av:145:HIS:HB2	1.94	0.50
1:ca:344:ARG:O	1:ca:345:TRP:HB2	2.12	0.50
1:fm:327:SER:OG	1:fm:328:LYS:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fz:317:GLY:O	1:fz:318:LYS:C	2.55	0.50
3:je:26:LYS:NZ	3:je:74:ASP:OD2	2.45	0.50
3:ks:26:LYS:NZ	3:ks:74:ASP:OD2	2.45	0.50
3:lf:26:LYS:NZ	3:lf:74:ASP:OD2	2.45	0.50
3:lh:26:LYS:NZ	3:lh:74:ASP:OD2	2.45	0.50
1:ca:101:ARG:HA	1:cb:370:ARG:HH22	1.75	0.50
1:de:327:SER:OG	1:de:328:LYS:N	2.44	0.50
1:eu:327:SER:OG	1:eu:328:LYS:N	2.44	0.50
1:ec:237:GLU:HB2	1:ej:466:ASN:HB3	1.94	0.50
3:mi:26:LYS:NZ	3:mi:74:ASP:OD2	2.45	0.50
1:cl:120:PRO:O	1:cl:121:THR:OG1	2.28	0.49
1:ei:198:ILE:O	1:ei:198:ILE:HG22	2.12	0.49
1:gh:112:CYS:HB3	1:gh:448:ILE:HG23	1.94	0.49
3:hp:26:LYS:NZ	3:hp:74:ASP:OD2	2.44	0.49
3:hs:26:LYS:NZ	3:hs:74:ASP:OD2	2.44	0.49
3:jl:26:LYS:NZ	3:jl:74:ASP:OD2	2.45	0.49
1:cg:184:GLU:HB2	1:cg:366:ARG:HH22	1.77	0.49
1:du:67:GLU:HB3	1:ed:274:LEU:CD2	2.41	0.49
1:ee:142:GLU:HB3	1:ee:145:HIS:HB2	1.94	0.49
1:gc:502:SER:OG	1:gc:503:ILE:N	2.45	0.49
1:hd:454:VAL:HB	1:hd:476:ARG:HB2	1.94	0.49
3:ny:79:THR:O	3:ny:80:GLY:C	2.55	0.49
1:ad:439:LYS:NZ	1:ad:440:GLY:O	2.45	0.49
1:gl:142:GLU:HB3	1:gl:145:HIS:HB2	1.95	0.49
1:hc:327:SER:OG	1:hc:328:LYS:N	2.44	0.49
3:iw:26:LYS:NZ	3:iw:74:ASP:OD2	2.45	0.49
3:kj:26:LYS:NZ	3:kj:74:ASP:OD2	2.45	0.49
3:mm:64:GLN:O	3:mm:66:THR:N	2.46	0.49
3:nn:26:LYS:NZ	3:nn:74:ASP:OD2	2.44	0.49
1:ah:131:TYR:HB3	1:ah:250:MET:HE2	1.94	0.49
1:aq:297:GLU:HG2	1:ar:250:MET:HE1	1.94	0.49
1:aq:521:ILE:O	1:ar:359:LYS:NZ	2.41	0.49
1:er:463:ASP:CG	1:er:465:LYS:HZ3	2.20	0.49
3:ik:26:LYS:NZ	3:ik:74:ASP:OD2	2.45	0.49
3:ku:26:LYS:NZ	3:ku:74:ASP:OD2	2.46	0.49
3:kz:26:LYS:NZ	3:kz:74:ASP:OD2	2.44	0.49
3:oe:26:LYS:NZ	3:oe:74:ASP:OD2	2.45	0.49
1:ay:134:ASP:OD1	1:ay:134:ASP:N	2.44	0.49
1:ay:260:GLU:HG2	1:bd:74:TYR:CE2	2.48	0.49
1:gc:328:LYS:NZ	1:gc:336:ASP:OD2	2.45	0.49
1:gr:328:LYS:NZ	1:gr:336:ASP:OD2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:he:140:PHE:O	2:he:141:SER:C	2.55	0.49
3:im:26:LYS:NZ	3:im:74:ASP:OD2	2.45	0.49
1:bx:121:THR:HG22	1:bx:260:GLU:HG2	1.95	0.49
1:ci:327:SER:OG	1:ci:328:LYS:N	2.44	0.49
1:cm:344:ARG:O	1:cm:345:TRP:HB2	2.12	0.49
1:cs:328:LYS:NZ	1:cs:336:ASP:OD2	2.45	0.49
1:do:327:SER:OG	1:do:328:LYS:N	2.44	0.49
1:ei:402:THR:OG1	1:ei:403:GLY:N	2.46	0.49
1:ek:67:GLU:HB2	1:ez:270:TYR:HA	1.94	0.49
1:fg:327:SER:OG	1:fg:328:LYS:N	2.44	0.49
1:fh:328:LYS:NZ	1:fh:336:ASP:OD2	2.45	0.49
1:ai:402:THR:OG1	1:ai:403:GLY:N	2.46	0.49
1:be:120:PRO:O	1:be:121:THR:OG1	2.31	0.49
1:bn:134:ASP:N	1:bn:134:ASP:OD1	2.42	0.49
1:df:328:LYS:NZ	1:df:336:ASP:OD2	2.45	0.49
1:fy:118:ASN:OD1	1:fy:118:ASN:N	2.46	0.49
1:ge:344:ARG:O	1:ge:345:TRP:HB2	2.12	0.49
2:hk:208:ASP:OD2	2:hk:212:LYS:NZ	2.46	0.49
3:kj:79:THR:O	3:kj:80:GLY:C	2.56	0.49
3:lq:64:GLN:O	3:lq:66:THR:N	2.46	0.49
3:oa:26:LYS:NZ	3:oa:74:ASP:OD2	2.45	0.49
1:ak:521:ILE:O	1:al:359:LYS:NZ	2.41	0.49
1:an:351:LYS:NZ	1:an:390:ASP:O	2.41	0.49
1:db:351:LYS:NZ	1:db:395:TYR:O	2.42	0.49
1:ec:395:TYR:CG	1:ec:396:ALA:N	2.80	0.49
1:gl:83:GLN:NE2	3:my:36:SER:OG	2.45	0.49
3:kg:64:GLN:O	3:kg:66:THR:N	2.46	0.49
1:cb:328:LYS:NZ	1:cb:336:ASP:OD2	2.40	0.49
1:fe:327:SER:OG	1:fe:328:LYS:N	2.45	0.49
3:mg:64:GLN:O	3:mg:66:THR:N	2.46	0.49
1:ag:395:TYR:CG	1:ag:396:ALA:N	2.80	0.49
1:ai:327:SER:OG	1:ai:328:LYS:N	2.46	0.49
1:au:118:ASN:OD1	1:au:118:ASN:N	2.45	0.49
1:bb:328:LYS:NZ	1:bb:336:ASP:OD2	2.42	0.49
1:bg:93:PRO:O	1:bg:94:ALA:C	2.56	0.49
1:bi:344:ARG:O	1:bi:345:TRP:HB2	2.11	0.49
1:bl:344:ARG:O	1:bl:345:TRP:CB	2.61	0.49
1:de:402:THR:OG1	1:de:403:GLY:N	2.46	0.49
1:gb:262:LYS:NZ	1:gc:226:GLU:OE2	2.45	0.49
1:gk:344:ARG:O	1:gk:345:TRP:HB2	2.13	0.49
2:hg:286:GLY:C	2:hg:288:LEU:H	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:hm:227:VAL:N	2:hm:231:THR:OG1	2.46	0.49
3:kp:26:LYS:NZ	3:kp:74:ASP:OD2	2.46	0.49
1:ae:267:LYS:NZ	1:af:237:GLU:OE2	2.46	0.48
1:aq:394:SER:O	1:aq:395:TYR:C	2.56	0.48
1:bm:351:LYS:NZ	1:bm:394:SER:O	2.46	0.48
1:do:328:LYS:NZ	1:do:336:ASP:OD2	2.46	0.48
1:dy:128:ARG:HG2	1:dy:484:PHE:HE1	1.78	0.48
1:fn:145:HIS:NE2	1:fn:487:SER:O	2.46	0.48
3:ii:26:LYS:NZ	3:ii:74:ASP:OD2	2.45	0.48
3:lk:64:GLN:O	3:lk:66:THR:N	2.46	0.48
1:ai:315:GLN:HB2	1:ai:514:ARG:HG3	1.94	0.48
1:ba:439:LYS:NZ	1:ba:440:GLY:O	2.46	0.48
1:bs:72:HIS:HB2	1:bt:260:GLU:CD	2.37	0.48
1:ct:351:LYS:NZ	1:ct:395:TYR:O	2.46	0.48
1:du:439:LYS:NZ	1:du:440:GLY:O	2.46	0.48
1:fz:114:VAL:O	1:fz:115:GLN:C	2.54	0.48
2:he:227:VAL:N	2:he:231:THR:OG1	2.46	0.48
3:kb:14:GLU:OE2	3:kg:16:LYS:NZ	2.47	0.48
3:lt:26:LYS:NZ	3:lt:74:ASP:OD2	2.46	0.48
3:lu:26:LYS:NZ	3:lu:74:ASP:OD2	2.46	0.48
1:bo:327:SER:OG	1:bo:328:LYS:N	2.45	0.48
1:by:83:GLN:NE2	3:jf:36:SER:OG	2.46	0.48
1:fp:273:GLU:OE2	1:gf:474:LYS:NZ	2.42	0.48
1:fq:505:ASN:OD1	1:fq:505:ASN:N	2.43	0.48
1:gb:456:LEU:H	1:gb:475:THR:HG22	1.79	0.48
2:hn:298:LEU:HB2	2:hn:302:ALA:HB3	1.95	0.48
3:kk:79:THR:O	3:kk:80:GLY:C	2.56	0.48
1:bd:344:ARG:O	1:bd:345:TRP:HB2	2.12	0.48
1:dd:278:LEU:HD21	1:dd:284:MET:HB2	1.95	0.48
1:dd:345:TRP:HE1	1:de:344:ARG:H	1.62	0.48
1:er:71:ASP:HB2	1:et:230:THR:HB	1.95	0.48
1:fg:278:LEU:HD21	1:fg:284:MET:HB2	1.95	0.48
1:ge:328:LYS:NZ	1:ge:336:ASP:OD2	2.46	0.48
3:nc:26:LYS:NZ	3:nc:74:ASP:OD2	2.46	0.48
1:bm:327:SER:OG	1:bm:328:LYS:N	2.45	0.48
1:dy:407:ASP:OD1	1:dy:410:LYS:NZ	2.44	0.48
1:em:439:LYS:NZ	1:em:440:GLY:O	2.46	0.48
1:fe:345:TRP:CZ2	1:fe:347:GLY:HA3	2.49	0.48
1:fj:85:SER:HB3	3:mu:32:PHE:CE1	2.49	0.48
3:kr:64:GLN:O	3:kr:66:THR:N	2.46	0.48
1:ai:474:LYS:NZ	1:aw:273:GLU:OE2	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:bu:72:HIS:HB2	1:bv:260:GLU:CD	2.38	0.48
1:bx:131:TYR:HE2	1:bx:143:ALA:HA	1.78	0.48
1:cg:344:ARG:O	1:cg:345:TRP:HB2	2.13	0.48
1:eb:486:GLU:C	1:eb:488:ALA:H	2.22	0.48
1:fq:502:SER:OG	1:fq:503:ILE:N	2.47	0.48
1:gh:409:THR:OG1	1:gh:410:LYS:N	2.47	0.48
2:hm:219:ILE:HD11	2:hm:322:TYR:CZ	2.49	0.48
2:hn:227:VAL:N	2:hn:231:THR:OG1	2.46	0.48
3:ig:64:GLN:O	3:ig:66:THR:N	2.47	0.48
3:nu:26:LYS:NZ	3:nu:74:ASP:OD2	2.46	0.48
1:am:142:GLU:HB3	1:am:145:HIS:HB2	1.95	0.48
1:ao:328:LYS:NZ	1:ao:336:ASP:OD2	2.41	0.48
1:co:85:SER:HB3	3:ju:32:PHE:CE1	2.49	0.48
1:eq:250:MET:HE1	1:ev:297:GLU:HG3	1.96	0.48
1:fj:237:GLU:HG2	1:fj:247:TRP:HD1	1.78	0.48
2:he:46:ASN:H	2:hf:23:ASN:HD22	1.61	0.48
3:iu:79:THR:O	3:iu:80:GLY:C	2.57	0.48
3:ja:64:GLN:O	3:ja:66:THR:N	2.47	0.48
3:jt:26:LYS:NZ	3:jt:74:ASP:OD2	2.46	0.48
1:cp:351:LYS:NZ	1:cp:390:ASP:O	2.43	0.48
2:he:67:LYS:NZ	2:he:264:GLU:OE1	2.47	0.48
3:ii:64:GLN:O	3:ii:66:THR:N	2.47	0.48
3:jg:64:GLN:O	3:jg:66:THR:N	2.46	0.48
1:bq:454:VAL:HB	1:bq:476:ARG:HB2	1.96	0.48
1:cp:91:ILE:HA	1:cz:125:PHE:HZ	1.78	0.48
1:dm:439:LYS:NZ	1:dm:440:GLY:O	2.45	0.48
1:dy:134:ASP:C	1:dy:134:ASP:OD1	2.56	0.48
3:ij:26:LYS:NZ	3:ij:74:ASP:OD2	2.46	0.48
3:kv:26:LYS:NZ	3:kv:74:ASP:OD2	2.47	0.48
3:mu:26:LYS:NZ	3:mu:74:ASP:OD2	2.47	0.48
3:nf:64:GLN:O	3:nf:66:THR:N	2.47	0.48
3:ny:79:THR:OG1	3:ny:80:GLY:N	2.47	0.48
1:af:317:GLY:O	1:af:318:LYS:C	2.57	0.48
1:bs:401:ALA:O	1:bt:420:LYS:NZ	2.46	0.48
1:bt:83:GLN:NE2	3:jc:36:SER:OG	2.47	0.48
1:by:486:GLU:O	1:by:488:ALA:N	2.46	0.48
1:ce:502:SER:OG	1:ce:503:ILE:N	2.46	0.48
1:cs:327:SER:OG	1:cs:328:LYS:N	2.46	0.48
1:dp:266:LEU:HD21	1:dq:155:SER:HB3	1.96	0.48
1:eo:146:PRO:HB2	1:eo:366:ARG:O	2.14	0.48
1:fa:327:SER:OG	1:fa:328:LYS:N	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fj:134:ASP:OD1	1:fj:134:ASP:N	2.42	0.48
1:fv:131:TYR:HB3	1:fv:250:MET:HE2	1.96	0.48
2:hj:352:ASP:O	2:hj:353:ASP:C	2.57	0.48
3:ms:26:LYS:NZ	3:ms:74:ASP:OD2	2.47	0.48
1:as:226:GLU:OE2	1:ax:262:LYS:NZ	2.46	0.47
1:bw:72:HIS:HB2	1:bx:260:GLU:CD	2.39	0.47
1:bx:78:ASN:O	1:bx:80:ALA:N	2.47	0.47
1:co:273:GLU:OE2	1:gn:474:LYS:NZ	2.39	0.47
1:dc:327:SER:OG	1:dc:328:LYS:N	2.45	0.47
1:dw:264:ARG:HD2	1:dw:302:ILE:HG13	1.96	0.47
1:dx:317:GLY:O	1:dx:318:LYS:C	2.57	0.47
1:ew:260:GLU:HG2	1:fb:74:TYR:CE1	2.49	0.47
1:ex:83:GLN:NE2	3:lt:36:SER:OG	2.47	0.47
1:fm:344:ARG:O	1:fm:345:TRP:CB	2.62	0.47
1:gh:439:LYS:NZ	1:gh:440:GLY:O	2.44	0.47
1:gq:297:GLU:HB3	1:gr:250:MET:HE1	1.95	0.47
1:gq:402:THR:OG1	1:gq:403:GLY:N	2.47	0.47
2:he:352:ASP:O	2:he:353:ASP:C	2.57	0.47
3:jf:26:LYS:NZ	3:jf:74:ASP:OD2	2.46	0.47
1:be:260:GLU:HG2	1:bj:74:TYR:CE1	2.49	0.47
1:bz:398:GLN:HE21	1:ca:351:LYS:HD2	1.79	0.47
1:ch:463:ASP:CG	1:ch:465:LYS:HZ3	2.21	0.47
1:cm:278:LEU:HD21	1:cm:284:MET:HB2	1.96	0.47
1:eb:154:PHE:CZ	1:eb:248:ASN:HB3	2.49	0.47
1:eb:317:GLY:O	1:eb:318:LYS:C	2.57	0.47
1:fv:294:LEU:HA	1:fw:250:MET:HE3	1.95	0.47
1:hd:121:THR:HA	1:hd:259:ILE:O	2.14	0.47
2:hn:240:TYR:HE1	2:hn:421:PRO:HG2	1.80	0.47
3:hq:64:GLN:O	3:hq:66:THR:N	2.48	0.47
3:mm:79:THR:O	3:mm:80:GLY:C	2.57	0.47
3:ny:26:LYS:NZ	3:ny:74:ASP:OD2	2.46	0.47
1:ar:317:GLY:HA2	1:ar:514:ARG:HE	1.77	0.47
1:as:521:ILE:O	1:at:359:LYS:NZ	2.45	0.47
1:co:430:LYS:NZ	1:cp:223:GLU:OE1	2.47	0.47
1:dd:454:VAL:HB	1:dd:476:ARG:HB2	1.96	0.47
1:fq:474:LYS:NZ	1:ge:273:GLU:OE2	2.39	0.47
3:im:30:VAL:O	3:im:31:ALA:C	2.57	0.47
1:aj:134:ASP:OD1	1:aj:134:ASP:N	2.41	0.47
1:ba:93:PRO:O	1:ba:94:ALA:C	2.58	0.47
1:bc:402:THR:OG1	1:bc:403:GLY:N	2.47	0.47
1:cy:521:ILE:O	1:cz:359:LYS:NZ	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:do:454:VAL:HB	1:do:476:ARG:HB2	1.95	0.47
1:eg:402:THR:OG1	1:eg:403:GLY:N	2.47	0.47
1:eg:502:SER:OG	1:eg:503:ILE:N	2.47	0.47
1:fk:93:PRO:O	1:fk:94:ALA:C	2.57	0.47
1:gl:344:ARG:O	1:gl:345:TRP:HB2	2.13	0.47
1:gl:446:ALA:HB3	1:gl:449:TYR:CE1	2.48	0.47
1:hd:270:TYR:HE2	1:hd:275:ALA:HB2	1.80	0.47
2:hk:239:SER:OG	2:hk:240:TYR:N	2.48	0.47
3:ku:64:GLN:O	3:ku:66:THR:N	2.47	0.47
3:la:64:GLN:O	3:la:66:THR:N	2.47	0.47
3:lg:64:GLN:O	3:lg:66:THR:N	2.48	0.47
3:lo:64:GLN:O	3:lo:66:THR:N	2.47	0.47
3:mz:30:VAL:O	3:mz:31:ALA:C	2.57	0.47
3:ob:26:LYS:NZ	3:ob:74:ASP:OD2	2.47	0.47
1:al:417:LEU:HB3	1:al:421:TYR:HB2	1.96	0.47
1:au:474:LYS:NZ	1:bu:273:GLU:OE2	2.44	0.47
1:cp:439:LYS:NZ	1:cp:440:GLY:O	2.44	0.47
1:fs:402:THR:OG1	1:fs:403:GLY:N	2.47	0.47
1:fu:439:LYS:NZ	1:fu:440:GLY:O	2.45	0.47
1:gj:486:GLU:O	1:gj:488:ALA:N	2.48	0.47
3:jf:79:THR:O	3:jf:80:GLY:C	2.57	0.47
3:jq:64:GLN:O	3:jq:66:THR:N	2.48	0.47
3:jr:64:GLN:O	3:jr:66:THR:N	2.47	0.47
1:ao:327:SER:OG	1:ao:328:LYS:N	2.45	0.47
1:au:439:LYS:NZ	1:au:440:GLY:O	2.43	0.47
1:aw:402:THR:OG1	1:aw:403:GLY:N	2.47	0.47
1:cq:136:VAL:HG22	1:cq:253:ARG:HG3	1.96	0.47
1:cr:344:ARG:O	1:cr:345:TRP:HB2	2.14	0.47
1:dk:344:ARG:O	1:dk:345:TRP:HB2	2.13	0.47
1:gs:131:TYR:CB	1:gs:250:MET:HB3	2.44	0.47
3:iy:64:GLN:O	3:iy:66:THR:N	2.48	0.47
3:jp:26:LYS:NZ	3:jp:74:ASP:OD2	2.48	0.47
3:lm:30:VAL:O	3:lm:31:ALA:C	2.58	0.47
1:ag:344:ARG:O	1:ag:345:TRP:HB2	2.14	0.47
1:ah:231:SER:HB3	1:al:71:ASP:HB2	1.97	0.47
1:ao:278:LEU:HD21	1:ao:284:MET:HB2	1.96	0.47
1:bm:72:HIS:HB2	1:bn:260:GLU:CD	2.40	0.47
1:bn:269:ALA:O	1:bq:66:ALA:N	2.47	0.47
1:ci:114:VAL:H	1:ci:443:GLU:HG2	1.80	0.47
1:cm:93:PRO:O	1:cm:94:ALA:C	2.58	0.47
1:cv:262:LYS:NZ	1:cw:226:GLU:OE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:de:409:THR:OG1	1:de:410:LYS:N	2.48	0.47
1:dj:502:SER:OG	1:dj:503:ILE:N	2.48	0.47
1:dw:344:ARG:O	1:dw:345:TRP:HB2	2.15	0.47
1:dy:118:ASN:OD1	1:dy:118:ASN:N	2.47	0.47
1:ed:118:ASN:OD1	1:ed:118:ASN:N	2.48	0.47
1:fk:327:SER:OG	1:fk:328:LYS:N	2.46	0.47
1:fw:502:SER:OG	1:fw:503:ILE:N	2.48	0.47
1:fy:184:GLU:HB2	1:fy:366:ARG:HH22	1.80	0.47
1:fy:297:GLU:HG2	1:fz:250:MET:HE1	1.95	0.47
1:gm:131:TYR:HB3	1:gm:250:MET:HB3	1.97	0.47
1:gp:344:ARG:O	1:gp:345:TRP:HB2	2.14	0.47
3:im:64:GLN:O	3:im:66:THR:N	2.48	0.47
3:iz:26:LYS:NZ	3:iz:74:ASP:OD2	2.47	0.47
3:ki:64:GLN:O	3:ki:66:THR:N	2.48	0.47
3:ko:64:GLN:O	3:ko:66:THR:N	2.48	0.47
3:nn:64:GLN:O	3:nn:66:THR:N	2.47	0.47
1:ae:328:LYS:NZ	1:ae:336:ASP:OD2	2.43	0.47
1:cc:521:ILE:O	1:cd:359:LYS:NZ	2.47	0.47
1:co:199:ASP:OD2	1:co:207:LYS:NZ	2.48	0.47
1:cs:439:LYS:NZ	1:cs:440:GLY:O	2.45	0.47
1:dv:266:LEU:HD21	1:dw:155:SER:HB3	1.97	0.47
1:eg:344:ARG:O	1:eg:345:TRP:HB2	2.15	0.47
1:eu:93:PRO:O	1:eu:94:ALA:C	2.58	0.47
1:fd:521:ILE:O	1:fe:359:LYS:NZ	2.39	0.47
1:hd:319:SER:N	1:hd:322:THR:OG1	2.46	0.47
2:hk:248:ARG:HG2	2:hk:287:TRP:CZ3	2.49	0.47
3:ly:79:THR:O	3:ly:80:GLY:C	2.58	0.47
3:me:64:GLN:O	3:me:66:THR:N	2.47	0.47
1:ar:328:LYS:NZ	1:ar:336:ASP:OD2	2.42	0.47
1:dh:521:ILE:O	1:di:359:LYS:NZ	2.48	0.47
1:dq:351:LYS:NZ	1:dq:395:TYR:O	2.37	0.47
1:ed:131:TYR:CE1	1:ed:143:ALA:HA	2.50	0.47
2:hn:341:PHE:O	2:hn:343:ALA:N	2.48	0.47
3:hx:26:LYS:NZ	3:hx:74:ASP:OD2	2.47	0.47
3:ie:64:GLN:O	3:ie:66:THR:N	2.47	0.47
3:od:26:LYS:NZ	3:od:74:ASP:OD2	2.48	0.47
1:ae:439:LYS:NZ	1:ae:440:GLY:O	2.47	0.47
1:ao:125:PHE:CZ	1:ca:91:ILE:HG12	2.49	0.47
1:au:404:PHE:CZ	1:au:417:LEU:HA	2.47	0.47
1:bc:345:TRP:CG	1:bc:346:ALA:N	2.83	0.47
1:bz:344:ARG:O	1:bz:345:TRP:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ca:344:ARG:O	1:ca:345:TRP:CB	2.63	0.47
1:cq:380:ARG:NH2	1:cq:408:THR:OG1	2.48	0.47
1:dq:84:THR:OG1	1:dq:85:SER:N	2.47	0.47
1:eb:118:ASN:OD1	1:eb:118:ASN:N	2.47	0.47
1:fk:230:THR:O	1:fk:234:GLU:HB2	2.14	0.47
2:hk:352:ASP:O	2:hk:353:ASP:C	2.57	0.47
3:hy:64:GLN:O	3:hy:66:THR:N	2.48	0.47
3:jb:40:LYS:H	3:jb:72:ASN:HD21	1.62	0.47
3:jl:64:GLN:O	3:jl:66:THR:N	2.48	0.47
3:jo:64:GLN:O	3:jo:66:THR:N	2.48	0.47
3:kb:64:GLN:O	3:kb:66:THR:N	2.48	0.47
3:ln:35:TYR:HE1	3:ln:41:ILE:HD12	1.79	0.47
3:lt:64:GLN:O	3:lt:66:THR:N	2.48	0.47
1:br:502:SER:OG	1:br:503:ILE:N	2.48	0.46
1:eb:486:GLU:HG3	1:eb:509:LYS:HB3	1.97	0.46
1:gp:317:GLY:O	1:gp:318:LYS:C	2.59	0.46
1:gy:439:LYS:NZ	1:gy:440:GLY:O	2.46	0.46
2:hf:227:VAL:N	2:hf:231:THR:OG1	2.48	0.46
3:ik:64:GLN:O	3:ik:66:THR:N	2.48	0.46
3:in:30:VAL:O	3:in:31:ALA:C	2.57	0.46
1:aa:142:GLU:HB3	1:aa:145:HIS:HB2	1.98	0.46
1:ay:483:PRO:O	1:ay:484:PHE:HB2	2.16	0.46
1:cg:278:LEU:HD21	1:cg:284:MET:HB2	1.97	0.46
1:ff:474:LYS:NZ	1:gl:273:GLU:OE2	2.44	0.46
1:fr:344:ARG:O	1:fr:345:TRP:CB	2.62	0.46
1:gj:123:GLN:HG3	1:gj:124:VAL:N	2.30	0.46
2:hi:181:VAL:H	2:hi:370:GLN:HG2	1.80	0.46
3:jw:30:VAL:O	3:jw:31:ALA:C	2.57	0.46
3:kd:30:VAL:O	3:kd:31:ALA:C	2.58	0.46
3:kx:64:GLN:O	3:kx:66:THR:N	2.48	0.46
3:lz:26:LYS:NZ	3:lz:74:ASP:OD2	2.47	0.46
1:by:142:GLU:HB3	1:by:145:HIS:HB2	1.97	0.46
1:cg:407:ASP:HB3	1:ch:372:GLU:HG3	1.98	0.46
1:cw:454:VAL:HB	1:cw:476:ARG:HB2	1.97	0.46
1:ef:502:SER:OG	1:ef:503:ILE:N	2.47	0.46
1:ei:521:ILE:O	1:ej:359:LYS:NZ	2.47	0.46
1:en:327:SER:OG	1:en:328:LYS:N	2.48	0.46
1:fc:120:PRO:O	1:fc:121:THR:OG1	2.32	0.46
1:fx:72:HIS:HB2	1:fy:260:GLU:CD	2.40	0.46
2:hm:243:ALA:HB3	2:hm:244:PRO:CD	2.45	0.46
3:kh:30:VAL:O	3:kh:31:ALA:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:of:64:GLN:O	3:of:66:THR:N	2.48	0.46
1:bn:250:MET:SD	1:bn:250:MET:C	2.98	0.46
1:by:121:THR:HG22	1:by:260:GLU:HG2	1.96	0.46
1:dj:134:ASP:OD1	1:dj:134:ASP:N	2.47	0.46
1:ds:521:ILE:O	1:dt:359:LYS:NZ	2.48	0.46
1:dv:121:THR:HG22	1:dv:260:GLU:HB3	1.97	0.46
1:fh:114:VAL:O	1:fh:115:GLN:C	2.58	0.46
3:il:26:LYS:NZ	3:il:74:ASP:OD2	2.48	0.46
3:js:64:GLN:O	3:js:66:THR:N	2.48	0.46
1:am:133:LYS:HG2	1:am:249:GLU:HG3	1.96	0.46
1:am:398:GLN:OE1	1:am:398:GLN:N	2.48	0.46
1:ar:317:GLY:O	1:ar:318:LYS:C	2.59	0.46
1:aw:454:VAL:HB	1:aw:476:ARG:HB2	1.97	0.46
1:bl:105:ASN:HB2	1:bl:412:VAL:HG23	1.98	0.46
1:bo:142:GLU:HB3	1:bo:145:HIS:HB2	1.98	0.46
1:by:131:TYR:HB3	1:by:250:MET:HE2	1.98	0.46
1:bz:402:THR:OG1	1:bz:403:GLY:N	2.48	0.46
1:de:203:THR:OG1	1:de:204:ASP:N	2.48	0.46
1:er:237:GLU:HG2	1:er:247:TRP:CD1	2.51	0.46
1:ga:268:ALA:O	1:gj:66:ALA:N	2.48	0.46
2:hn:243:ALA:HB3	2:hn:244:PRO:CD	2.45	0.46
3:iq:30:VAL:O	3:iq:31:ALA:C	2.59	0.46
3:jw:79:THR:O	3:jw:80:GLY:C	2.58	0.46
3:ks:64:GLN:O	3:ks:66:THR:N	2.48	0.46
3:lc:64:GLN:O	3:lc:66:THR:N	2.49	0.46
3:lq:30:VAL:O	3:lq:31:ALA:C	2.59	0.46
3:nh:64:GLN:O	3:nh:66:THR:N	2.49	0.46
3:np:64:GLN:O	3:np:66:THR:N	2.48	0.46
1:ai:228:MET:O	1:ai:229:ALA:C	2.57	0.46
1:am:117:MET:HB2	1:am:453:TYR:HB2	1.98	0.46
1:ao:439:LYS:NZ	1:ao:440:GLY:O	2.46	0.46
1:as:262:LYS:NZ	1:at:226:GLU:OE2	2.49	0.46
1:av:317:GLY:O	1:av:318:LYS:C	2.59	0.46
1:ce:444:MET:SD	1:ce:449:TYR:OH	2.74	0.46
1:dc:402:THR:OG1	1:dc:403:GLY:N	2.49	0.46
1:eh:120:PRO:O	1:eh:121:THR:OG1	2.29	0.46
1:ei:456:LEU:H	1:ei:475:THR:HG22	1.80	0.46
1:er:439:LYS:NZ	1:er:440:GLY:O	2.46	0.46
1:fl:145:HIS:CD2	1:fl:490:GLN:HG2	2.51	0.46
3:kk:30:VAL:O	3:kk:31:ALA:C	2.59	0.46
3:li:64:GLN:O	3:li:66:THR:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:oe:64:GLN:O	3:oe:66:THR:N	2.49	0.46
1:ad:93:PRO:O	1:ad:94:ALA:C	2.57	0.46
1:bf:93:PRO:O	1:bf:94:ALA:C	2.59	0.46
1:cb:317:GLY:O	1:cb:318:LYS:C	2.58	0.46
1:ex:439:LYS:NZ	1:ex:440:GLY:O	2.43	0.46
1:fb:319:SER:OG	1:fb:514:ARG:NH2	2.49	0.46
1:fn:502:SER:OG	1:fn:503:ILE:N	2.48	0.46
1:fr:121:THR:HA	1:fr:259:ILE:O	2.16	0.46
1:gq:294:LEU:HA	1:gr:250:MET:CE	2.45	0.46
1:gt:439:LYS:NZ	1:gt:440:GLY:O	2.48	0.46
2:ho:243:ALA:HB3	2:ho:244:PRO:CD	2.45	0.46
1:bi:327:SER:OG	1:bi:328:LYS:N	2.42	0.46
1:dy:155:SER:HB3	1:ed:266:LEU:HG	1.97	0.46
1:ec:266:LEU:CG	1:ed:155:SER:HB3	2.46	0.46
1:eu:72:HIS:HB2	1:ev:260:GLU:CD	2.41	0.46
1:ey:93:PRO:O	1:ey:94:ALA:C	2.58	0.46
1:fa:121:THR:HG22	1:fa:260:GLU:HB3	1.97	0.46
1:gq:121:THR:HG22	1:gq:260:GLU:HG2	1.97	0.46
2:hm:239:SER:OG	2:hm:240:TYR:N	2.48	0.46
3:ie:30:VAL:O	3:ie:31:ALA:C	2.58	0.46
3:jh:79:THR:O	3:jh:80:GLY:C	2.58	0.46
3:ju:64:GLN:O	3:ju:66:THR:N	2.49	0.46
3:ka:64:GLN:O	3:ka:66:THR:N	2.49	0.46
3:ko:30:VAL:O	3:ko:31:ALA:C	2.59	0.46
1:ab:71:ASP:OD2	1:ab:74:TYR:OH	2.30	0.46
1:ai:345:TRP:CG	1:ai:346:ALA:N	2.83	0.46
1:at:474:LYS:NZ	1:bh:273:GLU:OE2	2.38	0.46
1:bm:502:SER:OG	1:bm:503:ILE:N	2.49	0.46
1:cw:502:SER:OG	1:cw:503:ILE:N	2.48	0.46
1:eo:351:LYS:NZ	1:eo:395:TYR:O	2.46	0.46
1:fk:328:LYS:NZ	1:fk:336:ASP:OD2	2.42	0.46
1:ft:450:TYR:CZ	1:ft:452:PRO:HG3	2.50	0.46
1:ge:93:PRO:O	1:ge:94:ALA:C	2.59	0.46
1:gg:344:ARG:O	1:gg:345:TRP:HB2	2.16	0.46
1:gp:301:GLU:OE1	1:gq:155:SER:OG	2.30	0.46
1:gz:351:LYS:NZ	1:gz:390:ASP:O	2.48	0.46
3:ic:30:VAL:O	3:ic:31:ALA:C	2.58	0.46
3:if:64:GLN:O	3:if:66:THR:N	2.49	0.46
3:ig:79:THR:O	3:ig:80:GLY:C	2.59	0.46
3:ir:26:LYS:NZ	3:ir:74:ASP:OD2	2.49	0.46
3:ir:30:VAL:O	3:ir:31:ALA:C	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:iw:64:GLN:O	3:iw:66:THR:N	2.49	0.46
3:nc:72:ASN:HD22	3:nc:72:ASN:C	2.24	0.46
3:nx:64:GLN:O	3:nx:66:THR:N	2.49	0.46
1:ag:317:GLY:O	1:ag:318:LYS:C	2.59	0.46
1:ah:131:TYR:HB3	1:ah:250:MET:HB3	1.98	0.46
1:aj:93:PRO:O	1:aj:94:ALA:C	2.60	0.46
1:bh:118:ASN:OD1	1:bh:118:ASN:N	2.48	0.46
1:ce:402:THR:OG1	1:ce:403:GLY:N	2.49	0.46
1:dh:301:GLU:OE1	1:di:155:SER:OG	2.23	0.46
1:dy:317:GLY:O	1:dy:318:LYS:C	2.59	0.46
1:ek:118:ASN:OD1	1:ek:118:ASN:N	2.48	0.46
1:en:344:ARG:O	1:en:345:TRP:CB	2.63	0.46
1:fb:120:PRO:O	1:fb:121:THR:OG1	2.31	0.46
1:fp:120:PRO:O	1:fp:121:THR:OG1	2.31	0.46
1:fy:114:VAL:O	1:fy:115:GLN:C	2.59	0.46
1:ga:74:TYR:OH	1:gc:229:ALA:HA	2.15	0.46
1:gy:454:VAL:HB	1:gy:476:ARG:HB2	1.98	0.46
1:hc:93:PRO:O	1:hc:94:ALA:C	2.59	0.46
3:hy:30:VAL:O	3:hy:31:ALA:C	2.59	0.46
3:iq:64:GLN:O	3:iq:66:THR:N	2.49	0.46
3:nk:26:LYS:NZ	3:nk:74:ASP:OD2	2.48	0.46
3:nm:31:ALA:O	3:nm:32:PHE:C	2.59	0.46
3:of:26:LYS:NZ	3:of:74:ASP:OD2	2.49	0.46
1:av:474:LYS:NZ	1:cb:273:GLU:OE2	2.38	0.45
1:bc:467:PHE:O	1:bc:467:PHE:CG	2.69	0.45
1:bd:236:GLN:HG2	1:bd:247:TRP:CE2	2.50	0.45
1:ck:444:MET:HA	1:ck:449:TYR:OH	2.16	0.45
1:cw:402:THR:OG1	1:cw:403:GLY:N	2.50	0.45
1:ef:345:TRP:HA	1:eg:341:ARG:O	2.15	0.45
1:eq:243:THR:OG1	1:eq:244:ASP:N	2.49	0.45
1:ev:134:ASP:OD1	1:ev:134:ASP:N	2.49	0.45
1:fi:262:LYS:NZ	1:fj:226:GLU:OE2	2.49	0.45
1:fx:266:LEU:CD2	1:fy:155:SER:HB3	2.46	0.45
1:ga:128:ARG:HD2	1:ga:253:ARG:NH1	2.30	0.45
1:gb:451:ALA:O	1:gb:477:TYR:HB2	2.15	0.45
3:id:79:THR:O	3:id:80:GLY:C	2.59	0.45
3:je:64:GLN:O	3:je:66:THR:N	2.49	0.45
3:jm:64:GLN:O	3:jm:66:THR:N	2.49	0.45
3:le:64:GLN:O	3:le:66:THR:N	2.49	0.45
3:lu:64:GLN:O	3:lu:66:THR:N	2.49	0.45
1:bf:439:LYS:NZ	1:bf:440:GLY:O	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:bi:198:ILE:O	1:bi:198:ILE:HG22	2.15	0.45
1:by:402:THR:OG1	1:by:403:GLY:N	2.49	0.45
1:da:262:LYS:NZ	1:db:226:GLU:OE2	2.49	0.45
1:fp:151:ASP:C	1:fp:151:ASP:OD1	2.58	0.45
1:fp:439:LYS:NZ	1:fp:440:GLY:O	2.46	0.45
1:fw:73:GLY:C	1:fw:75:ASN:N	2.74	0.45
1:fy:198:ILE:O	1:fy:198:ILE:HG22	2.17	0.45
1:gd:317:GLY:O	1:gd:318:LYS:C	2.59	0.45
1:go:502:SER:OG	1:go:503:ILE:N	2.49	0.45
3:ih:64:GLN:O	3:ih:66:THR:N	2.49	0.45
3:lu:30:VAL:O	3:lu:31:ALA:C	2.58	0.45
3:nb:64:GLN:O	3:nb:66:THR:N	2.49	0.45
3:og:64:GLN:O	3:og:66:THR:N	2.50	0.45
1:ak:267:LYS:NZ	1:al:237:GLU:OE2	2.47	0.45
1:az:120:PRO:O	1:az:121:THR:OG1	2.31	0.45
1:bo:203:THR:OG1	1:bo:204:ASP:N	2.49	0.45
1:cm:402:THR:OG1	1:cm:403:GLY:N	2.50	0.45
1:de:439:LYS:NZ	1:de:440:GLY:O	2.47	0.45
1:dm:120:PRO:O	1:dm:121:THR:OG1	2.33	0.45
1:du:502:SER:OG	1:du:503:ILE:N	2.50	0.45
1:en:344:ARG:O	1:en:345:TRP:HB2	2.16	0.45
1:gm:243:THR:OG1	1:gm:244:ASP:N	2.49	0.45
2:hn:239:SER:OG	2:hn:240:TYR:N	2.49	0.45
3:ld:30:VAL:O	3:ld:31:ALA:C	2.59	0.45
3:lg:30:VAL:O	3:lg:31:ALA:C	2.60	0.45
3:mo:64:GLN:O	3:mo:66:THR:N	2.49	0.45
3:mq:64:GLN:O	3:mq:66:THR:N	2.48	0.45
3:nl:64:GLN:O	3:nl:66:THR:N	2.49	0.45
3:ny:64:GLN:O	3:ny:66:THR:N	2.49	0.45
1:af:145:HIS:CD2	1:af:490:GLN:HG2	2.51	0.45
1:aj:317:GLY:O	1:aj:318:LYS:C	2.60	0.45
1:an:243:THR:OG1	1:an:244:ASP:N	2.50	0.45
1:ax:67:GLU:HG3	1:bb:135:PRO:HG2	1.98	0.45
1:be:243:THR:OG1	1:be:244:ASP:N	2.50	0.45
1:bf:72:HIS:HB2	1:bg:260:GLU:OE2	2.15	0.45
1:bt:317:GLY:O	1:bt:318:LYS:C	2.59	0.45
1:cj:72:HIS:HB2	1:ck:260:GLU:OE2	2.16	0.45
1:dt:505:ASN:OD1	1:dt:505:ASN:N	2.48	0.45
1:eq:490:GLN:N	1:eq:490:GLN:OE1	2.50	0.45
1:fs:203:THR:OG1	1:fs:204:ASP:N	2.50	0.45
1:ga:444:MET:HA	1:ga:449:TYR:OH	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:gd:72:HIS:HB2	1:ge:260:GLU:CD	2.40	0.45
1:gt:351:LYS:NZ	1:gt:395:TYR:O	2.35	0.45
1:hd:228:MET:O	1:hd:229:ALA:C	2.59	0.45
1:hd:315:GLN:HB2	1:hd:514:ARG:HD2	1.99	0.45
2:hg:227:VAL:N	2:hg:231:THR:OG1	2.50	0.45
2:hl:243:ALA:HB3	2:hl:244:PRO:CD	2.47	0.45
3:hq:30:VAL:O	3:hq:31:ALA:C	2.59	0.45
3:jc:79:THR:O	3:jc:80:GLY:C	2.59	0.45
3:mv:64:GLN:O	3:mv:66:THR:N	2.49	0.45
3:mx:64:GLN:O	3:mx:66:THR:N	2.50	0.45
1:al:505:ASN:OD1	1:al:505:ASN:N	2.47	0.45
1:am:344:ARG:O	1:am:345:TRP:HB2	2.16	0.45
1:bn:243:THR:OG1	1:bn:244:ASP:N	2.50	0.45
1:eb:93:PRO:O	1:eb:94:ALA:C	2.59	0.45
1:ed:131:TYR:HE1	1:ed:143:ALA:HA	1.80	0.45
1:ed:328:LYS:NZ	1:ed:336:ASP:OD2	2.43	0.45
1:ee:430:LYS:NZ	1:ef:223:GLU:OE2	2.46	0.45
1:fe:521:ILE:O	1:ff:359:LYS:NZ	2.43	0.45
2:hf:243:ALA:HB3	2:hf:244:PRO:CD	2.46	0.45
2:ho:40:VAL:HG12	2:ho:42:THR:HB	1.97	0.45
1:ag:93:PRO:HA	1:ah:121:THR:O	2.16	0.45
1:ai:502:SER:OG	1:ai:503:ILE:N	2.50	0.45
1:bn:118:ASN:OD1	1:bn:118:ASN:N	2.49	0.45
1:bq:456:LEU:H	1:bq:475:THR:HG22	1.82	0.45
1:ca:402:THR:OG1	1:ca:403:GLY:N	2.49	0.45
1:cc:279:ARG:HA	1:cc:279:ARG:HD3	1.83	0.45
1:ce:287:ASP:OD1	1:ce:287:ASP:N	2.49	0.45
1:cg:351:LYS:NZ	1:cg:390:ASP:O	2.41	0.45
1:cu:118:ASN:OD1	1:cu:118:ASN:N	2.48	0.45
1:cy:351:LYS:NZ	1:cy:395:TYR:O	2.36	0.45
1:db:521:ILE:O	1:dc:359:LYS:NZ	2.43	0.45
1:ek:142:GLU:HB3	1:ek:145:HIS:HB2	1.99	0.45
1:ey:266:LEU:CG	1:ez:155:SER:HB3	2.47	0.45
1:fh:482:ASN:O	1:fh:483:PRO:C	2.60	0.45
1:fi:133:LYS:HA	1:fi:249:GLU:HG3	1.99	0.45
1:fj:344:ARG:O	1:fj:345:TRP:CB	2.65	0.45
1:fq:142:GLU:HB3	1:fq:145:HIS:HB2	1.98	0.45
1:gq:344:ARG:O	1:gq:345:TRP:HB2	2.16	0.45
1:gz:446:ALA:HB3	1:gz:449:TYR:CE1	2.52	0.45
3:hr:64:GLN:O	3:hr:66:THR:N	2.50	0.45
3:ii:30:VAL:O	3:ii:31:ALA:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:io:79:THR:O	3:io:80:GLY:C	2.59	0.45
3:jr:48:THR:OG1	3:jr:49:PHE:N	2.49	0.45
3:ky:64:GLN:O	3:ky:66:THR:N	2.49	0.45
3:my:32:PHE:HB3	3:my:33:PRO:HD3	1.99	0.45
1:ay:155:SER:HB3	1:bd:266:LEU:CD2	2.46	0.45
1:bk:142:GLU:HB3	1:bk:145:HIS:HB2	1.97	0.45
1:bx:71:ASP:OD2	1:bz:230:THR:N	2.50	0.45
1:bz:344:ARG:O	1:bz:345:TRP:CB	2.65	0.45
1:cw:363:GLU:HG2	1:cw:514:ARG:HH12	1.81	0.45
1:cz:274:LEU:CD2	1:gr:67:GLU:HG2	2.47	0.45
1:dw:463:ASP:OD2	1:dw:465:LYS:NZ	2.44	0.45
1:ep:411:SER:OG	1:ep:412:VAL:N	2.50	0.45
1:fg:456:LEU:H	1:fg:475:THR:HG22	1.80	0.45
1:gc:521:ILE:O	1:gd:359:LYS:NZ	2.44	0.45
1:gf:243:THR:OG1	1:gf:244:ASP:N	2.50	0.45
1:gh:262:LYS:NZ	1:gi:226:GLU:OE2	2.49	0.45
1:gp:454:VAL:HB	1:gp:476:ARG:HB2	1.99	0.45
3:ht:30:VAL:O	3:ht:31:ALA:C	2.60	0.45
3:ij:30:VAL:O	3:ij:31:ALA:C	2.60	0.45
3:mp:64:GLN:O	3:mp:66:THR:N	2.50	0.45
3:mq:30:VAL:O	3:mq:31:ALA:C	2.58	0.45
3:nc:64:GLN:O	3:nc:66:THR:N	2.50	0.45
3:nw:79:THR:OG1	3:nw:80:GLY:N	2.50	0.45
1:aa:402:THR:OG1	1:aa:403:GLY:N	2.50	0.45
1:ah:439:LYS:NZ	1:ah:440:GLY:O	2.46	0.45
1:ao:502:SER:OG	1:ao:503:ILE:N	2.50	0.45
1:ca:203:THR:OG1	1:ca:204:ASP:N	2.49	0.45
1:ch:317:GLY:O	1:ch:318:LYS:C	2.59	0.45
1:cu:439:LYS:NZ	1:cu:440:GLY:O	2.46	0.45
1:cy:302:ILE:HD13	1:cy:477:TYR:CE1	2.52	0.45
1:dr:317:GLY:O	1:dr:318:LYS:C	2.60	0.45
1:dz:317:GLY:O	1:dz:318:LYS:C	2.60	0.45
1:dz:439:LYS:NZ	1:dz:440:GLY:O	2.46	0.45
1:ee:118:ASN:OD1	1:ee:118:ASN:N	2.48	0.45
1:es:439:LYS:NZ	1:es:440:GLY:O	2.46	0.45
1:fi:297:GLU:CB	1:fj:250:MET:HE1	2.47	0.45
1:gl:317:GLY:O	1:gl:318:LYS:C	2.60	0.45
1:gy:317:GLY:O	1:gy:318:LYS:C	2.59	0.45
2:hk:170:VAL:HG21	2:hk:345:TYR:CD2	2.52	0.45
3:hx:64:GLN:O	3:hx:66:THR:N	2.50	0.45
3:ij:64:GLN:O	3:ij:66:THR:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:jc:64:GLN:O	3:jc:66:THR:N	2.49	0.45
3:ji:79:THR:O	3:ji:80:GLY:C	2.60	0.45
3:lk:30:VAL:O	3:lk:31:ALA:C	2.60	0.45
3:nh:79:THR:O	3:nh:80:GLY:C	2.60	0.45
1:ai:297:GLU:HG2	1:aj:250:MET:HE1	1.99	0.45
1:an:301:GLU:OE2	1:ao:155:SER:OG	2.30	0.45
1:bq:118:ASN:OD1	1:bq:118:ASN:N	2.49	0.45
1:bu:134:ASP:OD1	1:bu:134:ASP:N	2.45	0.45
1:cr:345:TRP:HE1	1:cs:344:ARG:H	1.65	0.45
1:dn:409:THR:OG1	1:dn:410:LYS:N	2.48	0.45
1:er:270:TYR:HA	1:fa:67:GLU:HB2	1.99	0.45
1:es:448:ILE:HG12	1:es:513:PHE:CE2	2.52	0.45
1:ev:93:PRO:O	1:ev:94:ALA:C	2.59	0.45
1:fj:454:VAL:HB	1:fj:476:ARG:HB2	1.98	0.45
1:fm:346:ALA:O	1:fm:347:GLY:C	2.56	0.45
1:gc:456:LEU:H	1:gc:475:THR:HG22	1.82	0.45
1:gu:411:SER:OG	1:gu:412:VAL:N	2.49	0.45
2:hj:401:GLY:O	2:hj:402:ASP:C	2.59	0.45
3:jf:48:THR:OG1	3:jf:49:PHE:N	2.50	0.45
3:kl:64:GLN:O	3:kl:66:THR:N	2.50	0.45
3:li:30:VAL:O	3:li:31:ALA:C	2.60	0.45
3:lw:30:VAL:O	3:lw:31:ALA:C	2.60	0.45
3:nf:30:VAL:O	3:nf:31:ALA:C	2.60	0.45
1:aa:243:THR:OG1	1:aa:244:ASP:N	2.50	0.45
1:al:351:LYS:NZ	1:al:394:SER:O	2.49	0.45
1:be:155:SER:HB3	1:bj:266:LEU:HD21	1.99	0.45
1:br:198:ILE:O	1:br:198:ILE:HG22	2.16	0.45
1:ct:411:SER:OG	1:ct:412:VAL:N	2.50	0.45
1:fo:317:GLY:O	1:fo:318:LYS:C	2.60	0.45
1:gs:291:SER:HB2	1:gs:473:PHE:HE2	1.82	0.45
3:hw:30:VAL:O	3:hw:31:ALA:C	2.57	0.45
3:io:64:GLN:O	3:io:66:THR:N	2.50	0.45
3:jy:64:GLN:O	3:jy:66:THR:N	2.50	0.45
3:lc:79:THR:O	3:lc:80:GLY:C	2.60	0.45
3:mj:64:GLN:O	3:mj:66:THR:N	2.50	0.45
1:aw:444:MET:O	1:aw:449:TYR:OH	2.32	0.44
1:ba:266:LEU:HG	1:bb:155:SER:HB3	1.99	0.44
1:bi:93:PRO:O	1:bi:94:ALA:C	2.60	0.44
1:bu:203:THR:OG1	1:bu:204:ASP:N	2.50	0.44
1:cd:344:ARG:O	1:cd:345:TRP:HB2	2.17	0.44
1:dw:114:VAL:O	1:dw:115:GLN:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:dx:93:PRO:O	1:dx:94:ALA:C	2.59	0.44
1:fc:260:GLU:HG3	1:fc:261:ALA:N	2.32	0.44
1:ff:444:MET:O	1:ff:449:TYR:OH	2.29	0.44
1:ha:394:SER:O	1:ha:395:TYR:C	2.60	0.44
3:hu:64:GLN:O	3:hu:66:THR:N	2.50	0.44
3:it:63:ASN:OD1	3:it:63:ASN:N	2.51	0.44
3:jt:64:GLN:O	3:jt:66:THR:N	2.50	0.44
3:jz:64:GLN:O	3:jz:66:THR:N	2.49	0.44
3:kr:30:VAL:O	3:kr:31:ALA:C	2.59	0.44
3:ns:64:GLN:O	3:ns:66:THR:N	2.50	0.44
3:nt:26:LYS:NZ	3:nt:74:ASP:OD2	2.51	0.44
3:nv:23:ILE:HG13	3:nv:78:VAL:HG23	1.98	0.44
1:aa:226:GLU:OE2	1:af:262:LYS:NZ	2.48	0.44
1:ao:71:ASP:HB2	1:aq:230:THR:HB	1.98	0.44
1:ay:155:SER:HB3	1:bd:266:LEU:HD21	1.98	0.44
1:ba:250:MET:C	1:ba:250:MET:SD	3.01	0.44
1:br:409:THR:OG1	1:br:410:LYS:N	2.50	0.44
1:cf:345:TRP:CD1	1:cf:346:ALA:H	2.35	0.44
1:dc:502:SER:OG	1:dc:503:ILE:N	2.49	0.44
1:dx:145:HIS:CE1	1:dx:487:SER:O	2.70	0.44
1:fk:243:THR:OG1	1:fk:244:ASP:N	2.50	0.44
1:fl:270:TYR:HA	1:fo:67:GLU:HB2	1.99	0.44
1:gi:502:SER:OG	1:gi:503:ILE:N	2.50	0.44
1:gm:198:ILE:O	1:gm:199:ASP:C	2.60	0.44
1:gq:439:LYS:NZ	1:gq:440:GLY:O	2.47	0.44
1:hd:118:ASN:OD1	1:hd:118:ASN:N	2.48	0.44
3:jd:30:VAL:O	3:jd:31:ALA:C	2.60	0.44
3:kf:35:TYR:HE1	3:kf:41:ILE:HD12	1.83	0.44
3:mi:30:VAL:O	3:mi:31:ALA:C	2.60	0.44
3:og:30:VAL:O	3:og:31:ALA:C	2.59	0.44
1:av:243:THR:OG1	1:av:244:ASP:N	2.50	0.44
1:bt:456:LEU:H	1:bt:475:THR:HG22	1.83	0.44
1:cx:121:THR:HA	1:cx:259:ILE:O	2.18	0.44
1:dt:203:THR:OG1	1:dt:204:ASP:N	2.51	0.44
1:du:242:SER:OG	1:du:245:ASN:ND2	2.50	0.44
1:du:287:ASP:OD1	1:du:287:ASP:N	2.48	0.44
1:ec:328:LYS:NZ	1:ec:336:ASP:OD2	2.43	0.44
1:eu:198:ILE:O	1:eu:199:ASP:C	2.61	0.44
1:ev:344:ARG:O	1:ev:345:TRP:HB3	2.17	0.44
1:ez:243:THR:OG1	1:ez:244:ASP:N	2.50	0.44
1:fl:317:GLY:O	1:fl:318:LYS:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fo:134:ASP:OD1	1:fo:134:ASP:N	2.48	0.44
1:gb:134:ASP:OD1	1:gb:134:ASP:N	2.50	0.44
1:ge:243:THR:OG1	1:ge:244:ASP:N	2.50	0.44
1:gy:142:GLU:HB3	1:gy:145:HIS:HB2	1.98	0.44
3:mo:30:VAL:O	3:mo:31:ALA:C	2.60	0.44
3:my:79:THR:O	3:my:80:GLY:C	2.60	0.44
3:nd:64:GLN:O	3:nd:66:THR:N	2.50	0.44
3:nw:30:VAL:O	3:nw:31:ALA:C	2.60	0.44
3:nw:64:GLN:O	3:nw:66:THR:N	2.50	0.44
1:au:402:THR:OG1	1:au:403:GLY:N	2.49	0.44
1:bn:145:HIS:CD2	1:bn:490:GLN:HG2	2.53	0.44
1:bo:278:LEU:HD21	1:bo:284:MET:HB2	2.00	0.44
1:cb:85:SER:HB3	3:ir:32:PHE:CE1	2.53	0.44
1:ch:395:TYR:HB2	1:ch:396:ALA:H	1.69	0.44
1:da:136:VAL:HG22	1:da:253:ARG:HG3	1.99	0.44
1:ee:253:ARG:O	1:ee:495:ARG:NH2	2.50	0.44
1:ei:396:ALA:O	1:ei:397:ALA:HB2	2.18	0.44
1:et:278:LEU:HD21	1:et:284:MET:HB2	2.00	0.44
1:fj:344:ARG:O	1:fj:345:TRP:HB2	2.17	0.44
1:fo:402:THR:OG1	1:fo:403:GLY:N	2.49	0.44
1:fz:120:PRO:O	1:fz:121:THR:OG1	2.33	0.44
1:gx:134:ASP:OD1	1:gx:134:ASP:N	2.48	0.44
3:ic:64:GLN:O	3:ic:66:THR:N	2.50	0.44
3:jh:64:GLN:O	3:jh:66:THR:N	2.50	0.44
3:jo:30:VAL:O	3:jo:31:ALA:C	2.59	0.44
3:kv:64:GLN:O	3:kv:66:THR:N	2.50	0.44
3:le:30:VAL:O	3:le:31:ALA:C	2.61	0.44
3:lt:30:VAL:O	3:lt:31:ALA:C	2.61	0.44
3:me:79:THR:OG1	3:me:80:GLY:N	2.51	0.44
3:mk:26:LYS:NZ	3:mk:74:ASP:OD2	2.51	0.44
3:ms:30:VAL:O	3:ms:31:ALA:C	2.58	0.44
1:an:448:ILE:HG12	1:an:513:PHE:CE1	2.53	0.44
1:aw:203:THR:OG1	1:aw:204:ASP:N	2.50	0.44
1:bo:228:MET:O	1:bo:229:ALA:C	2.59	0.44
1:ci:118:ASN:OD1	1:ci:118:ASN:N	2.50	0.44
1:cm:243:THR:OG1	1:cm:244:ASP:N	2.49	0.44
1:db:495:ARG:NH2	1:gg:87:ALA:O	2.51	0.44
1:de:243:THR:OG1	1:de:244:ASP:N	2.50	0.44
1:dt:483:PRO:O	1:dt:484:PHE:HB2	2.18	0.44
1:dw:327:SER:OG	1:dw:328:LYS:N	2.45	0.44
1:dz:243:THR:OG1	1:dz:244:ASP:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ff:317:GLY:O	1:ff:318:LYS:C	2.61	0.44
1:ge:236:GLN:HG2	1:ge:247:TRP:CD2	2.52	0.44
1:go:317:GLY:O	1:go:318:LYS:C	2.61	0.44
1:gr:456:LEU:H	1:gr:475:THR:HG22	1.82	0.44
1:gz:118:ASN:OD1	1:gz:118:ASN:N	2.50	0.44
1:hd:317:GLY:O	1:hd:318:LYS:C	2.58	0.44
3:jl:30:VAL:O	3:jl:31:ALA:C	2.60	0.44
3:kp:30:VAL:O	3:kp:31:ALA:C	2.61	0.44
3:la:26:LYS:NZ	3:la:74:ASP:OD2	2.50	0.44
3:lm:64:GLN:O	3:lm:66:THR:N	2.50	0.44
3:lx:26:LYS:NZ	3:lx:74:ASP:OD2	2.50	0.44
3:ma:64:GLN:O	3:ma:66:THR:N	2.50	0.44
3:me:30:VAL:O	3:me:31:ALA:C	2.60	0.44
3:mn:64:GLN:O	3:mn:66:THR:N	2.50	0.44
3:mt:79:THR:O	3:mt:80:GLY:C	2.61	0.44
1:ad:317:GLY:O	1:ad:318:LYS:C	2.60	0.44
1:ap:349:SER:OG	1:aq:341:ARG:NH2	2.50	0.44
1:ay:490:GLN:OE1	1:ay:490:GLN:N	2.50	0.44
1:bf:83:GLN:NE2	3:ij:36:SER:OG	2.51	0.44
1:cb:411:SER:OG	1:cb:412:VAL:N	2.50	0.44
1:cf:262:LYS:NZ	1:cg:226:GLU:OE2	2.48	0.44
1:dg:155:SER:HB3	1:dl:266:LEU:HG	2.00	0.44
1:dg:243:THR:OG1	1:dg:244:ASP:N	2.51	0.44
1:eo:456:LEU:H	1:eo:475:THR:HG22	1.82	0.44
1:fa:243:THR:OG1	1:fa:244:ASP:N	2.50	0.44
1:fd:448:ILE:HG12	1:fd:513:PHE:CE2	2.52	0.44
1:fm:250:MET:SD	1:fm:250:MET:C	3.01	0.44
1:ft:317:GLY:O	1:ft:318:LYS:C	2.61	0.44
1:gl:121:THR:HA	1:gl:259:ILE:O	2.17	0.44
1:gx:317:GLY:O	1:gx:318:LYS:C	2.61	0.44
1:ha:317:GLY:O	1:ha:318:LYS:C	2.61	0.44
3:hv:30:VAL:O	3:hv:31:ALA:C	2.61	0.44
3:is:30:VAL:O	3:is:31:ALA:C	2.59	0.44
3:iu:30:VAL:O	3:iu:31:ALA:C	2.60	0.44
3:jf:64:GLN:O	3:jf:66:THR:N	2.51	0.44
3:jz:32:PHE:N	3:jz:33:PRO:HD2	2.33	0.44
3:kd:26:LYS:NZ	3:kd:74:ASP:OD2	2.50	0.44
3:kf:63:ASN:OD1	3:kf:63:ASN:N	2.51	0.44
3:kg:30:VAL:O	3:kg:31:ALA:C	2.60	0.44
3:lx:79:THR:O	3:lx:80:GLY:C	2.60	0.44
3:mt:64:GLN:O	3:mt:66:THR:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:nd:32:PHE:N	3:nd:33:PRO:HD2	2.33	0.44
3:nn:30:VAL:O	3:nn:31:ALA:C	2.61	0.44
1:aa:267:LYS:NZ	1:ab:237:GLU:OE1	2.50	0.44
1:al:358:ASP:HA	1:al:421:TYR:OH	2.17	0.44
1:au:521:ILE:O	1:av:359:LYS:NZ	2.51	0.44
1:ay:142:GLU:HB3	1:ay:145:HIS:HB2	2.00	0.44
1:ba:118:ASN:OD1	1:ba:118:ASN:N	2.49	0.44
1:bj:411:SER:OG	1:bj:412:VAL:N	2.51	0.44
1:br:134:ASP:OD1	1:br:134:ASP:N	2.48	0.44
1:bt:243:THR:OG1	1:bt:244:ASP:N	2.50	0.44
1:cc:199:ASP:OD2	1:cc:207:LYS:NZ	2.48	0.44
1:cy:278:LEU:CD2	1:cy:284:MET:HB2	2.48	0.44
1:ex:265:GLN:OE1	1:ex:474:LYS:NZ	2.48	0.44
1:fb:317:GLY:O	1:fb:318:LYS:C	2.61	0.44
1:gi:253:ARG:O	1:gi:254:ILE:C	2.60	0.44
1:gj:134:ASP:OD1	1:gj:134:ASP:C	2.60	0.44
1:gk:454:VAL:HB	1:gk:476:ARG:HB2	1.99	0.44
1:gp:490:GLN:OE1	1:gp:490:GLN:N	2.50	0.44
1:ha:456:LEU:H	1:ha:475:THR:HG22	1.83	0.44
3:ky:30:VAL:O	3:ky:31:ALA:C	2.60	0.44
3:mb:79:THR:O	3:mb:80:GLY:C	2.61	0.44
3:mz:64:GLN:O	3:mz:66:THR:N	2.51	0.44
1:ae:456:LEU:H	1:ae:475:THR:HG22	1.83	0.44
1:as:118:ASN:OD1	1:as:118:ASN:N	2.50	0.44
1:az:409:THR:OG1	1:az:410:LYS:N	2.51	0.44
1:bl:409:THR:OG1	1:bl:410:LYS:N	2.50	0.44
1:ca:145:HIS:CD2	1:ca:490:GLN:HG2	2.53	0.44
1:cg:456:LEU:H	1:cg:475:THR:HG22	1.83	0.44
1:ea:99:VAL:CG2	1:eb:483:PRO:HG3	2.25	0.44
1:en:502:SER:OG	1:en:503:ILE:N	2.51	0.44
1:ff:243:THR:OG1	1:ff:244:ASP:N	2.51	0.44
1:fm:243:THR:OG1	1:fm:244:ASP:N	2.49	0.44
1:fn:243:THR:OG1	1:fn:244:ASP:N	2.51	0.44
1:ft:394:SER:O	1:ft:395:TYR:C	2.60	0.44
1:gb:521:ILE:O	1:gc:359:LYS:NZ	2.48	0.44
1:gd:266:LEU:CD2	1:ge:155:SER:HB3	2.47	0.44
1:gd:456:LEU:H	1:gd:475:THR:HG22	1.83	0.44
1:gn:74:TYR:HE1	1:go:260:GLU:HG2	1.82	0.44
1:gy:402:THR:OG1	1:gy:403:GLY:N	2.49	0.44
3:ll:64:GLN:O	3:ll:65:ARG:C	2.60	0.44
3:lp:64:GLN:O	3:lp:66:THR:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:ls:64:GLN:O	3:ls:66:THR:N	2.50	0.44
3:lv:30:VAL:O	3:lv:31:ALA:C	2.60	0.44
3:nu:64:GLN:O	3:nu:66:THR:N	2.50	0.44
1:ck:319:SER:OG	1:ck:320:GLY:N	2.51	0.44
1:cu:199:ASP:OD2	1:cu:207:LYS:NZ	2.48	0.44
1:cw:243:THR:OG1	1:cw:244:ASP:N	2.51	0.44
1:dc:243:THR:OG1	1:dc:244:ASP:N	2.50	0.44
1:dd:317:GLY:O	1:dd:318:LYS:C	2.61	0.44
1:de:131:TYR:HE2	1:de:143:ALA:HA	1.83	0.44
1:du:317:GLY:HA2	1:du:514:ARG:HH11	1.83	0.44
1:eh:203:THR:OG1	1:eh:204:ASP:N	2.50	0.44
1:eo:120:PRO:O	1:eo:121:THR:OG1	2.34	0.44
1:fg:402:THR:OG1	1:fg:403:GLY:N	2.50	0.44
1:gi:327:SER:OG	1:gi:328:LYS:N	2.46	0.44
1:gq:118:ASN:OD1	1:gq:118:ASN:N	2.51	0.44
1:gt:344:ARG:O	1:gt:345:TRP:HB2	2.17	0.44
1:hb:402:THR:OG1	1:hb:403:GLY:N	2.51	0.44
3:ic:26:LYS:NZ	3:ic:74:ASP:OD2	2.47	0.44
3:ik:79:THR:O	3:ik:80:GLY:C	2.60	0.44
3:lb:64:GLN:O	3:lb:66:THR:N	2.51	0.44
3:lh:64:GLN:O	3:lh:66:THR:N	2.51	0.44
3:lj:64:GLN:O	3:lj:66:THR:N	2.50	0.44
3:lq:30:VAL:HG21	3:lq:68:TRP:CH2	2.53	0.44
3:lw:64:GLN:O	3:lw:66:THR:N	2.50	0.44
3:mj:79:THR:O	3:mj:80:GLY:C	2.60	0.44
3:my:30:VAL:O	3:my:31:ALA:C	2.61	0.44
1:an:344:ARG:O	1:an:345:TRP:CB	2.66	0.43
1:aw:456:LEU:H	1:aw:475:THR:HG22	1.83	0.43
1:ay:262:LYS:NZ	1:az:226:GLU:OE2	2.51	0.43
1:az:287:ASP:OD1	1:az:288:ALA:N	2.51	0.43
1:bk:243:THR:OG1	1:bk:244:ASP:N	2.51	0.43
1:bn:317:GLY:O	1:bn:318:LYS:C	2.60	0.43
1:by:502:SER:OG	1:by:503:ILE:N	2.51	0.43
1:bz:134:ASP:OD1	1:bz:134:ASP:N	2.50	0.43
1:ce:426:ASP:OD1	1:ce:426:ASP:C	2.60	0.43
1:cr:317:GLY:O	1:cr:318:LYS:C	2.60	0.43
1:cu:490:GLN:OE1	1:cu:490:GLN:N	2.49	0.43
1:db:409:THR:OG1	1:db:410:LYS:N	2.51	0.43
1:dj:317:GLY:O	1:dj:318:LYS:C	2.60	0.43
1:do:502:SER:OG	1:do:503:ILE:N	2.49	0.43
1:el:448:ILE:HG12	1:el:513:PHE:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ep:150:PRO:O	1:ep:151:ASP:C	2.60	0.43
1:fp:502:SER:OG	1:fp:503:ILE:N	2.50	0.43
1:ft:475:THR:OG1	1:ft:476:ARG:N	2.51	0.43
1:gi:96:MET:HA	1:gj:123:GLN:O	2.17	0.43
1:gn:228:MET:O	1:gn:229:ALA:C	2.61	0.43
1:gt:243:THR:OG1	1:gt:244:ASP:N	2.51	0.43
3:iv:30:VAL:O	3:iv:31:ALA:C	2.61	0.43
3:jh:30:VAL:O	3:jh:31:ALA:C	2.59	0.43
3:kb:30:VAL:O	3:kb:31:ALA:C	2.59	0.43
3:kq:64:GLN:O	3:kq:66:THR:N	2.51	0.43
3:lj:79:THR:O	3:lj:80:GLY:C	2.61	0.43
3:md:26:LYS:NZ	3:md:74:ASP:OD2	2.50	0.43
3:mi:64:GLN:O	3:mi:66:THR:N	2.51	0.43
3:na:30:VAL:O	3:na:31:ALA:C	2.61	0.43
3:nb:30:VAL:O	3:nb:31:ALA:C	2.60	0.43
3:nh:30:VAL:O	3:nh:31:ALA:C	2.59	0.43
3:ns:30:VAL:O	3:ns:31:ALA:C	2.61	0.43
1:aq:264:ARG:HG3	1:ar:155:SER:OG	2.18	0.43
1:as:317:GLY:O	1:as:318:LYS:C	2.59	0.43
1:aw:346:ALA:O	1:aw:347:GLY:C	2.60	0.43
1:az:99:VAL:HG21	1:ba:483:PRO:HG2	2.00	0.43
1:bb:317:GLY:O	1:bb:318:LYS:C	2.61	0.43
1:ct:336:ASP:C	1:ct:336:ASP:OD1	2.61	0.43
1:cx:317:GLY:O	1:cx:318:LYS:C	2.61	0.43
1:db:439:LYS:NZ	1:db:440:GLY:O	2.48	0.43
1:dc:203:THR:OG1	1:dc:204:ASP:N	2.49	0.43
1:eb:439:LYS:NZ	1:eb:440:GLY:O	2.46	0.43
1:eg:344:ARG:C	1:eg:345:TRP:CG	2.95	0.43
1:ek:120:PRO:O	1:ek:121:THR:OG1	2.36	0.43
1:et:243:THR:OG1	1:et:244:ASP:N	2.50	0.43
1:ew:317:GLY:O	1:ew:318:LYS:C	2.60	0.43
1:fc:402:THR:OG1	1:fc:403:GLY:N	2.51	0.43
1:fm:203:THR:OG1	1:fm:204:ASP:N	2.50	0.43
1:fm:394:SER:O	1:fm:395:TYR:C	2.59	0.43
1:gf:145:HIS:CG	1:gf:148:TYR:HD2	2.35	0.43
1:gm:250:MET:HE1	1:gr:297:GLU:HG3	2.01	0.43
1:gv:243:THR:OG1	1:gv:244:ASP:N	2.51	0.43
2:he:28:THR:HG1	2:hi:267:TYR:HH	1.65	0.43
3:hj:30:VAL:O	3:hj:31:ALA:C	2.61	0.43
3:km:64:GLN:O	3:km:66:THR:N	2.51	0.43
3:le:79:THR:O	3:le:80:GLY:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:lf:64:GLN:O	3:lf:66:THR:N	2.51	0.43
3:lo:79:THR:O	3:lo:80:GLY:C	2.61	0.43
3:oa:30:VAL:O	3:oa:31:ALA:C	2.60	0.43
1:ac:118:ASN:OD1	1:ac:118:ASN:N	2.49	0.43
1:ac:474:LYS:NZ	1:bc:273:GLU:OE2	2.45	0.43
1:ad:336:ASP:C	1:ad:336:ASP:OD1	2.61	0.43
1:bf:250:MET:SD	1:bf:250:MET:C	3.01	0.43
1:bo:250:MET:C	1:bo:250:MET:SD	3.02	0.43
1:bw:118:ASN:OD1	1:bw:118:ASN:N	2.48	0.43
1:cd:398:GLN:N	1:cd:398:GLN:OE1	2.50	0.43
1:ch:243:THR:OG1	1:ch:244:ASP:N	2.51	0.43
1:cm:198:ILE:O	1:cm:199:ASP:C	2.61	0.43
1:cp:409:THR:OG1	1:cp:410:LYS:N	2.51	0.43
1:da:317:GLY:O	1:da:318:LYS:C	2.61	0.43
1:ej:411:SER:OG	1:ej:412:VAL:N	2.51	0.43
1:ek:317:GLY:O	1:ek:318:LYS:C	2.59	0.43
1:en:317:GLY:O	1:en:318:LYS:C	2.59	0.43
1:fo:243:THR:OG1	1:fo:244:ASP:N	2.50	0.43
1:ft:101:ARG:HD2	1:ft:101:ARG:HA	1.64	0.43
1:go:439:LYS:NZ	1:go:440:GLY:O	2.47	0.43
1:hc:236:GLN:HG2	1:hc:247:TRP:CD2	2.53	0.43
2:hj:239:SER:OG	2:hj:240:TYR:N	2.50	0.43
2:hk:298:LEU:HB2	2:hk:302:ALA:HB3	2.00	0.43
3:hv:64:GLN:O	3:hv:66:THR:N	2.51	0.43
3:ig:30:VAL:O	3:ig:31:ALA:C	2.60	0.43
3:it:30:VAL:O	3:it:31:ALA:C	2.61	0.43
3:ja:30:VAL:O	3:ja:31:ALA:C	2.59	0.43
3:jd:64:GLN:O	3:jd:66:THR:N	2.51	0.43
3:jy:79:THR:OG1	3:jy:80:GLY:N	2.52	0.43
3:kp:64:GLN:O	3:kp:66:THR:N	2.51	0.43
3:mx:30:VAL:O	3:mx:31:ALA:C	2.61	0.43
1:bw:439:LYS:NZ	1:bw:440:GLY:O	2.49	0.43
1:cd:502:SER:OG	1:cd:503:ILE:N	2.52	0.43
1:ce:243:THR:OG1	1:ce:244:ASP:N	2.49	0.43
1:dc:317:GLY:O	1:dc:318:LYS:C	2.62	0.43
1:dg:260:GLU:HG2	1:dl:74:TYR:CE1	2.53	0.43
1:dv:266:LEU:CG	1:dw:155:SER:HB3	2.47	0.43
1:dv:394:SER:OG	1:dv:395:TYR:N	2.51	0.43
1:el:402:THR:OG1	1:el:403:GLY:N	2.51	0.43
1:em:404:PHE:HZ	1:em:417:LEU:HA	1.84	0.43
1:et:420:LYS:HE3	1:et:421:TYR:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:eu:250:MET:SD	1:eu:250:MET:C	3.01	0.43
1:ey:243:THR:OG1	1:ey:244:ASP:N	2.51	0.43
1:ez:317:GLY:O	1:ez:318:LYS:C	2.62	0.43
1:gm:287:ASP:OD1	1:gm:288:ALA:N	2.51	0.43
1:hb:93:PRO:O	1:hb:94:ALA:C	2.61	0.43
2:hi:140:PHE:O	2:hi:141:SER:C	2.60	0.43
3:hz:32:PHE:HB3	3:hz:33:PRO:HD3	2.00	0.43
3:hz:64:GLN:O	3:hz:66:THR:N	2.51	0.43
3:lb:30:VAL:O	3:lb:31:ALA:C	2.62	0.43
3:ly:64:GLN:O	3:ly:66:THR:N	2.52	0.43
3:mj:30:VAL:O	3:mj:31:ALA:C	2.62	0.43
1:aa:120:PRO:O	1:aa:121:THR:OG1	2.32	0.43
1:ae:118:ASN:OD1	1:ae:118:ASN:N	2.50	0.43
1:ao:125:PHE:CZ	1:ca:91:ILE:HA	2.53	0.43
1:ar:228:MET:O	1:ar:229:ALA:C	2.61	0.43
1:au:96:MET:N	1:av:123:GLN:O	2.49	0.43
1:bd:243:THR:OG1	1:bd:244:ASP:N	2.52	0.43
1:bs:243:THR:OG1	1:bs:244:ASP:N	2.50	0.43
1:ca:439:LYS:NZ	1:ca:442:ASN:O	2.49	0.43
1:co:520:GLY:O	1:cp:341:ARG:NH1	2.52	0.43
1:da:243:THR:OG1	1:da:244:ASP:N	2.51	0.43
1:dr:411:SER:OG	1:dr:412:VAL:N	2.52	0.43
1:dw:521:ILE:O	1:dx:359:LYS:NZ	2.45	0.43
1:ee:71:ASP:HB2	1:eg:231:SER:HB3	2.00	0.43
1:eg:344:ARG:O	1:eg:345:TRP:CB	2.67	0.43
1:el:118:ASN:OD1	1:el:118:ASN:N	2.50	0.43
1:fj:287:ASP:OD1	1:fj:287:ASP:N	2.51	0.43
1:gi:118:ASN:OD1	1:gi:118:ASN:N	2.51	0.43
1:gl:243:THR:OG1	1:gl:244:ASP:N	2.52	0.43
1:gm:345:TRP:CE2	1:gm:347:GLY:HA3	2.53	0.43
1:gt:336:ASP:C	1:gt:336:ASP:OD1	2.61	0.43
1:gu:228:MET:O	1:gu:229:ALA:C	2.60	0.43
1:gy:243:THR:OG1	1:gy:244:ASP:N	2.52	0.43
3:ik:35:TYR:HE1	3:ik:41:ILE:HD12	1.83	0.43
3:jk:79:THR:OG1	3:jk:80:GLY:N	2.52	0.43
3:kr:79:THR:O	3:kr:80:GLY:C	2.62	0.43
3:kt:64:GLN:O	3:kt:66:THR:N	2.51	0.43
3:ln:64:GLN:O	3:ln:66:THR:N	2.52	0.43
3:my:63:ASN:OD1	3:my:63:ASN:N	2.52	0.43
1:ag:273:GLU:OE2	1:bc:474:LYS:NZ	2.41	0.43
1:at:243:THR:OG1	1:at:244:ASP:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:au:502:SER:OG	1:au:503:ILE:N	2.51	0.43
1:bf:407:ASP:OD1	1:bf:410:LYS:NZ	2.47	0.43
1:bj:317:GLY:O	1:bj:318:LYS:C	2.62	0.43
1:bp:243:THR:OG1	1:bp:244:ASP:N	2.50	0.43
1:bs:228:MET:O	1:bs:229:ALA:C	2.62	0.43
1:cd:407:ASP:OD1	1:cd:410:LYS:NZ	2.45	0.43
1:cf:147:MET:HE3	1:cf:366:ARG:HH22	1.83	0.43
1:cp:502:SER:OG	1:cp:503:ILE:N	2.50	0.43
1:db:463:ASP:O	1:db:467:PHE:N	2.51	0.43
1:df:439:LYS:NZ	1:df:440:GLY:O	2.48	0.43
1:dm:317:GLY:O	1:dm:318:LYS:C	2.61	0.43
1:dp:134:ASP:OD1	1:dp:134:ASP:N	2.52	0.43
1:ea:394:SER:OG	1:ea:395:TYR:N	2.52	0.43
1:eq:402:THR:OG1	1:eq:403:GLY:N	2.49	0.43
1:gd:262:LYS:NZ	1:ge:226:GLU:OE2	2.49	0.43
1:gg:260:GLU:OE2	1:gl:72:HIS:HB2	2.18	0.43
1:gj:93:PRO:O	1:gk:123:GLN:HG2	2.18	0.43
1:gu:118:ASN:OD1	1:gu:118:ASN:N	2.50	0.43
1:gx:270:TYR:HB3	1:gx:290:LEU:CD1	2.49	0.43
1:gz:236:GLN:HG2	1:gz:247:TRP:CD2	2.53	0.43
3:hu:30:VAL:O	3:hu:31:ALA:C	2.62	0.43
3:im:79:THR:O	3:im:80:GLY:C	2.60	0.43
3:kk:30:VAL:O	3:kk:31:ALA:C	2.62	0.43
3:mg:30:VAL:O	3:mg:31:ALA:C	2.59	0.43
3:mt:30:VAL:O	3:mt:31:ALA:C	2.61	0.43
1:ad:278:LEU:HD21	1:ad:284:MET:HB2	2.01	0.43
1:ae:200:ALA:O	1:ae:201:GLY:C	2.62	0.43
1:aw:118:ASN:OD1	1:aw:118:ASN:N	2.44	0.43
1:bk:351:LYS:NZ	1:bk:395:TYR:O	2.46	0.43
1:ex:228:MET:HE3	1:ex:232:ILE:HG22	2.00	0.43
1:dh:317:GLY:O	1:dh:318:LYS:C	2.62	0.43
1:dn:344:ARG:O	1:dn:345:TRP:HB2	2.18	0.43
1:dr:394:SER:OG	1:dr:395:TYR:N	2.51	0.43
1:dv:344:ARG:O	1:dv:345:TRP:HB2	2.19	0.43
1:ek:243:THR:OG1	1:ek:244:ASP:N	2.52	0.43
1:fc:317:GLY:O	1:fc:318:LYS:C	2.61	0.43
1:fe:502:SER:OG	1:fe:503:ILE:N	2.51	0.43
1:fu:151:ASP:OD1	1:fu:151:ASP:C	2.62	0.43
1:fu:407:ASP:OD2	1:fu:410:LYS:NZ	2.46	0.43
1:fv:294:LEU:HA	1:fw:250:MET:CE	2.47	0.43
1:fw:317:GLY:O	1:fw:318:LYS:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:gb:72:HIS:HB2	1:gc:260:GLU:OE2	2.19	0.43
1:gj:444:MET:O	1:gj:449:TYR:OH	2.32	0.43
1:gn:439:LYS:NZ	1:gn:440:GLY:O	2.49	0.43
1:hc:402:THR:OG1	1:hc:403:GLY:N	2.51	0.43
2:he:140:PHE:O	2:he:140:PHE:CG	2.71	0.43
3:hw:26:LYS:NZ	3:hw:74:ASP:OD2	2.51	0.43
3:hw:64:GLN:O	3:hw:66:THR:N	2.52	0.43
3:jb:64:GLN:O	3:jb:66:THR:N	2.52	0.43
3:jc:30:VAL:O	3:jc:31:ALA:C	2.61	0.43
3:kc:79:THR:OG1	3:kc:80:GLY:N	2.52	0.43
3:ke:30:VAL:O	3:ke:31:ALA:C	2.62	0.43
3:la:30:VAL:O	3:la:31:ALA:C	2.61	0.43
3:ms:64:GLN:O	3:ms:66:THR:N	2.51	0.43
3:nz:79:THR:O	3:nz:80:GLY:C	2.61	0.43
1:ac:93:PRO:O	1:ac:94:ALA:C	2.61	0.43
1:ah:243:THR:OG1	1:ah:244:ASP:N	2.52	0.43
1:av:138:ALA:H	3:ir:38:VAL:HG13	1.83	0.43
1:av:203:THR:OG1	1:av:204:ASP:N	2.51	0.43
1:ay:402:THR:OG1	1:ay:403:GLY:N	2.50	0.43
1:az:343:ALA:CB	1:az:348:GLU:HG3	2.49	0.43
1:by:426:ASP:C	1:by:426:ASP:OD1	2.60	0.43
1:cd:118:ASN:OD1	1:cd:118:ASN:N	2.51	0.43
1:ck:249:GLU:OE1	1:ck:249:GLU:N	2.51	0.43
1:dl:138:ALA:H	3:kc:38:VAL:HG13	1.83	0.43
1:dq:198:ILE:HG22	1:dq:198:ILE:O	2.19	0.43
1:dx:439:LYS:NZ	1:dx:440:GLY:O	2.45	0.43
1:ep:407:ASP:OD1	1:ep:408:THR:N	2.52	0.43
1:ew:131:TYR:HB3	1:ew:250:MET:HB3	2.00	0.43
1:fh:411:SER:OG	1:fh:412:VAL:N	2.51	0.43
1:fs:267:LYS:NZ	1:ft:237:GLU:OE1	2.52	0.43
1:fv:243:THR:OG1	1:fv:244:ASP:N	2.52	0.43
1:gc:351:LYS:NZ	1:gc:394:SER:O	2.52	0.43
1:gr:317:GLY:O	1:gr:318:LYS:C	2.59	0.43
1:gz:521:ILE:O	1:ha:359:LYS:NZ	2.43	0.43
1:hc:141:LYS:HZ2	1:hc:151:ASP:CG	2.26	0.43
2:he:341:PHE:HE2	2:he:384:ASN:HA	1.84	0.43
2:ho:290:HIS:O	2:ho:291:LYS:C	2.62	0.43
3:ji:30:VAL:O	3:ji:31:ALA:C	2.61	0.43
3:kn:64:GLN:O	3:kn:66:THR:N	2.51	0.43
3:lc:30:VAL:O	3:lc:31:ALA:C	2.59	0.43
3:mk:79:THR:OG1	3:mk:80:GLY:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:nb:79:THR:OG1	3:nb:80:GLY:N	2.52	0.43
3:nq:26:LYS:NZ	3:nq:74:ASP:OD2	2.50	0.43
1:af:482:ASN:ND2	1:af:483:PRO:O	2.52	0.43
1:ap:203:THR:OG1	1:ap:204:ASP:N	2.51	0.43
1:aq:344:ARG:O	1:aq:345:TRP:CB	2.65	0.43
1:ay:344:ARG:O	1:ay:345:TRP:HB2	2.19	0.43
1:bg:123:GLN:OE1	1:bg:256:LYS:HD2	2.18	0.43
1:bs:407:ASP:OD1	1:bs:410:LYS:NZ	2.46	0.43
1:bu:263:SER:HB3	1:bu:476:ARG:HG2	2.01	0.43
1:cb:250:MET:SD	1:cb:250:MET:C	3.02	0.43
1:cf:319:SER:OG	1:cf:320:GLY:N	2.52	0.43
1:ck:317:GLY:O	1:ck:318:LYS:C	2.62	0.43
1:cp:150:PRO:O	1:cp:151:ASP:C	2.58	0.43
1:cr:395:TYR:HB2	1:cr:396:ALA:H	1.68	0.43
1:cyl:153:MET:HE2	1:cyl:225:ALA:HA	2.01	0.43
1:db:243:THR:OG1	1:db:244:ASP:N	2.52	0.43
1:dj:382:VAL:O	1:dj:382:VAL:HG12	2.19	0.43
1:do:118:ASN:OD1	1:do:118:ASN:N	2.49	0.43
1:dp:317:GLY:O	1:dp:318:LYS:C	2.61	0.43
1:du:395:TYR:CG	1:du:396:ALA:N	2.82	0.43
1:ee:439:LYS:NZ	1:ee:440:GLY:O	2.43	0.43
1:eu:444:MET:O	1:eu:449:TYR:OH	2.36	0.43
1:fc:439:LYS:NZ	1:fc:440:GLY:O	2.49	0.43
1:fi:266:LEU:HD13	1:fj:250:MET:HE2	2.00	0.43
1:fj:317:GLY:O	1:fj:318:LYS:C	2.60	0.43
1:fn:411:SER:OG	1:fn:412:VAL:N	2.51	0.43
1:gc:417:LEU:HB3	1:gc:421:TYR:HB2	2.00	0.43
1:gk:93:PRO:O	1:gk:94:ALA:C	2.62	0.43
1:gs:317:GLY:O	1:gs:318:LYS:C	2.61	0.43
1:gx:456:LEU:H	1:gx:475:THR:HG22	1.84	0.43
1:gx:502:SER:OG	1:gx:503:ILE:N	2.51	0.43
2:he:248:ARG:HG2	2:he:287:TRP:CZ3	2.54	0.43
3:ii:79:THR:OG1	3:ii:80:GLY:N	2.52	0.43
3:iu:79:THR:OG1	3:iu:80:GLY:N	2.52	0.43
3:jg:79:THR:O	3:jg:80:GLY:C	2.62	0.43
3:kp:79:THR:OG1	3:kp:80:GLY:N	2.52	0.43
3:la:32:PHE:N	3:la:33:PRO:HD2	2.34	0.43
3:ls:30:VAL:O	3:ls:31:ALA:C	2.59	0.43
3:ng:64:GLN:O	3:ng:66:THR:N	2.51	0.43
3:nj:30:VAL:O	3:nj:31:ALA:C	2.61	0.43
3:nq:79:THR:OG1	3:nq:80:GLY:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:ob:64:GLN:O	3:ob:66:THR:N	2.51	0.43
3:ob:79:THR:OG1	3:ob:80:GLY:N	2.52	0.43
1:aq:120:PRO:O	1:aq:121:THR:OG1	2.32	0.43
1:aw:278:LEU:HD21	1:aw:284:MET:HB2	1.99	0.43
1:ax:344:ARG:O	1:ax:345:TRP:CB	2.67	0.43
1:bb:134:ASP:OD1	1:bb:134:ASP:N	2.49	0.43
1:bc:131:TYR:CE2	1:bc:143:ALA:HA	2.54	0.43
1:bg:72:HIS:ND1	1:bg:78:ASN:O	2.50	0.43
1:cb:243:THR:OG1	1:cb:244:ASP:N	2.52	0.43
1:cl:134:ASP:OD1	1:cl:134:ASP:N	2.46	0.43
1:cr:409:THR:OG1	1:cr:410:LYS:N	2.51	0.43
1:df:317:GLY:O	1:df:318:LYS:C	2.60	0.43
1:df:474:LYS:NZ	1:dh:273:GLU:OE2	2.45	0.43
1:di:198:ILE:O	1:di:199:ASP:C	2.61	0.43
1:do:411:SER:OG	1:do:412:VAL:N	2.52	0.43
1:dq:243:THR:OG1	1:dq:244:ASP:N	2.52	0.43
1:ds:120:PRO:O	1:ds:121:THR:OG1	2.32	0.43
1:eb:243:THR:OG1	1:eb:244:ASP:N	2.52	0.43
1:eh:317:GLY:O	1:eh:318:LYS:C	2.60	0.43
1:ej:120:PRO:O	1:ej:121:THR:OG1	2.29	0.43
1:eo:521:ILE:O	1:ep:359:LYS:NZ	2.48	0.43
1:gg:454:VAL:HB	1:gg:476:ARG:HB2	2.01	0.43
1:gw:131:TYR:CE1	1:gw:141:LYS:HB2	2.54	0.43
2:hm:341:PHE:O	2:hm:343:ALA:N	2.52	0.43
3:jc:32:PHE:N	3:jc:33:PRO:HD2	2.33	0.43
3:jg:30:VAL:O	3:jg:31:ALA:C	2.61	0.43
3:ka:30:VAL:O	3:ka:31:ALA:C	2.62	0.43
3:kw:64:GLN:O	3:kw:66:THR:N	2.52	0.43
3:ls:79:THR:O	3:ls:80:GLY:C	2.60	0.43
3:mk:31:ALA:O	3:mk:32:PHE:C	2.62	0.43
3:mm:30:VAL:O	3:mm:31:ALA:C	2.61	0.43
3:mn:30:VAL:O	3:mn:31:ALA:C	2.61	0.43
1:ab:83:GLN:NE2	3:hu:36:SER:OG	2.52	0.42
1:aj:228:MET:SD	1:aj:232:ILE:HG23	2.59	0.42
1:ax:154:PHE:CZ	1:ax:248:ASN:HB3	2.53	0.42
1:ax:317:GLY:O	1:ax:318:LYS:C	2.62	0.42
1:ba:71:ASP:OD2	1:ba:74:TYR:OH	2.32	0.42
1:be:492:PRO:O	1:be:493:ALA:HB3	2.19	0.42
1:ct:228:MET:O	1:ct:229:ALA:C	2.60	0.42
1:dy:243:THR:OG1	1:dy:244:ASP:N	2.52	0.42
1:ea:96:MET:N	1:eb:123:GLN:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ec:266:LEU:CD2	1:ed:155:SER:HB3	2.49	0.42
1:em:402:THR:OG1	1:em:403:GLY:N	2.50	0.42
1:eu:243:THR:OG1	1:eu:244:ASP:N	2.52	0.42
1:gg:287:ASP:OD1	1:gg:288:ALA:N	2.52	0.42
1:gk:74:TYR:CE2	1:gl:260:GLU:HG2	2.53	0.42
1:hd:456:LEU:H	1:hd:475:THR:HG22	1.83	0.42
2:hi:322:TYR:CD2	2:hi:322:TYR:C	2.94	0.42
3:ia:64:GLN:O	3:ia:66:THR:N	2.52	0.42
3:ip:30:VAL:O	3:ip:31:ALA:C	2.62	0.42
3:ix:30:VAL:O	3:ix:31:ALA:C	2.61	0.42
3:je:30:VAL:O	3:je:31:ALA:C	2.61	0.42
3:kl:68:TRP:O	3:kl:69:ILE:C	2.61	0.42
3:kn:30:VAL:O	3:kn:31:ALA:C	2.62	0.42
3:lt:79:THR:OG1	3:lt:80:GLY:N	2.52	0.42
3:ms:79:THR:O	3:ms:80:GLY:C	2.61	0.42
3:nt:32:PHE:N	3:nt:33:PRO:HD2	2.34	0.42
3:nv:17:LEU:HD23	3:nv:78:VAL:HG21	1.99	0.42
1:am:365:ALA:HB2	1:am:372:GLU:HG2	2.01	0.42
1:ap:120:PRO:O	1:ap:121:THR:OG1	2.30	0.42
1:at:394:SER:O	1:at:395:TYR:C	2.62	0.42
1:be:198:ILE:HG22	1:be:198:ILE:O	2.19	0.42
1:be:317:GLY:O	1:be:318:LYS:C	2.61	0.42
1:cb:463:ASP:O	1:cb:467:PHE:N	2.52	0.42
1:cg:407:ASP:OD1	1:cg:410:LYS:NZ	2.45	0.42
1:ch:145:HIS:NE2	1:ch:487:SER:O	2.51	0.42
1:cj:145:HIS:HB3	1:cj:148:TYR:HB2	2.01	0.42
1:cu:142:GLU:HB3	1:cu:145:HIS:HB2	2.01	0.42
1:db:287:ASP:OD1	1:db:287:ASP:N	2.50	0.42
1:dj:456:LEU:H	1:dj:475:THR:HG22	1.83	0.42
1:dm:402:THR:OG1	1:dm:403:GLY:N	2.50	0.42
1:dn:134:ASP:OD1	1:dn:134:ASP:N	2.50	0.42
1:do:426:ASP:C	1:do:426:ASP:OD1	2.62	0.42
1:ds:184:GLU:HB3	1:ds:366:ARG:HH22	1.83	0.42
1:ed:278:LEU:HD21	1:ed:284:MET:HB2	2.01	0.42
1:fk:411:SER:OG	1:fk:412:VAL:N	2.51	0.42
1:fz:142:GLU:HB3	1:fz:145:HIS:HB2	2.01	0.42
1:fz:145:HIS:NE2	1:fz:487:SER:O	2.52	0.42
1:gz:243:THR:OG1	1:gz:244:ASP:N	2.52	0.42
1:gz:345:TRP:NE1	1:ha:344:ARG:H	2.18	0.42
1:hb:243:THR:OG1	1:hb:244:ASP:N	2.52	0.42
2:hg:59:ASN:HB3	2:hg:60:PRO:HD2	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:iu:32:PHE:HB3	3:iu:33:PRO:HD3	2.01	0.42
3:jn:79:THR:O	3:jn:80:GLY:C	2.61	0.42
3:jy:30:VAL:O	3:jy:31:ALA:C	2.61	0.42
3:jz:30:VAL:O	3:jz:31:ALA:C	2.62	0.42
3:km:30:VAL:O	3:km:31:ALA:C	2.61	0.42
3:lx:30:VAL:O	3:lx:31:ALA:C	2.61	0.42
3:lz:30:VAL:O	3:lz:31:ALA:C	2.62	0.42
3:nk:64:GLN:O	3:nk:66:THR:N	2.52	0.42
3:ns:79:THR:OG1	3:ns:80:GLY:N	2.52	0.42
3:oe:30:VAL:O	3:oe:31:ALA:C	2.60	0.42
1:ah:120:PRO:O	1:ah:121:THR:OG1	2.22	0.42
1:ah:317:GLY:O	1:ah:318:LYS:C	2.62	0.42
1:dh:134:ASP:OD1	1:dh:134:ASP:N	2.51	0.42
1:do:317:GLY:O	1:do:318:LYS:C	2.61	0.42
1:du:426:ASP:C	1:du:426:ASP:OD1	2.61	0.42
1:dy:502:SER:OG	1:dy:503:ILE:N	2.52	0.42
1:dz:273:GLU:OE2	1:ep:474:LYS:NZ	2.43	0.42
1:eo:502:SER:OG	1:eo:503:ILE:N	2.48	0.42
1:eq:317:GLY:O	1:eq:318:LYS:C	2.60	0.42
1:fd:231:SER:HB3	1:fh:71:ASP:OD2	2.19	0.42
1:fr:477:TYR:CG	1:fr:478:GLY:N	2.87	0.42
1:gc:228:MET:O	1:gc:229:ALA:C	2.61	0.42
1:gg:394:SER:OG	1:gg:395:TYR:N	2.52	0.42
1:gg:463:ASP:O	1:gg:467:PHE:N	2.52	0.42
1:gl:454:VAL:HB	1:gl:476:ARG:HB2	2.01	0.42
1:gv:344:ARG:O	1:gv:345:TRP:CB	2.67	0.42
1:gz:228:MET:O	1:gz:229:ALA:C	2.62	0.42
3:ib:63:ASN:OD1	3:ib:63:ASN:N	2.52	0.42
3:iv:64:GLN:O	3:iv:66:THR:N	2.53	0.42
3:ka:40:LYS:HB3	3:ka:72:ASN:HD21	1.85	0.42
3:ki:30:VAL:O	3:ki:31:ALA:C	2.60	0.42
3:kn:68:TRP:O	3:kn:69:ILE:C	2.61	0.42
3:mh:64:GLN:O	3:mh:66:THR:N	2.52	0.42
1:ae:243:THR:OG1	1:ae:244:ASP:N	2.53	0.42
1:af:243:THR:OG1	1:af:244:ASP:N	2.53	0.42
1:ah:402:THR:OG1	1:ah:403:GLY:N	2.51	0.42
1:ak:184:GLU:O	1:ak:185:THR:HB	2.19	0.42
1:at:448:ILE:HG12	1:at:513:PHE:CE2	2.54	0.42
1:bd:411:SER:OG	1:bd:412:VAL:N	2.51	0.42
1:bp:278:LEU:HD21	1:bp:284:MET:HB2	2.02	0.42
1:bs:317:GLY:O	1:bs:318:LYS:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:bt:407:ASP:OD2	1:bt:410:LYS:NZ	2.46	0.42
1:bv:72:HIS:C	1:bv:74:TYR:H	2.28	0.42
1:cc:96:MET:N	1:cd:123:GLN:O	2.50	0.42
1:cw:66:ALA:N	1:df:269:ALA:O	2.53	0.42
1:cw:145:HIS:CD2	1:cw:490:GLN:HE22	2.36	0.42
1:cx:398:GLN:N	1:cx:398:GLN:OE1	2.52	0.42
1:cz:502:SER:OG	1:cz:503:ILE:N	2.53	0.42
1:du:317:GLY:O	1:du:318:LYS:C	2.62	0.42
1:dx:250:MET:C	1:dx:250:MET:SD	3.03	0.42
1:eb:266:LEU:CG	1:ec:155:SER:HB3	2.49	0.42
1:ef:317:GLY:O	1:ef:318:LYS:C	2.62	0.42
1:eo:278:LEU:HD21	1:eo:284:MET:HB2	2.00	0.42
1:er:344:ARG:O	1:er:345:TRP:HB2	2.19	0.42
1:fd:351:LYS:HE3	1:fd:395:TYR:O	2.20	0.42
1:fn:142:GLU:HB3	1:fn:145:HIS:HB2	2.02	0.42
1:fp:344:ARG:O	1:fp:345:TRP:HB3	2.20	0.42
1:fu:483:PRO:O	1:fu:484:PHE:HB2	2.20	0.42
1:fz:243:THR:OG1	1:fz:244:ASP:N	2.52	0.42
1:ge:262:LYS:NZ	1:gf:226:GLU:OE2	2.50	0.42
1:gn:243:THR:OG1	1:gn:244:ASP:N	2.51	0.42
1:gs:243:THR:OG1	1:gs:244:ASP:N	2.53	0.42
2:hg:286:GLY:C	2:hg:288:LEU:N	2.78	0.42
2:hk:112:GLU:OE2	2:hk:136:LYS:NZ	2.49	0.42
3:in:64:GLN:O	3:in:66:THR:N	2.53	0.42
3:iz:30:VAL:O	3:iz:31:ALA:C	2.62	0.42
3:jf:30:VAL:O	3:jf:31:ALA:C	2.62	0.42
3:kt:30:VAL:O	3:kt:31:ALA:C	2.61	0.42
3:mf:64:GLN:O	3:mf:66:THR:N	2.52	0.42
3:nu:79:THR:O	3:nu:80:GLY:C	2.62	0.42
3:ny:30:VAL:O	3:ny:31:ALA:C	2.60	0.42
1:ag:344:ARG:O	1:ag:345:TRP:CB	2.68	0.42
1:al:345:TRP:CG	1:al:346:ALA:N	2.88	0.42
1:aq:198:ILE:O	1:aq:199:ASP:C	2.61	0.42
1:bg:79:ILE:O	1:bg:80:ALA:C	2.62	0.42
1:bx:253:ARG:O	1:bx:254:ILE:C	2.62	0.42
1:ce:394:SER:O	1:ce:395:TYR:C	2.62	0.42
1:cp:463:ASP:O	1:cp:467:PHE:N	2.52	0.42
1:cq:304:ARG:NH1	1:cr:150:PRO:O	2.52	0.42
1:ct:243:THR:OG1	1:ct:244:ASP:N	2.52	0.42
1:di:243:THR:OG1	1:di:244:ASP:N	2.53	0.42
1:dt:250:MET:SD	1:dt:250:MET:C	3.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:dw:344:ARG:O	1:dw:345:TRP:CB	2.67	0.42
1:ec:266:LEU:HD21	1:ed:155:SER:HB3	2.01	0.42
1:ec:444:MET:O	1:ec:449:TYR:OH	2.29	0.42
1:er:287:ASP:OD1	1:er:288:ALA:N	2.52	0.42
1:fj:409:THR:OG1	1:fj:410:LYS:N	2.50	0.42
1:fk:502:SER:OG	1:fk:503:ILE:N	2.52	0.42
1:fr:317:GLY:O	1:fr:318:LYS:C	2.60	0.42
1:ft:439:LYS:NZ	1:ft:442:ASN:O	2.49	0.42
1:ga:228:MET:O	1:ga:229:ALA:C	2.60	0.42
1:gp:344:ARG:O	1:gp:345:TRP:CB	2.66	0.42
1:gs:456:LEU:H	1:gs:475:THR:HG22	1.84	0.42
2:hk:290:HIS:O	2:hk:291:LYS:C	2.62	0.42
3:iw:30:VAL:O	3:iw:31:ALA:C	2.60	0.42
3:kc:30:VAL:O	3:kc:31:ALA:C	2.61	0.42
3:mb:30:VAL:O	3:mb:31:ALA:C	2.60	0.42
3:mp:30:VAL:O	3:mp:31:ALA:C	2.61	0.42
3:oc:30:VAL:O	3:oc:31:ALA:C	2.62	0.42
3:od:31:ALA:O	3:od:32:PHE:C	2.63	0.42
1:ae:74:TYR:CE1	1:af:260:GLU:HG2	2.54	0.42
1:ae:394:SER:OG	1:ae:395:TYR:N	2.53	0.42
1:ah:448:ILE:HG12	1:ah:513:PHE:HE2	1.85	0.42
1:am:439:LYS:NZ	1:am:440:GLY:O	2.44	0.42
1:be:446:ALA:HB3	1:be:449:TYR:CE1	2.54	0.42
1:bk:317:GLY:O	1:bk:318:LYS:C	2.61	0.42
1:bl:394:SER:OG	1:bl:395:TYR:N	2.51	0.42
1:bs:439:LYS:NZ	1:bs:440:GLY:O	2.47	0.42
1:bs:502:SER:OG	1:bs:503:ILE:N	2.53	0.42
1:cl:287:ASP:OD1	1:cl:288:ALA:N	2.53	0.42
1:cz:346:ALA:O	1:cz:347:GLY:C	2.62	0.42
1:da:521:ILE:HG22	1:da:521:ILE:O	2.19	0.42
1:dj:454:VAL:HB	1:dj:476:ARG:HB2	2.00	0.42
1:dl:344:ARG:O	1:dl:345:TRP:HB2	2.20	0.42
1:dn:344:ARG:O	1:dn:345:TRP:CB	2.67	0.42
1:dp:439:LYS:NZ	1:dp:440:GLY:O	2.49	0.42
1:ds:402:THR:OG1	1:ds:403:GLY:N	2.51	0.42
1:em:505:ASN:C	1:em:505:ASN:OD1	2.63	0.42
1:en:118:ASN:OD1	1:en:118:ASN:N	2.49	0.42
1:ep:317:GLY:O	1:ep:318:LYS:C	2.63	0.42
1:ev:411:SER:OG	1:ev:412:VAL:N	2.53	0.42
1:fb:411:SER:OG	1:fb:412:VAL:N	2.52	0.42
1:fn:394:SER:OG	1:fn:395:TYR:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fo:396:ALA:O	1:fo:397:ALA:HB2	2.18	0.42
1:fp:394:SER:OG	1:fp:395:TYR:N	2.50	0.42
1:fp:505:ASN:OD1	1:fp:505:ASN:N	2.47	0.42
1:ft:411:SER:OG	1:ft:412:VAL:N	2.51	0.42
1:ga:118:ASN:OD1	1:ga:118:ASN:N	2.52	0.42
1:gg:120:PRO:O	1:gg:121:THR:OG1	2.37	0.42
1:gh:463:ASP:O	1:gh:467:PHE:N	2.51	0.42
1:gr:243:THR:OG1	1:gr:244:ASP:N	2.53	0.42
1:gs:463:ASP:OD2	1:gs:465:LYS:NZ	2.44	0.42
2:ho:46:ASN:N	2:ho:46:ASN:OD1	2.44	0.42
3:jc:63:ASN:OD1	3:jc:63:ASN:N	2.53	0.42
3:ka:40:LYS:HB3	3:ka:72:ASN:ND2	2.34	0.42
1:aj:228:MET:HG2	1:aj:232:ILE:CG2	2.50	0.42
1:am:456:LEU:H	1:am:475:THR:HG22	1.84	0.42
1:aq:145:HIS:HD2	1:aq:490:GLN:HG2	1.85	0.42
1:at:328:LYS:NZ	1:at:336:ASP:OD2	2.48	0.42
1:bg:243:THR:OG1	1:bg:244:ASP:N	2.51	0.42
1:bl:243:THR:OG1	1:bl:244:ASP:N	2.52	0.42
1:bl:467:PHE:O	1:bl:467:PHE:CG	2.73	0.42
1:cc:439:LYS:NZ	1:cc:440:GLY:O	2.44	0.42
1:cj:454:VAL:HB	1:cj:476:ARG:HB2	2.01	0.42
1:cl:456:LEU:H	1:cl:475:THR:HG22	1.84	0.42
1:cy:463:ASP:O	1:cy:467:PHE:N	2.52	0.42
1:dg:72:HIS:HB2	1:dh:260:GLU:CD	2.45	0.42
1:dl:145:HIS:NE2	1:dl:487:SER:O	2.52	0.42
1:dm:243:THR:OG1	1:dm:244:ASP:N	2.52	0.42
1:fi:118:ASN:OD1	1:fi:118:ASN:N	2.52	0.42
1:fl:243:THR:OG1	1:fl:244:ASP:N	2.53	0.42
1:fm:317:GLY:O	1:fm:318:LYS:C	2.62	0.42
1:fr:134:ASP:OD1	1:fr:134:ASP:N	2.52	0.42
1:fw:439:LYS:NZ	1:fw:440:GLY:O	2.47	0.42
1:gj:96:MET:HE1	1:gk:256:LYS:HB2	2.01	0.42
1:go:131:TYR:CE1	1:go:141:LYS:HB2	2.54	0.42
1:gs:118:ASN:OD1	1:gs:118:ASN:N	2.50	0.42
1:ha:278:LEU:HD21	1:ha:284:MET:HB2	2.02	0.42
1:hb:120:PRO:O	1:hb:121:THR:OG1	2.35	0.42
3:iu:64:GLN:O	3:iu:66:THR:N	2.52	0.42
3:jg:69:ILE:HA	3:jg:72:ASN:HD22	1.84	0.42
3:ji:32:PHE:N	3:ji:33:PRO:HD2	2.35	0.42
3:jp:30:VAL:O	3:jp:31:ALA:C	2.62	0.42
3:ku:30:VAL:O	3:ku:31:ALA:C	2.61	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:mh:30:VAL:O	3:mh:31:ALA:C	2.62	0.42
3:nn:79:THR:OG1	3:nn:80:GLY:N	2.52	0.42
1:ay:243:THR:OG1	1:ay:244:ASP:N	2.51	0.42
1:bb:123:GLN:OE1	1:bb:256:LYS:HD2	2.20	0.42
1:bl:317:GLY:O	1:bl:318:LYS:C	2.62	0.42
1:bm:260:GLU:HB3	1:bm:500:MET:HE2	2.02	0.42
1:bo:93:PRO:O	1:bo:94:ALA:C	2.61	0.42
1:bq:84:THR:OG1	1:bq:85:SER:N	2.53	0.42
1:bv:145:HIS:NE2	1:bv:487:SER:O	2.53	0.42
1:bx:78:ASN:O	1:bx:79:ILE:C	2.63	0.42
1:cp:228:MET:O	1:cp:229:ALA:C	2.62	0.42
1:cu:72:HIS:HB2	1:cv:260:GLU:OE2	2.19	0.42
1:cu:446:ALA:HB3	1:cu:449:TYR:CE1	2.55	0.42
1:cy:490:GLN:OE1	1:cy:490:GLN:N	2.52	0.42
1:dl:243:THR:OG1	1:dl:244:ASP:N	2.52	0.42
1:dx:439:LYS:NZ	1:dx:442:ASN:O	2.47	0.42
1:ee:454:VAL:HG22	1:ee:476:ARG:HB2	2.02	0.42
1:ef:394:SER:OG	1:ef:395:TYR:N	2.52	0.42
1:ei:243:THR:OG1	1:ei:244:ASP:N	2.51	0.42
1:ex:463:ASP:O	1:ex:467:PHE:N	2.51	0.42
1:fj:88:VAL:HG13	1:gl:254:ILE:HB	2.01	0.42
1:fm:151:ASP:OD1	1:fm:189:TYR:HE2	2.03	0.42
1:gi:505:ASN:OD1	1:gi:505:ASN:C	2.62	0.42
1:gy:260:GLU:OE2	1:hd:72:HIS:HB2	2.19	0.42
3:ja:79:THR:OG1	3:ja:80:GLY:N	2.52	0.42
3:jw:64:GLN:O	3:jw:66:THR:N	2.52	0.42
3:lw:79:THR:OG1	3:lw:80:GLY:N	2.52	0.42
3:ng:30:VAL:O	3:ng:31:ALA:C	2.62	0.42
1:an:502:SER:OG	1:an:503:ILE:N	2.52	0.42
1:bd:317:GLY:O	1:bd:318:LYS:C	2.60	0.42
1:bo:114:VAL:O	1:bo:115:GLN:C	2.61	0.42
1:by:93:PRO:O	1:by:94:ALA:C	2.62	0.42
1:cm:490:GLN:OE1	1:cm:490:GLN:N	2.53	0.42
1:dj:67:GLU:HG3	1:dm:274:LEU:HD13	2.02	0.42
1:dy:67:GLU:HB2	1:et:270:TYR:HA	2.02	0.42
1:ee:317:GLY:O	1:ee:318:LYS:C	2.62	0.42
1:ek:249:GLU:OE1	1:ek:249:GLU:N	2.53	0.42
1:eo:317:GLY:O	1:eo:318:LYS:C	2.62	0.42
1:es:463:ASP:O	1:es:467:PHE:N	2.51	0.42
1:fd:243:THR:OG1	1:fd:244:ASP:N	2.52	0.42
1:ff:502:SER:OG	1:ff:503:ILE:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fm:74:TYR:CE2	1:fm:260:GLU:HG3	2.55	0.42
1:ft:118:ASN:OD1	1:ft:118:ASN:N	2.47	0.42
1:ft:243:THR:OG1	1:ft:244:ASP:N	2.53	0.42
1:gb:453:TYR:HB3	1:gb:476:ARG:O	2.20	0.42
1:gb:502:SER:OG	1:gb:503:ILE:N	2.52	0.42
1:gt:448:ILE:HG12	1:gt:513:PHE:CE2	2.55	0.42
1:gz:96:MET:N	1:ha:123:GLN:O	2.50	0.42
1:ha:502:SER:OG	1:ha:503:ILE:N	2.52	0.42
3:ik:30:VAL:O	3:ik:31:ALA:C	2.61	0.42
3:il:64:GLN:O	3:il:66:THR:N	2.52	0.42
3:jr:79:THR:O	3:jr:80:GLY:C	2.62	0.42
3:ju:30:VAL:O	3:ju:31:ALA:C	2.61	0.42
3:lf:30:VAL:O	3:lf:31:ALA:C	2.63	0.42
3:lo:30:VAL:O	3:lo:31:ALA:C	2.62	0.42
3:mn:63:ASN:OD1	3:mn:63:ASN:N	2.52	0.42
3:mo:79:THR:OG1	3:mo:80:GLY:N	2.53	0.42
3:mv:30:VAL:O	3:mv:31:ALA:C	2.62	0.42
1:aa:317:GLY:O	1:aa:318:LYS:C	2.62	0.42
1:ak:428:TYR:O	1:ak:430:LYS:NZ	2.52	0.42
1:am:243:THR:OG1	1:am:244:ASP:N	2.52	0.42
1:au:317:GLY:O	1:au:318:LYS:C	2.63	0.42
1:au:456:LEU:H	1:au:475:THR:HG22	1.85	0.42
1:bj:463:ASP:OD1	1:bj:463:ASP:C	2.63	0.42
1:bm:426:ASP:C	1:bm:426:ASP:OD1	2.61	0.42
1:bo:134:ASP:C	1:bo:134:ASP:OD1	2.59	0.42
1:cf:243:THR:OG1	1:cf:244:ASP:N	2.53	0.42
1:cl:317:GLY:O	1:cl:318:LYS:C	2.63	0.42
1:co:147:MET:HE3	1:co:366:ARG:HH22	1.85	0.42
1:cu:317:GLY:O	1:cu:318:LYS:C	2.63	0.42
1:eg:317:GLY:O	1:eg:318:LYS:C	2.63	0.42
1:ek:226:GLU:OE2	1:ep:262:LYS:NZ	2.52	0.42
1:em:502:SER:OG	1:em:503:ILE:N	2.49	0.42
1:er:243:THR:OG1	1:er:244:ASP:N	2.52	0.42
1:ev:145:HIS:NE2	1:ev:487:SER:O	2.51	0.42
1:ey:123:GLN:OE1	1:ey:256:LYS:HD2	2.20	0.42
1:fi:236:GLN:HG2	1:fi:247:TRP:CD2	2.55	0.42
1:fv:463:ASP:O	1:fv:467:PHE:N	2.52	0.42
1:gp:456:LEU:H	1:gp:475:THR:HG22	1.85	0.42
1:gu:317:GLY:O	1:gu:318:LYS:C	2.62	0.42
1:gx:344:ARG:O	1:gx:345:TRP:HB2	2.20	0.42
2:he:401:GLY:O	2:he:402:ASP:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:hh:241:ALA:O	2:hh:242:SER:C	2.63	0.42
2:hi:298:LEU:HB3	2:hi:302:ALA:HB3	2.02	0.42
2:hl:384:ASN:ND2	2:hl:387:THR:OG1	2.53	0.42
3:je:79:THR:OG1	3:je:80:GLY:N	2.53	0.42
3:jx:35:TYR:HE1	3:jx:41:ILE:HD12	1.85	0.42
3:ke:79:THR:OG1	3:ke:80:GLY:N	2.52	0.42
3:kn:31:ALA:O	3:kn:32:PHE:C	2.62	0.42
3:lz:64:GLN:O	3:lz:65:ARG:C	2.63	0.42
3:md:30:VAL:O	3:md:31:ALA:C	2.62	0.42
3:mp:31:ALA:O	3:mp:32:PHE:C	2.63	0.42
3:no:30:VAL:O	3:no:31:ALA:C	2.61	0.42
1:al:243:THR:OG1	1:al:244:ASP:N	2.53	0.41
1:aq:243:THR:OG1	1:aq:244:ASP:N	2.53	0.41
1:ay:521:ILE:O	1:az:359:LYS:NZ	2.53	0.41
1:bj:243:THR:OG1	1:bj:244:ASP:N	2.52	0.41
1:ce:198:ILE:O	1:ce:199:ASP:C	2.63	0.41
1:cf:72:HIS:HB2	1:cg:260:GLU:CD	2.45	0.41
1:ci:260:GLU:HG2	1:cn:74:TYR:CE1	2.55	0.41
1:cq:243:THR:OG1	1:cq:244:ASP:N	2.53	0.41
1:ct:317:GLY:O	1:ct:318:LYS:C	2.63	0.41
1:dq:131:TYR:CE1	1:dq:141:LYS:HB2	2.55	0.41
1:ee:198:ILE:HG12	1:ee:198:ILE:O	2.20	0.41
1:eh:95:VAL:HG22	1:eh:97:GLY:H	1.84	0.41
1:ep:243:THR:OG1	1:ep:244:ASP:N	2.53	0.41
1:fc:79:ILE:HG23	1:fd:121:THR:CG2	2.50	0.41
1:fq:426:ASP:C	1:fq:426:ASP:OD1	2.61	0.41
1:gm:345:TRP:CZ2	1:gm:347:GLY:HA3	2.55	0.41
1:gz:236:GLN:HG2	1:gz:247:TRP:CE2	2.55	0.41
1:hb:490:GLN:OE1	1:hb:490:GLN:N	2.51	0.41
3:hs:35:TYR:HE1	3:hs:41:ILE:HD12	1.85	0.41
3:hs:79:THR:OG1	3:hs:80:GLY:N	2.53	0.41
3:iq:79:THR:OG1	3:iq:80:GLY:N	2.53	0.41
3:iv:68:TRP:O	3:iv:69:ILE:C	2.63	0.41
3:iw:79:THR:OG1	3:iw:80:GLY:N	2.53	0.41
3:jg:26:LYS:NZ	3:jg:74:ASP:OD2	2.51	0.41
3:jm:30:VAL:O	3:jm:31:ALA:C	2.62	0.41
3:kk:79:THR:OG1	3:kk:80:GLY:N	2.53	0.41
3:kl:79:THR:OG1	3:kl:80:GLY:N	2.53	0.41
3:ko:79:THR:OG1	3:ko:80:GLY:N	2.53	0.41
3:mk:64:GLN:O	3:mk:66:THR:N	2.53	0.41
1:ai:254:ILE:HB	1:aw:88:VAL:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:au:273:GLU:OE2	1:bw:474:LYS:NZ	2.41	0.41
1:be:456:LEU:H	1:be:475:THR:HG22	1.85	0.41
1:bi:439:LYS:NZ	1:bi:440:GLY:O	2.48	0.41
1:bj:120:PRO:O	1:bj:121:THR:OG1	2.34	0.41
1:br:317:GLY:O	1:br:318:LYS:C	2.63	0.41
1:bu:198:ILE:O	1:bu:198:ILE:CG2	2.69	0.41
1:bz:317:GLY:O	1:bz:318:LYS:C	2.61	0.41
1:cj:93:PRO:O	1:cj:94:ALA:C	2.63	0.41
1:ck:243:THR:OG1	1:ck:244:ASP:N	2.53	0.41
1:cs:236:GLN:HG2	1:cs:247:TRP:CD2	2.55	0.41
1:cw:317:GLY:O	1:cw:318:LYS:C	2.62	0.41
1:dh:348:GLU:HG2	1:dh:396:ALA:HB2	2.02	0.41
1:dk:118:ASN:OD1	1:dk:118:ASN:N	2.52	0.41
1:dr:198:ILE:O	1:dr:199:ASP:C	2.63	0.41
1:ec:345:TRP:CD1	1:ed:348:GLU:HB3	2.55	0.41
1:ed:243:THR:OG1	1:ed:244:ASP:N	2.54	0.41
1:ed:317:GLY:O	1:ed:318:LYS:C	2.62	0.41
1:ee:243:THR:OG1	1:ee:244:ASP:N	2.51	0.41
1:ew:336:ASP:OD1	1:ew:336:ASP:C	2.63	0.41
1:fk:490:GLN:OE1	1:fk:490:GLN:N	2.50	0.41
1:fu:167:ALA:O	1:fu:168:ALA:C	2.63	0.41
1:gc:243:THR:OG1	1:gc:244:ASP:N	2.53	0.41
1:gc:411:SER:OG	1:gc:412:VAL:N	2.52	0.41
1:gi:287:ASP:OD1	1:gi:288:ALA:N	2.52	0.41
1:gl:120:PRO:O	1:gl:121:THR:OG1	2.37	0.41
1:gw:131:TYR:CE2	1:gw:143:ALA:HA	2.55	0.41
1:gw:198:ILE:O	1:gw:199:ASP:C	2.62	0.41
1:hd:243:THR:OG1	1:hd:244:ASP:N	2.52	0.41
2:hg:286:GLY:O	2:hg:288:LEU:N	2.53	0.41
3:hp:64:GLN:O	3:hp:66:THR:N	2.52	0.41
3:hr:30:VAL:O	3:hr:31:ALA:C	2.63	0.41
3:kf:26:LYS:NZ	3:kf:74:ASP:OD2	2.50	0.41
3:ks:30:VAL:O	3:ks:31:ALA:C	2.63	0.41
3:nf:79:THR:OG1	3:nf:80:GLY:N	2.53	0.41
3:ni:64:GLN:O	3:ni:66:THR:N	2.52	0.41
3:nj:79:THR:OG1	3:nj:80:GLY:N	2.53	0.41
3:nq:30:VAL:O	3:nq:31:ALA:C	2.62	0.41
1:ac:66:ALA:N	1:al:269:ALA:O	2.53	0.41
1:as:348:GLU:HG2	1:ax:345:TRP:CG	2.55	0.41
1:bl:118:ASN:OD1	1:bl:118:ASN:N	2.53	0.41
1:bw:317:GLY:O	1:bw:318:LYS:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:by:486:GLU:C	1:by:488:ALA:H	2.29	0.41
1:ch:180:HIS:CG	1:ch:181:PHE:N	2.88	0.41
1:cj:190:LEU:HB3	1:cj:221:LEU:HG	2.02	0.41
1:ck:411:SER:OG	1:ck:412:VAL:N	2.53	0.41
1:cl:439:LYS:NZ	1:cl:440:GLY:O	2.49	0.41
1:dg:287:ASP:OD1	1:dg:288:ALA:N	2.52	0.41
1:dr:142:GLU:HB3	1:dr:145:HIS:HB2	2.03	0.41
1:dt:287:ASP:OD1	1:dt:288:ALA:N	2.52	0.41
1:dv:345:TRP:CD1	1:dv:345:TRP:N	2.88	0.41
1:eo:243:THR:OG1	1:eo:244:ASP:N	2.53	0.41
1:er:483:PRO:O	1:er:484:PHE:HB2	2.20	0.41
1:et:336:ASP:OD1	1:et:336:ASP:C	2.63	0.41
1:eu:235:LEU:HA	1:eu:239:PHE:HB3	2.03	0.41
1:ev:138:ALA:H	3:le:38:VAL:HG13	1.85	0.41
1:ew:95:VAL:HG12	1:ew:97:GLY:H	1.84	0.41
1:ew:250:MET:HE2	1:fb:294:LEU:HD23	2.01	0.41
1:ew:407:ASP:OD1	1:ew:408:THR:N	2.53	0.41
1:fq:250:MET:SD	1:fq:250:MET:C	3.03	0.41
1:fr:426:ASP:OD1	1:fr:426:ASP:C	2.62	0.41
1:gc:358:ASP:HA	1:gc:421:TYR:OH	2.20	0.41
1:gu:426:ASP:C	1:gu:426:ASP:OD1	2.62	0.41
1:gu:446:ALA:HB3	1:gu:449:TYR:CE1	2.55	0.41
1:hc:198:ILE:O	1:hc:199:ASP:C	2.63	0.41
1:hc:345:TRP:CG	1:hc:346:ALA:N	2.88	0.41
2:hh:248:ARG:HG2	2:hh:287:TRP:CZ3	2.55	0.41
3:ik:32:PHE:N	3:ik:33:PRO:HD2	2.34	0.41
3:lg:26:LYS:NZ	3:lg:74:ASP:OD2	2.51	0.41
3:lu:79:THR:OG1	3:lu:80:GLY:N	2.52	0.41
3:lv:64:GLN:O	3:lv:66:THR:N	2.54	0.41
3:lz:79:THR:OG1	3:lz:80:GLY:N	2.53	0.41
3:mh:79:THR:O	3:mh:80:GLY:C	2.63	0.41
3:ne:30:VAL:O	3:ne:31:ALA:C	2.63	0.41
1:ab:134:ASP:OD1	1:ab:134:ASP:N	2.49	0.41
1:am:426:ASP:OD1	1:am:426:ASP:C	2.61	0.41
1:aw:262:LYS:NZ	1:ax:226:GLU:OE2	2.51	0.41
1:be:454:VAL:HB	1:be:476:ARG:HB2	2.01	0.41
1:bj:287:ASP:OD1	1:bj:288:ALA:N	2.53	0.41
1:bm:287:ASP:OD1	1:bm:288:ALA:N	2.52	0.41
1:br:134:ASP:O	1:br:135:PRO:C	2.62	0.41
1:bu:372:GLU:O	1:bu:373:GLY:C	2.64	0.41
1:cj:67:GLU:HB3	1:dk:270:TYR:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:cp:505:ASN:OD1	1:cp:505:ASN:C	2.63	0.41
1:db:407:ASP:OD2	1:db:410:LYS:NZ	2.42	0.41
1:dh:344:ARG:O	1:dh:345:TRP:HB2	2.20	0.41
1:dn:243:THR:OG1	1:dn:244:ASP:N	2.53	0.41
1:ek:71:ASP:OD2	1:em:230:THR:N	2.53	0.41
1:ek:74:TYR:CE1	1:el:260:GLU:HG2	2.55	0.41
1:ek:439:LYS:NZ	1:ek:440:GLY:O	2.49	0.41
1:en:250:MET:SD	1:en:250:MET:C	3.04	0.41
1:fa:483:PRO:O	1:fa:484:PHE:HB2	2.20	0.41
1:fr:243:THR:OG1	1:fr:244:ASP:N	2.52	0.41
1:fu:230:THR:N	1:fy:71:ASP:OD2	2.53	0.41
1:fz:395:TYR:HB2	1:fz:396:ALA:H	1.70	0.41
2:hi:344:PRO:HA	2:hi:379:TYR:HB3	2.02	0.41
3:jt:30:VAL:O	3:jt:31:ALA:C	2.62	0.41
3:ky:26:LYS:NZ	3:ky:74:ASP:OD2	2.50	0.41
3:lu:32:PHE:N	3:lu:33:PRO:HD2	2.35	0.41
3:mz:79:THR:OG1	3:mz:80:GLY:N	2.53	0.41
1:ac:502:SER:OG	1:ac:503:ILE:N	2.54	0.41
1:ae:317:GLY:O	1:ae:318:LYS:C	2.64	0.41
1:ag:243:THR:OG1	1:ag:244:ASP:N	2.53	0.41
1:ax:411:SER:OG	1:ax:412:VAL:N	2.53	0.41
1:ay:439:LYS:NZ	1:ay:440:GLY:O	2.45	0.41
1:bb:228:MET:O	1:bb:229:ALA:C	2.64	0.41
1:bl:336:ASP:C	1:bl:336:ASP:OD1	2.63	0.41
1:bo:253:ARG:O	1:bo:254:ILE:HB	2.21	0.41
1:bp:317:GLY:O	1:bp:318:LYS:C	2.63	0.41
1:bu:93:PRO:O	1:bu:94:ALA:C	2.63	0.41
1:cd:243:THR:OG1	1:cd:244:ASP:N	2.53	0.41
1:cf:287:ASP:OD1	1:cf:288:ALA:N	2.52	0.41
1:cj:474:LYS:NZ	1:cr:273:GLU:OE2	2.48	0.41
1:cv:287:ASP:OD1	1:cv:288:ALA:N	2.53	0.41
1:cw:327:SER:OG	1:cw:328:LYS:N	2.44	0.41
1:cx:86:GLY:O	1:dh:495:ARG:NH1	2.54	0.41
1:da:67:GLU:HB2	1:gg:270:TYR:HA	2.03	0.41
1:dp:243:THR:OG1	1:dp:244:ASP:N	2.53	0.41
1:dt:317:GLY:O	1:dt:318:LYS:C	2.62	0.41
1:ed:198:ILE:O	1:ed:199:ASP:C	2.64	0.41
1:ej:142:GLU:HG2	1:ej:145:HIS:HB2	2.02	0.41
1:ev:407:ASP:OD1	1:ev:408:THR:N	2.54	0.41
1:fl:407:ASP:OD1	1:fl:410:LYS:NZ	2.43	0.41
1:fw:198:ILE:O	1:fw:199:ASP:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fx:266:LEU:HD21	1:fy:155:SER:HB3	2.03	0.41
1:gc:317:GLY:O	1:gc:318:LYS:C	2.63	0.41
1:gc:490:GLN:OE1	1:gc:490:GLN:N	2.50	0.41
1:gn:253:ARG:O	1:gn:254:ILE:HB	2.20	0.41
1:go:426:ASP:C	1:go:426:ASP:OD1	2.62	0.41
1:gq:407:ASP:OD1	1:gq:410:LYS:NZ	2.46	0.41
1:gr:463:ASP:O	1:gr:467:PHE:N	2.52	0.41
1:gv:317:GLY:O	1:gv:318:LYS:C	2.63	0.41
1:gy:228:MET:O	1:gy:229:ALA:C	2.63	0.41
2:he:241:ALA:O	2:he:242:SER:C	2.63	0.41
2:hn:352:ASP:O	2:hn:353:ASP:CB	2.68	0.41
3:hs:32:PHE:N	3:hs:33:PRO:HD2	2.35	0.41
3:id:64:GLN:O	3:id:66:THR:N	2.53	0.41
3:ie:30:VAL:HG21	3:ie:68:TRP:CH2	2.56	0.41
3:is:64:GLN:O	3:is:66:THR:N	2.53	0.41
3:iz:79:THR:O	3:iz:80:GLY:C	2.62	0.41
3:jv:30:VAL:O	3:jv:31:ALA:C	2.62	0.41
3:kx:32:PHE:N	3:kx:33:PRO:HD2	2.35	0.41
3:lb:72:ASN:C	3:lb:72:ASN:HD22	2.29	0.41
3:le:79:THR:OG1	3:le:80:GLY:N	2.53	0.41
3:lj:30:VAL:O	3:lj:31:ALA:C	2.62	0.41
3:me:26:LYS:NZ	3:me:74:ASP:OD2	2.52	0.41
3:nd:30:VAL:O	3:nd:31:ALA:C	2.60	0.41
3:nv:79:THR:OG1	3:nv:80:GLY:N	2.53	0.41
1:ay:93:PRO:O	1:ay:94:ALA:C	2.63	0.41
1:az:243:THR:OG1	1:az:244:ASP:N	2.53	0.41
1:az:394:SER:O	1:az:395:TYR:C	2.63	0.41
1:bh:93:PRO:HA	1:bi:121:THR:O	2.20	0.41
1:bs:490:GLN:OE1	1:bs:490:GLN:N	2.51	0.41
1:bw:456:LEU:H	1:bw:475:THR:HG22	1.85	0.41
1:ct:145:HIS:NE2	1:ct:487:SER:O	2.52	0.41
1:df:93:PRO:O	1:df:94:ALA:C	2.64	0.41
1:do:243:THR:OG1	1:do:244:ASP:N	2.53	0.41
1:ds:327:SER:OG	1:ds:328:LYS:N	2.43	0.41
1:dt:243:THR:OG1	1:dt:244:ASP:N	2.54	0.41
1:du:250:MET:C	1:du:250:MET:SD	3.03	0.41
1:ei:120:PRO:O	1:ei:121:THR:OG1	2.31	0.41
1:em:67:GLU:HG3	1:ft:290:LEU:HD21	2.02	0.41
1:ev:243:THR:OG1	1:ev:244:ASP:N	2.54	0.41
1:ff:490:GLN:OE1	1:ff:490:GLN:N	2.52	0.41
1:fk:87:ALA:O	1:ga:495:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fw:287:ASP:OD1	1:fw:288:ALA:N	2.52	0.41
1:gq:243:THR:OG1	1:gq:244:ASP:N	2.53	0.41
1:gw:93:PRO:O	1:gw:94:ALA:C	2.64	0.41
2:hi:290:HIS:O	2:hi:291:LYS:C	2.63	0.41
3:iz:64:GLN:O	3:iz:66:THR:N	2.53	0.41
3:lk:79:THR:OG1	3:lk:80:GLY:N	2.53	0.41
1:ao:396:ALA:O	1:ao:397:ALA:HB2	2.20	0.41
1:ar:315:GLN:HB2	1:ar:514:ARG:HD2	2.02	0.41
1:as:243:THR:OG1	1:as:244:ASP:N	2.54	0.41
1:bo:287:ASP:OD1	1:bo:288:ALA:N	2.54	0.41
1:bw:396:ALA:O	1:bw:397:ALA:HB2	2.21	0.41
1:ca:317:GLY:O	1:ca:318:LYS:C	2.64	0.41
1:cc:243:THR:OG1	1:cc:244:ASP:N	2.53	0.41
1:cn:317:GLY:O	1:cn:318:LYS:C	2.61	0.41
1:cs:198:ILE:O	1:cs:199:ASP:C	2.63	0.41
1:cv:133:LYS:O	1:cv:133:LYS:HG2	2.21	0.41
1:da:93:PRO:O	1:da:94:ALA:C	2.63	0.41
1:dg:439:LYS:NZ	1:dg:440:GLY:O	2.50	0.41
1:du:344:ARG:O	1:du:345:TRP:HB2	2.21	0.41
1:dv:317:GLY:O	1:dv:318:LYS:C	2.63	0.41
1:dv:426:ASP:C	1:dv:426:ASP:OD1	2.63	0.41
1:ee:155:SER:HB3	1:ej:266:LEU:CD2	2.51	0.41
1:ef:336:ASP:C	1:ef:336:ASP:OD1	2.64	0.41
1:en:486:GLU:O	1:en:487:SER:C	2.63	0.41
1:es:145:HIS:NE2	1:es:487:SER:O	2.54	0.41
1:ex:317:GLY:O	1:ex:318:LYS:C	2.63	0.41
1:fa:93:PRO:O	1:fa:94:ALA:C	2.64	0.41
1:fg:134:ASP:C	1:fg:134:ASP:OD1	2.63	0.41
1:fs:344:ARG:O	1:fs:345:TRP:CB	2.68	0.41
1:fy:262:LYS:NZ	1:fz:226:GLU:OE2	2.51	0.41
1:gl:456:LEU:H	1:gl:475:THR:HG22	1.84	0.41
1:go:402:THR:OG1	1:go:403:GLY:N	2.50	0.41
1:gx:463:ASP:O	1:gx:467:PHE:N	2.53	0.41
1:gy:407:ASP:OD1	1:gy:408:THR:N	2.53	0.41
1:hb:483:PRO:O	1:hb:484:PHE:HB2	2.20	0.41
2:hf:28:THR:OG1	2:hf:29:ARG:N	2.51	0.41
2:hf:341:PHE:O	2:hf:343:ALA:N	2.53	0.41
2:hi:114:THR:N	2:hi:115:PRO:CD	2.82	0.41
2:hj:227:VAL:N	2:hj:231:THR:OG1	2.54	0.41
3:ib:30:VAL:O	3:ib:31:ALA:C	2.63	0.41
3:jq:30:VAL:O	3:jq:31:ALA:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:kl:30:VAL:O	3:kl:31:ALA:C	2.64	0.41
3:kq:68:TRP:O	3:kq:69:ILE:C	2.62	0.41
3:kw:79:THR:OG1	3:kw:80:GLY:N	2.53	0.41
3:ky:79:THR:OG1	3:ky:80:GLY:N	2.54	0.41
3:lm:30:VAL:HG21	3:lm:68:TRP:CH2	2.56	0.41
1:ba:317:GLY:O	1:ba:318:LYS:C	2.64	0.41
1:bl:120:PRO:O	1:bl:121:THR:OG1	2.38	0.41
1:bo:502:SER:OG	1:bo:503:ILE:N	2.54	0.41
1:bu:317:GLY:O	1:bu:318:LYS:C	2.64	0.41
1:bu:351:LYS:NZ	1:bu:394:SER:O	2.54	0.41
1:bv:243:THR:OG1	1:bv:244:ASP:N	2.53	0.41
1:bz:347:GLY:N	1:bz:398:GLN:OE1	2.53	0.41
1:cm:287:ASP:OD1	1:cm:288:ALA:N	2.54	0.41
1:cq:118:ASN:OD1	1:cq:118:ASN:N	2.50	0.41
1:cw:395:TYR:CG	1:cw:396:ALA:N	2.89	0.41
1:dn:118:ASN:OD1	1:dn:118:ASN:N	2.53	0.41
1:dw:287:ASP:OD1	1:dw:288:ALA:N	2.53	0.41
1:dx:273:GLU:H	1:dx:273:GLU:CD	2.29	0.41
1:ec:236:GLN:HG2	1:ec:247:TRP:CD2	2.56	0.41
1:ed:454:VAL:HB	1:ed:476:ARG:HB2	2.02	0.41
1:ef:118:ASN:OD1	1:ef:118:ASN:N	2.51	0.41
1:ek:484:PHE:O	1:ek:485:ALA:C	2.64	0.41
1:es:317:GLY:O	1:es:318:LYS:C	2.64	0.41
1:es:394:SER:O	1:es:395:TYR:C	2.64	0.41
1:et:287:ASP:OD1	1:et:288:ALA:N	2.53	0.41
1:ex:114:VAL:HA	1:ex:450:TYR:O	2.20	0.41
1:ex:474:LYS:NZ	2:hk:182:GLU:OE2	2.53	0.41
1:fj:481:ILE:HG23	1:fj:482:ASN:H	1.86	0.41
1:fp:345:TRP:CD1	1:fq:348:GLU:HB3	2.56	0.41
1:ga:407:ASP:OD2	1:ga:410:LYS:NZ	2.48	0.41
1:gb:505:ASN:N	1:gb:505:ASN:OD1	2.48	0.41
1:gg:317:GLY:O	1:gg:318:LYS:C	2.63	0.41
1:gh:344:ARG:O	1:gh:345:TRP:CB	2.68	0.41
1:gw:253:ARG:O	1:gw:254:ILE:C	2.62	0.41
2:hl:53:TYR:HD1	2:hl:53:TYR:HA	1.78	0.41
3:hu:79:THR:OG1	3:hu:80:GLY:N	2.53	0.41
3:jo:30:VAL:HG21	3:jo:68:TRP:CH2	2.56	0.41
3:kg:79:THR:OG1	3:kg:80:GLY:N	2.53	0.41
3:kp:68:TRP:O	3:kp:69:ILE:C	2.62	0.41
3:ld:64:GLN:O	3:ld:65:ARG:C	2.62	0.41
3:lp:30:VAL:O	3:lp:31:ALA:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:nk:79:THR:OG1	3:nk:80:GLY:N	2.53	0.41
1:ab:344:ARG:O	1:ab:345:TRP:HB3	2.20	0.41
1:ac:483:PRO:O	1:ac:484:PHE:HB2	2.21	0.41
1:am:67:GLU:CD	1:aw:251:GLY:HA3	2.45	0.41
1:am:118:ASN:N	1:am:118:ASN:OD1	2.49	0.41
1:ao:317:GLY:O	1:ao:318:LYS:C	2.64	0.41
1:ap:317:GLY:O	1:ap:318:LYS:C	2.62	0.41
1:ar:344:ARG:O	1:ar:345:TRP:HB2	2.21	0.41
1:ar:411:SER:OG	1:ar:412:VAL:N	2.54	0.41
1:au:198:ILE:O	1:au:199:ASP:C	2.62	0.41
1:az:317:GLY:O	1:az:318:LYS:C	2.63	0.41
1:bc:327:SER:OG	1:bc:328:LYS:N	2.54	0.41
1:be:264:ARG:HG3	1:bf:155:SER:OG	2.21	0.41
1:bh:267:LYS:O	1:bi:249:GLU:HB2	2.21	0.41
1:bi:317:GLY:O	1:bi:318:LYS:C	2.62	0.41
1:bt:426:ASP:C	1:bt:426:ASP:OD1	2.63	0.41
1:bv:411:SER:OG	1:bv:412:VAL:N	2.53	0.41
1:bx:77:THR:OG1	3:jd:5:ARG:NE	2.54	0.41
1:ca:394:SER:OG	1:ca:395:TYR:N	2.54	0.41
1:ci:456:LEU:H	1:ci:475:THR:HG22	1.84	0.41
1:cq:228:MET:O	1:cq:229:ALA:C	2.63	0.41
1:ct:456:LEU:H	1:ct:475:THR:HG22	1.84	0.41
1:de:133:LYS:HG3	1:de:133:LYS:O	2.21	0.41
1:de:236:GLN:HG2	1:de:247:TRP:CD2	2.55	0.41
1:dg:327:SER:OG	1:dg:328:LYS:N	2.53	0.41
1:dh:490:GLN:OE1	1:dh:490:GLN:N	2.53	0.41
1:di:444:MET:O	1:di:482:ASN:ND2	2.54	0.41
1:dl:125:PHE:CZ	1:dl:256:LYS:HD3	2.56	0.41
1:dl:407:ASP:OD1	1:dl:408:THR:N	2.54	0.41
1:dq:120:PRO:O	1:dq:121:THR:OG1	2.38	0.41
1:dt:502:SER:OG	1:dt:503:ILE:N	2.51	0.41
1:dv:336:ASP:OD1	1:dv:336:ASP:C	2.64	0.41
1:dx:243:THR:OG1	1:dx:244:ASP:N	2.54	0.41
1:dz:463:ASP:O	1:dz:467:PHE:N	2.53	0.41
1:ea:317:GLY:O	1:ea:318:LYS:C	2.63	0.41
1:en:243:THR:OG1	1:en:244:ASP:N	2.54	0.41
1:er:426:ASP:C	1:er:426:ASP:OD1	2.63	0.41
1:et:93:PRO:O	1:et:94:ALA:C	2.63	0.41
1:ey:267:LYS:HG3	1:ez:247:TRP:CE3	2.56	0.41
1:fa:439:LYS:NZ	1:fa:440:GLY:O	2.47	0.41
1:fe:345:TRP:CE2	1:fe:347:GLY:HA3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:fj:145:HIS:NE2	1:fj:487:SER:O	2.50	0.41
1:fo:198:ILE:HG22	1:fo:198:ILE:O	2.19	0.41
1:fq:463:ASP:O	1:fq:467:PHE:N	2.53	0.41
1:fw:118:ASN:OD1	1:fw:118:ASN:N	2.49	0.41
1:fx:243:THR:OG1	1:fx:244:ASP:N	2.54	0.41
1:fy:287:ASP:OD1	1:fy:288:ALA:N	2.54	0.41
1:gk:456:LEU:H	1:gk:475:THR:HG22	1.86	0.41
1:gm:131:TYR:CB	1:gm:250:MET:HB3	2.51	0.41
1:gm:131:TYR:HE1	1:gm:143:ALA:HA	1.85	0.41
1:gq:297:GLU:CB	1:gr:250:MET:HE1	2.51	0.41
1:gu:138:ALA:H	3:nu:38:VAL:HG13	1.85	0.41
1:gw:456:LEU:H	1:gw:475:THR:HG22	1.86	0.41
1:gz:394:SER:OG	1:gz:395:TYR:N	2.53	0.41
1:ha:118:ASN:OD1	1:ha:118:ASN:N	2.53	0.41
2:hj:290:HIS:O	2:hj:291:LYS:C	2.63	0.41
2:hk:241:ALA:O	2:hk:242:SER:C	2.63	0.41
2:hl:59:ASN:HB2	2:hl:60:PRO:HD2	2.03	0.41
3:hp:30:VAL:O	3:hp:31:ALA:C	2.64	0.41
3:hq:79:THR:O	3:hq:80:GLY:C	2.63	0.41
3:il:32:PHE:N	3:il:33:PRO:HD2	2.36	0.41
3:ix:44:ALA:HA	3:ix:76:TRP:HE1	1.86	0.41
3:kk:64:GLN:O	3:kk:66:THR:N	2.54	0.41
3:lb:68:TRP:O	3:lb:69:ILE:C	2.63	0.41
3:lp:68:TRP:O	3:lp:69:ILE:C	2.63	0.41
3:mc:30:VAL:O	3:mc:31:ALA:C	2.63	0.41
3:mf:30:VAL:O	3:mf:31:ALA:C	2.61	0.41
3:mk:30:VAL:O	3:mk:31:ALA:C	2.62	0.41
3:mo:26:LYS:NZ	3:mo:74:ASP:OD2	2.52	0.41
3:mq:26:LYS:NZ	3:mq:74:ASP:OD2	2.52	0.41
3:my:64:GLN:O	3:my:66:THR:N	2.54	0.41
3:no:79:THR:OG1	3:no:80:GLY:N	2.53	0.41
3:oe:79:THR:O	3:oe:80:GLY:C	2.64	0.41
1:ac:228:MET:O	1:ac:229:ALA:C	2.63	0.41
1:ai:250:MET:SD	1:ai:250:MET:C	3.04	0.41
1:at:521:ILE:O	1:au:359:LYS:NZ	2.50	0.41
1:bd:253:ARG:HB2	1:bd:254:ILE:H	1.78	0.41
1:bg:407:ASP:OD2	1:bg:410:LYS:NZ	2.46	0.41
1:bm:448:ILE:HG12	1:bm:513:PHE:CE2	2.56	0.41
1:bw:483:PRO:O	1:bw:484:PHE:HB2	2.20	0.41
1:ce:317:GLY:O	1:ce:318:LYS:C	2.64	0.41
1:cx:160:ALA:HB2	1:cx:228:MET:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:di:439:LYS:NZ	1:di:440:GLY:O	2.46	0.41
1:du:190:LEU:HB3	1:du:221:LEU:HG	2.03	0.41
1:dw:121:THR:HG22	1:dw:260:GLU:HG3	2.02	0.41
1:dw:236:GLN:HG2	1:dw:247:TRP:CD2	2.55	0.41
1:ed:83:GLN:NE2	3:lf:36:SER:OG	2.53	0.41
1:ej:243:THR:OG1	1:ej:244:ASP:N	2.53	0.41
1:eo:121:THR:HA	1:eo:259:ILE:O	2.20	0.41
1:ff:439:LYS:NZ	1:ff:440:GLY:O	2.48	0.41
1:fh:103:ILE:HA	1:fh:104:PRO:HD3	1.95	0.41
1:fz:351:LYS:NZ	1:fz:395:TYR:O	2.53	0.41
1:gb:344:ARG:O	1:gb:345:TRP:HB3	2.21	0.41
1:gt:448:ILE:HG12	1:gt:513:PHE:HE2	1.86	0.41
1:gy:273:GLU:O	1:gy:274:LEU:C	2.62	0.41
2:hg:384:ASN:HA	2:hg:385:PRO:HD3	1.95	0.41
3:hv:79:THR:O	3:hv:80:GLY:C	2.63	0.41
3:kh:68:TRP:O	3:kh:69:ILE:C	2.64	0.41
3:lo:79:THR:OG1	3:lo:80:GLY:N	2.54	0.41
3:ml:30:VAL:O	3:ml:31:ALA:C	2.64	0.41
3:mu:30:VAL:O	3:mu:31:ALA:C	2.63	0.41
3:nv:31:ALA:O	3:nv:32:PHE:C	2.63	0.41
1:ag:394:SER:O	1:ag:395:TYR:C	2.64	0.40
1:ag:468:GLN:HA	1:ag:469:PRO:HD3	1.97	0.40
1:ai:253:ARG:HH21	1:ai:495:ARG:HD2	1.85	0.40
1:ak:184:GLU:O	1:ak:185:THR:CB	2.68	0.40
1:bc:131:TYR:HE2	1:bc:143:ALA:HA	1.86	0.40
1:bw:236:GLN:HG2	1:bw:247:TRP:CD2	2.56	0.40
1:ce:505:ASN:OD1	1:ce:505:ASN:N	2.53	0.40
1:dc:253:ARG:O	1:dc:254:ILE:C	2.64	0.40
1:dc:372:GLU:O	1:dc:373:GLY:C	2.63	0.40
1:dd:344:ARG:O	1:dd:345:TRP:CB	2.69	0.40
1:dj:262:LYS:NZ	1:dk:226:GLU:OE2	2.49	0.40
1:dp:266:LEU:CD2	1:dq:155:SER:HB3	2.51	0.40
1:ea:463:ASP:O	1:ea:467:PHE:N	2.51	0.40
1:el:345:TRP:CG	1:el:346:ALA:N	2.88	0.40
1:em:456:LEU:H	1:em:475:THR:HG22	1.86	0.40
1:fh:71:ASP:OD1	1:fh:85:SER:OG	2.32	0.40
3:hz:79:THR:OG1	3:hz:80:GLY:N	2.54	0.40
3:jo:79:THR:OG1	3:jo:80:GLY:N	2.54	0.40
3:js:30:VAL:O	3:js:31:ALA:C	2.59	0.40
3:kl:79:THR:O	3:kl:80:GLY:C	2.64	0.40
3:lg:79:THR:OG1	3:lg:80:GLY:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:lv:72:ASN:C	3:lv:72:ASN:HD22	2.28	0.40
3:mh:26:LYS:NZ	3:mh:74:ASP:OD2	2.53	0.40
3:mp:79:THR:O	3:mp:80:GLY:C	2.64	0.40
3:nm:30:VAL:O	3:nm:31:ALA:C	2.61	0.40
3:nw:79:THR:O	3:nw:80:GLY:C	2.64	0.40
1:ad:118:ASN:OD1	1:ad:118:ASN:N	2.47	0.40
1:ak:439:LYS:NZ	1:ak:440:GLY:O	2.48	0.40
1:am:159:ALA:O	1:am:236:GLN:NE2	2.54	0.40
1:an:228:MET:O	1:an:229:ALA:C	2.62	0.40
1:aw:243:THR:OG1	1:aw:244:ASP:N	2.53	0.40
1:bg:121:THR:HG22	1:bg:260:GLU:HG2	2.03	0.40
1:bn:344:ARG:HG2	1:bn:348:GLU:OE1	2.22	0.40
1:br:407:ASP:OD2	1:br:410:LYS:NZ	2.46	0.40
1:br:505:ASN:C	1:br:505:ASN:OD1	2.64	0.40
1:bs:505:ASN:OD1	1:bs:505:ASN:C	2.64	0.40
1:dj:228:MET:O	1:dj:229:ALA:C	2.64	0.40
1:dl:456:LEU:H	1:dl:475:THR:HG22	1.86	0.40
1:ds:483:PRO:O	1:ds:484:PHE:HB2	2.21	0.40
1:ea:466:ASN:HB3	1:ef:237:GLU:HB2	2.02	0.40
1:ec:154:PHE:CZ	1:ec:248:ASN:HB3	2.57	0.40
1:em:267:LYS:HG3	1:en:247:TRP:CE3	2.56	0.40
1:eo:101:ARG:HD3	1:eo:101:ARG:HA	1.95	0.40
1:et:118:ASN:OD1	1:et:118:ASN:N	2.47	0.40
1:ez:263:SER:HB3	1:ez:476:ARG:HG2	2.03	0.40
1:fh:407:ASP:OD1	1:fh:408:THR:N	2.54	0.40
1:fs:243:THR:OG1	1:fs:244:ASP:N	2.51	0.40
1:fu:243:THR:OG1	1:fu:244:ASP:N	2.54	0.40
1:gc:426:ASP:OD1	1:gc:426:ASP:C	2.62	0.40
1:gg:456:LEU:H	1:gg:475:THR:HG22	1.86	0.40
1:go:243:THR:OG1	1:go:244:ASP:N	2.53	0.40
1:gq:287:ASP:OD1	1:gq:288:ALA:N	2.54	0.40
1:gr:407:ASP:OD1	1:gr:410:LYS:NZ	2.45	0.40
3:iy:79:THR:OG1	3:iy:80:GLY:N	2.54	0.40
3:jb:30:VAL:O	3:jb:31:ALA:C	2.64	0.40
3:jn:64:GLN:O	3:jn:66:THR:N	2.54	0.40
3:ka:32:PHE:N	3:ka:33:PRO:HD2	2.36	0.40
3:ke:31:ALA:O	3:ke:32:PHE:C	2.63	0.40
3:lg:31:ALA:O	3:lg:32:PHE:C	2.62	0.40
3:nt:30:VAL:O	3:nt:31:ALA:C	2.60	0.40
3:nu:32:PHE:N	3:nu:33:PRO:HD2	2.36	0.40
1:aa:341:ARG:O	1:af:345:TRP:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:aj:395:TYR:CD1	1:aj:395:TYR:C	2.97	0.40
1:aq:145:HIS:CD2	1:aq:490:GLN:HG2	2.56	0.40
1:as:456:LEU:H	1:as:475:THR:HG22	1.85	0.40
1:au:358:ASP:OD1	1:au:420:LYS:NZ	2.50	0.40
1:ax:407:ASP:OD1	1:ax:408:THR:N	2.53	0.40
1:ay:113:GLY:HA3	1:ay:449:TYR:HD1	1.86	0.40
1:bc:482:ASN:O	1:bc:483:PRO:C	2.63	0.40
1:bh:243:THR:OG1	1:bh:244:ASP:N	2.54	0.40
1:bx:486:GLU:O	1:bx:488:ALA:N	2.54	0.40
1:cf:237:GLU:HB2	1:dq:466:ASN:HB3	2.03	0.40
1:cn:243:THR:OG1	1:cn:244:ASP:N	2.54	0.40
1:cs:237:GLU:HB2	1:dl:466:ASN:HB3	2.04	0.40
1:cv:121:THR:HG22	1:cv:260:GLU:HG2	2.02	0.40
1:cx:71:ASP:OD2	1:cz:230:THR:N	2.55	0.40
1:cy:317:GLY:O	1:cy:318:LYS:C	2.64	0.40
1:dg:267:LYS:NZ	1:dh:237:GLU:OE1	2.54	0.40
1:dk:198:ILE:O	1:dk:199:ASP:C	2.64	0.40
1:eg:287:ASP:OD1	1:eg:288:ALA:N	2.53	0.40
1:eo:72:HIS:HB2	1:ep:260:GLU:CD	2.46	0.40
1:ey:404:PHE:HZ	1:ey:417:LEU:HA	1.86	0.40
1:ez:482:ASN:ND2	1:ez:483:PRO:O	2.55	0.40
1:fe:287:ASP:OD1	1:fe:288:ALA:N	2.54	0.40
1:fg:467:PHE:O	1:fg:467:PHE:CG	2.74	0.40
1:fj:439:LYS:NZ	1:fj:440:GLY:O	2.48	0.40
1:fl:93:PRO:CB	1:fm:121:THR:O	2.70	0.40
1:fp:317:GLY:O	1:fp:318:LYS:C	2.65	0.40
1:gg:103:ILE:HA	1:gg:104:PRO:HD3	1.97	0.40
1:gh:243:THR:OG1	1:gh:244:ASP:N	2.54	0.40
1:gj:71:ASP:OD2	1:gl:230:THR:N	2.54	0.40
1:gj:448:ILE:HG12	1:gj:513:PHE:CE2	2.56	0.40
1:gp:439:LYS:NZ	1:gp:440:GLY:O	2.51	0.40
2:ho:365:ASP:HB2	2:ho:368:SER:O	2.22	0.40
3:ia:79:THR:OG1	3:ia:80:GLY:N	2.53	0.40
3:im:79:THR:OG1	3:im:80:GLY:N	2.54	0.40
3:ke:32:PHE:N	3:ke:33:PRO:HD2	2.37	0.40
3:kv:30:VAL:O	3:kv:31:ALA:C	2.64	0.40
3:ma:79:THR:OG1	3:ma:80:GLY:N	2.54	0.40
3:ni:30:VAL:O	3:ni:31:ALA:C	2.65	0.40
3:nk:30:VAL:O	3:nk:31:ALA:C	2.61	0.40
3:nu:30:VAL:O	3:nu:31:ALA:C	2.63	0.40
3:od:79:THR:OG1	3:od:80:GLY:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:af:273:GLU:H	1:af:273:GLU:CD	2.30	0.40
1:aq:273:GLU:O	1:aq:274:LEU:C	2.64	0.40
1:at:118:ASN:OD1	1:at:118:ASN:N	2.50	0.40
1:aw:394:SER:OG	1:aw:395:TYR:N	2.55	0.40
1:az:198:ILE:O	1:az:199:ASP:C	2.63	0.40
1:bn:198:ILE:O	1:bn:199:ASP:C	2.64	0.40
1:br:463:ASP:O	1:br:467:PHE:N	2.52	0.40
1:ch:114:VAL:O	1:ch:115:GLN:C	2.62	0.40
1:cl:454:VAL:HB	1:cl:476:ARG:HB2	2.03	0.40
1:cp:198:ILE:HG22	1:cp:198:ILE:O	2.22	0.40
1:cv:317:GLY:O	1:cv:318:LYS:C	2.64	0.40
1:cw:72:HIS:HB2	1:cx:260:GLU:OE2	2.22	0.40
1:cx:463:ASP:O	1:cx:467:PHE:N	2.54	0.40
1:dq:154:PHE:CZ	1:dq:248:ASN:HB3	2.57	0.40
1:dz:448:ILE:HG12	1:dz:513:PHE:CE2	2.56	0.40
1:ee:394:SER:OG	1:ee:395:TYR:N	2.55	0.40
1:ef:490:GLN:OE1	1:ef:490:GLN:N	2.54	0.40
1:el:345:TRP:CD1	1:em:348:GLU:HB3	2.56	0.40
1:eq:456:LEU:H	1:eq:475:THR:HG22	1.87	0.40
1:ez:322:THR:HG23	1:ez:363:GLU:HG3	2.04	0.40
1:fi:456:LEU:H	1:fi:475:THR:HG22	1.87	0.40
1:fo:142:GLU:HB3	1:fo:145:HIS:HB2	2.03	0.40
1:fs:198:ILE:O	1:fs:198:ILE:CG2	2.70	0.40
1:ge:131:TYR:HB3	1:ge:250:MET:HE2	2.03	0.40
1:gj:133:LYS:NZ	1:gj:249:GLU:OE1	2.52	0.40
1:gl:287:ASP:OD1	1:gl:288:ALA:N	2.54	0.40
1:gm:483:PRO:O	1:gm:484:PHE:HB2	2.21	0.40
1:gp:120:PRO:O	1:gp:121:THR:OG1	2.36	0.40
1:gu:243:THR:OG1	1:gu:244:ASP:N	2.53	0.40
1:gw:344:ARG:O	1:gw:345:TRP:CB	2.69	0.40
2:hm:401:GLY:O	2:hm:402:ASP:C	2.65	0.40
3:ht:63:ASN:OD1	3:ht:63:ASN:N	2.52	0.40
3:ie:26:LYS:NZ	3:ie:74:ASP:OD2	2.52	0.40
3:it:64:GLN:O	3:it:65:ARG:C	2.64	0.40
3:jx:30:VAL:O	3:jx:31:ALA:C	2.64	0.40
3:la:79:THR:OG1	3:la:80:GLY:N	2.52	0.40
3:lp:79:THR:OG1	3:lp:80:GLY:N	2.53	0.40
3:mf:79:THR:OG1	3:mf:80:GLY:N	2.54	0.40
3:mn:79:THR:O	3:mn:80:GLY:C	2.64	0.40
3:ne:31:ALA:O	3:ne:32:PHE:C	2.65	0.40
3:nq:64:GLN:O	3:nq:66:THR:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ab:287:ASP:OD1	1:ab:288:ALA:N	2.52	0.40
1:af:372:GLU:O	1:af:373:GLY:C	2.65	0.40
1:ba:372:GLU:O	1:ba:373:GLY:C	2.65	0.40
1:bx:93:PRO:O	1:bx:94:ALA:C	2.65	0.40
1:cg:287:ASP:OD1	1:cg:288:ALA:N	2.53	0.40
1:cr:243:THR:OG1	1:cr:244:ASP:N	2.55	0.40
1:cy:287:ASP:OD1	1:cy:288:ALA:N	2.53	0.40
1:da:236:GLN:HG2	1:da:247:TRP:CE2	2.57	0.40
1:dh:154:PHE:CZ	1:dh:248:ASN:HB3	2.56	0.40
1:dp:273:GLU:O	1:dp:274:LEU:C	2.62	0.40
1:ed:456:LEU:H	1:ed:475:THR:HG22	1.85	0.40
1:eo:287:ASP:OD1	1:eo:287:ASP:N	2.50	0.40
1:ex:490:GLN:OE1	1:ex:490:GLN:N	2.54	0.40
1:fg:287:ASP:OD1	1:fg:288:ALA:N	2.54	0.40
1:fv:344:ARG:O	1:fv:345:TRP:CB	2.69	0.40
1:fx:439:LYS:NZ	1:fx:440:GLY:O	2.48	0.40
1:ge:467:PHE:CG	1:ge:467:PHE:O	2.74	0.40
1:gm:72:HIS:HB2	1:gn:260:GLU:CD	2.47	0.40
1:gn:345:TRP:CH2	1:go:395:TYR:O	2.75	0.40
3:ii:79:THR:O	3:ii:80:GLY:C	2.63	0.40
3:jl:33:PRO:HG2	3:jl:62:GLU:HG3	2.03	0.40
3:lj:68:TRP:O	3:lj:69:ILE:C	2.64	0.40
3:ls:79:THR:OG1	3:ls:80:GLY:N	2.54	0.40
3:nh:32:PHE:N	3:nh:33:PRO:HD2	2.37	0.40
3:np:30:VAL:O	3:np:31:ALA:C	2.61	0.40
3:np:32:PHE:N	3:np:33:PRO:HD2	2.37	0.40
3:nw:32:PHE:N	3:nw:33:PRO:HD2	2.36	0.40
3:nx:72:ASN:C	3:nx:72:ASN:HD22	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	aa	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	ab	454/521 (87%)	433 (95%)	16 (4%)	5 (1%)	11	38
1	ac	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	ad	454/521 (87%)	422 (93%)	29 (6%)	3 (1%)	18	47
1	ae	454/521 (87%)	432 (95%)	18 (4%)	4 (1%)	14	42
1	af	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42
1	ag	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	ah	454/521 (87%)	429 (94%)	19 (4%)	6 (1%)	9	33
1	ai	454/521 (87%)	425 (94%)	26 (6%)	3 (1%)	18	47
1	aj	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	ak	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42
1	al	454/521 (87%)	433 (95%)	17 (4%)	4 (1%)	14	42
1	am	454/521 (87%)	428 (94%)	24 (5%)	2 (0%)	30	59
1	an	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	ao	454/521 (87%)	425 (94%)	26 (6%)	3 (1%)	18	47
1	ap	454/521 (87%)	426 (94%)	26 (6%)	2 (0%)	30	59
1	aq	454/521 (87%)	424 (93%)	24 (5%)	6 (1%)	9	33
1	ar	454/521 (87%)	430 (95%)	22 (5%)	2 (0%)	30	59
1	as	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	at	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	au	454/521 (87%)	426 (94%)	24 (5%)	4 (1%)	14	42
1	av	454/521 (87%)	428 (94%)	22 (5%)	4 (1%)	14	42
1	aw	454/521 (87%)	423 (93%)	29 (6%)	2 (0%)	30	59
1	ax	454/521 (87%)	427 (94%)	25 (6%)	2 (0%)	30	59
1	ay	454/521 (87%)	428 (94%)	22 (5%)	4 (1%)	14	42
1	az	454/521 (87%)	428 (94%)	23 (5%)	3 (1%)	18	47
1	ba	454/521 (87%)	422 (93%)	29 (6%)	3 (1%)	18	47
1	bb	454/521 (87%)	433 (95%)	16 (4%)	5 (1%)	11	38
1	bc	454/521 (87%)	425 (94%)	26 (6%)	3 (1%)	18	47
1	bd	454/521 (87%)	430 (95%)	23 (5%)	1 (0%)	43	71
1	be	454/521 (87%)	427 (94%)	22 (5%)	5 (1%)	11	38
1	bf	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	bg	454/521 (87%)	426 (94%)	21 (5%)	7 (2%)	8	30
1	bh	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	bi	454/521 (87%)	423 (93%)	27 (6%)	4 (1%)	14	42
1	bj	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	bk	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	bl	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42
1	bm	454/521 (87%)	429 (94%)	19 (4%)	6 (1%)	9	33
1	bn	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42
1	bo	454/521 (87%)	427 (94%)	21 (5%)	6 (1%)	9	33
1	bp	454/521 (87%)	429 (94%)	19 (4%)	6 (1%)	9	33
1	bq	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	br	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	bs	454/521 (87%)	426 (94%)	23 (5%)	5 (1%)	11	38
1	bt	454/521 (87%)	424 (93%)	25 (6%)	5 (1%)	11	38
1	bu	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	bv	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	bw	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	bx	454/521 (87%)	427 (94%)	19 (4%)	8 (2%)	6	26
1	by	454/521 (87%)	424 (93%)	23 (5%)	7 (2%)	8	30
1	bz	454/521 (87%)	432 (95%)	17 (4%)	5 (1%)	11	38
1	ca	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	cb	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	cc	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	cd	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	ce	454/521 (87%)	423 (93%)	25 (6%)	6 (1%)	9	33
1	cf	454/521 (87%)	432 (95%)	20 (4%)	2 (0%)	30	59
1	cg	454/521 (87%)	428 (94%)	23 (5%)	3 (1%)	18	47
1	ch	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	ci	454/521 (87%)	430 (95%)	21 (5%)	3 (1%)	18	47
1	cj	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	ck	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	cl	454/521 (87%)	427 (94%)	21 (5%)	6 (1%)	9	33
1	cm	454/521 (87%)	427 (94%)	22 (5%)	5 (1%)	11	38
1	cn	454/521 (87%)	426 (94%)	24 (5%)	4 (1%)	14	42
1	co	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	cp	454/521 (87%)	424 (93%)	26 (6%)	4 (1%)	14	42
1	cq	454/521 (87%)	424 (93%)	24 (5%)	6 (1%)	9	33
1	cr	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	cs	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	ct	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	cu	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	cv	454/521 (87%)	428 (94%)	23 (5%)	3 (1%)	18	47
1	cw	454/521 (87%)	425 (94%)	22 (5%)	7 (2%)	8	30
1	cx	454/521 (87%)	423 (93%)	28 (6%)	3 (1%)	18	47
1	cy	454/521 (87%)	426 (94%)	23 (5%)	5 (1%)	11	38
1	cz	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	da	454/521 (87%)	430 (95%)	21 (5%)	3 (1%)	18	47
1	db	454/521 (87%)	426 (94%)	22 (5%)	6 (1%)	9	33
1	dc	454/521 (87%)	425 (94%)	26 (6%)	3 (1%)	18	47
1	dd	454/521 (87%)	427 (94%)	25 (6%)	2 (0%)	30	59
1	de	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	df	454/521 (87%)	430 (95%)	21 (5%)	3 (1%)	18	47
1	dg	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	dh	454/521 (87%)	429 (94%)	18 (4%)	7 (2%)	8	30
1	di	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	dj	454/521 (87%)	426 (94%)	26 (6%)	2 (0%)	30	59
1	dk	454/521 (87%)	426 (94%)	23 (5%)	5 (1%)	11	38
1	dl	454/521 (87%)	426 (94%)	25 (6%)	3 (1%)	18	47
1	dm	454/521 (87%)	432 (95%)	20 (4%)	2 (0%)	30	59
1	dn	454/521 (87%)	432 (95%)	18 (4%)	4 (1%)	14	42
1	do	454/521 (87%)	429 (94%)	22 (5%)	3 (1%)	18	47
1	dp	454/521 (87%)	422 (93%)	28 (6%)	4 (1%)	14	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	dq	454/521 (87%)	427 (94%)	22 (5%)	5 (1%)	11	38
1	dr	454/521 (87%)	429 (94%)	22 (5%)	3 (1%)	18	47
1	ds	454/521 (87%)	425 (94%)	24 (5%)	5 (1%)	11	38
1	dt	454/521 (87%)	430 (95%)	22 (5%)	2 (0%)	30	59
1	du	454/521 (87%)	431 (95%)	18 (4%)	5 (1%)	11	38
1	dv	454/521 (87%)	426 (94%)	25 (6%)	3 (1%)	18	47
1	dw	428/521 (82%)	400 (94%)	24 (6%)	4 (1%)	14	42
1	dx	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	dy	454/521 (87%)	428 (94%)	23 (5%)	3 (1%)	18	47
1	dz	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	ea	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	eb	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	ec	454/521 (87%)	426 (94%)	23 (5%)	5 (1%)	11	38
1	ed	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	ee	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
1	ef	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	eg	454/521 (87%)	428 (94%)	23 (5%)	3 (1%)	18	47
1	eh	454/521 (87%)	426 (94%)	25 (6%)	3 (1%)	18	47
1	ei	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	ej	454/521 (87%)	434 (96%)	17 (4%)	3 (1%)	18	47
1	ek	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	el	454/521 (87%)	429 (94%)	22 (5%)	3 (1%)	18	47
1	em	454/521 (87%)	423 (93%)	28 (6%)	3 (1%)	18	47
1	en	454/521 (87%)	424 (93%)	26 (6%)	4 (1%)	14	42
1	eo	454/521 (87%)	425 (94%)	24 (5%)	5 (1%)	11	38
1	ep	454/521 (87%)	426 (94%)	24 (5%)	4 (1%)	14	42
1	eq	454/521 (87%)	430 (95%)	21 (5%)	3 (1%)	18	47
1	er	454/521 (87%)	434 (96%)	17 (4%)	3 (1%)	18	47
1	es	454/521 (87%)	424 (93%)	26 (6%)	4 (1%)	14	42
1	et	454/521 (87%)	426 (94%)	24 (5%)	4 (1%)	14	42
1	eu	454/521 (87%)	425 (94%)	25 (6%)	4 (1%)	14	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ev	454/521 (87%)	432 (95%)	20 (4%)	2 (0%)	30	59
1	ew	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	ex	454/521 (87%)	430 (95%)	19 (4%)	5 (1%)	11	38
1	ey	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	ez	454/521 (87%)	430 (95%)	19 (4%)	5 (1%)	11	38
1	fa	454/521 (87%)	423 (93%)	27 (6%)	4 (1%)	14	42
1	fb	454/521 (87%)	428 (94%)	21 (5%)	5 (1%)	11	38
1	fc	454/521 (87%)	429 (94%)	23 (5%)	2 (0%)	30	59
1	fd	454/521 (87%)	429 (94%)	19 (4%)	6 (1%)	9	33
1	fe	454/521 (87%)	424 (93%)	27 (6%)	3 (1%)	18	47
1	ff	454/521 (87%)	432 (95%)	18 (4%)	4 (1%)	14	42
1	fg	454/521 (87%)	427 (94%)	22 (5%)	5 (1%)	11	38
1	fh	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	fi	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	fj	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42
1	fk	454/521 (87%)	429 (94%)	22 (5%)	3 (1%)	18	47
1	fl	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	fm	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	fn	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	fo	454/521 (87%)	428 (94%)	23 (5%)	3 (1%)	18	47
1	fp	454/521 (87%)	431 (95%)	19 (4%)	4 (1%)	14	42
1	fq	454/521 (87%)	423 (93%)	26 (6%)	5 (1%)	11	38
1	fr	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	fs	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	ft	454/521 (87%)	429 (94%)	22 (5%)	3 (1%)	18	47
1	fu	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	fv	454/521 (87%)	428 (94%)	21 (5%)	5 (1%)	11	38
1	fw	454/521 (87%)	424 (93%)	23 (5%)	7 (2%)	8	30
1	fx	454/521 (87%)	431 (95%)	18 (4%)	5 (1%)	11	38
1	fy	454/521 (87%)	426 (94%)	22 (5%)	6 (1%)	9	33
1	fz	454/521 (87%)	428 (94%)	22 (5%)	4 (1%)	14	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ga	454/521 (87%)	427 (94%)	23 (5%)	4 (1%)	14	42
1	gb	454/521 (87%)	431 (95%)	17 (4%)	6 (1%)	9	33
1	gc	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	gd	454/521 (87%)	430 (95%)	22 (5%)	2 (0%)	30	59
1	ge	454/521 (87%)	425 (94%)	23 (5%)	6 (1%)	9	33
1	gf	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	gg	454/521 (87%)	433 (95%)	17 (4%)	4 (1%)	14	42
1	gh	454/521 (87%)	426 (94%)	23 (5%)	5 (1%)	11	38
1	gi	454/521 (87%)	426 (94%)	24 (5%)	4 (1%)	14	42
1	gj	454/521 (87%)	423 (93%)	27 (6%)	4 (1%)	14	42
1	gk	454/521 (87%)	428 (94%)	20 (4%)	6 (1%)	9	33
1	gl	454/521 (87%)	431 (95%)	18 (4%)	5 (1%)	11	38
1	gm	454/521 (87%)	433 (95%)	17 (4%)	4 (1%)	14	42
1	gn	454/521 (87%)	427 (94%)	22 (5%)	5 (1%)	11	38
1	go	454/521 (87%)	426 (94%)	23 (5%)	5 (1%)	11	38
1	gp	454/521 (87%)	427 (94%)	26 (6%)	1 (0%)	43	71
1	gq	454/521 (87%)	429 (94%)	20 (4%)	5 (1%)	11	38
1	gr	454/521 (87%)	428 (94%)	21 (5%)	5 (1%)	11	38
1	gs	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	gt	454/521 (87%)	427 (94%)	21 (5%)	6 (1%)	9	33
1	gu	454/521 (87%)	431 (95%)	21 (5%)	2 (0%)	30	59
1	gv	454/521 (87%)	427 (94%)	24 (5%)	3 (1%)	18	47
1	gw	454/521 (87%)	430 (95%)	19 (4%)	5 (1%)	11	38
1	gx	454/521 (87%)	433 (95%)	20 (4%)	1 (0%)	43	71
1	gy	454/521 (87%)	429 (94%)	23 (5%)	2 (0%)	30	59
1	gz	454/521 (87%)	430 (95%)	20 (4%)	4 (1%)	14	42
1	ha	454/521 (87%)	429 (94%)	21 (5%)	4 (1%)	14	42
1	hb	454/521 (87%)	432 (95%)	19 (4%)	3 (1%)	18	47
1	hc	454/521 (87%)	425 (94%)	25 (6%)	4 (1%)	14	42
1	hd	454/521 (87%)	431 (95%)	20 (4%)	3 (1%)	18	47
2	he	413/427 (97%)	393 (95%)	16 (4%)	4 (1%)	12	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	hf	413/427 (97%)	389 (94%)	19 (5%)	5 (1%)	10	35
2	hg	413/427 (97%)	385 (93%)	24 (6%)	4 (1%)	12	40
2	hh	413/427 (97%)	386 (94%)	23 (6%)	4 (1%)	12	40
2	hi	413/427 (97%)	389 (94%)	20 (5%)	4 (1%)	12	40
2	hj	413/427 (97%)	389 (94%)	21 (5%)	3 (1%)	18	47
2	hk	413/427 (97%)	388 (94%)	20 (5%)	5 (1%)	10	35
2	hl	413/427 (97%)	384 (93%)	23 (6%)	6 (2%)	8	30
2	hm	413/427 (97%)	387 (94%)	19 (5%)	7 (2%)	7	28
2	hn	413/427 (97%)	390 (94%)	17 (4%)	6 (2%)	8	30
2	ho	413/427 (97%)	388 (94%)	20 (5%)	5 (1%)	10	35
3	hp	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	hq	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	hr	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	hs	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ht	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	hu	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	hv	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	hw	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	hx	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	hy	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	hz	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ia	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ib	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	ic	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	id	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ie	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	if	77/80 (96%)	72 (94%)	3 (4%)	2 (3%)	4	21
3	ig	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ih	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	ii	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ij	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	ik	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	il	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	im	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	in	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	io	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ip	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	iq	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ir	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	is	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	it	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	iu	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	iv	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	iw	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ix	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	iy	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	iz	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	ja	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jb	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jc	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jd	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	je	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	jf	77/80 (96%)	71 (92%)	5 (6%)	1 (1%)	9	33
3	jg	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	jh	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ji	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	jj	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	jk	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
3	jl	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jm	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jn	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	jo	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	jp	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	jq	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	jr	77/80 (96%)	70 (91%)	6 (8%)	1 (1%)	9	33
3	js	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	jt	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ju	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	jv	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	jw	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jx	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	jy	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	jz	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ka	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	kb	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	kc	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	kdl	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ke	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	kf	77/80 (96%)	73 (95%)	4 (5%)	0	100	100
3	kg	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	kh	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	ki	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	kj	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
3	kk	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	kl	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	km	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	kn	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ko	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	kp	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	kq	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	kr	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ks	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	kt	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	ku	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	kv	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	kw	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	kx	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ky	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	kz	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	la	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lb	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lc	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ld	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
3	le	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	lf	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lg	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	lh	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	li	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lj	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	lk	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ll	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	lm	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ln	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	lo	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	lp	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lq	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	lr	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	ls	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lt	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	lu	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lv	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	lw	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	lx	77/80 (96%)	73 (95%)	4 (5%)	0	100	100
3	ly	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	lz	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	ma	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	mb	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	mc	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	md	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	me	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mf	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	mg	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mh	77/80 (96%)	71 (92%)	5 (6%)	1 (1%)	9	33
3	mi	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mj	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	mk	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ml	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	mm	77/80 (96%)	76 (99%)	0	1 (1%)	9	33
3	mn	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mo	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mp	77/80 (96%)	72 (94%)	4 (5%)	1 (1%)	9	33
3	mq	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ms	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	mt	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mu	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	mv	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mw	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
3	mx	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	my	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	mz	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	na	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	nb	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	nc	77/80 (96%)	71 (92%)	5 (6%)	1 (1%)	9	33
3	nd	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ne	77/80 (96%)	73 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	nf	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ng	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	nh	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	ni	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	nj	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
3	nk	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	nl	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	nm	77/80 (96%)	73 (95%)	4 (5%)	0	100	100
3	nn	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	no	77/80 (96%)	75 (97%)	2 (3%)	0	100	100
3	np	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	nq	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	ns	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	nt	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	nu	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	nv	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	nw	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	nx	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ny	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	nz	77/80 (96%)	73 (95%)	4 (5%)	0	100	100
3	oa	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	ob	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	oc	77/80 (96%)	74 (96%)	2 (3%)	1 (1%)	9	33
3	od	77/80 (96%)	74 (96%)	3 (4%)	0	100	100
3	oe	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
3	of	77/80 (96%)	73 (95%)	3 (4%)	1 (1%)	9	33
3	og	77/80 (96%)	75 (97%)	1 (1%)	1 (1%)	9	33
All	All	102205/115363 (89%)	96599 (94%)	4674 (5%)	932 (1%)	16	42

All (932) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	aa	395	TYR

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Mol	Chain	Res	Type
1	ad	395	TYR
1	ag	254	ILE
1	ag	395	TYR
1	ai	254	ILE
1	ak	345	TRP
1	aq	481	ILE
1	as	105	ASN
1	as	254	ILE
1	as	395	TYR
1	av	254	ILE
1	av	345	TRP
1	aw	254	ILE
1	az	395	TYR
1	ba	345	TRP
1	bc	254	ILE
1	be	345	TRP
1	be	395	TYR
1	bf	345	TRP
1	bg	345	TRP
1	bh	345	TRP
1	bj	254	ILE
1	bj	345	TRP
1	bj	395	TYR
1	bk	345	TRP
1	bm	254	ILE
1	bm	395	TYR
1	bn	395	TYR
1	bp	395	TYR
1	bq	254	ILE
1	bq	345	TRP
1	br	345	TRP
1	bs	395	TYR
1	bt	345	TRP
1	bt	395	TYR
1	bu	345	TRP
1	bu	395	TYR
1	bv	395	TYR
1	bw	254	ILE
1	bw	345	TRP
1	bx	79	ILE
1	bx	254	ILE
1	by	345	TRP

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Mol	Chain	Res	Type
1	by	395	TYR
1	by	487	SER
1	bz	395	TYR
1	cb	395	TYR
1	cc	345	TRP
1	ce	395	TYR
1	ch	395	TYR
1	ci	254	ILE
1	ci	345	TRP
1	cj	345	TRP
1	cl	395	TYR
1	cm	395	TYR
1	cn	254	ILE
1	cp	345	TRP
1	cp	395	TYR
1	cq	254	ILE
1	cq	395	TYR
1	cr	395	TYR
1	cs	395	TYR
1	ct	395	TYR
1	cv	345	TRP
1	cw	395	TYR
1	cy	395	TYR
1	da	254	ILE
1	da	395	TYR
1	db	345	TRP
1	dc	254	ILE
1	dc	345	TRP
1	df	254	ILE
1	dg	254	ILE
1	dg	395	TYR
1	dh	395	TYR
1	di	254	ILE
1	di	345	TRP
1	dk	395	TYR
1	dl	254	ILE
1	do	345	TRP
1	dp	345	TRP
1	dq	395	TYR
1	dr	254	ILE
1	ds	345	TRP
1	du	254	ILE

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Mol	Chain	Res	Type
1	dy	395	TYR
1	dz	345	TRP
1	dz	395	TYR
1	eb	345	TRP
1	ed	345	TRP
1	ee	254	ILE
1	ee	345	TRP
1	ef	345	TRP
1	eh	345	TRP
1	ek	254	ILE
1	el	395	TYR
1	em	345	TRP
1	eo	345	TRP
1	eq	345	TRP
1	es	395	TYR
1	et	254	ILE
1	ev	254	ILE
1	ex	395	TYR
1	ey	345	TRP
1	ez	345	TRP
1	ez	395	TYR
1	fa	395	TYR
1	fc	345	TRP
1	fd	345	TRP
1	fd	395	TYR
1	fe	395	TYR
1	ff	345	TRP
1	fg	395	TYR
1	fh	345	TRP
1	fi	254	ILE
1	fi	345	TRP
1	fl	345	TRP
1	fl	395	TYR
1	fn	254	ILE
1	fo	254	ILE
1	fo	345	TRP
1	fs	395	TYR
1	ft	395	TYR
1	fu	254	ILE
1	fu	345	TRP
1	fu	395	TYR
1	fv	395	TYR

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Mol	Chain	Res	Type
1	fw	395	TYR
1	fx	345	TRP
1	fx	395	TYR
1	fy	395	TYR
1	fz	395	TYR
1	ga	254	ILE
1	ga	345	TRP
1	gc	345	TRP
1	gc	395	TYR
1	gd	345	TRP
1	ge	395	TYR
1	gi	254	ILE
1	gi	345	TRP
1	gi	395	TYR
1	gj	395	TYR
1	gj	487	SER
1	gk	254	ILE
1	gl	254	ILE
1	gn	345	TRP
1	gn	395	TYR
1	go	254	ILE
1	go	345	TRP
1	gq	395	TYR
1	gr	395	TYR
1	gt	395	TYR
1	gu	254	ILE
1	gu	345	TRP
1	gw	254	ILE
1	ha	345	TRP
1	ha	395	TYR
1	hb	345	TRP
1	hc	395	TYR
2	hf	243	ALA
2	hf	342	TYR
2	hg	342	TYR
2	hh	342	TYR
2	hk	342	TYR
2	hl	243	ALA
2	hm	243	ALA
2	hn	243	ALA
2	hn	353	ASP
2	ho	243	ALA

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Mol	Chain	Res	Type
2	ho	342	TYR
3	hp	65	ARG
3	hq	65	ARG
3	hr	65	ARG
3	hs	65	ARG
3	hu	65	ARG
3	hv	65	ARG
3	hw	65	ARG
3	hx	65	ARG
3	hy	65	ARG
3	hz	65	ARG
3	ia	65	ARG
3	ic	65	ARG
3	id	65	ARG
3	ie	65	ARG
3	if	65	ARG
3	ig	65	ARG
3	ih	65	ARG
3	ii	65	ARG
3	ij	65	ARG
3	ik	65	ARG
3	il	65	ARG
3	im	65	ARG
3	in	65	ARG
3	io	65	ARG
3	iq	65	ARG
3	ir	65	ARG
3	is	65	ARG
3	iu	65	ARG
3	iv	65	ARG
3	iw	65	ARG
3	ix	65	ARG
3	iy	65	ARG
3	iz	65	ARG
3	ja	65	ARG
3	jb	65	ARG
3	jc	65	ARG
3	jd	65	ARG
3	je	65	ARG
3	jf	65	ARG
3	jg	65	ARG
3	jh	65	ARG

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Mol	Chain	Res	Type
3	ji	65	ARG
3	jl	65	ARG
3	jm	65	ARG
3	jn	65	ARG
3	jo	65	ARG
3	jq	65	ARG
3	jr	65	ARG
3	js	65	ARG
3	jt	65	ARG
3	ju	65	ARG
3	jw	65	ARG
3	jy	65	ARG
3	jz	65	ARG
3	ka	65	ARG
3	kb	65	ARG
3	ke	65	ARG
3	kg	65	ARG
3	ki	65	ARG
3	kk	65	ARG
3	kl	65	ARG
3	km	65	ARG
3	kn	65	ARG
3	ko	65	ARG
3	kp	65	ARG
3	kq	65	ARG
3	kr	65	ARG
3	ks	65	ARG
3	kt	65	ARG
3	ku	65	ARG
3	65	ARG	
3	kw	65	ARG
3	kx	65	ARG
3	ky	65	ARG
3	kz	65	ARG
3	la	65	ARG
3	lb	65	ARG
3	lc	65	ARG
3	le	65	ARG
3	lf	65	ARG
3	lg	65	ARG
3	lh	65	ARG
3	li	65	ARG

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Mol	Chain	Res	Type
3	lj	65	ARG
3	lk	65	ARG
3	ll	65	ARG
3	lm	65	ARG
3	ln	65	ARG
3	lo	65	ARG
3	lp	65	ARG
3	lq	65	ARG
3	ls	65	ARG
3	lt	65	ARG
3	lu	65	ARG
3	lv	65	ARG
3	lw	65	ARG
3	ly	65	ARG
3	ma	65	ARG
3	me	65	ARG
3	mf	65	ARG
3	mg	65	ARG
3	mh	65	ARG
3	mi	65	ARG
3	mj	65	ARG
3	mk	65	ARG
3	mm	65	ARG
3	mn	65	ARG
3	mo	65	ARG
3	mp	65	ARG
3	mq	65	ARG
3	ms	65	ARG
3	mt	65	ARG
3	mv	65	ARG
3	mx	65	ARG
3	my	65	ARG
3	mz	65	ARG
3	nb	65	ARG
3	nc	65	ARG
3	nd	65	ARG
3	nf	65	ARG
3	ng	65	ARG
3	nh	65	ARG
3	ni	65	ARG
3	nk	65	ARG
3	nl	65	ARG

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Mol	Chain	Res	Type
3	nn	65	ARG
3	np	65	ARG
3	nq	65	ARG
3	ns	65	ARG
3	nt	65	ARG
3	nu	65	ARG
3	nw	65	ARG
3	nx	65	ARG
3	ny	65	ARG
3	oa	65	ARG
3	ob	65	ARG
3	oc	65	ARG
3	oe	65	ARG
3	of	65	ARG
3	og	65	ARG
1	aa	199	ASP
1	ac	254	ILE
1	ac	345	TRP
1	ac	395	TYR
1	ad	254	ILE
1	ad	345	TRP
1	ae	94	ALA
1	ae	345	TRP
1	af	345	TRP
1	af	395	TYR
1	ah	254	ILE
1	ah	345	TRP
1	aj	254	ILE
1	ak	185	THR
1	am	254	ILE
1	aq	199	ASP
1	aq	395	TYR
1	as	345	TRP
1	at	254	ILE
1	at	395	TYR
1	au	254	ILE
1	au	345	TRP
1	ba	254	ILE
1	ba	395	TYR
1	bb	345	TRP
1	bd	254	ILE
1	bf	237	GLU

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Mol	Chain	Res	Type
1	bh	254	ILE
1	bi	254	ILE
1	bk	199	ASP
1	bl	345	TRP
1	bn	254	ILE
1	bo	395	TYR
1	bp	345	TRP
1	bq	502	SER
1	bs	94	ALA
1	bs	345	TRP
1	bt	254	ILE
1	by	254	ILE
1	bz	254	ILE
1	ca	345	TRP
1	cb	345	TRP
1	cc	395	TYR
1	cd	254	ILE
1	ce	94	ALA
1	ce	254	ILE
1	ce	345	TRP
1	ch	345	TRP
1	ck	345	TRP
1	ck	395	TYR
1	cm	199	ASP
1	cn	345	TRP
1	co	345	TRP
1	cp	254	ILE
1	cq	345	TRP
1	cs	199	ASP
1	cu	254	ILE
1	cu	345	TRP
1	cv	254	ILE
1	cw	254	ILE
1	cw	345	TRP
1	cx	254	ILE
1	cy	254	ILE
1	da	345	TRP
1	de	345	TRP
1	de	395	TYR
1	dg	345	TRP
1	dj	345	TRP
1	dk	199	ASP

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Mol	Chain	Res	Type
1	dm	345	TRP
1	dn	254	ILE
1	dn	345	TRP
1	dq	345	TRP
1	dr	345	TRP
1	dt	345	TRP
1	du	395	TYR
1	dv	254	ILE
1	dy	254	ILE
1	dy	345	TRP
1	dz	254	ILE
1	ec	395	TYR
1	ef	254	ILE
1	eg	254	ILE
1	eh	254	ILE
1	eh	395	TYR
1	ej	345	TRP
1	ek	345	TRP
1	em	254	ILE
1	en	345	TRP
1	eo	395	TYR
1	ep	345	TRP
1	ep	395	TYR
1	et	395	TYR
1	eu	199	ASP
1	ex	254	ILE
1	ex	345	TRP
1	ey	254	ILE
1	ez	254	ILE
1	fa	254	ILE
1	fb	345	TRP
1	fe	254	ILE
1	fe	345	TRP
1	ff	254	ILE
1	fj	254	ILE
1	fk	254	ILE
1	fk	345	TRP
1	fn	345	TRP
1	fp	254	ILE
1	fq	345	TRP
1	fq	395	TYR
1	fq	487	SER

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Mol	Chain	Res	Type
1	fr	254	ILE
1	fr	395	TYR
1	fw	254	ILE
1	gb	254	ILE
1	ge	254	ILE
1	gf	345	TRP
1	gg	254	ILE
1	gh	254	ILE
1	gj	254	ILE
1	gj	345	TRP
1	gk	395	TYR
1	gk	487	SER
1	gl	345	TRP
1	gl	395	TYR
1	gp	254	ILE
1	gr	345	TRP
1	gt	94	ALA
1	gt	254	ILE
1	gw	199	ASP
1	gy	254	ILE
1	gy	345	TRP
1	hc	199	ASP
2	he	340	ILE
2	he	342	TYR
2	hf	340	ILE
2	hk	25	VAL
2	hl	342	TYR
2	hm	130	ILE
2	hn	342	TYR
3	if	19	GLY
3	kd	65	ARG
1	aa	345	TRP
1	ab	199	ASP
1	ab	254	ILE
1	ab	395	TYR
1	ae	254	ILE
1	af	94	ALA
1	ai	94	ALA
1	aj	199	ASP
1	ak	254	ILE
1	al	199	ASP
1	al	254	ILE

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Mol	Chain	Res	Type
1	am	199	ASP
1	an	254	ILE
1	an	345	TRP
1	an	395	TYR
1	ao	94	ALA
1	ao	254	ILE
1	ap	254	ILE
1	ap	345	TRP
1	aq	254	ILE
1	ar	94	ALA
1	ar	254	ILE
1	at	94	ALA
1	av	432	ASP
1	ax	254	ILE
1	ay	94	ALA
1	ay	345	TRP
1	az	254	ILE
1	bb	94	ALA
1	bb	395	TYR
1	bc	199	ASP
1	be	493	ALA
1	be	495	ARG
1	bg	254	ILE
1	bg	487	SER
1	bg	495	ARG
1	bh	395	TYR
1	bi	395	TYR
1	bj	199	ASP
1	bl	254	ILE
1	bm	199	ASP
1	bn	94	ALA
1	bn	199	ASP
1	bo	345	TRP
1	bp	254	ILE
1	bq	501	PRO
1	bs	199	ASP
1	bs	254	ILE
1	bu	254	ILE
1	bv	254	ILE
1	bv	345	TRP
1	bx	94	ALA
1	bx	487	SER

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Mol	Chain	Res	Type
1	by	199	ASP
1	bz	94	ALA
1	bz	199	ASP
1	bz	345	TRP
1	cc	199	ASP
1	cc	254	ILE
1	cd	199	ASP
1	cd	395	TYR
1	cf	94	ALA
1	cf	254	ILE
1	cg	254	ILE
1	cg	395	TYR
1	ch	254	ILE
1	cj	254	ILE
1	cj	395	TYR
1	cl	199	ASP
1	cl	254	ILE
1	cl	345	TRP
1	cl	495	ARG
1	cm	254	ILE
1	cn	199	ASP
1	co	199	ASP
1	cq	124	VAL
1	cq	199	ASP
1	cq	487	SER
1	cr	254	ILE
1	ct	345	TRP
1	cu	199	ASP
1	cu	495	ARG
1	cw	94	ALA
1	cw	199	ASP
1	db	254	ILE
1	dc	94	ALA
1	dd	254	ILE
1	de	254	ILE
1	df	199	ASP
1	dh	199	ASP
1	dh	345	TRP
1	di	199	ASP
1	dj	254	ILE
1	dk	254	ILE
1	dl	199	ASP

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Mol	Chain	Res	Type
1	dl	269	ALA
1	dm	495	ARG
1	dn	432	ASP
1	do	199	ASP
1	do	254	ILE
1	dp	254	ILE
1	dq	94	ALA
1	dq	254	ILE
1	dr	199	ASP
1	du	495	ARG
1	dv	199	ASP
1	dw	94	ALA
1	dw	254	ILE
1	ea	254	ILE
1	ea	345	TRP
1	eb	199	ASP
1	eb	487	SER
1	ec	199	ASP
1	ec	254	ILE
1	ec	345	TRP
1	ed	199	ASP
1	ed	254	ILE
1	eg	199	ASP
1	ei	254	ILE
1	ei	487	SER
1	eo	254	ILE
1	ep	199	ASP
1	eq	199	ASP
1	er	254	ILE
1	er	395	TYR
1	es	454	VAL
1	et	199	ASP
1	et	495	ARG
1	eu	345	TRP
1	ew	345	TRP
1	ey	199	ASP
1	ey	487	SER
1	fb	199	ASP
1	fd	254	ILE
1	fd	495	ARG
1	ff	94	ALA
1	fg	254	ILE

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Mol	Chain	Res	Type
1	fg	487	SER
1	fj	94	ALA
1	fj	345	TRP
1	fj	495	ARG
1	fk	199	ASP
1	fm	345	TRP
1	fm	395	TYR
1	fm	487	SER
1	fq	94	ALA
1	fr	94	ALA
1	fr	199	ASP
1	fs	254	ILE
1	fs	345	TRP
1	ft	254	ILE
1	ft	345	TRP
1	fu	495	ARG
1	fv	199	ASP
1	fw	199	ASP
1	fw	501	PRO
1	fw	502	SER
1	fx	254	ILE
1	fy	254	ILE
1	fy	345	TRP
1	fz	254	ILE
1	gb	199	ASP
1	gb	345	TRP
1	gc	199	ASP
1	ge	199	ASP
1	gf	199	ASP
1	gg	199	ASP
1	gh	94	ALA
1	gh	199	ASP
1	gl	199	ASP
1	gm	199	ASP
1	gm	254	ILE
1	gm	345	TRP
1	gq	254	ILE
1	gr	254	ILE
1	gs	199	ASP
1	gt	199	ASP
1	gt	345	TRP
1	gv	254	ILE

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Mol	Chain	Res	Type
1	gw	345	TRP
1	hb	254	ILE
1	hc	254	ILE
1	hd	199	ASP
2	he	364	VAL
2	hg	340	ILE
2	hg	357	VAL
2	hh	364	VAL
2	hi	340	ILE
2	hi	342	TYR
2	hi	357	VAL
2	hj	357	VAL
2	hl	340	ILE
2	hm	340	ILE
2	hm	357	VAL
2	hn	364	VAL
2	ho	340	ILE
1	aa	495	ARG
1	ab	345	TRP
1	ae	487	SER
1	af	254	ILE
1	ag	503	ILE
1	ah	199	ASP
1	ah	395	TYR
1	ah	495	ARG
1	ak	199	ASP
1	al	237	GLU
1	al	432	ASP
1	an	495	ARG
1	aq	345	TRP
1	aq	487	SER
1	as	495	ARG
1	at	345	TRP
1	au	199	ASP
1	aw	495	ARG
1	ax	345	TRP
1	bb	254	ILE
1	bb	487	SER
1	bf	254	ILE
1	bf	395	TYR
1	bg	199	ASP
1	bh	199	ASP

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Mol	Chain	Res	Type
1	bi	432	ASP
1	bk	254	ILE
1	bk	495	ARG
1	bm	269	ALA
1	bo	254	ILE
1	bo	487	SER
1	bo	495	ARG
1	br	254	ILE
1	bt	432	ASP
1	bt	495	ARG
1	bw	495	ARG
1	bx	345	TRP
1	bx	395	TYR
1	by	94	ALA
1	by	269	ALA
1	ca	487	SER
1	cb	254	ILE
1	ce	199	ASP
1	cg	487	SER
1	ci	495	ARG
1	ck	94	ALA
1	ck	254	ILE
1	cn	482	ASN
1	co	94	ALA
1	co	254	ILE
1	cr	94	ALA
1	cs	254	ILE
1	cs	432	ASP
1	cw	487	SER
1	cx	94	ALA
1	cx	495	ARG
1	cz	199	ASP
1	cz	254	ILE
1	cz	495	ARG
1	db	199	ASP
1	de	495	ARG
1	dh	94	ALA
1	dh	254	ILE
1	dk	237	GLU
1	dk	432	ASP
1	dn	487	SER
1	dp	94	ALA

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Mol	Chain	Res	Type
1	dp	495	ARG
1	ds	116	PRO
1	dv	94	ALA
1	dw	345	TRP
1	dw	495	ARG
1	dx	199	ASP
1	dx	345	TRP
1	ea	94	ALA
1	eb	254	ILE
1	ec	495	ARG
1	ef	432	ASP
1	ej	254	ILE
1	ej	432	ASP
1	ek	199	ASP
1	el	254	ILE
1	en	254	ILE
1	en	432	ASP
1	ep	254	ILE
1	es	254	ILE
1	eu	254	ILE
1	eu	432	ASP
1	ev	199	ASP
1	ew	495	ARG
1	fa	487	SER
1	fb	94	ALA
1	fb	254	ILE
1	fc	254	ILE
1	fd	94	ALA
1	fd	199	ASP
1	fg	495	ARG
1	fh	254	ILE
1	fi	199	ASP
1	fl	254	ILE
1	fl	487	SER
1	fm	254	ILE
1	fo	495	ARG
1	fp	199	ASP
1	fp	495	ARG
1	fr	495	ARG
1	fs	487	SER
1	fw	94	ALA
1	fw	495	ARG

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Mol	Chain	Res	Type
1	fx	495	ARG
1	fy	94	ALA
1	fy	487	SER
1	ga	199	ASP
1	gb	94	ALA
1	gb	453	TYR
1	gc	254	ILE
1	gd	254	ILE
1	ge	495	ARG
1	gf	254	ILE
1	gh	345	TRP
1	gh	495	ARG
1	gi	199	ASP
1	gk	432	ASP
1	gl	94	ALA
1	gm	495	ARG
1	gn	495	ARG
1	go	199	ASP
1	gs	254	ILE
1	gs	345	TRP
1	gw	487	SER
1	gx	254	ILE
1	gz	254	ILE
1	gz	487	SER
1	hc	432	ASP
2	he	357	VAL
2	hf	364	VAL
2	hg	364	VAL
2	hi	364	VAL
2	hj	364	VAL
2	hk	364	VAL
2	hl	357	VAL
2	hl	364	VAL
2	hm	364	VAL
2	ho	364	VAL
1	aa	254	ILE
1	ab	94	ALA
1	ag	199	ASP
1	ah	432	ASP
1	ai	432	ASP
1	aj	345	TRP
1	ao	345	TRP

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Mol	Chain	Res	Type
1	au	94	ALA
1	ay	199	ASP
1	ay	254	ILE
1	be	254	ILE
1	bf	494	SER
1	bl	495	ARG
1	bm	345	TRP
1	bm	432	ASP
1	bo	432	ASP
1	bp	269	ALA
1	bp	495	ARG
1	br	94	ALA
1	bx	495	ARG
1	ca	254	ILE
1	cd	345	TRP
1	ce	432	ASP
1	ch	432	ASP
1	cl	487	SER
1	cm	185	THR
1	cm	487	SER
1	cp	432	ASP
1	ct	254	ILE
1	cv	432	ASP
1	cw	432	ASP
1	cy	199	ASP
1	cy	345	TRP
1	cy	495	ARG
1	db	94	ALA
1	db	432	ASP
1	db	495	ARG
1	dd	345	TRP
1	df	345	TRP
1	dg	199	ASP
1	dh	432	ASP
1	dq	432	ASP
1	ds	254	ILE
1	ds	395	TYR
1	dt	254	ILE
1	du	345	TRP
1	dx	254	ILE
1	eg	495	ARG
1	ei	94	ALA

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Mol	Chain	Res	Type
1	eo	94	ALA
1	eq	254	ILE
1	er	199	ASP
1	es	345	TRP
1	ew	199	ASP
1	ew	254	ILE
1	ex	94	ALA
1	ex	269	ALA
1	ez	94	ALA
1	fb	396	ALA
1	fh	269	ALA
1	fp	487	SER
1	fq	254	ILE
1	fv	254	ILE
1	fx	94	ALA
1	fz	345	TRP
1	fz	432	ASP
1	gb	487	SER
1	gg	345	TRP
1	gk	185	THR
1	gn	254	ILE
1	go	94	ALA
1	go	432	ASP
1	gq	345	TRP
1	gr	94	ALA
1	gr	432	ASP
1	gs	495	ARG
1	gt	432	ASP
1	gv	94	ALA
1	gv	345	TRP
1	gw	432	ASP
1	gz	345	TRP
1	gz	432	ASP
1	ha	254	ILE
1	hb	494	SER
1	hd	254	ILE
1	hd	345	TRP
2	hf	357	VAL
2	hh	340	ILE
2	hh	357	VAL
2	hj	340	ILE
2	hk	340	ILE

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Mol	Chain	Res	Type
2	hk	357	VAL
2	hl	333	GLU
2	hm	342	TYR
2	hn	340	ILE
2	ho	357	VAL
1	av	94	ALA
1	az	345	TRP
1	bg	94	ALA
1	bh	432	ASP
1	bi	94	ALA
1	bl	94	ALA
1	bp	94	ALA
1	bx	432	ASP
1	dh	487	SER
1	ds	199	ASP
1	du	199	ASP
1	dx	94	ALA
1	ee	495	ARG
1	ek	492	PRO
1	el	345	TRP
1	em	432	ASP
1	en	495	ARG
1	eo	432	ASP
1	ey	94	ALA
1	ez	432	ASP
1	fa	432	ASP
1	ff	199	ASP
1	fg	94	ALA
1	fh	94	ALA
1	fn	432	ASP
1	fv	345	TRP
1	fv	432	ASP
1	ga	495	ARG
1	ge	432	ASP
1	ge	487	SER
1	gg	94	ALA
1	gk	94	ALA
1	gn	487	SER
1	gq	199	ASP
1	gq	432	ASP
1	ha	432	ASP
1	bg	79	ILE

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Mol	Chain	Res	Type
1	ei	198	ILE
2	hm	291	LYS
1	br	198	ILE
1	fy	198	ILE
1	fh	482	ASN
2	hn	292	PRO
1	bc	482	ASN

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	aa	345/400 (86%)	345 (100%)	0	100	100
1	ab	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ac	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ad	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ae	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	af	345/400 (86%)	345 (100%)	0	100	100
1	ag	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ah	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ai	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	aj	345/400 (86%)	345 (100%)	0	100	100
1	ak	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	al	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	am	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	an	345/400 (86%)	345 (100%)	0	100	100
1	ao	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ap	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	aq	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ar	345/400 (86%)	345 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	as	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	at	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	au	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	av	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	aw	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ax	345/400 (86%)	345 (100%)	0	100	100
1	ay	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	az	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ba	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bb	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	bc	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	bd	345/400 (86%)	345 (100%)	0	100	100
1	be	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	bf	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bg	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bh	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	bi	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bj	345/400 (86%)	345 (100%)	0	100	100
1	bk	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bl	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bm	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bn	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bo	345/400 (86%)	345 (100%)	0	100	100
1	bp	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bq	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	br	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	bs	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bt	345/400 (86%)	345 (100%)	0	100	100
1	bu	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	bv	345/400 (86%)	345 (100%)	0	100	100
1	bw	345/400 (86%)	343 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	bx	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	by	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	bz	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	ca	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	cb	345/400 (86%)	345 (100%)	0	100	100
1	cc	345/400 (86%)	345 (100%)	0	100	100
1	cd	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ce	345/400 (86%)	345 (100%)	0	100	100
1	cf	345/400 (86%)	345 (100%)	0	100	100
1	cg	345/400 (86%)	345 (100%)	0	100	100
1	ch	345/400 (86%)	345 (100%)	0	100	100
1	ci	345/400 (86%)	345 (100%)	0	100	100
1	cj	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	ck	345/400 (86%)	345 (100%)	0	100	100
1	cl	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	cm	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	cn	345/400 (86%)	345 (100%)	0	100	100
1	co	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	cp	345/400 (86%)	345 (100%)	0	100	100
1	cq	345/400 (86%)	345 (100%)	0	100	100
1	cr	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	cs	345/400 (86%)	345 (100%)	0	100	100
1	ct	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	cu	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	cv	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	cw	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	cx	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	cy	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	cz	345/400 (86%)	345 (100%)	0	100	100
1	da	345/400 (86%)	345 (100%)	0	100	100
1	db	345/400 (86%)	343 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	dc	345/400 (86%)	345 (100%)	0	100	100
1	dd	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	de	345/400 (86%)	345 (100%)	0	100	100
1	df	345/400 (86%)	345 (100%)	0	100	100
1	dg	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	dh	345/400 (86%)	345 (100%)	0	100	100
1	di	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	dj	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	dk	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	dl	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	dm	345/400 (86%)	341 (99%)	4 (1%)	63	72
1	dn	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	do	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	dp	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	dq	345/400 (86%)	345 (100%)	0	100	100
1	dr	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ds	345/400 (86%)	345 (100%)	0	100	100
1	dt	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	du	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	dv	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	dw	329/400 (82%)	328 (100%)	1 (0%)	86	84
1	dx	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	dy	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	dz	345/400 (86%)	345 (100%)	0	100	100
1	ea	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	eb	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ec	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ed	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ee	345/400 (86%)	345 (100%)	0	100	100
1	ef	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	eg	345/400 (86%)	342 (99%)	3 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	eh	345/400 (86%)	341 (99%)	4 (1%)	63	72
1	ei	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ej	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ek	345/400 (86%)	345 (100%)	0	100	100
1	el	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	em	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	en	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	eo	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ep	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	eq	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	er	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	es	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	et	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	eu	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ev	345/400 (86%)	345 (100%)	0	100	100
1	ew	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	ex	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ey	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	ez	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	fa	345/400 (86%)	345 (100%)	0	100	100
1	fb	345/400 (86%)	345 (100%)	0	100	100
1	fc	345/400 (86%)	341 (99%)	4 (1%)	63	72
1	fd	345/400 (86%)	345 (100%)	0	100	100
1	fe	345/400 (86%)	345 (100%)	0	100	100
1	ff	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fg	345/400 (86%)	345 (100%)	0	100	100
1	fh	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fi	345/400 (86%)	341 (99%)	4 (1%)	63	72
1	fj	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	fk	345/400 (86%)	345 (100%)	0	100	100
1	fl	345/400 (86%)	343 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	fm	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fn	345/400 (86%)	345 (100%)	0	100	100
1	fo	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fp	345/400 (86%)	345 (100%)	0	100	100
1	fq	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fr	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	fs	345/400 (86%)	340 (99%)	5 (1%)	59	70
1	ft	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fu	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fv	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fw	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fx	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	fy	345/400 (86%)	345 (100%)	0	100	100
1	fz	345/400 (86%)	345 (100%)	0	100	100
1	ga	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	gb	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gc	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gd	345/400 (86%)	345 (100%)	0	100	100
1	ge	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gf	345/400 (86%)	345 (100%)	0	100	100
1	gg	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	gh	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gi	345/400 (86%)	345 (100%)	0	100	100
1	gj	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gk	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gl	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gm	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gn	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	go	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gp	345/400 (86%)	345 (100%)	0	100	100
1	gq	345/400 (86%)	343 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	gr	345/400 (86%)	345 (100%)	0	100	100
1	gs	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	gt	345/400 (86%)	339 (98%)	6 (2%)	53	67
1	gu	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	gv	345/400 (86%)	343 (99%)	2 (1%)	78	80
1	gw	345/400 (86%)	345 (100%)	0	100	100
1	gx	345/400 (86%)	345 (100%)	0	100	100
1	gy	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	gz	345/400 (86%)	341 (99%)	4 (1%)	63	72
1	ha	345/400 (86%)	345 (100%)	0	100	100
1	hb	345/400 (86%)	342 (99%)	3 (1%)	70	76
1	hc	345/400 (86%)	344 (100%)	1 (0%)	86	84
1	hd	345/400 (86%)	344 (100%)	1 (0%)	86	84
2	he	350/361 (97%)	348 (99%)	2 (1%)	78	80
2	hf	350/361 (97%)	347 (99%)	3 (1%)	70	76
2	hg	350/361 (97%)	349 (100%)	1 (0%)	86	84
2	hh	350/361 (97%)	349 (100%)	1 (0%)	86	84
2	hi	350/361 (97%)	349 (100%)	1 (0%)	86	84
2	hj	350/361 (97%)	350 (100%)	0	100	100
2	hk	350/361 (97%)	349 (100%)	1 (0%)	86	84
2	hl	350/361 (97%)	348 (99%)	2 (1%)	78	80
2	hm	350/361 (97%)	348 (99%)	2 (1%)	78	80
2	hn	350/361 (97%)	349 (100%)	1 (0%)	86	84
2	ho	350/361 (97%)	349 (100%)	1 (0%)	86	84
3	hp	66/67 (98%)	66 (100%)	0	100	100
3	hq	66/67 (98%)	66 (100%)	0	100	100
3	hr	66/67 (98%)	66 (100%)	0	100	100
3	hs	66/67 (98%)	66 (100%)	0	100	100
3	ht	66/67 (98%)	66 (100%)	0	100	100
3	hu	66/67 (98%)	66 (100%)	0	100	100
3	hv	66/67 (98%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	hw	66/67 (98%)	66 (100%)	0	100	100
3	hx	66/67 (98%)	66 (100%)	0	100	100
3	hy	66/67 (98%)	66 (100%)	0	100	100
3	hz	66/67 (98%)	66 (100%)	0	100	100
3	ia	66/67 (98%)	66 (100%)	0	100	100
3	ib	66/67 (98%)	66 (100%)	0	100	100
3	ic	66/67 (98%)	66 (100%)	0	100	100
3	id	66/67 (98%)	66 (100%)	0	100	100
3	ie	66/67 (98%)	66 (100%)	0	100	100
3	if	66/67 (98%)	66 (100%)	0	100	100
3	ig	66/67 (98%)	66 (100%)	0	100	100
3	ih	66/67 (98%)	66 (100%)	0	100	100
3	ii	66/67 (98%)	66 (100%)	0	100	100
3	ij	66/67 (98%)	66 (100%)	0	100	100
3	ik	66/67 (98%)	66 (100%)	0	100	100
3	il	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	im	66/67 (98%)	66 (100%)	0	100	100
3	in	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	io	66/67 (98%)	66 (100%)	0	100	100
3	ip	66/67 (98%)	66 (100%)	0	100	100
3	iq	66/67 (98%)	66 (100%)	0	100	100
3	ir	66/67 (98%)	66 (100%)	0	100	100
3	is	66/67 (98%)	66 (100%)	0	100	100
3	it	66/67 (98%)	66 (100%)	0	100	100
3	iu	66/67 (98%)	66 (100%)	0	100	100
3	iv	66/67 (98%)	66 (100%)	0	100	100
3	iw	66/67 (98%)	66 (100%)	0	100	100
3	ix	66/67 (98%)	66 (100%)	0	100	100
3	iy	66/67 (98%)	66 (100%)	0	100	100
3	iz	66/67 (98%)	66 (100%)	0	100	100
3	ja	66/67 (98%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	jb	66/67 (98%)	66 (100%)	0	100	100
3	jc	66/67 (98%)	66 (100%)	0	100	100
3	jd	66/67 (98%)	66 (100%)	0	100	100
3	je	66/67 (98%)	66 (100%)	0	100	100
3	jf	66/67 (98%)	66 (100%)	0	100	100
3	jg	66/67 (98%)	66 (100%)	0	100	100
3	jh	66/67 (98%)	66 (100%)	0	100	100
3	ji	66/67 (98%)	66 (100%)	0	100	100
3	jj	66/67 (98%)	66 (100%)	0	100	100
3	jk	66/67 (98%)	66 (100%)	0	100	100
3	jl	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	jm	66/67 (98%)	66 (100%)	0	100	100
3	jn	66/67 (98%)	66 (100%)	0	100	100
3	jo	66/67 (98%)	66 (100%)	0	100	100
3	jp	66/67 (98%)	66 (100%)	0	100	100
3	jq	66/67 (98%)	66 (100%)	0	100	100
3	jr	66/67 (98%)	66 (100%)	0	100	100
3	js	66/67 (98%)	66 (100%)	0	100	100
3	jt	66/67 (98%)	66 (100%)	0	100	100
3	ju	66/67 (98%)	66 (100%)	0	100	100
3	jv	66/67 (98%)	66 (100%)	0	100	100
3	jw	66/67 (98%)	66 (100%)	0	100	100
3	jx	66/67 (98%)	66 (100%)	0	100	100
3	jy	66/67 (98%)	66 (100%)	0	100	100
3	jz	66/67 (98%)	66 (100%)	0	100	100
3	ka	66/67 (98%)	66 (100%)	0	100	100
3	kb	66/67 (98%)	66 (100%)	0	100	100
3	kc	66/67 (98%)	66 (100%)	0	100	100
3	kd	66/67 (98%)	66 (100%)	0	100	100
3	ke	66/67 (98%)	66 (100%)	0	100	100
3	kf	66/67 (98%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	kg	66/67 (98%)	66 (100%)	0	100	100
3	kh	66/67 (98%)	66 (100%)	0	100	100
3	ki	66/67 (98%)	66 (100%)	0	100	100
3	kj	66/67 (98%)	66 (100%)	0	100	100
3	kk	66/67 (98%)	66 (100%)	0	100	100
3	kl	66/67 (98%)	66 (100%)	0	100	100
3	km	66/67 (98%)	66 (100%)	0	100	100
3	kn	66/67 (98%)	66 (100%)	0	100	100
3	ko	66/67 (98%)	66 (100%)	0	100	100
3	kp	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	kq	66/67 (98%)	66 (100%)	0	100	100
3	kr	66/67 (98%)	66 (100%)	0	100	100
3	ks	66/67 (98%)	66 (100%)	0	100	100
3	kt	66/67 (98%)	66 (100%)	0	100	100
3	ku	66/67 (98%)	66 (100%)	0	100	100
3	kv	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	kw	66/67 (98%)	66 (100%)	0	100	100
3	kx	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	ky	66/67 (98%)	66 (100%)	0	100	100
3	kz	66/67 (98%)	66 (100%)	0	100	100
3	la	66/67 (98%)	66 (100%)	0	100	100
3	lb	66/67 (98%)	66 (100%)	0	100	100
3	lc	66/67 (98%)	66 (100%)	0	100	100
3	ld	66/67 (98%)	66 (100%)	0	100	100
3	le	66/67 (98%)	66 (100%)	0	100	100
3	lf	66/67 (98%)	66 (100%)	0	100	100
3	lg	66/67 (98%)	66 (100%)	0	100	100
3	lh	66/67 (98%)	66 (100%)	0	100	100
3	li	66/67 (98%)	66 (100%)	0	100	100
3	lj	66/67 (98%)	66 (100%)	0	100	100
3	lk	66/67 (98%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	ll	66/67 (98%)	66 (100%)	0	100	100
3	lm	66/67 (98%)	66 (100%)	0	100	100
3	ln	66/67 (98%)	66 (100%)	0	100	100
3	lo	66/67 (98%)	66 (100%)	0	100	100
3	lp	66/67 (98%)	66 (100%)	0	100	100
3	lq	66/67 (98%)	66 (100%)	0	100	100
3	lr	66/67 (98%)	66 (100%)	0	100	100
3	ls	66/67 (98%)	66 (100%)	0	100	100
3	lt	66/67 (98%)	66 (100%)	0	100	100
3	lu	66/67 (98%)	66 (100%)	0	100	100
3	lv	66/67 (98%)	64 (97%)	2 (3%)	36	59
3	lw	66/67 (98%)	66 (100%)	0	100	100
3	lx	66/67 (98%)	66 (100%)	0	100	100
3	ly	66/67 (98%)	66 (100%)	0	100	100
3	lz	66/67 (98%)	66 (100%)	0	100	100
3	ma	66/67 (98%)	66 (100%)	0	100	100
3	mb	66/67 (98%)	66 (100%)	0	100	100
3	mc	66/67 (98%)	66 (100%)	0	100	100
3	md	66/67 (98%)	66 (100%)	0	100	100
3	me	66/67 (98%)	66 (100%)	0	100	100
3	mf	66/67 (98%)	66 (100%)	0	100	100
3	mg	66/67 (98%)	66 (100%)	0	100	100
3	mh	66/67 (98%)	66 (100%)	0	100	100
3	mi	66/67 (98%)	66 (100%)	0	100	100
3	mj	66/67 (98%)	66 (100%)	0	100	100
3	mk	66/67 (98%)	66 (100%)	0	100	100
3	ml	66/67 (98%)	66 (100%)	0	100	100
3	mm	66/67 (98%)	66 (100%)	0	100	100
3	mn	66/67 (98%)	66 (100%)	0	100	100
3	mo	66/67 (98%)	66 (100%)	0	100	100
3	mp	66/67 (98%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	mq	66/67 (98%)	66 (100%)	0	100	100
3	ms	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	mt	66/67 (98%)	66 (100%)	0	100	100
3	mu	66/67 (98%)	66 (100%)	0	100	100
3	mv	66/67 (98%)	66 (100%)	0	100	100
3	mw	66/67 (98%)	66 (100%)	0	100	100
3	mx	66/67 (98%)	66 (100%)	0	100	100
3	my	66/67 (98%)	66 (100%)	0	100	100
3	mz	66/67 (98%)	66 (100%)	0	100	100
3	na	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	nb	66/67 (98%)	66 (100%)	0	100	100
3	nc	66/67 (98%)	66 (100%)	0	100	100
3	nd	66/67 (98%)	66 (100%)	0	100	100
3	ne	66/67 (98%)	66 (100%)	0	100	100
3	nf	66/67 (98%)	66 (100%)	0	100	100
3	ng	66/67 (98%)	66 (100%)	0	100	100
3	nh	66/67 (98%)	66 (100%)	0	100	100
3	ni	66/67 (98%)	66 (100%)	0	100	100
3	nj	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	nk	66/67 (98%)	66 (100%)	0	100	100
3	nl	66/67 (98%)	66 (100%)	0	100	100
3	nm	66/67 (98%)	66 (100%)	0	100	100
3	nn	66/67 (98%)	66 (100%)	0	100	100
3	no	66/67 (98%)	66 (100%)	0	100	100
3	np	66/67 (98%)	66 (100%)	0	100	100
3	nq	66/67 (98%)	66 (100%)	0	100	100
3	ns	66/67 (98%)	66 (100%)	0	100	100
3	nt	66/67 (98%)	66 (100%)	0	100	100
3	nu	66/67 (98%)	66 (100%)	0	100	100
3	nv	66/67 (98%)	65 (98%)	1 (2%)	57	69
3	nw	66/67 (98%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	nx	66/67 (98%)	66 (100%)	0	100	100
3	ny	66/67 (98%)	66 (100%)	0	100	100
3	nz	66/67 (98%)	66 (100%)	0	100	100
3	oa	66/67 (98%)	66 (100%)	0	100	100
3	ob	66/67 (98%)	66 (100%)	0	100	100
3	oc	66/67 (98%)	66 (100%)	0	100	100
3	od	66/67 (98%)	66 (100%)	0	100	100
3	oe	66/67 (98%)	66 (100%)	0	100	100
3	of	66/67 (98%)	66 (100%)	0	100	100
3	og	66/67 (98%)	65 (98%)	1 (2%)	57	69
All	All	79356/89895 (88%)	79096 (100%)	260 (0%)	84	84

All (260) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	ab	372	GLU
1	ac	101	ARG
1	ac	305	GLU
1	ad	360	GLU
1	ae	460	ARG
1	ag	112	CYS
1	ah	101	ARG
1	ah	360	GLU
1	ai	514	ARG
1	ak	279	ARG
1	ak	360	GLU
1	ak	363	GLU
1	al	348	GLU
1	al	476	ARG
1	am	249	GLU
1	am	495	ARG
1	ao	142	GLU
1	ap	305	GLU
1	aq	263	SER
1	as	249	GLU
1	as	463	ASP
1	at	101	ARG
1	at	360	GLU

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Mol	Chain	Res	Type
1	au	260	GLU
1	av	142	GLU
1	av	360	GLU
1	av	372	GLU
1	aw	187	THR
1	aw	484	PHE
1	ay	142	GLU
1	ay	305	GLU
1	az	101	ARG
1	ba	483	PRO
1	bb	142	GLU
1	bb	305	GLU
1	bb	495	ARG
1	bc	142	GLU
1	bc	260	GLU
1	be	372	GLU
1	be	514	ARG
1	bf	360	GLU
1	bg	79	ILE
1	bh	142	GLU
1	bh	372	GLU
1	bi	360	GLU
1	bk	360	GLU
1	bl	360	GLU
1	bm	372	GLU
1	bn	345	TRP
1	bp	514	ARG
1	bq	372	GLU
1	br	279	ARG
1	br	363	GLU
1	bs	249	GLU
1	bu	249	GLU
1	bu	360	GLU
1	bu	363	GLU
1	bw	112	CYS
1	bw	372	GLU
1	bx	67	GLU
1	bx	483	PRO
1	by	253	ARG
1	bz	142	GLU
1	bz	153	MET
1	bz	495	ARG

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Mol	Chain	Res	Type
1	ca	253	ARG
1	ca	360	GLU
1	ca	363	GLU
1	cd	360	GLU
1	cd	514	ARG
1	cj	101	ARG
1	cj	305	GLU
1	cj	360	GLU
1	cl	142	GLU
1	cm	360	GLU
1	cm	363	GLU
1	co	249	GLU
1	co	495	ARG
1	co	514	ARG
1	cr	297	GLU
1	ct	67	GLU
1	cu	112	CYS
1	cv	360	GLU
1	cw	360	GLU
1	cx	145	HIS
1	cx	249	GLU
1	cx	514	ARG
1	cy	153	MET
1	cy	360	GLU
1	cy	450	TYR
1	db	360	GLU
1	db	514	ARG
1	dd	153	MET
1	dd	476	ARG
1	dd	514	ARG
1	dg	363	GLU
1	di	360	GLU
1	dj	279	ARG
1	dj	297	GLU
1	dj	360	GLU
1	dk	360	GLU
1	dl	249	GLU
1	dl	305	GLU
1	dm	142	GLU
1	dm	236	GLN
1	dm	249	GLU
1	dm	363	GLU

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Mol	Chain	Res	Type
1	dn	101	ARG
1	dn	305	GLU
1	do	278	LEU
1	do	360	GLU
1	do	363	GLU
1	dp	279	ARG
1	dp	372	GLU
1	dr	67	GLU
1	dt	67	GLU
1	du	67	GLU
1	du	360	GLU
1	dv	463	ASP
1	dw	264	ARG
1	dx	112	CYS
1	dy	101	ARG
1	ea	305	GLU
1	eb	360	GLU
1	eb	481	ILE
1	ec	305	GLU
1	ed	142	GLU
1	ed	273	GLU
1	ef	142	GLU
1	ef	372	GLU
1	eg	142	GLU
1	eg	278	LEU
1	eg	305	GLU
1	eh	278	LEU
1	eh	341	ARG
1	eh	372	GLU
1	eh	482	ASN
1	ei	305	GLU
1	ei	363	GLU
1	ej	341	ARG
1	el	249	GLU
1	el	483	PRO
1	em	142	GLU
1	en	142	GLU
1	en	305	GLU
1	eo	67	GLU
1	eo	101	ARG
1	ep	260	GLU
1	eq	372	GLU

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Mol	Chain	Res	Type
1	er	258	VAL
1	er	372	GLU
1	es	67	GLU
1	et	142	GLU
1	et	341	ARG
1	et	345	TRP
1	eu	67	GLU
1	ew	250	MET
1	ew	360	GLU
1	ex	372	GLU
1	ey	363	GLU
1	ez	142	GLU
1	ez	305	GLU
1	ez	360	GLU
1	fc	249	GLU
1	fc	260	GLU
1	fc	372	GLU
1	fc	474	LYS
1	ff	514	ARG
1	fh	260	GLU
1	fi	101	ARG
1	fi	112	CYS
1	fi	249	GLU
1	fi	366	ARG
1	fj	112	CYS
1	fj	463	ASP
1	fl	234	GLU
1	fl	450	TYR
1	fm	305	GLU
1	fo	443	GLU
1	fq	372	GLU
1	fr	260	GLU
1	fr	305	GLU
1	fs	142	GLU
1	fs	318	LYS
1	fs	360	GLU
1	fs	363	GLU
1	fs	372	GLU
1	ft	115	GLN
1	fu	249	GLU
1	fv	360	GLU
1	fw	345	TRP

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Mol	Chain	Res	Type
1	fx	260	GLU
1	ga	67	GLU
1	ga	101	ARG
1	ga	249	GLU
1	gb	360	GLU
1	gc	67	GLU
1	ge	360	GLU
1	gg	260	GLU
1	gg	514	ARG
1	gh	112	CYS
1	gj	142	GLU
1	gk	476	ARG
1	gl	463	ASP
1	gm	345	TRP
1	gn	360	GLU
1	go	278	LEU
1	gq	67	GLU
1	gq	360	GLU
1	gs	250	MET
1	gt	142	GLU
1	gt	184	GLU
1	gt	279	ARG
1	gt	360	GLU
1	gt	370	ARG
1	gt	463	ASP
1	gu	249	GLU
1	gu	278	LEU
1	gv	217	GLU
1	gv	260	GLU
1	gy	249	GLU
1	gy	260	GLU
1	gy	476	ARG
1	gz	249	GLU
1	gz	278	LEU
1	gz	360	GLU
1	gz	372	GLU
1	hb	101	ARG
1	hb	278	LEU
1	hb	476	ARG
1	hc	372	GLU
1	hd	360	GLU
2	he	209	GLU

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Mol	Chain	Res	Type
2	he	293	GLU
2	hf	53	TYR
2	hf	174	LYS
2	hf	248	ARG
2	hg	53	TYR
2	hh	209	GLU
2	hi	248	ARG
2	hk	81	ARG
2	hl	53	TYR
2	hl	293	GLU
2	hm	53	TYR
2	hm	314	CYS
2	hn	182	GLU
2	ho	205	GLU
3	il	14	GLU
3	in	5	ARG
3	jl	62	GLU
3	kp	14	GLU
3	kv	78	VAL
3	kx	61	GLU
3	lv	14	GLU
3	lv	62	GLU
3	ms	14	GLU
3	na	72	ASN
3	nj	14	GLU
3	nv	78	VAL
3	og	62	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (553) such sidechains are listed below:

Mol	Chain	Res	Type
1	aa	157	GLN
1	aa	384	ASN
1	aa	427	GLN
1	ab	83	GLN
1	ab	367	GLN
1	ab	384	ASN
1	ac	115	GLN
1	ac	157	GLN
1	ac	315	GLN
1	ac	482	ASN
1	ad	157	GLN

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Mol	Chain	Res	Type
1	ad	311	ASN
1	ad	497	GLN
1	ae	157	GLN
1	ae	183	GLN
1	ae	257	GLN
1	ae	282	HIS
1	af	123	GLN
1	af	183	GLN
1	ah	83	GLN
1	ah	183	GLN
1	ah	257	GLN
1	ah	384	ASN
1	ai	236	GLN
1	aj	115	GLN
1	ak	257	GLN
1	ak	497	GLN
1	al	83	GLN
1	al	157	GLN
1	al	183	GLN
1	al	257	GLN
1	am	384	ASN
1	an	83	GLN
1	an	257	GLN
1	an	311	ASN
1	an	384	ASN
1	ao	183	GLN
1	ao	282	HIS
1	ap	157	GLN
1	aq	157	GLN
1	aq	257	GLN
1	aq	497	GLN
1	ar	384	ASN
1	as	157	GLN
1	as	257	GLN
1	as	497	GLN
1	at	183	GLN
1	at	257	GLN
1	at	367	GLN
1	au	78	ASN
1	av	83	GLN
1	aw	157	GLN
1	aw	257	GLN

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Mol	Chain	Res	Type
1	ax	157	GLN
1	ay	157	GLN
1	ay	257	GLN
1	az	78	ASN
1	az	83	GLN
1	az	157	GLN
1	az	257	GLN
1	az	315	GLN
1	az	367	GLN
1	az	482	ASN
1	bb	72	HIS
1	bb	384	ASN
1	bc	257	GLN
1	bd	183	GLN
1	bd	257	GLN
1	bd	384	ASN
1	be	257	GLN
1	be	427	GLN
1	bf	83	GLN
1	bg	83	GLN
1	bg	482	ASN
1	bi	171	GLN
1	bi	257	GLN
1	bk	157	GLN
1	bk	257	GLN
1	bl	183	GLN
1	bl	257	GLN
1	bl	384	ASN
1	bl	497	GLN
1	bm	115	GLN
1	bm	157	GLN
1	bm	171	GLN
1	bn	257	GLN
1	bo	367	GLN
1	bp	157	GLN
1	bq	83	GLN
1	bq	157	GLN
1	br	367	GLN
1	bs	183	GLN
1	bs	240	ASN
1	bt	83	GLN
1	bu	83	GLN

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Mol	Chain	Res	Type
1	bu	157	GLN
1	bw	83	GLN
1	bw	257	GLN
1	bw	497	GLN
1	bx	72	HIS
1	bx	83	GLN
1	bx	157	GLN
1	bx	257	GLN
1	bx	384	ASN
1	bx	482	ASN
1	by	83	GLN
1	by	183	GLN
1	bz	157	GLN
1	bz	257	GLN
1	bz	282	HIS
1	ca	115	GLN
1	ca	257	GLN
1	cb	183	GLN
1	cc	183	GLN
1	cc	257	GLN
1	cc	427	GLN
1	cd	157	GLN
1	cd	257	GLN
1	cd	367	GLN
1	ce	115	GLN
1	ce	157	GLN
1	ce	183	GLN
1	cf	157	GLN
1	cf	431	GLN
1	cf	497	GLN
1	cg	157	GLN
1	cg	183	GLN
1	cg	257	GLN
1	cg	497	GLN
1	ch	171	GLN
1	ch	183	GLN
1	ch	195	GLN
1	ch	257	GLN
1	ci	115	GLN
1	ci	257	GLN
1	ci	497	GLN
1	cj	115	GLN

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Mol	Chain	Res	Type
1	cj	171	GLN
1	cj	257	GLN
1	cj	367	GLN
1	cj	384	ASN
1	ck	83	GLN
1	ck	257	GLN
1	ck	356	GLN
1	ck	497	GLN
1	cm	157	GLN
1	cm	257	GLN
1	cm	497	GLN
1	cn	83	GLN
1	cn	157	GLN
1	cn	384	ASN
1	co	115	GLN
1	co	157	GLN
1	co	257	GLN
1	co	482	ASN
1	cp	367	GLN
1	cq	157	GLN
1	cq	257	GLN
1	cs	115	GLN
1	cs	157	GLN
1	ct	83	GLN
1	ct	497	GLN
1	cu	115	GLN
1	cu	157	GLN
1	cu	236	GLN
1	cu	257	GLN
1	cu	315	GLN
1	cu	367	GLN
1	cu	384	ASN
1	cv	115	GLN
1	cv	367	GLN
1	cv	384	ASN
1	cw	157	GLN
1	cw	257	GLN
1	cw	356	GLN
1	cw	427	GLN
1	cx	257	GLN
1	cx	384	ASN
1	cy	257	GLN

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Mol	Chain	Res	Type
1	cz	83	GLN
1	cz	157	GLN
1	cz	384	ASN
1	db	367	GLN
1	db	384	ASN
1	dc	157	GLN
1	dd	157	GLN
1	dd	384	ASN
1	de	183	GLN
1	de	257	GLN
1	de	367	GLN
1	de	497	GLN
1	dg	157	GLN
1	dg	257	GLN
1	dg	490	GLN
1	dh	115	GLN
1	dh	257	GLN
1	dh	367	GLN
1	dh	398	GLN
1	dh	497	GLN
1	di	157	GLN
1	di	183	GLN
1	di	282	HIS
1	dk	157	GLN
1	dk	257	GLN
1	dk	497	GLN
1	dl	72	HIS
1	dl	83	GLN
1	dl	497	GLN
1	dm	236	GLN
1	dm	257	GLN
1	dm	367	GLN
1	dm	490	GLN
1	dn	183	GLN
1	dn	257	GLN
1	dn	367	GLN
1	dn	384	ASN
1	dn	431	GLN
1	dp	384	ASN
1	dq	257	GLN
1	dr	115	GLN
1	dr	236	GLN

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Mol	Chain	Res	Type
1	dr	257	GLN
1	ds	427	GLN
1	dt	83	GLN
1	dt	157	GLN
1	dt	257	GLN
1	dt	367	GLN
1	dt	497	GLN
1	du	115	GLN
1	du	157	GLN
1	dv	335	GLN
1	dv	431	GLN
1	dw	257	GLN
1	dw	282	HIS
1	dw	367	GLN
1	dw	482	ASN
1	dx	145	HIS
1	dx	265	GLN
1	dx	282	HIS
1	dx	384	ASN
1	dy	157	GLN
1	dy	384	ASN
1	dz	83	GLN
1	dz	115	GLN
1	dz	367	GLN
1	ea	497	GLN
1	eb	257	GLN
1	ec	157	GLN
1	ec	257	GLN
1	ec	282	HIS
1	ed	83	GLN
1	ed	157	GLN
1	ed	384	ASN
1	ee	257	GLN
1	ef	83	GLN
1	eg	183	GLN
1	eh	265	GLN
1	ei	157	GLN
1	ei	257	GLN
1	ej	78	ASN
1	ej	83	GLN
1	ej	183	GLN
1	ej	236	GLN

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Mol	Chain	Res	Type
1	ej	257	GLN
1	ej	384	ASN
1	ek	183	GLN
1	el	83	GLN
1	el	183	GLN
1	el	257	GLN
1	el	367	GLN
1	em	183	GLN
1	en	83	GLN
1	eo	72	HIS
1	eo	157	GLN
1	ep	257	GLN
1	ep	497	GLN
1	eq	157	GLN
1	eq	257	GLN
1	eq	497	GLN
1	er	83	GLN
1	er	384	ASN
1	es	257	GLN
1	es	497	GLN
1	et	83	GLN
1	et	384	ASN
1	eu	257	GLN
1	ev	257	GLN
1	ew	183	GLN
1	ew	431	GLN
1	ex	83	GLN
1	ey	83	GLN
1	ey	236	GLN
1	ez	157	GLN
1	ez	384	ASN
1	fa	384	ASN
1	fb	157	GLN
1	fb	183	GLN
1	fb	257	GLN
1	fb	282	HIS
1	fc	157	GLN
1	fd	183	GLN
1	fd	367	GLN
1	fe	83	GLN
1	ff	157	GLN
1	ff	257	GLN

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Mol	Chain	Res	Type
1	fg	171	GLN
1	fg	195	GLN
1	fg	257	GLN
1	fg	367	GLN
1	fh	90	GLN
1	fh	157	GLN
1	fi	115	GLN
1	fi	157	GLN
1	fi	183	GLN
1	fi	265	GLN
1	fi	384	ASN
1	fj	83	GLN
1	fj	157	GLN
1	fj	236	GLN
1	fj	257	GLN
1	fj	367	GLN
1	fj	427	GLN
1	fk	482	ASN
1	fm	83	GLN
1	fm	157	GLN
1	fn	157	GLN
1	fn	384	ASN
1	fn	497	GLN
1	fo	183	GLN
1	fp	157	GLN
1	fp	257	GLN
1	fr	157	GLN
1	fr	257	GLN
1	fr	265	GLN
1	fs	83	GLN
1	fs	466	ASN
1	fs	482	ASN
1	ft	115	GLN
1	ft	482	ASN
1	fu	183	GLN
1	fu	384	ASN
1	fu	490	GLN
1	fv	83	GLN
1	fv	367	GLN
1	fv	384	ASN
1	fw	183	GLN
1	fy	115	GLN

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Mol	Chain	Res	Type
1	fy	257	GLN
1	fy	384	ASN
1	fy	427	GLN
1	fy	497	GLN
1	gb	83	GLN
1	gb	195	GLN
1	gb	257	GLN
1	gb	367	GLN
1	gb	398	GLN
1	gc	257	GLN
1	gc	384	ASN
1	gd	157	GLN
1	gd	257	GLN
1	gd	490	GLN
1	ge	83	GLN
1	ge	157	GLN
1	ge	431	GLN
1	ge	482	ASN
1	gf	384	ASN
1	gg	157	GLN
1	gg	257	GLN
1	gg	384	ASN
1	gh	257	GLN
1	gh	367	GLN
1	gh	384	ASN
1	gi	83	GLN
1	gi	257	GLN
1	gj	240	ASN
1	gj	315	GLN
1	gj	367	GLN
1	gk	265	GLN
1	gk	482	ASN
1	gl	83	GLN
1	gl	497	GLN
1	gm	157	GLN
1	gm	335	GLN
1	gm	384	ASN
1	gm	482	ASN
1	gn	265	GLN
1	gn	367	GLN
1	gn	384	ASN
1	gn	497	GLN

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Mol	Chain	Res	Type
1	gp	115	GLN
1	gp	384	ASN
1	gq	367	GLN
1	gq	384	ASN
1	gr	83	GLN
1	gr	157	GLN
1	gs	157	GLN
1	gs	183	GLN
1	gs	257	GLN
1	gt	183	GLN
1	gt	257	GLN
1	gt	367	GLN
1	gu	183	GLN
1	gv	83	GLN
1	gv	115	GLN
1	gv	257	GLN
1	gv	398	GLN
1	gw	83	GLN
1	gw	257	GLN
1	gw	497	GLN
1	gz	72	HIS
1	gz	282	HIS
1	gz	367	GLN
1	gz	384	ASN
1	ha	482	ASN
1	hb	115	GLN
1	hb	157	GLN
1	hb	183	GLN
1	hc	257	GLN
1	hc	367	GLN
1	hc	497	GLN
1	hd	83	GLN
2	he	167	GLN
2	he	216	GLN
2	hf	47	GLN
2	hf	96	ASN
2	hf	167	GLN
2	hf	211	ASN
2	hf	260	HIS
2	hg	96	ASN
2	hg	167	GLN
2	hg	211	ASN

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Mol	Chain	Res	Type
2	hg	300	GLN
2	hh	17	ASN
2	hh	167	GLN
2	hh	260	HIS
2	hh	262	GLN
2	hh	317	ASN
2	hi	17	ASN
2	hi	47	GLN
2	hi	211	ASN
2	hi	216	GLN
2	hi	260	HIS
2	hj	211	ASN
2	hj	260	HIS
2	hj	356	HIS
2	hk	96	ASN
2	hl	167	GLN
2	hl	190	ASN
2	hl	260	HIS
2	hl	317	ASN
2	hm	47	GLN
2	hn	96	ASN
2	hn	167	GLN
2	hn	260	HIS
2	hn	300	GLN
2	ho	167	GLN
2	ho	211	ASN
2	ho	300	GLN
3	hp	72	ASN
3	hs	64	GLN
3	ht	64	GLN
3	hw	64	GLN
3	hy	64	GLN
3	ia	64	GLN
3	ic	64	GLN
3	id	72	ASN
3	if	15	GLN
3	ih	64	GLN
3	ii	64	GLN
3	ij	64	GLN
3	im	64	GLN
3	it	64	GLN
3	ix	64	GLN

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Mol	Chain	Res	Type
3	ix	72	ASN
3	ja	64	GLN
3	jb	64	GLN
3	jc	64	GLN
3	jd	64	GLN
3	je	64	GLN
3	jh	72	ASN
3	ji	64	GLN
3	jj	64	GLN
3	jn	15	GLN
3	jn	64	GLN
3	jo	64	GLN
3	jp	64	GLN
3	jq	64	GLN
3	jr	64	GLN
3	js	64	GLN
3	jt	64	GLN
3	ju	64	GLN
3	jw	64	GLN
3	jz	64	GLN
3	ka	64	GLN
3	ka	72	ASN
3	kb	64	GLN
3	kf	64	GLN
3	kg	64	GLN
3	kh	64	GLN
3	ki	64	GLN
3	kk	64	GLN
3	ko	64	GLN
3	kq	64	GLN
3	ks	64	GLN
3	kv	64	GLN
3	kw	64	GLN
3	kx	64	GLN
3	ky	64	GLN
3	kz	64	GLN
3	lc	64	GLN
3	ld	64	GLN
3	lg	45	HIS
3	lh	64	GLN
3	li	15	GLN
3	lk	64	GLN

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Mol	Chain	Res	Type
3	lm	64	GLN
3	ln	64	GLN
3	lp	15	GLN
3	lp	64	GLN
3	lp	72	ASN
3	lq	64	GLN
3	lr	15	GLN
3	lt	64	GLN
3	lw	64	GLN
3	lx	64	GLN
3	lx	72	ASN
3	lz	15	GLN
3	lz	64	GLN
3	mf	63	ASN
3	mh	64	GLN
3	mm	64	GLN
3	ms	64	GLN
3	mt	64	GLN
3	mv	64	GLN
3	mz	64	GLN
3	nf	64	GLN
3	ng	15	GLN
3	nh	64	GLN
3	ni	64	GLN
3	nk	64	GLN
3	nk	72	ASN
3	nl	15	GLN
3	nm	64	GLN
3	nn	64	GLN
3	np	64	GLN
3	nt	64	GLN
3	nu	64	GLN
3	ny	64	GLN
3	nz	64	GLN
3	oa	64	GLN
3	od	64	GLN
3	oe	64	GLN
3	og	64	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

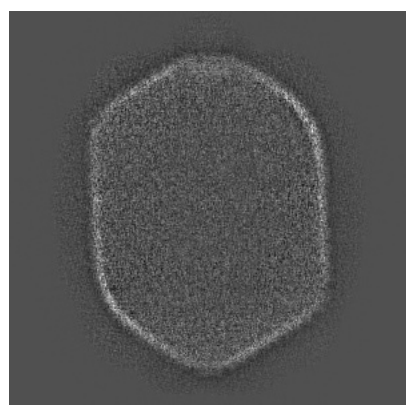
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32109. These allow visual inspection of the internal detail of the map and identification of artifacts.

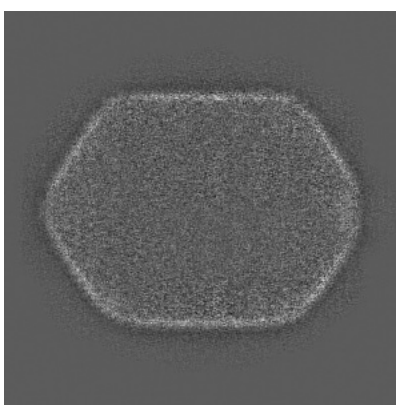
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

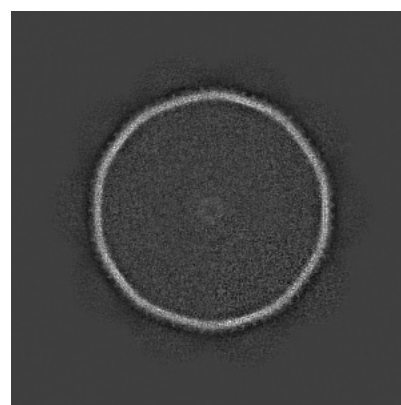
6.1.1 Primary map



X



Y

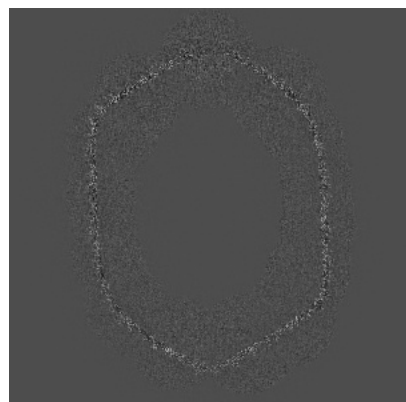


Z

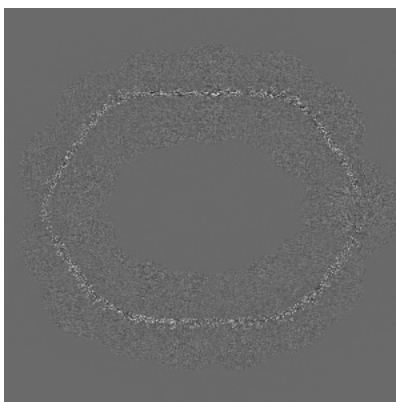
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

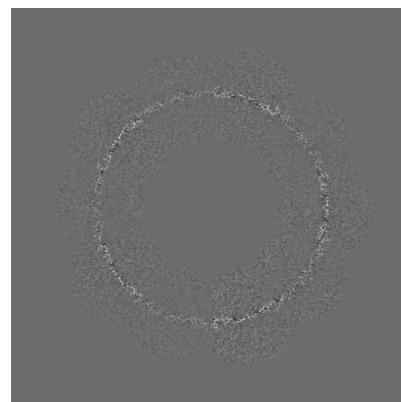
6.2.1 Primary map



X Index: 480



Y Index: 480

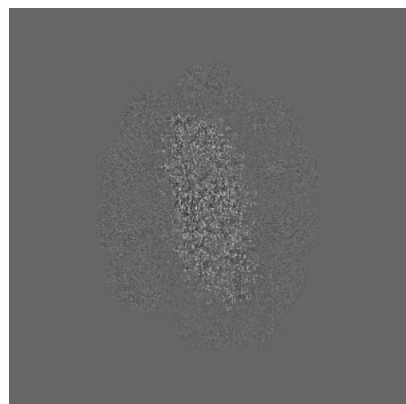


Z Index: 480

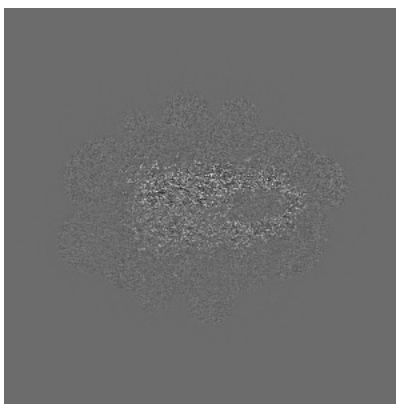
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

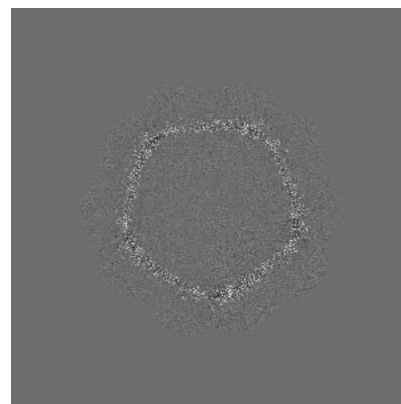
6.3.1 Primary map



X Index: 750



Y Index: 212

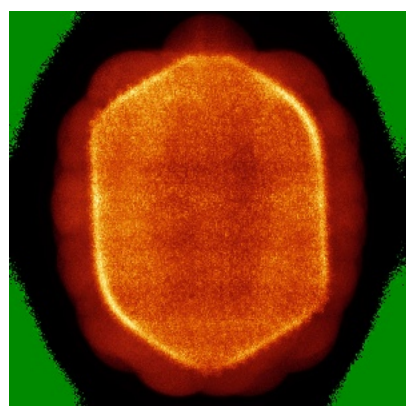


Z Index: 750

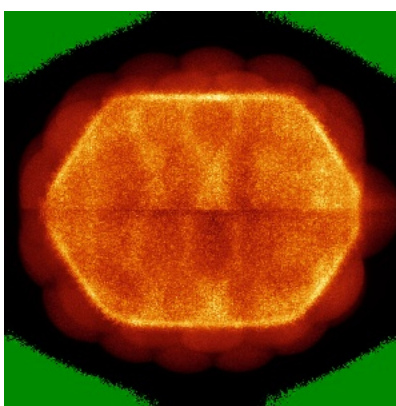
The images above show the largest variance slices of the map in three orthogonal directions.

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

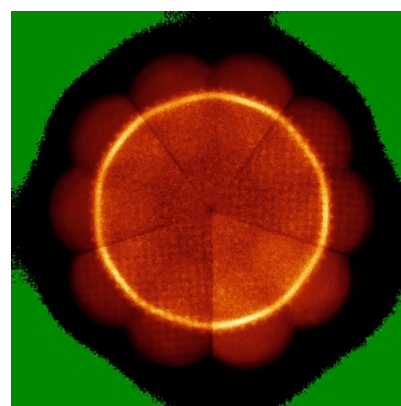
6.4.1 Primary map



X



Y

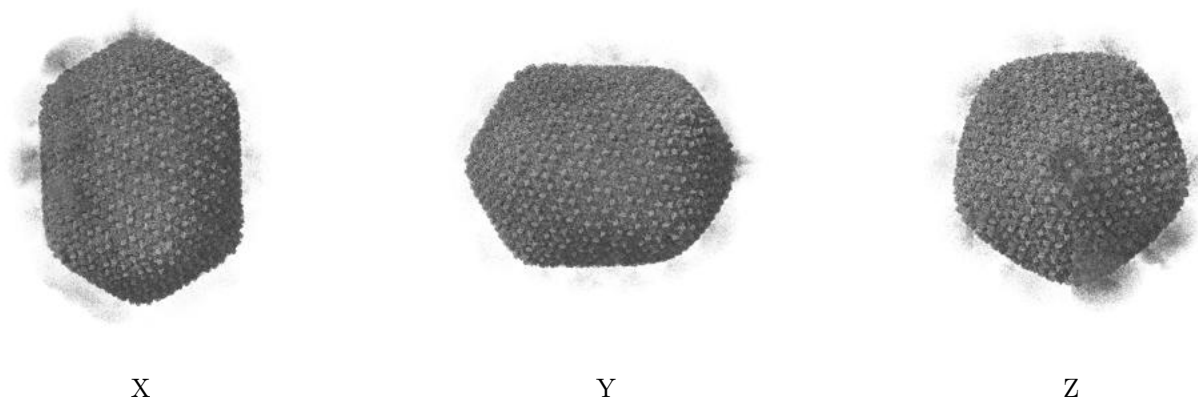


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

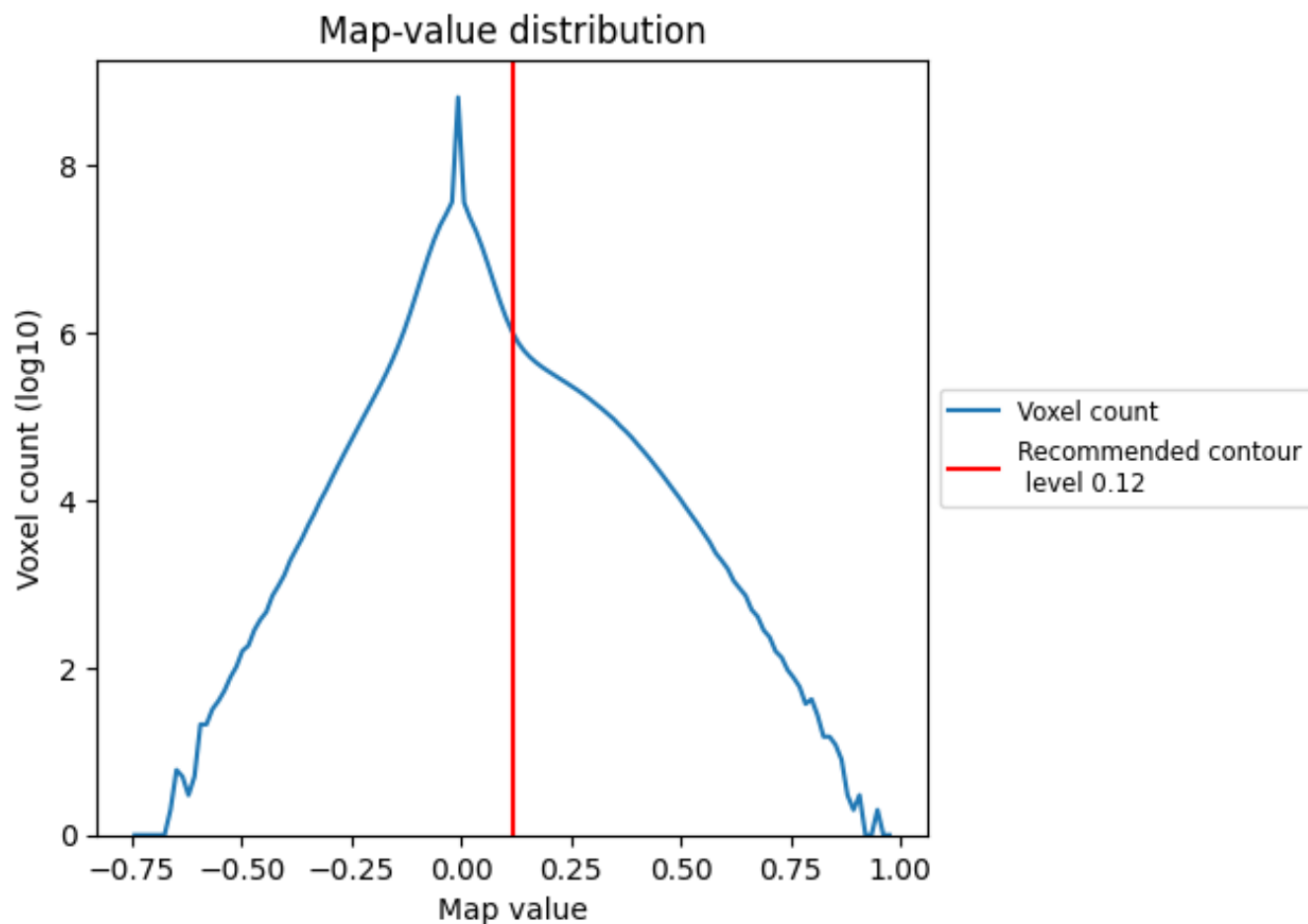
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

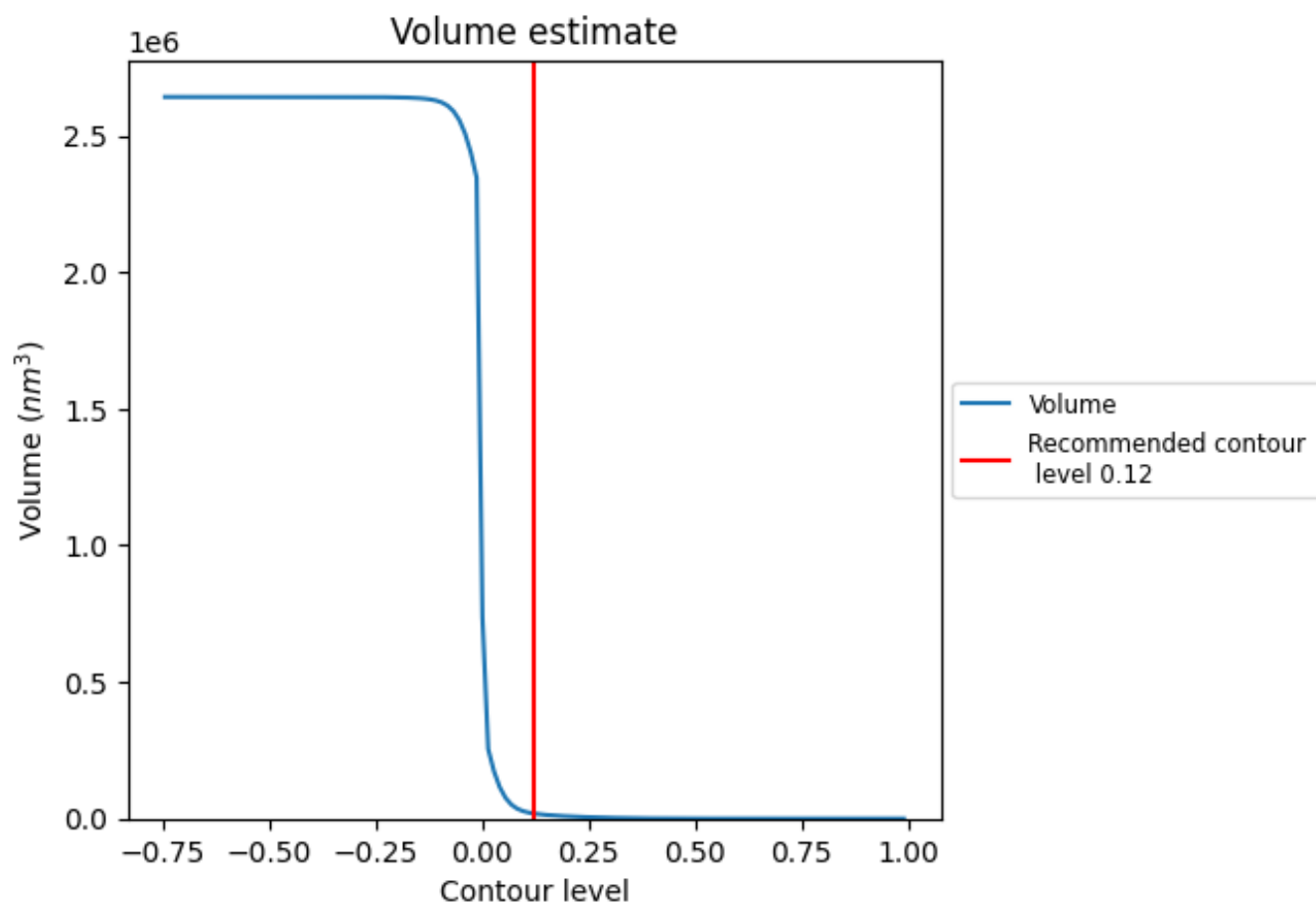
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

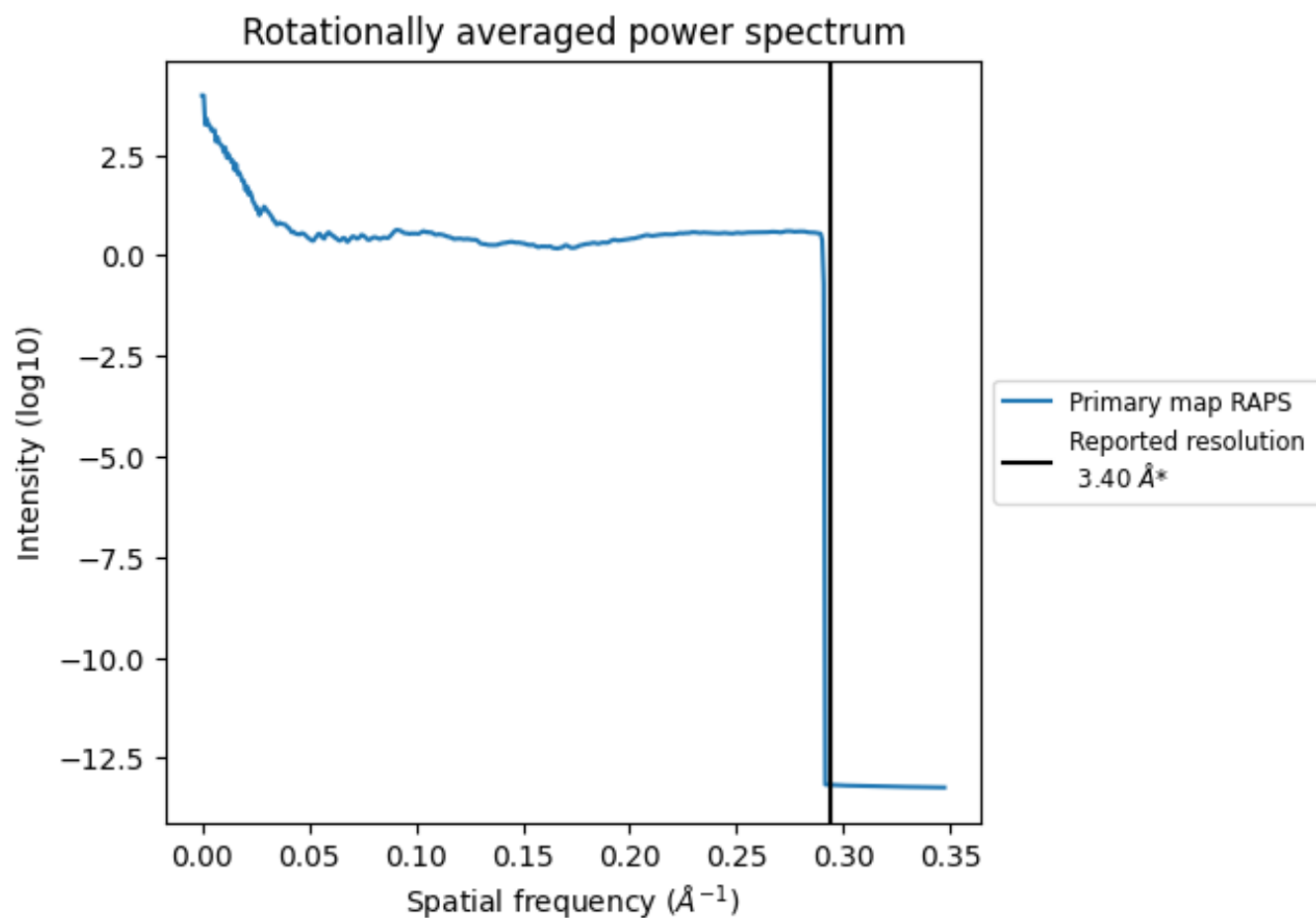
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 19040 nm³; this corresponds to an approximate mass of 17199 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

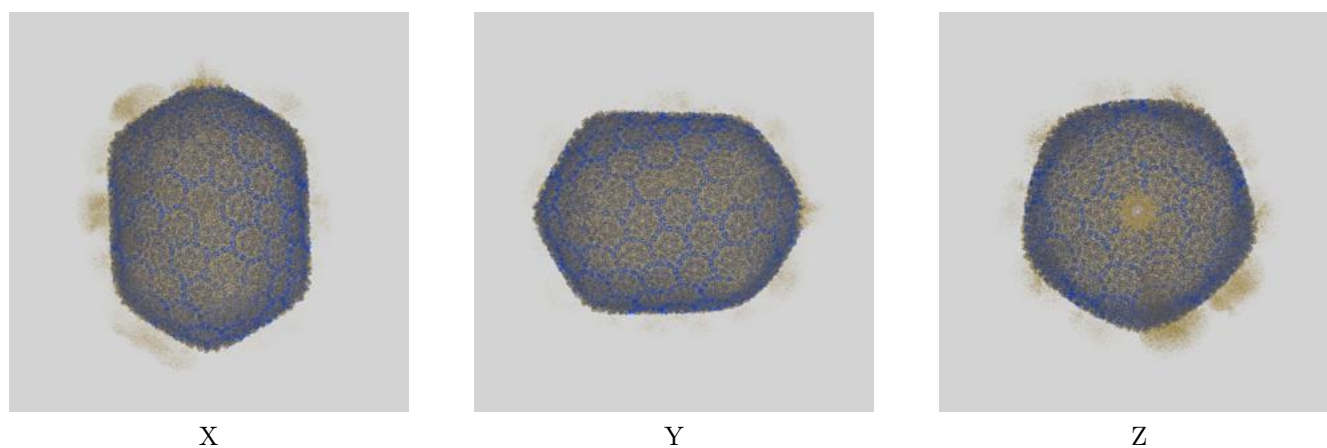
This section contains information regarding the fit between EMDB map EMD-32109 and PDB model 7VS5. Per-residue inclusion information can be found in section 3 on page 45.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



9.1.2 Map-model assembly overlay [i](#)



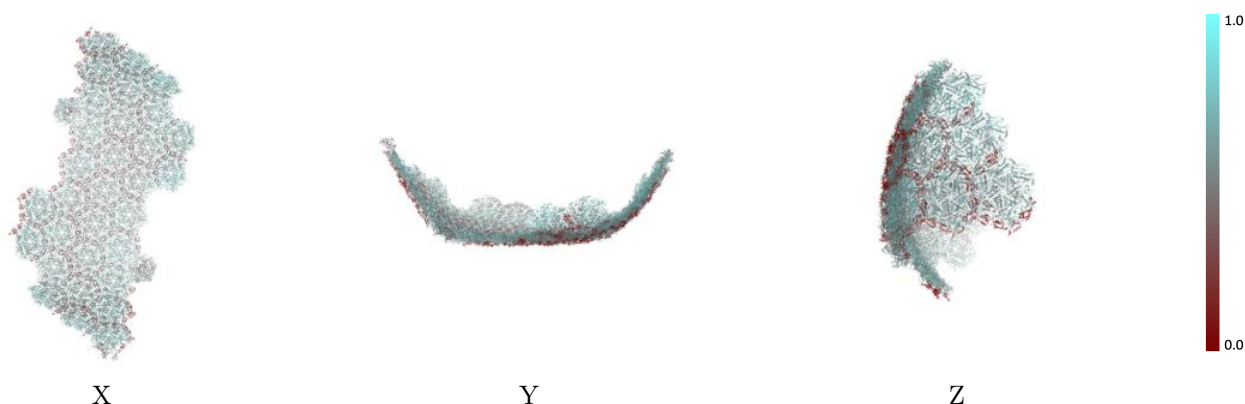
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



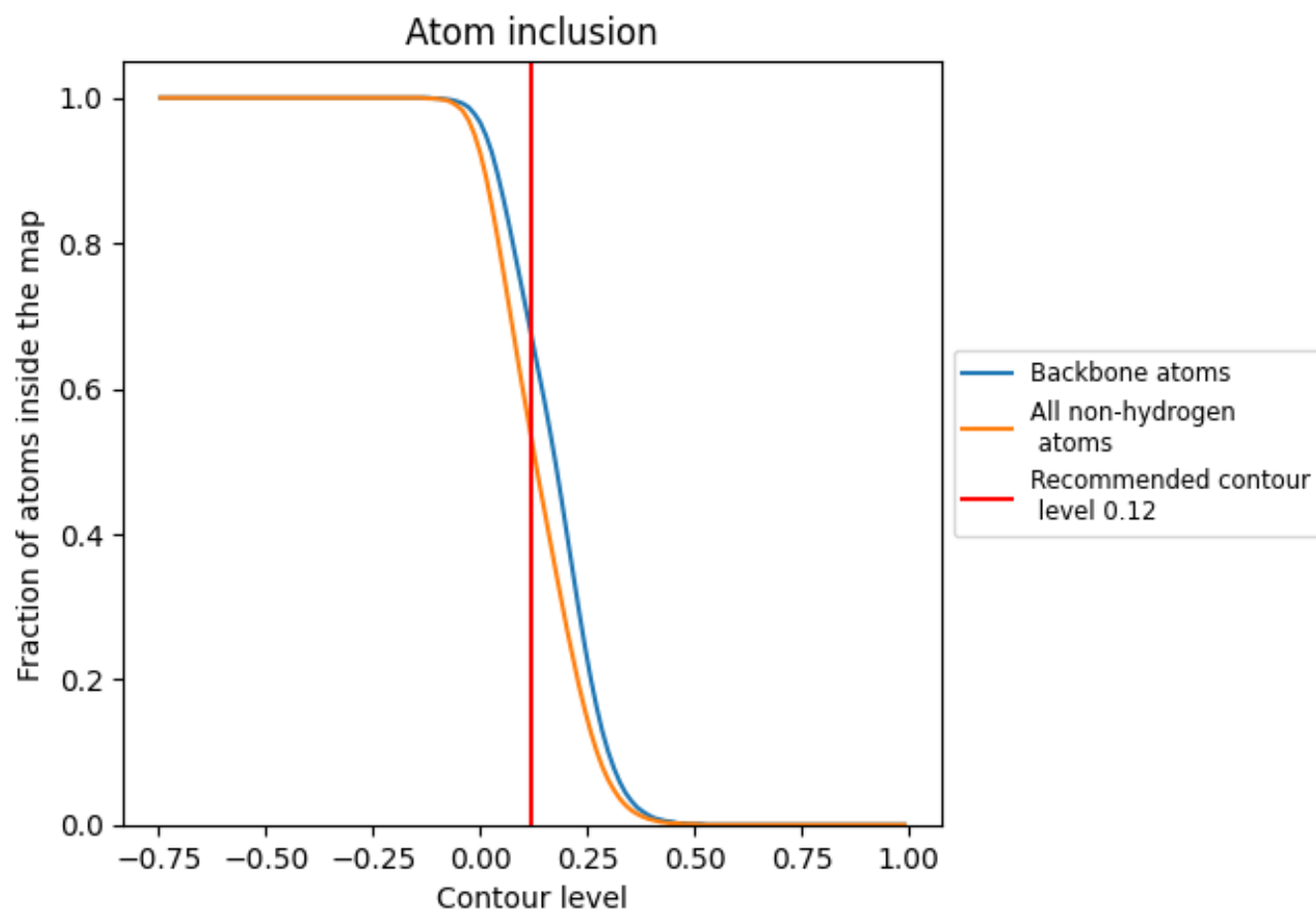
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 53% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5310	 0.4110
aa	 0.6410	 0.4500
ab	 0.6440	 0.4540
ac	 0.6290	 0.4510
ad	 0.6480	 0.4510
ae	 0.6210	 0.4420
af	 0.6080	 0.4390
ag	 0.6150	 0.4320
ah	 0.5430	 0.4180
ai	 0.5370	 0.4310
aj	 0.5580	 0.4400
ak	 0.5830	 0.4450
al	 0.6200	 0.4390
am	 0.5860	 0.4360
an	 0.6040	 0.4480
ao	 0.6080	 0.4490
ap	 0.6040	 0.4390
aq	 0.6210	 0.4400
ar	 0.6070	 0.4430
as	 0.6120	 0.4240
at	 0.5910	 0.4240
au	 0.5420	 0.4120
av	 0.5740	 0.4300
aw	 0.5890	 0.4340
ax	 0.5760	 0.4230
ay	 0.6070	 0.4480
az	 0.6070	 0.4480
ba	 0.6170	 0.4360
bb	 0.6140	 0.4370
bc	 0.6070	 0.4360
bd	 0.6090	 0.4360
be	 0.6310	 0.4540
bf	 0.6190	 0.4460
bg	 0.6470	 0.4420
bh	 0.6300	 0.4470



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Chain	Atom inclusion	Q-score
bi	 0.6160	 0.4420
bj	 0.6380	 0.4410
bk	 0.6460	 0.4370
bl	 0.6390	 0.4460
bm	 0.6380	 0.4480
bn	 0.6490	 0.4450
bo	 0.6550	 0.4410
bp	 0.6580	 0.4500
bq	 0.5880	 0.4150
br	 0.6200	 0.4230
bs	 0.6060	 0.4170
bt	 0.5740	 0.4120
bu	 0.5110	 0.4020
bv	 0.5470	 0.4130
bw	 0.5960	 0.4400
bx	 0.5630	 0.4250
by	 0.5990	 0.4360
bz	 0.6070	 0.4380
ca	 0.6060	 0.4390
cb	 0.6050	 0.4390
cc	 0.6130	 0.4300
cd	 0.6410	 0.4360
ce	 0.6470	 0.4270
cf	 0.6270	 0.4350
cg	 0.6050	 0.4260
ch	 0.5950	 0.4260
ci	 0.5780	 0.4030
cj	 0.5210	 0.3920
ck	 0.5790	 0.4010
cl	 0.6340	 0.4180
cm	 0.6350	 0.4240
cn	 0.6160	 0.4200
co	 0.5920	 0.4150
cp	 0.5720	 0.4050
cq	 0.5470	 0.3920
cr	 0.5140	 0.3840
cs	 0.5050	 0.3970
ct	 0.5700	 0.4100
cu	 0.5700	 0.4070
cv	 0.5510	 0.4060
cw	 0.5500	 0.4110
cx	 0.5440	 0.4080

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Chain	Atom inclusion	Q-score
cy	0.5310	0.4020
cz	0.5650	0.4100
da	0.5540	0.4170
db	0.5990	0.4300
dc	0.6040	0.4270
dd	0.5810	0.4070
de	0.5750	0.3930
df	0.5640	0.4020
dg	0.5190	0.3820
dh	0.5330	0.4050
di	0.5690	0.3920
dj	0.6480	0.4030
dk	0.5910	0.4020
dl	0.5420	0.3920
dm	0.6290	0.4340
dn	0.6280	0.4260
do	0.6240	0.4230
dp	0.6180	0.4200
dq	0.6010	0.4270
dr	0.6180	0.4320
ds	0.5710	0.4130
dt	0.5600	0.4290
du	0.5550	0.4370
dv	0.5750	0.4340
dw	0.5820	0.4280
dx	0.5900	0.4110
dy	0.6120	0.4470
dz	0.6330	0.4500
ea	0.6420	0.4450
eb	0.6450	0.4450
ec	0.6420	0.4470
ed	0.6130	0.4440
ee	0.6780	0.4480
ef	0.6660	0.4550
eg	0.6410	0.4490
eh	0.6330	0.4470
ei	0.6680	0.4450
ej	0.6940	0.4550
ek	0.6150	0.4410
el	0.6050	0.4310
em	0.6010	0.4380
en	0.6110	0.4440

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Chain	Atom inclusion	Q-score
eo	 0.6450	 0.4450
ep	 0.6360	 0.4390
eq	 0.6130	 0.4340
er	 0.6220	 0.4380
es	 0.6060	 0.4400
et	 0.6180	 0.4470
eu	 0.6200	 0.4400
ev	 0.6150	 0.4350
ew	 0.6160	 0.4460
ex	 0.6110	 0.4380
ey	 0.6420	 0.4460
ez	 0.6380	 0.4480
fa	 0.6280	 0.4470
fb	 0.6340	 0.4470
fc	 0.6200	 0.4330
fd	 0.5810	 0.4290
fe	 0.6060	 0.4370
ff	 0.6200	 0.4290
fg	 0.6230	 0.4400
fh	 0.6340	 0.4460
fi	 0.6060	 0.4160
fj	 0.5930	 0.4170
fk	 0.5370	 0.4110
fl	 0.5380	 0.4180
fm	 0.5710	 0.4300
fn	 0.5710	 0.4200
fo	 0.6120	 0.4350
fp	 0.5940	 0.4270
fq	 0.6530	 0.4420
fr	 0.6560	 0.4420
fs	 0.6440	 0.4390
ft	 0.6400	 0.4500
fu	 0.6520	 0.4310
fv	 0.6260	 0.4360
fw	 0.6010	 0.4230
fx	 0.6010	 0.4220
fy	 0.6350	 0.4190
fz	 0.6340	 0.4140
ga	 0.5430	 0.4100
gb	 0.4950	 0.4060
gc	 0.5240	 0.4090
gd	 0.5750	 0.4170

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Chain	Atom inclusion	Q-score
ge	 0.6070	 0.4280
gf	 0.6100	 0.4230
gg	 0.5300	 0.3810
gh	 0.5530	 0.4000
gi	 0.5530	 0.3930
gj	 0.5330	 0.3740
gk	 0.5040	 0.3700
gl	 0.5050	 0.3660
gm	 0.6280	 0.4270
gn	 0.6180	 0.4310
go	 0.6120	 0.4290
gp	 0.5820	 0.4240
gq	 0.5790	 0.4280
gr	 0.6150	 0.4250
gs	 0.5130	 0.3970
gt	 0.5270	 0.4040
gu	 0.5670	 0.4110
gv	 0.6070	 0.4140
gw	 0.5930	 0.3880
gx	 0.5490	 0.3940
gy	 0.6200	 0.4230
gz	 0.6410	 0.4100
ha	 0.6750	 0.4090
hb	 0.6830	 0.4200
hc	 0.6570	 0.4270
hd	 0.6120	 0.4220
he	 0.5230	 0.4120
hf	 0.5150	 0.4120
hg	 0.5190	 0.4100
hh	 0.5280	 0.4200
hi	 0.5280	 0.4170
hj	 0.5300	 0.4020
hk	 0.5440	 0.3970
hl	 0.5650	 0.3930
hm	 0.5500	 0.4050
hn	 0.5600	 0.4180
ho	 0.4430	 0.3960
hp	 0.1610	 0.3340
hq	 0.3490	 0.4020
hr	 0.1250	 0.3660
hs	 0.0820	 0.3390
ht	 0.0390	 0.3410

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Chain	Atom inclusion	Q-score
hu	 0.0970	 0.3150
hv	 0.2320	 0.3690
hw	 0.1660	 0.3680
hx	 0.1780	 0.3590
hy	 0.1090	 0.3500
hz	 0.2590	 0.3470
ia	 0.1930	 0.3410
ib	 0.1880	 0.3910
ic	 0.2750	 0.3610
id	 0.0260	 0.3640
ie	 0.1090	 0.3560
if	 0.0920	 0.3440
ig	 0.1170	 0.3630
ih	 0.3040	 0.3810
ii	 0.1950	 0.3690
ij	 0.3330	 0.3750
ik	 0.2270	 0.3670
il	 0.0480	 0.3220
im	 0.1410	 0.3510
in	 0.0970	 0.3490
io	 0.0390	 0.3040
ip	 0.1250	 0.3680
iq	 0.0450	 0.3060
ir	 0.0690	 0.3280
is	 0.0850	 0.3240
it	 0.1290	 0.3610
iu	 0.1510	 0.3460
iv	 0.0870	 0.3450
iw	 0.0680	 0.3320
ix	 0.0150	 0.3290
iy	 0.0300	 0.3230
iz	 0.2330	 0.3540
ja	 0.3310	 0.4040
jb	 0.0160	 0.3460
jc	 0.0030	 0.2720
jd	 0.1090	 0.3620
je	 0.1370	 0.3570
jf	 0.1800	 0.3750
jg	 0.2690	 0.3730
jh	 0.0970	 0.3070
ji	 0.1090	 0.3170
jj	 0.1090	 0.3120

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Chain	Atom inclusion	Q-score
jk	0.1040	0.3250
jl	0.2330	0.3570
jm	0.1240	0.3580
jn	0.0920	0.3160
jo	0.0900	0.3160
jp	0.0190	0.3040
jq	0.0480	0.2950
jr	0.1780	0.3620
js	0.2240	0.3500
jt	0.1110	0.3020
ju	0.1290	0.3220
jv	0.0390	0.3160
jw	0.0550	0.3060
jx	0.1900	0.3280
jy	0.1410	0.3110
jz	0.0180	0.2470
ka	0.0110	0.2560
kb	0.0950	0.2890
kc	0.0530	0.2920
kd	0.0400	0.2610
ke	0.0560	0.2540
kf	0.0800	0.2910
kg	0.1190	0.2830
kh	0.1590	0.3360
ki	0.1300	0.3270
kj	0.0480	0.2260
kk	0.0630	0.2270
kl	0.0160	0.2720
km	0.0020	0.2700
kn	0.0580	0.3000
ko	0.0340	0.2700
kp	0.0150	0.2780
kq	0.0640	0.2830
kr	0.0630	0.2810
ks	0.1190	0.3150
kt	0.1030	0.3100
ku	0.1290	0.3280
kv	0.0100	0.2520
kw	0.0160	0.2560
kx	0.0190	0.2000
ky	0.0000	0.1780
kz	0.0180	0.1810

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Chain	Atom inclusion	Q-score
la	 0.2480	 0.3480
lb	 0.0900	 0.3270
lc	 0.1380	 0.3200
ld	 0.1210	 0.3600
le	 0.1720	 0.3540
lf	 0.2540	 0.3690
lg	 0.0560	 0.3450
lh	 0.2280	 0.3620
li	 0.1690	 0.3410
lj	 0.1980	 0.3550
lk	 0.2060	 0.3610
ll	 0.1770	 0.3520
lm	 0.2140	 0.3760
ln	 0.1930	 0.3320
lo	 0.1240	 0.3420
lp	 0.2150	 0.3440
lq	 0.3070	 0.3450
lr	 0.2190	 0.3690
ls	 0.1720	 0.3600
lt	 0.4210	 0.3940
lu	 0.3220	 0.3610
lv	 0.0690	 0.3270
lw	 0.1900	 0.3580
lx	 0.1190	 0.3500
ly	 0.0950	 0.3190
lz	 0.1720	 0.3600
ma	 0.1210	 0.3390
mb	 0.0550	 0.3330
mc	 0.1170	 0.3720
md	 0.1820	 0.3570
me	 0.2880	 0.3720
mf	 0.2650	 0.3480
mg	 0.2410	 0.3710
mh	 0.1240	 0.3120
mi	 0.2170	 0.3620
mj	 0.2850	 0.3720
mk	 0.3440	 0.3750
ml	 0.0770	 0.3400
mm	 0.0220	 0.3130
mn	 0.2440	 0.3380
mo	 0.2730	 0.3580
mp	 0.2690	 0.3500

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Chain	Atom inclusion	Q-score
mq	 0.3910	 0.3850
ms	 0.0800	 0.3220
mt	 0.0640	 0.3440
mu	 0.0720	 0.2690
mv	 0.0790	 0.2990
mw	 0.1480	 0.3570
mx	 0.1130	 0.3260
my	 0.0580	 0.3050
mz	 0.0760	 0.3010
na	 0.0130	 0.2930
nb	 0.0220	 0.2690
nc	 0.1510	 0.3370
nd	 0.1610	 0.3630
ne	 0.0660	 0.3110
nf	 0.1090	 0.2800
ng	 0.2040	 0.3520
nh	 0.0550	 0.2950
ni	 0.0110	 0.2740
nj	 0.0110	 0.2560
nk	 0.0560	 0.3190
nl	 0.0710	 0.2830
nm	 0.0420	 0.2720
nn	 0.0900	 0.2880
no	 0.1510	 0.3400
np	 0.1010	 0.3550
nq	 0.1240	 0.3010
ns	 0.1610	 0.2900
nt	 0.0060	 0.2260
nu	 0.0050	 0.1990
nv	 0.1370	 0.2860
nw	 0.1990	 0.3080
nx	 0.0660	 0.3170
ny	 0.0510	 0.3210
nz	 0.0300	 0.2830
oa	 0.0290	 0.2920
ob	 0.0350	 0.2100
oc	 0.0190	 0.2520
od	 0.1030	 0.2500
oe	 0.0580	 0.2160
of	 0.0270	 0.2860
og	 0.0500	 0.2520