



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 07:00 AM UTC

PDB ID : 3J6R / pdb_00003j6r
EMDB ID : EMD-5932
Title : Electron cryo-microscopy of Human Papillomavirus Type 16 capsid
Authors : Cardone, G.; Moyer, A.L.; Cheng, N.; Thompson, C.D.; Dvoretzky, I.; Lowy, D.R.; Schiller, J.T.; Steven, A.C.; Buck, C.B.; Trus, B.L.
Deposited on : 2014-03-20
Resolution : 9.10 Å(reported)
Based on initial model : 1DZL

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:

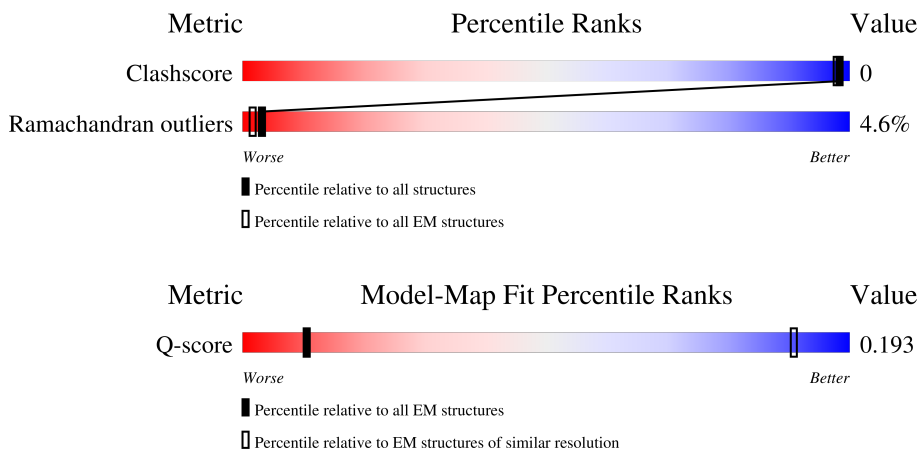
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.10 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	-
Q-score	-	25397	244 (8.60 - 9.60)

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	A	478	 55% 41% 5% 1% 1%
1	B	478	 54% 42% 5% 1% 1%
1	C	478	 54% 44% 5% 1% 1%
1	D	478	 54% 42% 5% 1% 1%
1	E	478	 54% 43% 5% 1% 1%

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Mol	Chain	Length	Quality of chain
1	F	478	58% 38%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17214 atoms, of which 5748 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 L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	478	Total	C	H	N	O	0	0
			2869	956	958	478	477		
1	A	478	Total	C	H	N	O	0	0
			2869	956	958	478	477		
1	E	478	Total	C	H	N	O	0	0
			2869	956	958	478	477		
1	D	478	Total	C	H	N	O	0	0
			2869	956	958	478	477		
1	C	478	Total	C	H	N	O	0	0
			2869	956	958	478	477		
1	F	478	Total	C	H	N	O	0	0
			2869	956	958	478	477		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	GLN	ASN	conflict	UNP Q4VRM0
B	181	GLN	ASN	conflict	UNP Q4VRM0
B	472	LEU	ALA	conflict	UNP Q4VRM0
A	177	GLN	ASN	conflict	UNP Q4VRM0
A	181	GLN	ASN	conflict	UNP Q4VRM0
A	472	LEU	ALA	conflict	UNP Q4VRM0
E	177	GLN	ASN	conflict	UNP Q4VRM0
E	181	GLN	ASN	conflict	UNP Q4VRM0
E	472	LEU	ALA	conflict	UNP Q4VRM0
D	177	GLN	ASN	conflict	UNP Q4VRM0
D	181	GLN	ASN	conflict	UNP Q4VRM0
D	472	LEU	ALA	conflict	UNP Q4VRM0
C	177	GLN	ASN	conflict	UNP Q4VRM0
C	181	GLN	ASN	conflict	UNP Q4VRM0
C	472	LEU	ALA	conflict	UNP Q4VRM0
F	177	GLN	ASN	conflict	UNP Q4VRM0
F	181	GLN	ASN	conflict	UNP Q4VRM0
F	472	LEU	ALA	conflict	UNP Q4VRM0

3 Residue-property plots

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

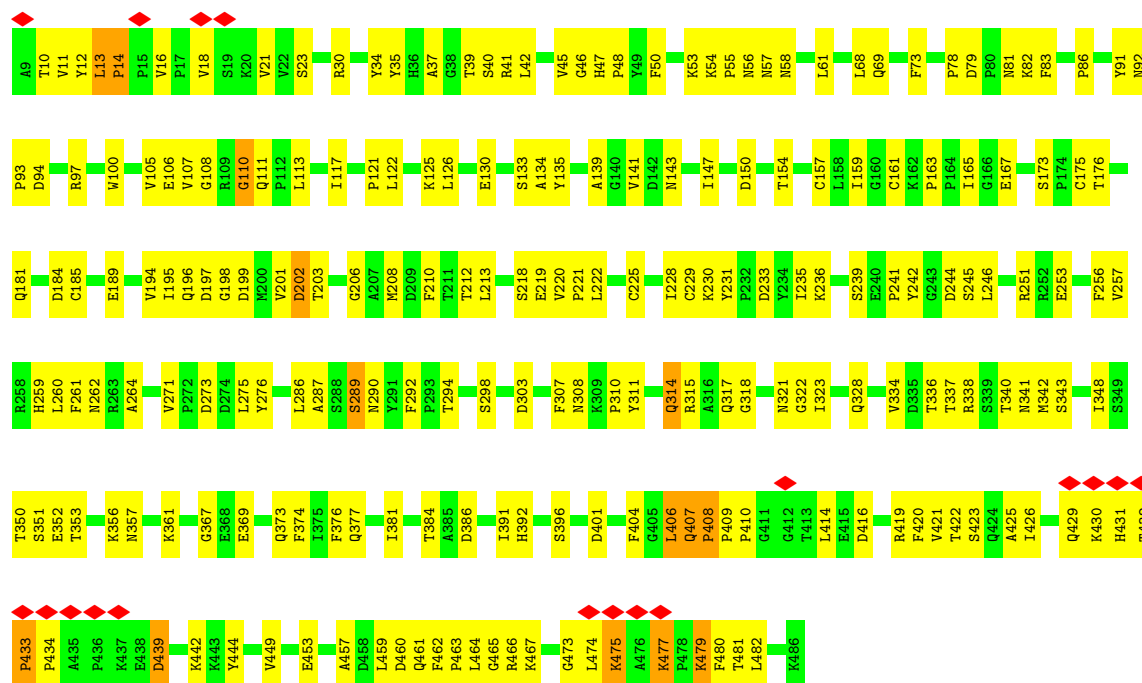
• Molecule 1: Major capsid protein L1



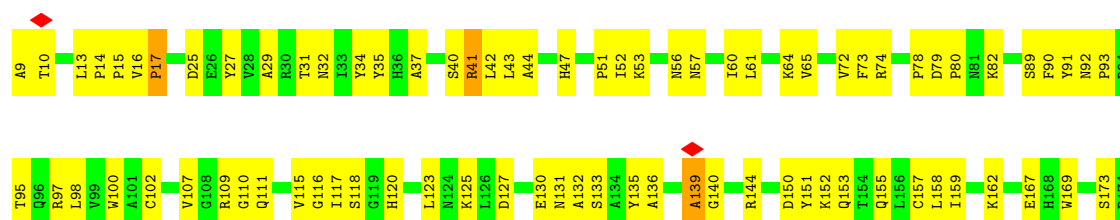
• Molecule 1: Major capsid protein L1

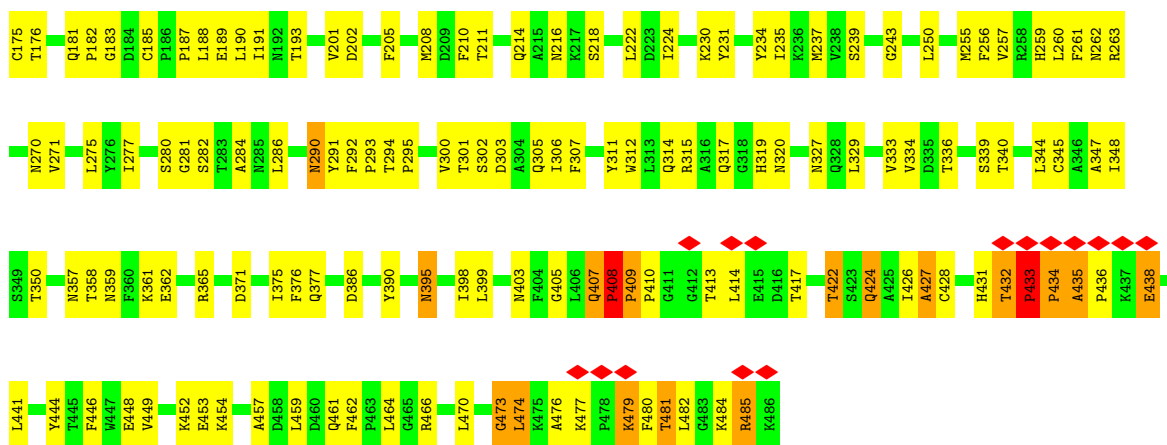


- Molecule 1: Major capsid protein L1

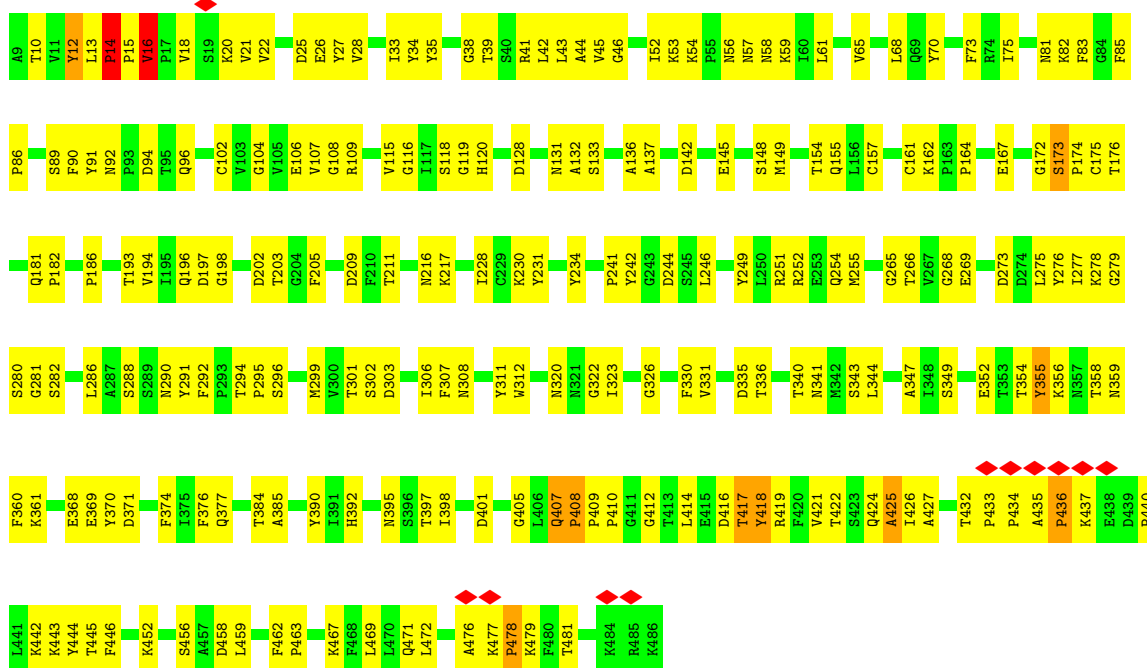


- Molecule 1: Major capsid protein L1

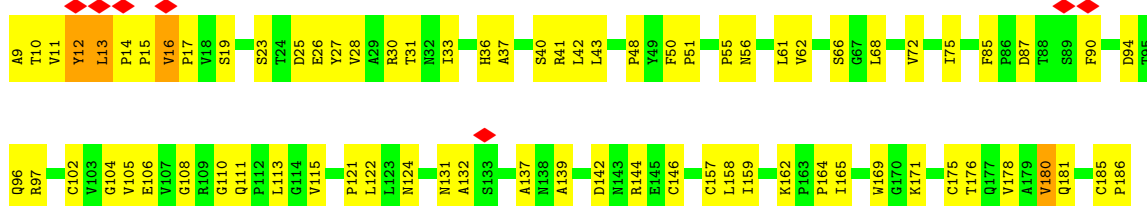


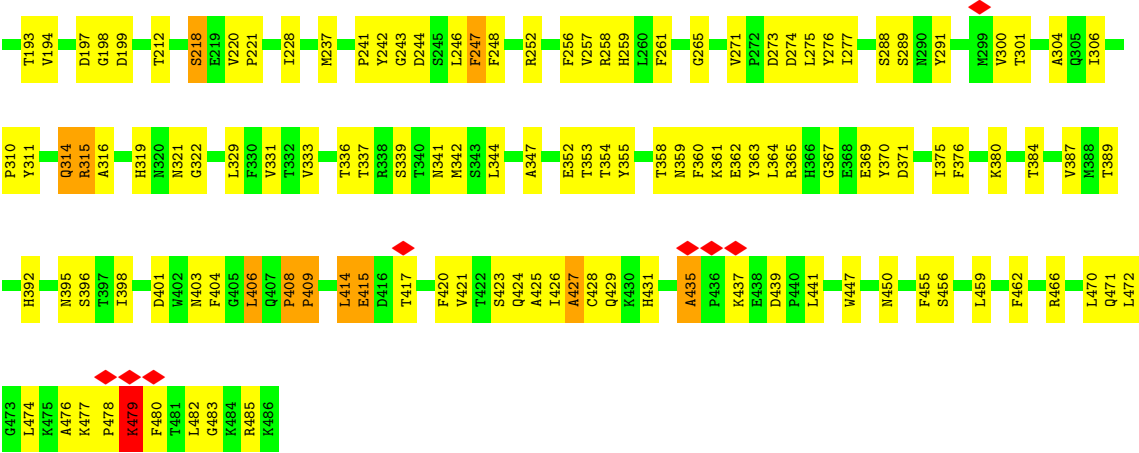


• Molecule 1: Major capsid protein L1



• Molecule 1: Major capsid protein L1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	5952	Depositor
Resolution determination method	FSC 0.33 CUT-OFF	Depositor
CTF correction method	each micrograph	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	537	Depositor
Maximum defocus (nm)	2175	Depositor
Magnification	38000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	3846.000	Depositor
Minimum map value	-2226.000	Depositor
Average map value	22.884	Depositor
Map value standard deviation	535.923	Depositor
Recommended contour level	800	Depositor
Map size ($\text{\AA}$)	720.51, 720.51, 720.51	wwPDB
Map dimensions	511, 511, 511	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.41, 1.41, 1.41	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	A	2.50	97/1910 (5.1%)	2.90	200/2386 (8.4%)
1	B	2.55	98/1910 (5.1%)	2.93	207/2386 (8.7%)
1	C	2.58	110/1910 (5.8%)	2.81	190/2386 (8.0%)
1	D	2.62	125/1910 (6.5%)	2.83	174/2386 (7.3%)
1	E	2.63	112/1910 (5.9%)	2.88	208/2386 (8.7%)
1	F	2.53	102/1910 (5.3%)	2.85	181/2386 (7.6%)
All	All	2.57	644/11460 (5.6%)	2.87	1160/14316 (8.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	13
1	B	0	10
1	C	0	13
1	D	0	15
1	E	0	9
1	F	0	11
All	All	0	71

All (644) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	85	PHE	CA-C	-18.56	1.37	1.52
1	A	143	ASN	CA-C	-10.94	1.40	1.53
1	C	149	MET	CA-C	-10.11	1.39	1.52
1	C	137	ALA	CA-C	9.90	1.57	1.52
1	A	305	GLN	C-N	9.85	1.44	1.33
1	C	290	ASN	N-CA	-9.84	1.33	1.46
1	A	115	VAL	CA-C	-9.53	1.44	1.52
1	E	163	PRO	CA-C	-9.43	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	197	ASP	CA-C	-9.43	1.40	1.52
1	D	73	PHE	CA-C	-9.34	1.41	1.52
1	E	439	ASP	C-N	9.17	1.41	1.33
1	B	374	PHE	CA-C	-9.06	1.41	1.52
1	D	408	PRO	C-N	8.99	1.44	1.33
1	E	197	ASP	N-CA	-8.96	1.34	1.46
1	C	347	ALA	CA-C	-8.87	1.41	1.52
1	E	350	THR	CA-C	-8.86	1.42	1.52
1	B	220	VAL	CA-C	-8.83	1.45	1.52
1	C	445	THR	CA-C	-8.79	1.41	1.52
1	E	315	ARG	CA-C	-8.69	1.42	1.53
1	B	273	ASP	CA-C	-8.67	1.43	1.53
1	C	360	PHE	CA-C	-8.65	1.41	1.52
1	D	214	GLN	N-CA	-8.62	1.35	1.46
1	C	312	TRP	CA-C	-8.62	1.41	1.52
1	A	245	SER	CA-C	-8.59	1.41	1.52
1	F	277	ILE	C-N	8.56	1.45	1.33
1	C	162	LYS	C-N	8.54	1.43	1.33
1	F	162	LYS	C-N	8.41	1.43	1.33
1	C	230	LYS	CA-C	-8.37	1.42	1.52
1	C	28	VAL	CA-C	-8.33	1.42	1.52
1	F	169	TRP	CA-C	-8.30	1.42	1.52
1	A	164	PRO	N-CA	-8.30	1.36	1.47
1	F	61	LEU	CA-C	-8.25	1.42	1.52
1	B	65	VAL	CA-C	-8.23	1.42	1.52
1	D	92	ASN	C-N	8.21	1.43	1.33
1	F	27	TYR	C-N	8.13	1.44	1.33
1	C	43	LEU	CA-C	-8.13	1.42	1.52
1	F	51	PRO	CA-C	-8.11	1.42	1.52
1	B	147	ILE	CA-C	-8.07	1.42	1.52
1	E	338	ARG	CA-C	-8.05	1.42	1.52
1	F	365	ARG	CA-C	-8.04	1.42	1.52
1	A	395	ASN	CA-C	-8.03	1.43	1.52
1	F	316	ALA	CA-C	-8.01	1.42	1.52
1	F	198	GLY	C-N	7.97	1.43	1.33
1	B	146	CYS	N-CA	-7.91	1.36	1.46
1	A	92	ASN	CA-C	-7.90	1.46	1.52
1	D	347	ALA	CA-C	-7.90	1.42	1.52
1	D	359	ASN	CA-C	-7.89	1.42	1.52
1	E	184	ASP	CA-C	-7.89	1.43	1.52
1	C	59	LYS	CA-C	-7.87	1.43	1.52
1	E	256	PHE	C-N	7.84	1.43	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	359	ASN	N-CA	-7.83	1.36	1.46
1	D	167	GLU	CA-C	-7.83	1.43	1.52
1	C	254	GLN	CA-C	-7.80	1.43	1.52
1	B	21	VAL	C-N	7.76	1.43	1.33
1	E	482	LEU	C-N	7.71	1.44	1.33
1	A	156	LEU	CA-C	-7.68	1.43	1.52
1	B	26	GLU	CA-C	-7.66	1.42	1.52
1	C	119	GLY	CA-C	-7.61	1.42	1.51
1	B	408	PRO	CA-C	7.60	1.59	1.52
1	F	90	PHE	N-CA	-7.57	1.36	1.46
1	E	55	PRO	N-CA	-7.52	1.42	1.47
1	D	91	TYR	N-CA	-7.50	1.37	1.46
1	B	47	HIS	N-CA	-7.50	1.38	1.46
1	C	249	TYR	CA-C	-7.48	1.43	1.52
1	D	408	PRO	CA-C	-7.47	1.45	1.52
1	F	165	ILE	CA-C	-7.45	1.43	1.52
1	C	53	LYS	C-N	7.45	1.45	1.33
1	E	122	LEU	CA-C	-7.44	1.42	1.53
1	E	195	ILE	CA-C	-7.37	1.44	1.52
1	F	258	ARG	CA-C	-7.37	1.43	1.52
1	D	262	ASN	CA-C	-7.36	1.43	1.52
1	D	435	ALA	N-CA	-7.36	1.35	1.46
1	E	113	LEU	N-CA	-7.35	1.37	1.46
1	B	464	LEU	CA-C	-7.34	1.43	1.52
1	D	56	ASN	C-N	7.30	1.42	1.33
1	E	218	SER	CA-C	7.29	1.60	1.52
1	C	148	SER	CA-C	-7.29	1.43	1.52
1	C	38	GLY	CA-C	-7.28	1.42	1.51
1	F	113	LEU	CA-C	-7.28	1.43	1.52
1	B	79	ASP	CA-C	-7.25	1.45	1.52
1	D	182	PRO	N-CA	-7.24	1.38	1.47
1	A	161	CYS	N-CA	-7.22	1.39	1.46
1	D	208	MET	C-N	7.22	1.43	1.33
1	E	165	ILE	C-N	7.21	1.44	1.33
1	B	383	LEU	CA-C	-7.18	1.44	1.52
1	A	231	TYR	CA-C	7.17	1.59	1.52
1	B	375	ILE	C-N	7.16	1.42	1.33
1	A	261	PHE	C-O	-7.16	1.15	1.23
1	A	427	ALA	CA-C	-7.15	1.43	1.52
1	A	119	GLY	N-CA	-7.14	1.37	1.45
1	E	292	PHE	C-N	-7.13	1.25	1.33
1	F	180	VAL	CA-C	-7.13	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	412	GLY	C-N	7.11	1.43	1.33
1	A	129	THR	N-CA	-7.10	1.36	1.46
1	C	107	VAL	C-N	7.09	1.41	1.33
1	C	456	SER	N-CA	-7.09	1.37	1.46
1	E	230	LYS	CA-C	-7.08	1.43	1.52
1	B	188	LEU	CA-C	-7.08	1.44	1.52
1	D	127	ASP	C-N	7.05	1.43	1.33
1	D	222	LEU	CA-C	-7.04	1.43	1.52
1	B	345	CYS	CA-C	-7.02	1.43	1.52
1	C	25	ASP	N-CA	-7.01	1.37	1.46
1	A	88	THR	CA-C	-7.00	1.44	1.52
1	F	363	TYR	CA-C	-7.00	1.44	1.52
1	B	190	LEU	CA-C	-7.00	1.44	1.52
1	F	193	THR	C-N	7.00	1.42	1.33
1	E	39	THR	CA-C	-6.99	1.44	1.52
1	D	43	LEU	CA-C	-6.98	1.44	1.52
1	D	334	VAL	CA-C	-6.95	1.44	1.52
1	C	255	MET	CA-C	-6.95	1.43	1.52
1	E	430	LYS	CA-C	-6.94	1.43	1.52
1	D	282	SER	C-N	6.93	1.43	1.33
1	A	10	THR	C-N	6.91	1.43	1.33
1	B	289	SER	N-CA	-6.90	1.36	1.46
1	C	306	ILE	C-N	6.89	1.43	1.33
1	A	388	MET	CA-C	-6.89	1.43	1.52
1	D	250	LEU	C-N	6.88	1.42	1.33
1	D	312	TRP	CA-C	-6.88	1.44	1.52
1	C	408	PRO	CA-C	6.88	1.58	1.52
1	E	273	ASP	N-CA	-6.87	1.40	1.46
1	F	137	ALA	N-CA	-6.85	1.37	1.46
1	A	356	LYS	N-CA	-6.83	1.38	1.46
1	E	251	ARG	CA-C	-6.83	1.44	1.52
1	D	37	ALA	CA-C	-6.82	1.44	1.52
1	B	20	LYS	N-CA	-6.82	1.37	1.46
1	F	228	ILE	CA-C	-6.81	1.44	1.52
1	B	481	THR	C-N	6.80	1.43	1.33
1	E	100	TRP	CA-C	-6.79	1.44	1.52
1	F	361	LYS	N-CA	-6.78	1.37	1.46
1	D	144	ARG	N-CA	-6.77	1.37	1.46
1	C	286	LEU	CA-C	-6.76	1.44	1.52
1	A	443	LYS	C-N	6.73	1.42	1.33
1	A	84	GLY	N-CA	-6.73	1.37	1.45
1	A	359	ASN	N-CA	-6.73	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	470	LEU	N-CA	-6.72	1.37	1.46
1	D	72	VAL	N-CA	-6.71	1.38	1.46
1	D	234	TYR	CA-C	6.69	1.61	1.52
1	B	69	GLN	N-CA	-6.67	1.37	1.45
1	F	97	ARG	CA-C	-6.67	1.43	1.52
1	F	291	TYR	CA-C	-6.66	1.44	1.52
1	F	367	GLY	CA-C	-6.66	1.47	1.52
1	A	462	PHE	C-N	6.66	1.43	1.34
1	B	154	THR	C-O	-6.66	1.16	1.23
1	A	90	PHE	CA-C	-6.65	1.44	1.52
1	D	16	VAL	CA-C	-6.65	1.47	1.53
1	D	293	PRO	CA-C	-6.65	1.43	1.52
1	B	173	SER	CA-C	-6.64	1.44	1.52
1	C	28	VAL	N-CA	6.64	1.54	1.46
1	D	311	TYR	N-CA	-6.63	1.38	1.46
1	B	153	GLN	CA-C	-6.62	1.44	1.52
1	D	173	SER	CA-C	-6.62	1.45	1.52
1	F	122	LEU	C-N	6.62	1.42	1.33
1	B	482	LEU	CA-C	-6.62	1.44	1.52
1	E	235	ILE	N-CA	-6.62	1.38	1.46
1	F	252	ARG	N-CA	-6.61	1.38	1.46
1	A	308	ASN	CA-C	-6.60	1.44	1.52
1	C	203	THR	N-CA	-6.59	1.37	1.46
1	F	331	VAL	CA-C	-6.59	1.44	1.52
1	C	288	SER	C-N	6.59	1.42	1.33
1	E	83	PHE	C-N	6.57	1.43	1.33
1	B	260	LEU	CA-C	-6.55	1.44	1.52
1	E	12	TYR	N-CA	-6.54	1.37	1.45
1	E	414	LEU	N-CA	-6.53	1.38	1.46
1	E	30	ARG	C-N	6.52	1.42	1.33
1	E	117	ILE	CA-C	-6.51	1.44	1.52
1	C	361	LYS	CA-C	-6.50	1.44	1.52
1	A	280	SER	N-CA	-6.49	1.38	1.46
1	F	43	LEU	N-CA	-6.49	1.37	1.46
1	D	115	VAL	CA-C	-6.47	1.44	1.52
1	C	446	PHE	N-CA	-6.47	1.37	1.45
1	A	240	GLU	C-N	-6.46	1.28	1.33
1	A	109	ARG	CA-C	-6.46	1.45	1.52
1	E	376	PHE	CA-C	-6.45	1.44	1.52
1	A	53	LYS	N-CA	-6.44	1.38	1.45
1	C	369	GLU	CA-C	-6.44	1.44	1.52
1	E	377	GLN	N-CA	-6.43	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	322	GLY	C-N	6.41	1.39	1.33
1	B	266	THR	C-N	6.39	1.41	1.33
1	E	337	THR	CA-C	-6.36	1.44	1.52
1	B	302	SER	C-N	6.36	1.42	1.33
1	B	223	ASP	C-O	-6.35	1.16	1.24
1	F	375	ILE	C-N	6.35	1.42	1.33
1	E	391	ILE	C-N	6.35	1.42	1.34
1	F	17	PRO	C-N	6.34	1.41	1.34
1	D	271	VAL	C-N	6.34	1.42	1.33
1	A	399	LEU	CA-C	-6.33	1.44	1.52
1	B	265	GLY	C-N	6.33	1.42	1.33
1	A	21	VAL	N-CA	-6.32	1.38	1.46
1	F	139	ALA	CA-C	-6.32	1.45	1.52
1	C	102	CYS	C-N	6.29	1.41	1.33
1	F	322	GLY	C-N	6.29	1.41	1.33
1	F	75	ILE	N-CA	-6.28	1.38	1.46
1	C	392	HIS	C-N	6.28	1.42	1.33
1	E	348	ILE	N-CA	-6.28	1.38	1.46
1	F	429	GLN	C-N	6.28	1.42	1.33
1	B	312	TRP	CA-C	-6.27	1.44	1.52
1	D	255	MET	CA-C	-6.26	1.45	1.52
1	D	52	ILE	CA-C	-6.26	1.44	1.52
1	C	432	THR	C-N	6.26	1.40	1.33
1	F	43	LEU	CA-C	-6.26	1.44	1.52
1	E	422	THR	CA-C	6.25	1.60	1.52
1	A	32	ASN	C-N	6.25	1.41	1.33
1	C	106	GLU	CA-C	-6.25	1.45	1.52
1	D	262	ASN	C-N	6.23	1.42	1.33
1	E	139	ALA	N-CA	6.23	1.53	1.45
1	D	159	ILE	C-N	6.22	1.42	1.33
1	E	56	ASN	CA-C	-6.22	1.44	1.52
1	D	357	ASN	C-N	6.21	1.42	1.33
1	C	269	GLU	C-N	6.21	1.42	1.33
1	E	391	ILE	C-O	6.21	1.31	1.24
1	E	135	TYR	CA-C	-6.20	1.45	1.52
1	E	220	VAL	N-CA	6.19	1.52	1.46
1	A	233	ASP	CA-C	-6.18	1.46	1.53
1	F	146	CYS	CA-C	-6.18	1.45	1.52
1	F	300	VAL	C-O	-6.17	1.17	1.23
1	E	276	TYR	CA-C	-6.17	1.45	1.52
1	C	280	SER	C-N	6.16	1.42	1.33
1	F	380	LYS	CA-C	-6.16	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	376	PHE	CA-C	-6.16	1.45	1.52
1	D	187	PRO	CA-C	-6.16	1.44	1.52
1	D	120	HIS	C-N	-6.16	1.27	1.34
1	D	375	ILE	N-CA	-6.14	1.39	1.46
1	C	22	VAL	N-CA	-6.14	1.38	1.46
1	D	485	ARG	N-CA	6.13	1.54	1.46
1	C	56	ASN	C-N	6.12	1.42	1.33
1	B	212	THR	CA-C	6.12	1.60	1.52
1	F	257	VAL	C-N	6.12	1.42	1.33
1	C	46	GLY	C-O	-6.11	1.18	1.24
1	A	72	VAL	CA-C	-6.11	1.44	1.52
1	F	274	ASP	C-N	6.10	1.43	1.33
1	B	164	PRO	C-N	6.10	1.42	1.33
1	D	123	LEU	C-N	6.09	1.41	1.33
1	A	248	PHE	C-N	6.08	1.41	1.33
1	F	347	ALA	CA-C	-6.08	1.45	1.52
1	A	158	LEU	CA-C	-6.07	1.45	1.52
1	E	46	GLY	C-N	6.07	1.40	1.33
1	E	275	LEU	C-N	6.04	1.41	1.33
1	D	434	PRO	CA-C	6.04	1.60	1.52
1	A	355	TYR	N-CA	-6.04	1.38	1.46
1	A	132	ALA	C-N	6.03	1.42	1.33
1	B	361	LYS	C-N	6.03	1.41	1.33
1	E	161	CYS	C-O	-6.03	1.16	1.24
1	E	462	PHE	N-CA	-6.02	1.40	1.45
1	F	248	PHE	N-CA	-6.02	1.38	1.46
1	B	96	GLN	N-CA	-6.01	1.38	1.46
1	F	439	ASP	CA-C	-6.01	1.46	1.53
1	F	466	ARG	CA-C	-6.01	1.45	1.52
1	B	156	LEU	N-CA	-6.00	1.38	1.46
1	A	156	LEU	C-O	-6.00	1.16	1.23
1	C	419	ARG	C-N	6.00	1.41	1.33
1	D	301	THR	N-CA	-5.99	1.39	1.46
1	F	186	PRO	CA-C	5.99	1.57	1.52
1	C	116	GLY	CA-C	-5.98	1.43	1.51
1	D	98	LEU	CA-C	-5.97	1.45	1.52
1	C	437	LYS	CA-C	-5.97	1.45	1.52
1	A	463	PRO	CA-C	-5.97	1.43	1.52
1	C	39	THR	CA-C	-5.97	1.45	1.52
1	D	327	ASN	C-N	5.96	1.42	1.33
1	A	196	GLN	C-N	5.96	1.41	1.33
1	B	257	VAL	C-N	5.95	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	134	ALA	CA-C	-5.94	1.45	1.52
1	E	429	GLN	C-N	5.94	1.41	1.33
1	A	367	GLY	C-N	5.93	1.41	1.33
1	D	295	PRO	CA-C	-5.93	1.45	1.52
1	B	367	GLY	CA-C	-5.93	1.48	1.52
1	B	149	MET	C-N	5.92	1.41	1.33
1	A	118	SER	C-N	5.92	1.41	1.33
1	D	42	LEU	CA-C	-5.92	1.45	1.52
1	B	324	CYS	N-CA	-5.91	1.38	1.46
1	F	333	VAL	N-CA	-5.91	1.39	1.46
1	F	144	ARG	N-CA	-5.91	1.39	1.46
1	D	61	LEU	C-N	5.90	1.40	1.33
1	E	189	GLU	C-O	-5.90	1.17	1.24
1	A	366	HIS	C-N	5.89	1.38	1.33
1	F	456	SER	C-N	5.89	1.42	1.33
1	B	418	TYR	C-O	-5.89	1.18	1.24
1	A	247	PHE	CA-C	-5.89	1.44	1.52
1	D	319	HIS	CA-C	5.89	1.60	1.52
1	C	426	ILE	C-N	5.88	1.42	1.33
1	D	358	THR	CA-C	-5.87	1.45	1.52
1	F	48	PRO	C-N	5.87	1.42	1.33
1	D	202	ASP	C-N	5.87	1.41	1.33
1	B	470	LEU	N-CA	-5.86	1.39	1.46
1	C	343	SER	CA-C	-5.86	1.45	1.52
1	B	52	ILE	N-CA	-5.86	1.39	1.46
1	F	37	ALA	C-N	5.86	1.39	1.33
1	F	164	PRO	C-N	5.85	1.40	1.33
1	E	242	TYR	CA-C	-5.85	1.45	1.52
1	F	275	LEU	C-N	5.85	1.40	1.33
1	C	266	THR	C-N	5.85	1.41	1.34
1	B	136	ALA	CA-C	-5.85	1.45	1.52
1	E	92	ASN	C-N	5.84	1.38	1.33
1	D	271	VAL	CA-C	-5.84	1.47	1.52
1	E	57	ASN	CA-C	-5.84	1.45	1.52
1	F	176	THR	N-CA	5.84	1.53	1.46
1	D	390	TYR	C-N	5.83	1.41	1.33
1	F	456	SER	CA-C	-5.83	1.45	1.52
1	A	410	PRO	N-CA	-5.83	1.39	1.47
1	E	338	ARG	C-N	5.82	1.41	1.33
1	C	277	ILE	CA-C	-5.82	1.45	1.52
1	B	95	THR	N-CA	5.82	1.53	1.46
1	B	341	ASN	CA-C	-5.81	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	245	SER	CA-C	-5.81	1.44	1.52
1	E	353	THR	C-N	5.81	1.41	1.33
1	F	247	PHE	C-N	5.81	1.41	1.33
1	E	167	GLU	CA-C	-5.80	1.45	1.52
1	D	277	ILE	C-N	5.78	1.41	1.33
1	B	33	ILE	CA-C	-5.78	1.45	1.52
1	E	54	LYS	C-N	-5.78	1.29	1.33
1	D	44	ALA	CA-C	-5.77	1.45	1.52
1	E	271	VAL	N-CA	-5.77	1.41	1.45
1	F	358	THR	C-N	5.76	1.41	1.33
1	E	97	ARG	CA-C	-5.76	1.45	1.52
1	C	94	ASP	CA-C	-5.76	1.45	1.52
1	B	66	SER	N-CA	-5.75	1.39	1.46
1	B	354	THR	N-CA	-5.74	1.38	1.45
1	E	467	LYS	C-N	5.74	1.41	1.33
1	D	371	ASP	C-N	5.74	1.41	1.33
1	A	236	LYS	C-N	5.74	1.41	1.34
1	C	291	TYR	N-CA	-5.74	1.39	1.46
1	A	451	LEU	C-N	5.73	1.41	1.33
1	F	124	ASN	N-CA	-5.73	1.39	1.46
1	B	92	ASN	CA-C	-5.72	1.46	1.53
1	B	480	PHE	C-N	5.72	1.41	1.33
1	A	279	GLY	C-N	5.72	1.41	1.33
1	F	36	HIS	N-CA	5.72	1.53	1.45
1	E	125	LYS	N-CA	-5.72	1.38	1.45
1	E	157	CYS	N-CA	-5.72	1.39	1.46
1	E	290	ASN	CA-C	-5.72	1.46	1.53
1	B	191	ILE	CA-C	-5.71	1.45	1.52
1	D	181	GLN	CA-C	-5.71	1.45	1.52
1	A	145	GLU	C-N	5.71	1.41	1.33
1	C	52	ILE	N-CA	-5.70	1.39	1.46
1	D	377	GLN	N-CA	-5.70	1.39	1.46
1	D	446	PHE	C-N	5.70	1.41	1.33
1	A	25	ASP	CA-C	-5.69	1.45	1.52
1	D	131	ASN	C-N	5.69	1.40	1.33
1	B	274	ASP	N-CA	-5.67	1.42	1.47
1	C	254	GLN	C-N	5.67	1.40	1.33
1	B	141	VAL	CA-C	-5.67	1.45	1.52
1	D	41	ARG	CA-C	-5.67	1.45	1.52
1	D	185	CYS	C-N	5.67	1.40	1.33
1	C	370	TYR	N-CA	-5.67	1.38	1.45
1	F	96	GLN	CA-C	-5.67	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	236	LYS	CA-C	-5.67	1.45	1.52
1	A	377	GLN	CA-C	-5.67	1.45	1.52
1	F	62	VAL	CA-C	5.66	1.58	1.52
1	B	233	ASP	C-N	5.65	1.41	1.33
1	E	50	PHE	CA-C	5.64	1.59	1.52
1	C	27	TYR	N-CA	-5.64	1.38	1.46
1	E	194	VAL	CA-C	-5.64	1.46	1.52
1	C	193	THR	CA-C	-5.64	1.45	1.52
1	F	329	LEU	CA-C	-5.64	1.45	1.52
1	C	115	VAL	CA-C	-5.63	1.46	1.52
1	F	248	PHE	C-N	5.63	1.40	1.33
1	B	197	ASP	C-N	5.62	1.42	1.33
1	B	177	GLN	CA-C	-5.62	1.45	1.52
1	A	207	ALA	N-CA	-5.62	1.39	1.46
1	B	447	TRP	CA-C	-5.62	1.45	1.52
1	D	202	ASP	N-CA	-5.62	1.38	1.46
1	C	52	ILE	CA-C	-5.61	1.45	1.52
1	E	466	ARG	C-N	5.60	1.41	1.34
1	B	76	HIS	CA-C	-5.60	1.46	1.52
1	C	335	ASP	CA-C	-5.60	1.46	1.52
1	E	416	ASP	N-CA	-5.59	1.38	1.46
1	D	426	ILE	C-N	5.59	1.41	1.33
1	B	94	ASP	N-CA	-5.58	1.38	1.45
1	B	44	ALA	N-CA	-5.58	1.39	1.46
1	E	352	GLU	C-N	5.58	1.40	1.33
1	D	188	LEU	CA-C	-5.58	1.46	1.52
1	E	202	ASP	N-CA	-5.57	1.39	1.46
1	D	211	THR	C-N	5.57	1.41	1.33
1	F	237	MET	N-CA	-5.57	1.39	1.46
1	A	41	ARG	CA-C	-5.57	1.45	1.52
1	A	357	ASN	N-CA	-5.56	1.39	1.46
1	E	93	PRO	CA-C	5.56	1.58	1.52
1	C	33	ILE	CA-C	5.55	1.59	1.52
1	D	461	GLN	CA-C	-5.55	1.44	1.52
1	A	203	THR	N-CA	-5.54	1.38	1.45
1	F	157	CYS	CA-C	-5.54	1.45	1.52
1	D	257	VAL	CA-C	-5.54	1.46	1.52
1	E	233	ASP	CA-C	-5.53	1.46	1.53
1	E	246	LEU	CA-C	-5.53	1.45	1.52
1	A	316	ALA	N-CA	-5.53	1.38	1.45
1	F	362	GLU	C-N	5.53	1.41	1.33
1	E	386	ASP	CA-C	-5.52	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	331	VAL	C-N	5.52	1.40	1.33
1	A	11	VAL	C-N	5.52	1.41	1.33
1	E	459	LEU	N-CA	5.52	1.53	1.45
1	F	30	ARG	C-N	5.51	1.41	1.33
1	F	164	PRO	CA-C	5.51	1.60	1.52
1	D	57	ASN	CA-C	-5.51	1.45	1.52
1	E	73	PHE	CA-C	-5.50	1.46	1.52
1	E	18	VAL	N-CA	5.50	1.53	1.46
1	D	95	THR	C-O	-5.50	1.16	1.24
1	C	132	ALA	N-CA	-5.49	1.38	1.46
1	E	143	ASN	C-N	5.49	1.40	1.33
1	A	362	GLU	CA-C	-5.49	1.45	1.52
1	D	320	ASN	C-O	-5.49	1.17	1.23
1	E	16	VAL	CA-C	-5.49	1.47	1.52
1	B	166	GLY	C-N	5.48	1.41	1.33
1	C	252	ARG	CA-C	-5.48	1.45	1.52
1	F	56	ASN	CA-C	-5.48	1.45	1.52
1	E	58	ASN	C-N	5.47	1.40	1.33
1	D	74	ARG	CA-C	-5.47	1.45	1.52
1	C	155	GLN	N-CA	-5.47	1.39	1.46
1	C	242	TYR	C-N	5.47	1.41	1.33
1	C	295	PRO	CA-C	5.47	1.59	1.52
1	E	384	THR	C-N	5.47	1.41	1.33
1	C	330	PHE	CA-C	-5.47	1.46	1.52
1	C	323	ILE	CA-C	-5.47	1.46	1.52
1	A	286	LEU	C-N	5.47	1.40	1.33
1	F	472	LEU	CA-C	-5.46	1.45	1.52
1	D	118	SER	N-CA	-5.46	1.38	1.45
1	A	361	LYS	N-CA	-5.46	1.39	1.46
1	C	157	CYS	N-CA	-5.46	1.39	1.45
1	B	373	GLN	CA-C	-5.46	1.46	1.52
1	D	344	LEU	CA-C	-5.46	1.46	1.52
1	E	208	MET	C-N	-5.45	1.26	1.33
1	E	42	LEU	CA-C	-5.45	1.46	1.52
1	B	299	MET	CA-C	-5.45	1.45	1.52
1	C	331	VAL	N-CA	-5.44	1.39	1.46
1	E	374	PHE	N-CA	-5.44	1.39	1.45
1	B	117	ILE	CA-C	-5.44	1.46	1.52
1	A	216	ASN	N-CA	-5.44	1.39	1.46
1	C	352	GLU	C-N	5.44	1.41	1.33
1	E	159	ILE	CA-C	5.43	1.59	1.52
1	D	314	GLN	C-N	5.43	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	473	GLY	CA-C	-5.43	1.44	1.51
1	A	220	VAL	CA-C	-5.43	1.47	1.52
1	D	64	LYS	CA-C	-5.43	1.46	1.52
1	E	110	GLY	C-N	5.42	1.41	1.33
1	C	463	PRO	C-N	5.42	1.41	1.33
1	E	135	TYR	N-CA	-5.42	1.39	1.46
1	B	243	GLY	CA-C	-5.42	1.46	1.51
1	C	22	VAL	CA-C	-5.42	1.45	1.52
1	B	21	VAL	CA-C	-5.42	1.45	1.52
1	C	196	GLN	C-N	5.41	1.41	1.33
1	D	301	THR	CA-C	-5.41	1.47	1.53
1	F	42	LEU	CA-C	-5.41	1.45	1.52
1	A	242	TYR	CA-C	-5.41	1.45	1.52
1	A	376	PHE	C-O	-5.41	1.17	1.24
1	F	194	VAL	CA-C	-5.41	1.46	1.52
1	B	248	PHE	C-N	5.41	1.40	1.33
1	E	203	THR	N-CA	-5.40	1.39	1.46
1	E	328	GLN	CA-C	-5.40	1.46	1.52
1	B	150	ASP	CA-C	-5.40	1.46	1.52
1	B	207	ALA	C-N	5.39	1.40	1.33
1	F	171	LYS	CA-C	-5.39	1.46	1.52
1	C	296	SER	CA-C	-5.39	1.46	1.52
1	C	86	PRO	C-N	5.39	1.41	1.33
1	D	43	LEU	C-N	5.39	1.40	1.33
1	F	304	ALA	C-N	5.38	1.40	1.33
1	C	268	GLY	N-CA	-5.36	1.37	1.45
1	A	304	ALA	C-N	5.36	1.40	1.33
1	D	371	ASP	N-CA	-5.36	1.39	1.46
1	F	144	ARG	C-N	5.36	1.40	1.33
1	D	44	ALA	C-N	5.35	1.40	1.33
1	D	155	GLN	N-CA	-5.35	1.39	1.46
1	F	31	THR	CA-C	5.35	1.59	1.52
1	A	76	HIS	CA-C	-5.35	1.46	1.52
1	A	437	LYS	C-N	5.35	1.40	1.33
1	C	374	PHE	N-CA	-5.34	1.39	1.46
1	F	301	THR	CA-C	-5.34	1.46	1.52
1	B	147	ILE	C-N	5.34	1.41	1.33
1	C	15	PRO	N-CA	-5.34	1.41	1.47
1	A	330	PHE	CA-C	-5.33	1.46	1.52
1	D	82	LYS	C-N	5.33	1.38	1.33
1	D	110	GLY	N-CA	-5.33	1.37	1.45
1	F	55	PRO	CA-C	5.33	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	462	PHE	CA-C	-5.33	1.47	1.52
1	A	147	ILE	CA-C	-5.32	1.46	1.52
1	C	384	THR	CA-C	-5.32	1.46	1.52
1	F	13	LEU	N-CA	5.32	1.56	1.46
1	B	69	GLN	CA-C	5.32	1.59	1.52
1	E	21	VAL	N-CA	-5.31	1.40	1.46
1	E	147	ILE	CA-C	-5.31	1.46	1.52
1	D	292	PHE	C-O	-5.31	1.18	1.24
1	D	340	THR	CA-C	-5.31	1.45	1.52
1	F	121	PRO	C-O	-5.31	1.17	1.24
1	F	218	SER	CA-C	5.31	1.59	1.52
1	B	458	ASP	CA-C	-5.31	1.46	1.52
1	F	243	GLY	C-O	-5.31	1.16	1.23
1	F	369	GLU	C-N	5.31	1.40	1.33
1	B	193	THR	C-O	5.31	1.30	1.23
1	E	361	LYS	C-N	5.30	1.40	1.33
1	C	92	ASN	CA-C	-5.30	1.47	1.52
1	D	190	LEU	CA-C	-5.30	1.46	1.52
1	F	158	LEU	CA-C	-5.30	1.46	1.52
1	A	431	HIS	C-N	5.30	1.40	1.33
1	C	173	SER	CA-C	-5.30	1.46	1.52
1	C	186	PRO	CA-C	-5.30	1.47	1.52
1	D	270	ASN	N-CA	5.30	1.52	1.46
1	E	342	MET	CA-C	-5.29	1.46	1.52
1	A	485	ARG	C-N	5.29	1.40	1.33
1	C	20	LYS	N-CA	-5.28	1.40	1.46
1	C	81	ASN	C-N	5.28	1.41	1.33
1	F	131	ASN	C-N	5.28	1.42	1.33
1	B	338	ARG	CA-C	-5.28	1.46	1.52
1	D	125	LYS	C-N	5.28	1.41	1.33
1	E	343	SER	CA-C	-5.28	1.46	1.52
1	D	44	ALA	N-CA	-5.28	1.39	1.46
1	D	329	LEU	N-CA	-5.28	1.39	1.46
1	D	230	LYS	C-N	5.28	1.40	1.33
1	C	209	ASP	C-N	5.28	1.42	1.33
1	B	199	ASP	CA-C	-5.27	1.45	1.52
1	A	54	LYS	C-N	-5.27	1.28	1.33
1	C	340	THR	C-N	5.27	1.40	1.33
1	A	418	TYR	C-N	5.27	1.40	1.33
1	C	118	SER	C-N	5.27	1.39	1.33
1	B	77	LEU	CA-C	-5.27	1.47	1.52
1	D	175	CYS	N-CA	-5.27	1.39	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	271	VAL	CA-C	-5.27	1.47	1.52
1	E	311	TYR	C-N	5.26	1.40	1.33
1	C	12	TYR	N-CA	-5.26	1.36	1.46
1	D	261	PHE	CA-C	-5.26	1.46	1.52
1	E	61	LEU	CA-C	-5.25	1.46	1.52
1	B	149	MET	N-CA	-5.25	1.39	1.46
1	A	343	SER	C-N	5.25	1.41	1.33
1	A	139	ALA	CA-C	-5.25	1.46	1.53
1	B	157	CYS	C-N	5.24	1.40	1.33
1	E	463	PRO	CA-C	-5.24	1.44	1.52
1	F	164	PRO	C-O	5.24	1.30	1.24
1	C	216	ASN	C-N	5.24	1.41	1.33
1	C	142	ASP	CA-C	-5.23	1.46	1.53
1	C	308	ASN	CA-C	-5.23	1.45	1.52
1	E	287	ALA	N-CA	-5.23	1.39	1.46
1	E	121	PRO	N-CA	-5.22	1.40	1.47
1	D	97	ARG	CA-C	5.22	1.58	1.52
1	F	361	LYS	CA-C	-5.22	1.46	1.52
1	B	271	VAL	CA-C	-5.21	1.49	1.53
1	A	351	SER	CA-C	-5.21	1.45	1.52
1	C	44	ALA	C-N	5.21	1.39	1.33
1	B	372	LEU	CA-C	-5.21	1.46	1.52
1	E	105	VAL	CA-C	-5.21	1.46	1.52
1	B	63	PRO	N-CA	5.21	1.53	1.47
1	E	430	LYS	C-N	5.20	1.40	1.33
1	F	220	VAL	CA-C	5.20	1.57	1.52
1	D	191	ILE	C-O	-5.20	1.18	1.24
1	C	401	ASP	C-N	5.20	1.40	1.33
1	E	406	LEU	C-N	5.20	1.40	1.33
1	E	261	PHE	CA-C	-5.20	1.46	1.52
1	A	201	VAL	C-N	5.19	1.41	1.33
1	C	198	GLY	C-N	5.19	1.40	1.33
1	D	15	PRO	C-N	5.19	1.38	1.33
1	E	143	ASN	N-CA	-5.19	1.40	1.46
1	D	159	ILE	CA-C	-5.19	1.46	1.52
1	F	146	CYS	C-O	-5.19	1.17	1.24
1	E	126	LEU	CA-C	-5.18	1.45	1.52
1	C	467	LYS	N-CA	-5.18	1.39	1.46
1	D	348	ILE	CA-C	-5.18	1.45	1.52
1	B	395	ASN	C-N	5.18	1.40	1.33
1	E	37	ALA	C-O	-5.18	1.17	1.23
1	D	424	GLN	C-N	5.18	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	136	ALA	C-N	5.18	1.41	1.34
1	F	478	PRO	N-CA	-5.18	1.40	1.47
1	D	79	ASP	C-O	5.17	1.28	1.24
1	D	361	LYS	N-CA	-5.17	1.39	1.46
1	B	270	ASN	CA-C	-5.17	1.46	1.52
1	B	400	GLU	N-CA	5.17	1.52	1.46
1	D	375	ILE	CA-C	-5.17	1.46	1.52
1	E	367	GLY	CA-C	-5.17	1.48	1.52
1	A	459	LEU	CA-C	-5.17	1.46	1.52
1	A	182	PRO	CA-C	-5.16	1.45	1.52
1	F	110	GLY	CA-C	-5.16	1.44	1.51
1	E	34	TYR	C-N	-5.16	1.26	1.33
1	B	205	PHE	CA-C	-5.16	1.45	1.52
1	D	305	GLN	C-N	5.16	1.39	1.33
1	C	34	TYR	CA-C	-5.16	1.46	1.52
1	E	154	THR	C-N	5.15	1.40	1.33
1	D	243	GLY	CA-C	-5.15	1.45	1.51
1	D	286	LEU	CA-C	-5.15	1.46	1.52
1	A	27	TYR	N-CA	5.14	1.51	1.46
1	C	444	TYR	N-CA	-5.14	1.39	1.45
1	D	185	CYS	N-CA	5.14	1.51	1.45
1	A	303	ASP	C-N	5.14	1.41	1.33
1	D	307	PHE	C-N	5.14	1.41	1.33
1	C	244	ASP	C-N	5.14	1.41	1.34
1	E	414	LEU	C-N	5.13	1.40	1.33
1	F	406	LEU	C-O	-5.12	1.17	1.24
1	A	241	PRO	CA-C	-5.12	1.47	1.52
1	D	407	GLN	C-N	5.12	1.39	1.33
1	E	40	SER	CA-C	-5.12	1.46	1.52
1	C	175	CYS	C-N	5.12	1.40	1.33
1	C	251	ARG	CA-C	-5.12	1.46	1.52
1	A	86	PRO	C-N	5.11	1.40	1.33
1	F	344	LEU	C-N	5.11	1.39	1.33
1	B	133	SER	C-N	5.11	1.39	1.33
1	D	47	HIS	CA-C	-5.11	1.45	1.52
1	D	386	ASP	CA-C	-5.11	1.46	1.52
1	D	441	LEU	CA-C	-5.10	1.46	1.52
1	C	436	PRO	CA-C	-5.10	1.45	1.52
1	B	310	PRO	C-O	-5.10	1.18	1.23
1	B	334	VAL	CA-C	-5.10	1.46	1.52
1	A	483	GLY	CA-C	-5.09	1.47	1.52
1	D	40	SER	N-CA	-5.09	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	344	LEU	C-N	5.09	1.39	1.33
1	A	307	PHE	CA-C	-5.09	1.46	1.52
1	F	354	THR	C-N	5.09	1.40	1.33
1	A	44	ALA	C-N	5.09	1.39	1.33
1	C	174	PRO	N-CA	-5.09	1.40	1.47
1	F	261	PHE	N-CA	-5.08	1.39	1.45
1	A	364	LEU	C-O	-5.08	1.17	1.23
1	D	92	ASN	CA-C	-5.08	1.47	1.52
1	A	381	ILE	N-CA	-5.08	1.39	1.46
1	E	198	GLY	C-N	5.07	1.40	1.33
1	F	256	PHE	N-CA	-5.07	1.39	1.46
1	B	413	THR	C-N	5.07	1.40	1.33
1	C	355	TYR	C-N	5.07	1.40	1.33
1	D	216	ASN	CA-C	-5.07	1.46	1.52
1	D	237	MET	CA-C	5.06	1.59	1.52
1	C	38	GLY	N-CA	-5.06	1.38	1.45
1	A	331	VAL	N-CA	-5.06	1.39	1.46
1	D	449	VAL	C-N	5.06	1.40	1.33
1	F	104	GLY	C-N	5.06	1.40	1.33
1	D	60	ILE	N-CA	-5.05	1.40	1.46
1	F	115	VAL	C-N	5.05	1.39	1.33
1	B	447	TRP	C-N	5.05	1.40	1.33
1	A	242	TYR	C-N	5.05	1.40	1.33
1	F	72	VAL	CA-C	-5.05	1.46	1.52
1	D	193	THR	C-O	-5.04	1.17	1.23
1	B	105	VAL	C-O	-5.04	1.18	1.23
1	A	33	ILE	C-O	-5.04	1.18	1.24
1	D	339	SER	CA-C	-5.04	1.46	1.52
1	C	154	THR	N-CA	-5.04	1.40	1.46
1	C	42	LEU	C-N	-5.04	1.26	1.33
1	A	268	GLY	C-N	5.03	1.40	1.33
1	E	173	SER	CA-C	-5.03	1.46	1.52
1	A	353	THR	C-N	5.03	1.39	1.33
1	B	188	LEU	N-CA	-5.03	1.40	1.46
1	B	416	ASP	CA-C	-5.03	1.42	1.52
1	B	356	LYS	CA-C	-5.02	1.46	1.52
1	E	408	PRO	CA-C	5.02	1.56	1.52
1	D	189	GLU	C-O	-5.01	1.18	1.23
1	C	75	ILE	CA-C	-5.01	1.46	1.52
1	C	390	TYR	C-O	-5.01	1.18	1.24
1	F	26	GLU	N-CA	-5.01	1.40	1.46
1	F	471	GLN	N-CA	-5.01	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	260	LEU	C-N	5.00	1.40	1.33
1	A	334	VAL	CA-C	-5.00	1.46	1.52
1	D	405	GLY	N-CA	5.00	1.52	1.45
1	D	444	TYR	C-N	5.00	1.40	1.33
1	A	179	ALA	N-CA	-5.00	1.40	1.46
1	E	206	GLY	N-CA	-5.00	1.35	1.45

All (1160) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	306	ILE	N-CA-C	-13.17	101.23	111.90
1	F	220	VAL	N-CA-C	-13.01	98.52	109.19
1	C	409	PRO	CA-C-O	-12.73	111.73	120.90
1	A	433	PRO	N-CA-C	12.39	122.37	110.47
1	B	420	PHE	CA-C-N	12.02	143.34	121.70
1	B	420	PHE	C-N-CA	12.02	143.34	121.70
1	D	462	PHE	N-CA-C	-11.37	95.75	110.07
1	E	408	PRO	CA-C-N	11.36	132.08	120.38
1	E	408	PRO	C-N-CA	11.36	132.08	120.38
1	B	15	PRO	CA-C-N	11.35	142.14	121.70
1	B	15	PRO	C-N-CA	11.35	142.14	121.70
1	B	395	ASN	CA-C-N	11.25	135.79	120.38
1	B	395	ASN	C-N-CA	11.25	135.79	120.38
1	F	485	ARG	CA-C-N	11.21	141.88	121.70
1	F	485	ARG	C-N-CA	11.21	141.88	121.70
1	B	223	ASP	N-CA-C	11.17	123.46	111.28
1	F	306	ILE	N-CA-C	-11.00	102.43	113.10
1	A	408	PRO	N-CA-C	10.93	122.28	110.58
1	C	354	THR	O-C-N	10.77	134.42	122.15
1	B	430	LYS	N-CA-C	10.46	122.26	111.07
1	F	212	THR	N-CA-C	-10.46	101.07	114.04
1	D	111	GLN	CA-C-N	10.30	131.64	120.11
1	D	111	GLN	C-N-CA	10.30	131.64	120.11
1	A	353	THR	N-CA-C	-10.26	100.76	113.28
1	C	359	ASN	N-CA-C	-10.24	99.30	112.93
1	B	240	GLU	CA-C-O	-10.22	111.59	119.46
1	C	409	PRO	O-C-N	10.21	126.01	121.31
1	D	176	THR	N-CA-C	-9.87	101.33	113.97
1	F	424	GLN	O-C-N	9.87	129.59	120.71
1	F	431	HIS	CA-C-N	9.83	139.39	121.70
1	F	431	HIS	C-N-CA	9.83	139.39	121.70
1	D	408	PRO	CA-C-N	9.71	130.38	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	408	PRO	C-N-CA	9.71	130.38	120.38
1	B	409	PRO	CA-C-N	9.70	131.97	119.84
1	B	409	PRO	C-N-CA	9.70	131.97	119.84
1	F	221	PRO	CA-C-N	9.69	133.26	120.28
1	F	221	PRO	C-N-CA	9.69	133.26	120.28
1	B	177	GLN	CA-C-O	-9.68	110.16	120.42
1	C	409	PRO	N-CA-C	9.62	119.71	110.47
1	E	479	LYS	CA-C-N	9.61	139.00	121.70
1	E	479	LYS	C-N-CA	9.61	139.00	121.70
1	C	61	LEU	N-CA-C	-9.41	101.70	113.55
1	A	339	SER	CA-C-N	9.37	139.44	121.54
1	A	339	SER	C-N-CA	9.37	139.44	121.54
1	B	431	HIS	CA-C-N	9.37	138.56	121.70
1	B	431	HIS	C-N-CA	9.37	138.56	121.70
1	F	132	ALA	CA-C-N	9.28	133.07	120.54
1	F	132	ALA	C-N-CA	9.28	133.07	120.54
1	D	181	GLN	CA-C-N	9.24	129.32	119.90
1	D	181	GLN	C-N-CA	9.24	129.32	119.90
1	E	212	THR	CA-C-N	9.23	132.65	120.28
1	E	212	THR	C-N-CA	9.23	132.65	120.28
1	E	47	HIS	O-C-N	-9.20	115.41	121.85
1	D	438	GLU	N-CA-C	-9.18	94.29	109.07
1	E	442	LYS	O-C-N	9.16	131.25	122.18
1	B	464	LEU	CA-C-N	9.11	130.28	119.99
1	B	464	LEU	C-N-CA	9.11	130.28	119.99
1	F	470	LEU	CA-C-N	9.11	133.39	120.28
1	F	470	LEU	C-N-CA	9.11	133.39	120.28
1	F	16	VAL	CA-C-N	9.09	129.16	119.89
1	F	16	VAL	C-N-CA	9.09	129.16	119.89
1	A	10	THR	CA-C-O	-9.06	111.31	120.82
1	F	408	PRO	O-C-N	-8.96	116.94	121.15
1	F	359	ASN	CA-C-N	8.86	134.21	122.42
1	F	359	ASN	C-N-CA	8.86	134.21	122.42
1	A	47	HIS	CA-C-O	-8.82	111.69	119.72
1	B	357	ASN	N-CA-C	-8.80	102.09	113.17
1	E	323	ILE	N-CA-C	-8.79	97.42	109.55
1	E	404	PHE	N-CA-C	-8.77	101.93	114.12
1	E	336	THR	CA-C-N	8.75	132.34	120.44
1	E	336	THR	C-N-CA	8.75	132.34	120.44
1	E	341	ASN	N-CA-C	-8.74	94.65	108.90
1	A	194	VAL	CA-C-N	8.73	133.71	121.66
1	A	194	VAL	C-N-CA	8.73	133.71	121.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	474	LEU	CA-C-N	8.65	137.27	121.70
1	D	474	LEU	C-N-CA	8.65	137.27	121.70
1	C	294	THR	CA-C-O	-8.63	112.81	119.46
1	F	483	GLY	CA-C-N	8.62	137.21	121.70
1	F	483	GLY	C-N-CA	8.62	137.21	121.70
1	D	428	CYS	CA-C-N	8.57	137.13	121.70
1	D	428	CYS	C-N-CA	8.57	137.13	121.70
1	A	473	GLY	CA-C-N	8.54	133.38	120.82
1	A	473	GLY	C-N-CA	8.54	133.38	120.82
1	A	14	PRO	N-CA-C	8.50	121.08	110.70
1	E	462	PHE	N-CA-C	-8.49	98.40	108.25
1	B	313	LEU	CA-C-N	8.49	132.51	120.28
1	B	313	LEU	C-N-CA	8.49	132.51	120.28
1	B	50	PHE	N-CA-C	-8.47	98.42	108.25
1	E	298	SER	CA-C-N	8.47	133.16	121.05
1	E	298	SER	C-N-CA	8.47	133.16	121.05
1	D	422	THR	CA-C-O	-8.46	111.93	120.82
1	B	459	LEU	N-CA-C	-8.44	101.40	113.21
1	D	302	SER	N-CA-C	-8.41	103.13	112.72
1	D	169	TRP	CA-C-O	8.38	129.33	120.36
1	B	415	GLU	CA-C-N	8.35	136.73	121.70
1	B	415	GLU	C-N-CA	8.35	136.73	121.70
1	C	358	THR	N-CA-C	-8.33	102.67	112.92
1	B	271	VAL	O-C-N	-8.32	114.33	121.57
1	D	292	PHE	CA-C-N	8.32	128.08	119.76
1	D	292	PHE	C-N-CA	8.32	128.08	119.76
1	B	290	ASN	N-CA-C	-8.29	101.17	112.03
1	A	258	ARG	N-CA-C	-8.27	102.35	111.36
1	A	433	PRO	O-C-N	-8.25	117.52	121.31
1	F	427	ALA	O-C-N	-8.25	109.81	123.00
1	B	120	HIS	CA-C-N	8.23	127.91	119.19
1	B	120	HIS	C-N-CA	8.23	127.91	119.19
1	B	235	ILE	N-CA-C	8.22	118.31	110.42
1	E	433	PRO	CA-C-N	8.20	130.09	119.84
1	E	433	PRO	C-N-CA	8.20	130.09	119.84
1	C	205	PHE	N-CA-C	-8.20	102.31	112.88
1	A	406	LEU	CA-C-N	8.18	136.42	121.70
1	A	406	LEU	C-N-CA	8.18	136.42	121.70
1	D	294	THR	CA-C-N	8.14	128.09	120.03
1	D	294	THR	C-N-CA	8.14	128.09	120.03
1	E	94	ASP	N-CA-C	-8.14	103.48	113.41
1	D	116	GLY	CA-C-O	-8.13	114.26	121.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	301	THR	N-CA-C	-8.12	96.73	109.07
1	C	54	LYS	CA-C-O	-8.10	113.32	119.32
1	C	10	THR	CA-C-N	8.06	136.22	121.70
1	C	10	THR	C-N-CA	8.06	136.22	121.70
1	A	83	PHE	CA-C-N	8.05	128.97	120.43
1	A	83	PHE	C-N-CA	8.05	128.97	120.43
1	C	244	ASP	CA-C-N	8.04	132.52	120.31
1	C	244	ASP	C-N-CA	8.04	132.52	120.31
1	E	477	LYS	CA-C-O	-8.03	113.37	120.60
1	E	271	VAL	CA-C-O	-8.00	115.78	119.94
1	E	401	ASP	CA-C-N	7.98	130.82	120.44
1	E	401	ASP	C-N-CA	7.98	130.82	120.44
1	A	303	ASP	N-CA-C	-7.96	103.14	113.17
1	F	431	HIS	O-C-N	-7.95	112.01	122.59
1	D	300	VAL	CA-C-O	-7.95	111.73	120.71
1	B	425	ALA	CA-C-N	7.94	135.98	121.70
1	B	425	ALA	C-N-CA	7.94	135.98	121.70
1	A	45	VAL	N-CA-C	-7.92	93.93	107.24
1	E	465	GLY	CA-C-N	7.91	130.73	120.44
1	E	465	GLY	C-N-CA	7.91	130.73	120.44
1	C	336	THR	N-CA-C	-7.88	103.88	113.97
1	D	350	THR	N-CA-C	-7.87	103.23	112.92
1	F	429	GLN	N-CA-C	-7.85	97.48	109.41
1	C	433	PRO	CA-C-N	7.84	127.80	120.03
1	C	433	PRO	C-N-CA	7.84	127.80	120.03
1	F	14	PRO	N-CA-C	7.83	120.25	110.70
1	A	12	TYR	CA-C-N	7.81	135.76	121.70
1	A	12	TYR	C-N-CA	7.81	135.76	121.70
1	A	181	GLN	CA-C-N	7.77	129.55	119.84
1	A	181	GLN	C-N-CA	7.77	129.55	119.84
1	B	181	GLN	CA-C-O	-7.77	112.66	120.66
1	B	10	THR	CA-C-N	7.76	135.67	121.70
1	B	10	THR	C-N-CA	7.76	135.67	121.70
1	C	397	THR	CA-C-N	7.75	130.33	120.56
1	C	397	THR	C-N-CA	7.75	130.33	120.56
1	D	395	ASN	CA-C-N	7.74	131.43	120.28
1	D	395	ASN	C-N-CA	7.74	131.43	120.28
1	D	57	ASN	CA-C-N	7.74	131.28	120.29
1	D	57	ASN	C-N-CA	7.74	131.28	120.29
1	E	201	VAL	N-CA-C	-7.72	101.63	110.05
1	F	367	GLY	CA-C-N	7.71	133.64	122.77
1	F	367	GLY	C-N-CA	7.71	133.64	122.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	55	PRO	N-CA-C	-7.71	103.86	114.80
1	F	421	VAL	O-C-N	-7.70	115.10	123.18
1	D	256	PHE	O-C-N	-7.69	111.88	122.81
1	C	21	VAL	CA-C-N	7.69	130.81	120.50
1	C	21	VAL	C-N-CA	7.69	130.81	120.50
1	E	130	GLU	N-CA-C	-7.69	102.54	112.23
1	F	384	THR	CA-C-O	-7.69	112.06	120.36
1	E	150	ASP	N-CA-C	-7.66	99.13	110.46
1	F	289	SER	N-CA-C	-7.63	101.28	110.44
1	C	341	ASN	N-CA-C	-7.60	96.51	108.90
1	F	474	LEU	N-CA-C	-7.59	95.89	108.34
1	A	108	GLY	O-C-N	-7.58	116.47	122.99
1	D	16	VAL	N-CA-C	-7.58	99.49	107.60
1	F	429	GLN	CA-C-N	7.58	135.34	121.70
1	F	429	GLN	C-N-CA	7.58	135.34	121.70
1	C	108	GLY	O-C-N	7.57	130.69	122.96
1	E	434	PRO	O-C-N	-7.54	112.46	122.64
1	B	137	ALA	N-CA-C	-7.52	103.67	114.12
1	D	173	SER	CA-C-O	-7.52	113.67	119.46
1	A	456	SER	N-CA-C	-7.51	98.38	108.74
1	E	462	PHE	CA-C-N	7.49	127.02	118.85
1	E	462	PHE	C-N-CA	7.49	127.02	118.85
1	C	107	VAL	O-C-N	-7.48	114.98	122.99
1	E	83	PHE	N-CA-C	-7.46	102.26	112.03
1	E	474	LEU	CA-C-N	7.45	135.12	121.70
1	E	474	LEU	C-N-CA	7.45	135.12	121.70
1	C	371	ASP	N-CA-C	-7.45	97.29	108.99
1	A	479	LYS	N-CA-C	-7.45	103.31	114.64
1	B	333	VAL	CA-C-O	-7.45	112.33	120.67
1	C	472	LEU	CA-C-O	7.44	128.37	120.70
1	B	454	LYS	CA-C-O	7.43	128.27	119.28
1	E	225	CYS	N-CA-C	-7.42	102.34	111.40
1	A	233	ASP	CA-C-N	7.41	130.21	120.28
1	A	233	ASP	C-N-CA	7.41	130.21	120.28
1	A	142	ASP	CA-C-O	-7.40	112.83	122.45
1	C	91	TYR	N-CA-C	-7.40	97.81	109.50
1	D	256	PHE	CA-C-N	7.39	131.74	122.43
1	D	256	PHE	C-N-CA	7.39	131.74	122.43
1	F	450	ASN	CA-C-O	-7.37	112.45	120.92
1	B	111	GLN	CA-C-N	7.36	128.35	120.11
1	B	111	GLN	C-N-CA	7.36	128.35	120.11
1	E	433	PRO	N-CA-C	7.36	119.68	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	225	CYS	N-CA-C	-7.35	103.34	111.36
1	F	273	ASP	N-CA-C	-7.35	104.34	112.72
1	D	25	ASP	CA-C-N	7.35	131.49	120.17
1	D	25	ASP	C-N-CA	7.35	131.49	120.17
1	D	414	LEU	CA-C-N	7.35	134.93	121.70
1	D	414	LEU	C-N-CA	7.35	134.93	121.70
1	F	342	MET	N-CA-C	-7.35	97.43	109.40
1	D	205	PHE	N-CA-C	-7.33	101.88	111.71
1	D	306	ILE	N-CA-C	-7.33	104.15	111.77
1	E	294	THR	N-CA-C	-7.32	99.06	109.24
1	E	185	CYS	CA-C-N	7.31	127.91	120.38
1	E	185	CYS	C-N-CA	7.31	127.91	120.38
1	C	422	THR	CA-C-N	7.31	134.86	121.70
1	C	422	THR	C-N-CA	7.31	134.86	121.70
1	E	230	LYS	N-CA-C	-7.30	98.21	109.24
1	A	39	THR	N-CA-C	-7.30	97.92	109.23
1	E	434	PRO	CA-C-N	7.30	134.84	121.70
1	E	434	PRO	C-N-CA	7.30	134.84	121.70
1	A	290	ASN	CA-C-N	7.29	131.19	120.90
1	A	290	ASN	C-N-CA	7.29	131.19	120.90
1	A	424	GLN	N-CA-C	-7.29	95.26	110.80
1	D	133	SER	N-CA-C	-7.29	104.25	113.72
1	A	13	LEU	CA-C-N	7.28	127.88	120.38
1	A	13	LEU	C-N-CA	7.28	127.88	120.38
1	E	482	LEU	O-C-N	-7.28	111.36	123.00
1	E	321	ASN	N-CA-C	-7.27	103.56	113.30
1	A	334	VAL	N-CA-C	-7.25	97.68	108.12
1	B	393	SER	CA-C-O	7.24	128.22	120.55
1	F	50	PHE	CA-C-N	7.23	127.80	119.99
1	F	50	PHE	C-N-CA	7.23	127.80	119.99
1	D	31	THR	N-CA-C	-7.22	98.33	109.52
1	F	106	GLU	N-CA-C	-7.21	97.20	109.24
1	C	410	PRO	CA-C-N	7.20	134.67	121.70
1	C	410	PRO	C-N-CA	7.20	134.67	121.70
1	B	107	VAL	CA-C-N	7.19	128.55	121.57
1	B	107	VAL	C-N-CA	7.19	128.55	121.57
1	A	141	VAL	CA-C-N	7.18	133.70	122.78
1	A	141	VAL	C-N-CA	7.18	133.70	122.78
1	D	79	ASP	CA-C-O	-7.18	113.89	120.50
1	E	82	LYS	N-CA-C	-7.18	104.08	112.92
1	D	333	VAL	N-CA-C	-7.17	97.78	108.46
1	F	427	ALA	CA-C-N	7.16	134.59	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	427	ALA	C-N-CA	7.16	134.59	121.70
1	B	77	LEU	O-C-N	-7.15	115.65	121.80
1	D	449	VAL	CA-C-O	-7.15	112.62	120.48
1	C	18	VAL	O-C-N	-7.15	115.62	123.20
1	C	132	ALA	N-CA-C	-7.14	98.79	108.86
1	E	105	VAL	N-CA-C	-7.14	97.74	108.17
1	C	322	GLY	N-CA-C	-7.14	105.20	115.27
1	E	86	PRO	N-CA-C	-7.14	104.67	114.80
1	A	91	TYR	CA-C-N	7.12	132.10	122.56
1	A	91	TYR	C-N-CA	7.12	132.10	122.56
1	A	231	TYR	N-CA-C	-7.11	97.98	109.58
1	D	481	THR	CA-C-N	7.11	134.50	121.70
1	D	481	THR	C-N-CA	7.11	134.50	121.70
1	D	32	ASN	N-CA-C	-7.11	104.49	113.02
1	E	420	PHE	CA-C-N	7.10	134.48	121.70
1	E	420	PHE	C-N-CA	7.10	134.48	121.70
1	E	461	GLN	CA-C-N	7.09	134.65	122.38
1	E	461	GLN	C-N-CA	7.09	134.65	122.38
1	B	460	ASP	N-CA-C	-7.09	104.63	113.28
1	A	20	LYS	CA-C-N	7.08	131.51	122.37
1	A	20	LYS	C-N-CA	7.08	131.51	122.37
1	A	358	THR	CA-C-N	7.07	129.76	120.28
1	A	358	THR	C-N-CA	7.07	129.76	120.28
1	A	363	TYR	N-CA-C	-7.07	97.10	108.55
1	A	232	PRO	CA-C-O	-7.06	113.29	121.34
1	A	433	PRO	CA-C-O	-7.05	115.82	120.90
1	A	220	VAL	CA-C-N	7.05	128.65	119.84
1	A	220	VAL	C-N-CA	7.05	128.65	119.84
1	D	432	THR	CA-C-N	-7.04	113.13	120.38
1	D	432	THR	C-N-CA	-7.04	113.13	120.38
1	E	79	ASP	O-C-N	-7.03	113.56	121.43
1	C	356	LYS	N-CA-C	-7.03	97.95	108.99
1	B	181	GLN	N-CA-C	-7.03	98.02	109.82
1	A	79	ASP	N-CA-C	-7.02	100.80	109.65
1	C	462	PHE	CA-C-N	7.01	126.64	119.56
1	C	462	PHE	C-N-CA	7.01	126.64	119.56
1	B	381	ILE	N-CA-C	-7.01	97.40	107.77
1	D	107	VAL	O-C-N	7.01	132.06	122.88
1	B	233	ASP	O-C-N	7.00	130.47	122.55
1	A	331	VAL	N-CA-C	-7.00	97.41	107.77
1	E	286	LEU	N-CA-C	-7.00	98.33	109.59
1	A	394	MET	N-CA-C	6.99	118.69	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	231	TYR	N-CA-C	-6.99	99.59	110.14
1	D	183	GLY	CA-C-N	6.98	133.32	121.87
1	D	183	GLY	C-N-CA	6.98	133.32	121.87
1	A	277	ILE	N-CA-C	-6.95	98.57	108.58
1	C	462	PHE	N-CA-C	-6.95	99.83	110.32
1	D	362	GLU	N-CA-C	6.94	119.79	110.35
1	A	215	ALA	N-CA-C	-6.93	104.63	113.23
1	D	231	TYR	N-CA-C	-6.93	98.31	109.40
1	B	358	THR	N-CA-C	-6.93	104.40	112.92
1	C	299	MET	N-CA-C	-6.93	99.31	110.32
1	B	270	ASN	CA-C-N	6.90	127.56	122.59
1	B	270	ASN	C-N-CA	6.90	127.56	122.59
1	A	193	THR	CA-C-N	6.90	130.01	120.49
1	A	193	THR	C-N-CA	6.90	130.01	120.49
1	D	53	LYS	N-CA-C	-6.90	99.72	110.42
1	E	181	GLN	N-CA-C	-6.89	99.22	108.11
1	E	473	GLY	N-CA-C	-6.88	105.41	111.95
1	D	413	THR	N-CA-C	-6.88	98.84	109.24
1	B	231	TYR	CA-C-O	-6.87	111.79	120.04
1	D	454	LYS	CA-C-N	6.85	130.44	120.71
1	D	454	LYS	C-N-CA	6.85	130.44	120.71
1	D	27	TYR	CA-C-O	6.85	126.06	118.52
1	B	94	ASP	N-CA-C	-6.84	103.08	113.89
1	C	359	ASN	O-C-N	6.84	131.34	122.03
1	F	459	LEU	N-CA-C	-6.84	102.83	113.02
1	A	120	HIS	CA-C-N	6.84	126.53	119.56
1	A	120	HIS	C-N-CA	6.84	126.53	119.56
1	A	92	ASN	CA-C-O	6.84	124.92	119.59
1	B	184	ASP	N-CA-C	-6.83	98.79	109.72
1	E	457	ALA	N-CA-C	-6.82	104.70	113.16
1	A	327	ASN	CA-C-O	-6.82	113.94	121.84
1	F	414	LEU	CA-C-N	6.81	133.96	121.70
1	F	414	LEU	C-N-CA	6.81	133.96	121.70
1	C	472	LEU	O-C-N	-6.79	114.75	122.09
1	A	63	PRO	CA-C-O	-6.79	113.58	121.86
1	C	481	THR	O-C-N	-6.77	115.01	123.27
1	F	376	PHE	CA-C-N	6.77	132.10	122.09
1	F	376	PHE	C-N-CA	6.77	132.10	122.09
1	A	57	ASN	CA-C-N	6.75	129.65	120.54
1	A	57	ASN	C-N-CA	6.75	129.65	120.54
1	F	398	ILE	O-C-N	-6.75	115.33	121.87
1	F	68	LEU	N-CA-C	-6.74	104.68	113.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	386	ASP	CA-C-N	6.73	129.04	120.56
1	B	386	ASP	C-N-CA	6.73	129.04	120.56
1	F	331	VAL	N-CA-C	-6.72	98.70	108.11
1	E	81	ASN	N-CA-C	-6.72	105.24	113.50
1	E	82	LYS	CA-C-N	6.72	132.09	121.08
1	E	82	LYS	C-N-CA	6.72	132.09	121.08
1	F	311	TYR	CA-C-N	6.72	131.57	122.84
1	F	311	TYR	C-N-CA	6.72	131.57	122.84
1	F	435	ALA	N-CA-C	6.69	119.14	109.84
1	E	242	TYR	N-CA-C	6.69	118.57	111.28
1	C	83	PHE	O-C-N	6.69	130.75	122.86
1	F	437	LYS	CA-C-N	6.68	132.22	123.00
1	F	437	LYS	C-N-CA	6.68	132.22	123.00
1	B	319	HIS	N-CA-C	-6.68	104.08	111.36
1	B	296	SER	CA-C-N	6.66	127.70	120.44
1	B	296	SER	C-N-CA	6.66	127.70	120.44
1	A	452	LYS	N-CA-C	-6.65	105.14	112.72
1	F	409	PRO	N-CA-C	6.65	118.82	110.70
1	E	464	LEU	CA-C-N	6.64	127.49	119.99
1	E	464	LEU	C-N-CA	6.64	127.49	119.99
1	D	398	ILE	O-C-N	6.64	128.31	121.87
1	F	61	LEU	N-CA-C	-6.64	105.06	113.43
1	D	135	TYR	CA-C-N	6.64	130.77	120.75
1	D	135	TYR	C-N-CA	6.64	130.77	120.75
1	E	317	GLN	O-C-N	6.64	130.69	122.86
1	F	322	GLY	CA-C-N	6.63	129.45	120.63
1	F	322	GLY	C-N-CA	6.63	129.45	120.63
1	B	334	VAL	N-CA-C	-6.63	98.58	108.46
1	E	431	HIS	N-CA-C	-6.62	97.47	108.34
1	C	216	ASN	CA-C-N	6.62	131.53	122.19
1	C	216	ASN	C-N-CA	6.62	131.53	122.19
1	E	225	CYS	CA-C-N	6.62	129.15	120.28
1	E	225	CYS	C-N-CA	6.62	129.15	120.28
1	D	201	VAL	CA-C-N	6.62	131.89	121.56
1	D	201	VAL	C-N-CA	6.62	131.89	121.56
1	E	261	PHE	N-CA-C	-6.61	99.29	109.14
1	E	271	VAL	CA-C-N	6.61	126.64	119.90
1	E	271	VAL	C-N-CA	6.61	126.64	119.90
1	B	368	GLU	CA-C-O	-6.60	112.15	120.20
1	D	14	PRO	CA-C-N	6.59	127.11	119.99
1	D	14	PRO	C-N-CA	6.59	127.11	119.99
1	A	385	ALA	CA-C-O	6.59	127.53	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	414	LEU	CA-C-N	6.59	133.56	121.70
1	C	414	LEU	C-N-CA	6.59	133.56	121.70
1	A	446	PHE	O-C-N	-6.58	116.11	123.48
1	D	144	ARG	O-C-N	-6.58	116.11	123.48
1	B	201	VAL	CA-C-N	6.58	134.11	121.54
1	B	201	VAL	C-N-CA	6.58	134.11	121.54
1	A	62	VAL	CA-C-O	-6.58	111.14	119.95
1	C	471	GLN	CA-C-O	6.58	127.53	120.10
1	A	170	GLY	N-CA-C	-6.57	104.90	112.79
1	A	58	ASN	CA-C-N	6.57	130.20	120.87
1	A	58	ASN	C-N-CA	6.57	130.20	120.87
1	A	319	HIS	CA-C-N	6.57	131.81	122.09
1	A	319	HIS	C-N-CA	6.57	131.81	122.09
1	E	219	GLU	CA-C-O	-6.57	113.46	120.42
1	E	422	THR	CA-C-N	6.57	133.52	121.70
1	E	422	THR	C-N-CA	6.57	133.52	121.70
1	C	10	THR	O-C-N	-6.56	114.70	123.23
1	A	432	THR	CA-C-N	6.55	124.44	119.66
1	A	432	THR	C-N-CA	6.55	124.44	119.66
1	B	401	ASP	CA-C-N	6.55	129.06	120.28
1	B	401	ASP	C-N-CA	6.55	129.06	120.28
1	C	303	ASP	N-CA-C	-6.55	105.33	113.38
1	F	447	TRP	CA-C-N	6.54	130.05	120.82
1	F	447	TRP	C-N-CA	6.54	130.05	120.82
1	A	387	VAL	O-C-N	6.54	128.56	121.83
1	A	442	LYS	CA-C-O	-6.53	114.44	121.56
1	C	322	GLY	CA-C-N	6.53	130.97	121.18
1	C	322	GLY	C-N-CA	6.53	130.97	121.18
1	C	452	LYS	N-CA-C	-6.53	104.89	112.92
1	E	257	VAL	N-CA-C	-6.52	98.23	107.75
1	A	322	GLY	N-CA-C	-6.51	106.08	115.27
1	E	303	ASP	N-CA-C	-6.51	105.07	114.12
1	B	441	LEU	O-C-N	-6.51	114.94	123.21
1	F	9	ALA	CA-C-N	6.51	133.41	121.70
1	F	9	ALA	C-N-CA	6.51	133.41	121.70
1	D	281	GLY	O-C-N	-6.50	117.48	122.88
1	B	129	THR	CA-C-N	6.49	129.50	120.29
1	B	129	THR	C-N-CA	6.49	129.50	120.29
1	D	139	ALA	N-CA-C	-6.49	96.98	110.80
1	F	426	ILE	O-C-N	-6.49	114.46	122.57
1	B	320	ASN	CA-C-O	-6.48	113.90	120.96
1	A	427	ALA	CA-C-N	6.48	133.36	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	427	ALA	C-N-CA	6.48	133.36	121.70
1	A	101	ALA	CA-C-N	-6.48	113.06	122.19
1	A	101	ALA	C-N-CA	-6.48	113.06	122.19
1	E	351	SER	CA-C-O	6.47	125.87	119.08
1	D	459	LEU	N-CA-C	-6.47	104.59	114.16
1	A	262	ASN	CA-C-O	-6.46	113.86	120.71
1	F	352	GLU	N-CA-C	-6.46	97.70	108.75
1	F	33	ILE	CA-C-N	6.45	133.18	122.73
1	F	33	ILE	C-N-CA	6.45	133.18	122.73
1	B	220	VAL	O-C-N	6.45	127.31	121.57
1	A	72	VAL	N-CA-C	-6.45	98.33	107.75
1	A	298	SER	O-C-N	6.45	130.20	122.85
1	D	479	LYS	O-C-N	-6.45	114.02	122.59
1	A	257	VAL	CA-C-N	6.44	129.44	120.29
1	A	257	VAL	C-N-CA	6.44	129.44	120.29
1	B	387	VAL	CA-C-N	6.44	128.91	120.28
1	B	387	VAL	C-N-CA	6.44	128.91	120.28
1	C	53	LYS	N-CA-C	-6.43	99.69	109.85
1	B	422	THR	CA-C-N	6.43	133.27	121.70
1	B	422	THR	C-N-CA	6.43	133.27	121.70
1	D	284	ALA	N-CA-C	-6.42	105.02	112.92
1	A	431	HIS	O-C-N	-6.42	114.05	122.59
1	C	83	PHE	CA-C-N	6.42	126.19	120.10
1	C	83	PHE	C-N-CA	6.42	126.19	120.10
1	F	480	PHE	CA-C-N	6.42	133.25	121.70
1	F	480	PHE	C-N-CA	6.42	133.25	121.70
1	D	375	ILE	N-CA-C	-6.41	99.49	108.27
1	E	83	PHE	O-C-N	6.41	128.90	122.30
1	C	279	GLY	O-C-N	-6.41	115.16	122.85
1	F	242	TYR	N-CA-C	-6.40	105.10	114.39
1	E	35	TYR	N-CA-C	-6.40	99.57	109.24
1	E	23	SER	CA-C-O	-6.40	114.58	121.56
1	C	422	THR	CA-C-O	-6.39	114.11	120.70
1	D	261	PHE	N-CA-C	-6.38	99.63	109.14
1	D	150	ASP	N-CA-C	-6.38	101.07	110.52
1	C	56	ASN	N-CA-C	-6.38	103.84	111.69
1	B	341	ASN	N-CA-C	-6.38	98.80	109.07
1	C	469	LEU	N-CA-C	-6.38	104.41	111.36
1	A	141	VAL	N-CA-C	-6.36	98.49	108.86
1	C	424	GLN	N-CA-C	6.36	120.17	111.39
1	C	281	GLY	CA-C-N	6.36	129.32	120.29
1	C	281	GLY	C-N-CA	6.36	129.32	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	162	LYS	CA-C-N	6.35	126.92	120.38
1	F	162	LYS	C-N-CA	6.35	126.92	120.38
1	A	315	ARG	N-CA-C	-6.34	99.67	109.24
1	C	194	VAL	CA-C-N	6.34	129.60	120.98
1	C	194	VAL	C-N-CA	6.34	129.60	120.98
1	C	424	GLN	CA-C-N	6.34	133.11	121.70
1	C	424	GLN	C-N-CA	6.34	133.11	121.70
1	D	82	LYS	N-CA-C	-6.34	105.41	113.02
1	F	12	TYR	CA-C-N	6.34	133.11	121.70
1	F	12	TYR	C-N-CA	6.34	133.11	121.70
1	D	218	SER	CA-C-N	6.33	128.77	120.28
1	D	218	SER	C-N-CA	6.33	128.77	120.28
1	C	478	PRO	CA-C-N	6.33	133.10	121.70
1	C	478	PRO	C-N-CA	6.33	133.10	121.70
1	C	172	GLY	CA-C-N	6.33	137.24	121.80
1	C	172	GLY	C-N-CA	6.33	137.24	121.80
1	B	219	GLU	N-CA-C	-6.33	103.91	111.69
1	B	177	GLN	CA-C-N	6.32	131.79	123.06
1	B	177	GLN	C-N-CA	6.32	131.79	123.06
1	A	454	LYS	N-CA-C	-6.32	105.20	113.17
1	C	109	ARG	N-CA-C	-6.32	103.75	112.03
1	F	66	SER	N-CA-C	-6.32	100.02	108.74
1	F	315	ARG	N-CA-C	-6.32	97.34	110.80
1	B	414	LEU	CA-C-N	6.31	133.06	121.70
1	B	414	LEU	C-N-CA	6.31	133.06	121.70
1	C	68	LEU	N-CA-C	-6.31	105.53	112.72
1	E	78	PRO	CA-C-O	-6.30	114.38	122.13
1	E	460	ASP	N-CA-C	-6.30	106.22	114.04
1	E	133	SER	N-CA-C	-6.30	105.75	113.50
1	A	365	ARG	N-CA-C	-6.30	99.83	109.41
1	E	189	GLU	O-C-N	-6.29	115.95	123.31
1	D	34	TYR	N-CA-C	-6.29	97.56	108.69
1	A	277	ILE	CA-C-N	6.29	129.76	120.90
1	A	277	ILE	C-N-CA	6.29	129.76	120.90
1	F	359	ASN	O-C-N	-6.29	114.23	122.59
1	A	481	THR	CA-C-N	6.27	132.99	121.70
1	A	481	THR	C-N-CA	6.27	132.99	121.70
1	E	404	PHE	CA-C-O	6.27	125.80	118.90
1	F	40	SER	N-CA-C	-6.27	105.57	113.72
1	E	159	ILE	N-CA-C	-6.26	99.10	108.12
1	C	443	LYS	CA-C-O	6.26	125.41	118.52
1	B	135	TYR	N-CA-C	-6.25	104.36	112.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	483	GLY	CA-C-N	6.25	132.95	121.70
1	A	483	GLY	C-N-CA	6.25	132.95	121.70
1	F	353	THR	CA-C-N	6.25	131.00	122.19
1	F	353	THR	C-N-CA	6.25	131.00	122.19
1	A	29	ALA	N-CA-C	-6.25	98.34	108.52
1	E	55	PRO	N-CA-C	-6.24	106.69	114.68
1	C	349	SER	N-CA-C	-6.24	99.58	109.07
1	B	311	TYR	CA-C-O	6.24	127.03	120.36
1	E	18	VAL	CA-C-N	6.24	132.93	121.70
1	E	18	VAL	C-N-CA	6.24	132.93	121.70
1	D	431	HIS	CA-C-O	-6.23	112.62	120.28
1	C	83	PHE	CA-C-O	-6.23	114.77	121.56
1	C	361	LYS	CA-C-N	6.22	130.15	120.75
1	C	361	LYS	C-N-CA	6.22	130.15	120.75
1	F	441	LEU	N-CA-C	-6.21	104.18	112.94
1	F	336	THR	CA-C-N	6.19	128.57	120.28
1	F	336	THR	C-N-CA	6.19	128.57	120.28
1	B	271	VAL	CA-C-N	6.18	126.51	119.83
1	B	271	VAL	C-N-CA	6.18	126.51	119.83
1	D	345	CYS	O-C-N	6.17	130.02	123.42
1	B	271	VAL	CA-C-O	-6.17	115.51	119.15
1	E	68	LEU	N-CA-C	-6.17	105.60	112.57
1	D	303	ASP	CA-C-N	6.16	131.23	122.72
1	D	303	ASP	C-N-CA	6.16	131.23	122.72
1	B	441	LEU	CA-C-N	6.16	132.78	121.70
1	B	441	LEU	C-N-CA	6.16	132.78	121.70
1	E	421	VAL	CA-C-N	6.16	131.16	121.56
1	E	421	VAL	C-N-CA	6.16	131.16	121.56
1	A	349	SER	N-CA-C	-6.15	99.62	108.60
1	F	105	VAL	N-CA-C	-6.15	99.19	108.17
1	E	218	SER	CA-C-O	6.15	125.28	118.52
1	A	168	HIS	N-CA-C	-6.15	99.39	108.79
1	D	275	LEU	O-C-N	6.15	129.68	122.24
1	C	15	PRO	CA-C-N	6.14	132.75	121.70
1	C	15	PRO	C-N-CA	6.14	132.75	121.70
1	F	370	TYR	N-CA-C	-6.14	99.35	108.99
1	A	425	ALA	CA-C-N	6.13	132.74	121.70
1	A	425	ALA	C-N-CA	6.13	132.74	121.70
1	B	481	THR	N-CA-C	-6.13	97.74	110.80
1	D	317	GLN	CA-C-O	-6.13	114.89	121.94
1	A	421	VAL	CA-C-N	6.13	132.73	121.70
1	A	421	VAL	C-N-CA	6.13	132.73	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	392	HIS	CA-C-N	6.13	128.41	120.44
1	E	392	HIS	C-N-CA	6.13	128.41	120.44
1	D	97	ARG	N-CA-C	-6.12	99.74	109.23
1	A	10	THR	CA-C-N	6.11	132.69	121.70
1	A	10	THR	C-N-CA	6.11	132.69	121.70
1	A	265	GLY	CA-C-N	6.10	129.37	120.71
1	A	265	GLY	C-N-CA	6.10	129.37	120.71
1	A	27	TYR	N-CA-C	-6.09	105.14	114.16
1	C	128	ASP	CA-C-O	-6.09	114.05	121.36
1	A	45	VAL	O-C-N	-6.09	117.13	123.03
1	F	360	PHE	N-CA-C	6.08	118.20	108.41
1	A	364	LEU	N-CA-C	-6.08	100.72	110.14
1	E	432	THR	N-CA-C	-6.06	102.43	110.07
1	C	418	TYR	CA-C-O	-6.06	110.49	120.80
1	E	461	GLN	N-CA-C	-6.06	101.16	109.71
1	D	117	ILE	CA-C-O	-6.06	115.27	120.96
1	D	35	TYR	N-CA-C	-6.05	100.03	109.72
1	D	290	ASN	CA-C-N	6.05	129.31	120.71
1	D	290	ASN	C-N-CA	6.05	129.31	120.71
1	B	240	GLU	O-C-N	6.05	126.45	121.31
1	B	407	GLN	CA-C-N	6.05	126.61	120.38
1	B	407	GLN	C-N-CA	6.05	126.61	120.38
1	B	68	LEU	CA-C-O	6.05	126.64	119.56
1	A	166	GLY	N-CA-C	-6.04	101.02	112.51
1	A	306	ILE	O-C-N	6.04	127.53	122.09
1	B	311	TYR	N-CA-C	-6.04	98.89	108.73
1	C	425	ALA	CA-C-N	6.04	132.57	121.70
1	C	425	ALA	C-N-CA	6.04	132.57	121.70
1	D	17	PRO	CA-C-N	6.03	132.56	121.70
1	D	17	PRO	C-N-CA	6.03	132.56	121.70
1	B	468	PHE	CA-C-N	6.03	128.85	120.29
1	B	468	PHE	C-N-CA	6.03	128.85	120.29
1	C	296	SER	CA-C-N	6.03	133.22	121.41
1	C	296	SER	C-N-CA	6.03	133.22	121.41
1	F	37	ALA	CA-C-O	-6.03	115.00	121.45
1	F	115	VAL	CA-C-N	6.03	125.83	120.10
1	F	115	VAL	C-N-CA	6.03	125.83	120.10
1	A	440	PRO	N-CA-C	-6.02	100.06	112.47
1	B	234	TYR	CA-C-N	6.02	128.15	120.56
1	B	234	TYR	C-N-CA	6.02	128.15	120.56
1	B	133	SER	N-CA-C	-6.02	97.99	110.80
1	C	241	PRO	CA-C-O	-6.01	109.66	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	289	SER	CA-C-N	6.01	130.26	120.23
1	E	289	SER	C-N-CA	6.01	130.26	120.23
1	F	341	ASN	N-CA-C	-6.01	99.20	109.24
1	A	244	ASP	CA-C-N	6.01	128.33	120.28
1	A	244	ASP	C-N-CA	6.01	128.33	120.28
1	E	253	GLU	CA-C-O	-6.01	114.26	120.99
1	F	121	PRO	N-CA-C	-6.00	105.84	114.18
1	F	111	GLN	N-CA-C	-6.00	102.82	108.22
1	D	136	ALA	CA-C-N	6.00	129.39	120.87
1	D	136	ALA	C-N-CA	6.00	129.39	120.87
1	C	427	ALA	CA-C-N	5.99	131.09	122.40
1	C	427	ALA	C-N-CA	5.99	131.09	122.40
1	D	175	CYS	O-C-N	-5.99	116.35	123.06
1	B	216	ASN	N-CA-C	-5.99	104.33	111.69
1	B	399	LEU	CA-C-N	5.99	128.79	120.29
1	B	399	LEU	C-N-CA	5.99	128.79	120.29
1	E	416	ASP	N-CA-C	-5.98	100.49	108.74
1	B	333	VAL	O-C-N	5.98	129.50	123.10
1	E	221	PRO	N-CA-C	5.98	120.62	111.11
1	C	231	TYR	CA-C-N	5.98	125.92	119.76
1	C	231	TYR	C-N-CA	5.98	125.92	119.76
1	E	229	CYS	N-CA-C	-5.98	100.55	110.17
1	E	175	CYS	CA-C-N	5.97	128.57	120.44
1	E	175	CYS	C-N-CA	5.97	128.57	120.44
1	F	479	LYS	CA-C-N	5.97	132.45	121.70
1	F	479	LYS	C-N-CA	5.97	132.45	121.70
1	B	86	PRO	N-CA-C	-5.97	107.04	114.68
1	A	34	TYR	N-CA-C	-5.97	100.07	109.50
1	E	307	PHE	CA-C-O	-5.97	114.68	121.72
1	F	244	ASP	CA-C-N	5.97	128.27	120.28
1	F	244	ASP	C-N-CA	5.97	128.27	120.28
1	C	14	PRO	N-CA-C	5.96	117.98	110.70
1	A	427	ALA	O-C-N	-5.96	114.66	122.59
1	B	183	GLY	N-CA-C	-5.96	107.03	115.43
1	B	228	ILE	N-CA-C	-5.96	99.83	108.71
1	B	267	VAL	CA-C-O	5.96	127.91	121.36
1	B	462	PHE	CA-C-N	5.96	125.66	119.05
1	B	462	PHE	C-N-CA	5.96	125.66	119.05
1	C	252	ARG	N-CA-C	-5.96	98.15	108.69
1	A	239	SER	CA-C-N	5.95	128.67	120.39
1	A	239	SER	C-N-CA	5.95	128.67	120.39
1	C	45	VAL	O-C-N	-5.95	117.26	123.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	356	LYS	N-CA-C	-5.94	99.66	108.99
1	F	274	ASP	N-CA-C	-5.94	104.56	112.94
1	E	121	PRO	N-CA-C	5.94	121.67	113.65
1	E	262	ASN	N-CA-C	-5.94	99.32	109.24
1	A	216	ASN	N-CA-C	-5.93	104.74	111.14
1	C	265	GLY	O-C-N	5.93	130.41	122.70
1	C	104	GLY	O-C-N	-5.92	118.77	123.27
1	C	398	ILE	CA-C-N	5.92	128.80	120.28
1	C	398	ILE	C-N-CA	5.92	128.80	120.28
1	E	290	ASN	N-CA-C	-5.92	103.47	112.99
1	E	45	VAL	N-CA-C	-5.91	97.31	107.24
1	A	469	LEU	CA-C-N	5.91	128.12	120.44
1	A	469	LEU	C-N-CA	5.91	128.12	120.44
1	D	434	PRO	O-C-N	5.91	130.62	122.64
1	A	435	ALA	CA-C-N	5.90	126.09	120.31
1	A	435	ALA	C-N-CA	5.90	126.09	120.31
1	F	15	PRO	CA-C-N	5.90	132.32	121.70
1	F	15	PRO	C-N-CA	5.90	132.32	121.70
1	F	198	GLY	CA-C-O	-5.90	112.67	119.10
1	E	233	ASP	CA-C-N	5.89	128.17	120.28
1	E	233	ASP	C-N-CA	5.89	128.17	120.28
1	A	387	VAL	CA-C-N	5.88	128.17	120.28
1	A	387	VAL	C-N-CA	5.88	128.17	120.28
1	C	301	THR	N-CA-C	-5.88	100.62	108.74
1	C	275	LEU	O-C-N	5.88	128.85	122.15
1	D	452	LYS	N-CA-C	-5.88	104.98	113.21
1	B	120	HIS	CA-C-O	-5.87	114.38	119.72
1	E	429	GLN	CA-C-N	5.87	130.16	120.94
1	E	429	GLN	C-N-CA	5.87	130.16	120.94
1	F	392	HIS	N-CA-C	5.87	117.68	111.28
1	B	379	CYS	CA-C-O	-5.86	114.94	121.51
1	D	413	THR	CA-C-N	5.86	132.25	121.70
1	D	413	THR	C-N-CA	5.86	132.25	121.70
1	C	385	ALA	CA-C-N	5.86	129.21	120.31
1	C	385	ALA	C-N-CA	5.86	129.21	120.31
1	E	453	GLU	N-CA-C	-5.85	103.87	111.71
1	D	235	ILE	O-C-N	-5.85	116.19	121.87
1	C	96	GLN	O-C-N	5.85	129.68	123.42
1	A	221	PRO	CA-C-N	5.85	128.12	120.28
1	A	221	PRO	C-N-CA	5.85	128.12	120.28
1	C	59	LYS	CA-C-N	5.84	128.47	120.35
1	C	59	LYS	C-N-CA	5.84	128.47	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	265	GLY	N-CA-C	-5.84	104.07	111.72
1	F	384	THR	CA-C-N	5.84	128.10	120.28
1	F	384	THR	C-N-CA	5.84	128.10	120.28
1	C	12	TYR	CA-C-N	5.84	132.21	121.70
1	C	12	TYR	C-N-CA	5.84	132.21	121.70
1	A	136	ALA	N-CA-C	-5.84	99.54	108.76
1	A	465	GLY	CA-C-N	5.83	128.10	120.28
1	A	465	GLY	C-N-CA	5.83	128.10	120.28
1	F	16	VAL	O-C-N	-5.83	113.67	123.00
1	B	169	TRP	CA-C-N	5.83	128.71	121.83
1	B	169	TRP	C-N-CA	5.83	128.71	121.83
1	F	246	LEU	O-C-N	-5.83	116.40	123.10
1	D	329	LEU	N-CA-C	-5.82	98.39	108.69
1	B	231	TYR	N-CA-C	-5.82	101.36	110.14
1	C	57	ASN	N-CA-C	-5.81	98.42	110.80
1	C	469	LEU	CA-C-N	5.81	128.87	120.79
1	C	469	LEU	C-N-CA	5.81	128.87	120.79
1	C	419	ARG	CA-C-N	5.81	132.16	121.70
1	C	419	ARG	C-N-CA	5.81	132.16	121.70
1	C	131	ASN	N-CA-C	-5.81	99.19	109.06
1	D	417	THR	CA-C-N	5.81	132.15	121.70
1	D	417	THR	C-N-CA	5.81	132.15	121.70
1	C	326	GLY	O-C-N	-5.81	116.29	122.56
1	A	97	ARG	N-CA-C	-5.80	100.50	109.14
1	E	107	VAL	CA-C-N	5.80	126.22	120.31
1	E	107	VAL	C-N-CA	5.80	126.22	120.31
1	B	410	PRO	CA-C-N	5.78	132.10	121.70
1	B	410	PRO	C-N-CA	5.78	132.10	121.70
1	A	248	PHE	N-CA-C	-5.78	98.87	108.75
1	C	241	PRO	O-C-N	5.78	130.44	122.64
1	D	336	THR	N-CA-C	-5.77	105.56	113.30
1	D	231	TYR	O-C-N	-5.77	116.26	121.39
1	E	210	PHE	N-CA-C	-5.76	104.79	113.89
1	C	278	LYS	CA-C-O	-5.76	114.86	121.19
1	B	170	GLY	N-CA-C	-5.74	103.82	112.60
1	B	180	VAL	N-CA-C	-5.74	99.80	108.17
1	F	102	CYS	CA-C-N	5.74	130.69	122.72
1	F	102	CYS	C-N-CA	5.74	130.69	122.72
1	C	273	ASP	N-CA-C	-5.73	105.62	113.30
1	F	474	LEU	O-C-N	-5.73	116.56	123.27
1	F	108	GLY	N-CA-C	-5.72	102.65	111.64
1	D	102	CYS	CA-C-N	5.72	130.39	121.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	102	CYS	C-N-CA	5.72	130.39	121.35
1	B	59	LYS	CA-C-N	5.72	128.38	120.49
1	B	59	LYS	C-N-CA	5.72	128.38	120.49
1	E	53	LYS	O-C-N	-5.72	115.02	122.97
1	D	271	VAL	O-C-N	-5.72	113.74	120.66
1	A	144	ARG	N-CA-C	-5.71	100.66	109.52
1	D	16	VAL	CA-C-O	-5.71	113.67	119.89
1	F	478	PRO	CA-C-O	-5.71	114.70	121.67
1	D	427	ALA	CA-C-N	5.71	131.98	121.70
1	D	427	ALA	C-N-CA	5.71	131.98	121.70
1	D	263	ARG	CA-C-O	5.71	126.99	120.54
1	F	178	VAL	CA-C-N	5.70	130.85	121.39
1	F	178	VAL	C-N-CA	5.70	130.85	121.39
1	E	50	PHE	N-CA-C	-5.68	103.11	108.22
1	C	412	GLY	CA-C-N	5.68	131.93	121.70
1	C	412	GLY	C-N-CA	5.68	131.93	121.70
1	E	410	PRO	CA-C-N	5.68	131.92	121.70
1	E	410	PRO	C-N-CA	5.68	131.92	121.70
1	F	9	ALA	CA-C-O	-5.68	111.15	120.80
1	E	322	GLY	N-CA-C	-5.67	106.70	116.01
1	E	422	THR	O-C-N	-5.67	116.75	123.11
1	E	241	PRO	CA-C-N	5.67	127.88	120.28
1	E	241	PRO	C-N-CA	5.67	127.88	120.28
1	D	280	SER	N-CA-C	-5.67	99.80	108.76
1	F	482	LEU	CA-C-O	-5.67	114.59	121.05
1	C	355	TYR	CA-C-N	5.66	131.87	121.85
1	C	355	TYR	C-N-CA	5.66	131.87	121.85
1	E	141	VAL	N-CA-C	-5.66	100.03	108.46
1	C	217	LYS	O-C-N	5.66	130.00	122.41
1	A	201	VAL	CA-C-N	5.66	132.35	121.54
1	A	201	VAL	C-N-CA	5.66	132.35	121.54
1	C	302	SER	N-CA-C	-5.65	106.39	113.28
1	B	128	ASP	O-C-N	5.65	129.66	123.22
1	D	92	ASN	N-CA-C	-5.65	94.17	108.40
1	F	423	SER	CA-C-N	5.64	129.60	121.98
1	F	423	SER	C-N-CA	5.64	129.60	121.98
1	C	104	GLY	CA-C-O	5.64	126.14	121.06
1	A	277	ILE	O-C-N	-5.64	116.52	122.95
1	B	206	GLY	CA-C-O	-5.63	117.39	122.57
1	D	210	PHE	N-CA-C	-5.63	104.62	113.02
1	D	320	ASN	O-C-N	-5.63	115.94	122.87
1	A	159	ILE	N-CA-C	-5.62	100.03	108.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	221	PRO	N-CA-C	5.62	120.05	111.11
1	E	213	LEU	N-CA-C	-5.61	105.17	111.28
1	F	415	GLU	CA-C-N	5.61	131.80	121.70
1	F	415	GLU	C-N-CA	5.61	131.80	121.70
1	C	384	THR	O-C-N	-5.61	116.65	123.10
1	F	142	ASP	CA-C-O	-5.61	114.71	120.54
1	A	10	THR	O-C-N	5.61	127.84	122.07
1	B	88	THR	N-CA-C	-5.60	105.13	112.41
1	B	126	LEU	CA-C-O	5.60	128.52	120.51
1	A	120	HIS	CA-C-O	-5.60	114.62	119.72
1	C	282	SER	CA-C-N	5.60	131.94	122.65
1	C	282	SER	C-N-CA	5.60	131.94	122.65
1	E	419	ARG	O-C-N	-5.59	114.75	122.30
1	D	162	LYS	N-CA-C	-5.59	99.83	108.55
1	A	71	ARG	CA-C-O	-5.59	114.48	120.46
1	A	29	ALA	CA-C-O	5.58	126.46	120.32
1	F	175	CYS	N-CA-C	-5.58	102.20	110.46
1	A	258	ARG	CA-C-O	-5.58	114.50	120.42
1	E	294	THR	CA-C-N	5.58	126.06	120.14
1	E	294	THR	C-N-CA	5.58	126.06	120.14
1	D	345	CYS	CA-C-O	-5.57	115.27	121.23
1	E	134	ALA	CA-C-N	5.57	130.85	123.00
1	E	134	ALA	C-N-CA	5.57	130.85	123.00
1	B	295	PRO	CA-C-O	-5.56	115.12	121.96
1	E	236	LYS	CA-C-N	5.56	128.77	120.31
1	E	236	LYS	C-N-CA	5.56	128.77	120.31
1	B	402	TRP	N-CA-C	-5.56	105.22	111.28
1	E	106	GLU	N-CA-C	-5.56	100.33	109.40
1	B	316	ALA	CA-C-O	-5.56	115.28	121.51
1	B	404	PHE	CA-C-O	-5.56	114.03	120.31
1	A	18	VAL	N-CA-C	5.56	115.69	110.30
1	B	483	GLY	CA-C-O	-5.56	114.83	121.83
1	E	444	TYR	CA-C-O	-5.55	115.29	121.23
1	D	426	ILE	CA-C-N	5.55	131.70	121.70
1	D	426	ILE	C-N-CA	5.55	131.70	121.70
1	C	276	TYR	CA-C-N	5.55	129.31	122.37
1	C	276	TYR	C-N-CA	5.55	129.31	122.37
1	C	368	GLU	N-CA-C	-5.55	99.24	108.34
1	E	307	PHE	CA-C-N	5.55	132.14	121.54
1	E	307	PHE	C-N-CA	5.55	132.14	121.54
1	F	75	ILE	N-CA-C	-5.55	100.59	108.58
1	F	456	SER	N-CA-C	-5.55	99.62	109.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	428	CYS	CA-C-N	5.55	131.69	121.70
1	B	428	CYS	C-N-CA	5.55	131.69	121.70
1	C	292	PHE	CA-C-O	-5.54	114.57	120.28
1	B	261	PHE	O-C-N	5.54	129.56	123.25
1	F	337	THR	CA-C-N	-5.54	115.18	122.99
1	F	337	THR	C-N-CA	-5.54	115.18	122.99
1	A	441	LEU	N-CA-C	-5.54	105.51	114.09
1	E	14	PRO	CA-C-N	-5.54	112.92	119.84
1	E	14	PRO	C-N-CA	-5.54	112.92	119.84
1	B	32	ASN	CA-C-N	5.53	129.29	122.37
1	B	32	ASN	C-N-CA	5.53	129.29	122.37
1	B	260	LEU	CA-C-N	5.53	131.32	121.75
1	B	260	LEU	C-N-CA	5.53	131.32	121.75
1	A	225	CYS	N-CA-C	-5.53	106.53	113.28
1	A	411	GLY	CA-C-N	5.53	131.65	121.70
1	A	411	GLY	C-N-CA	5.53	131.65	121.70
1	D	182	PRO	O-C-N	-5.53	115.87	122.89
1	B	221	PRO	CA-C-N	5.53	127.69	120.28
1	B	221	PRO	C-N-CA	5.53	127.69	120.28
1	B	151	TYR	CA-C-N	5.52	132.09	121.54
1	B	151	TYR	C-N-CA	5.52	132.09	121.54
1	D	239	SER	CA-C-N	5.52	128.72	120.83
1	D	239	SER	C-N-CA	5.52	128.72	120.83
1	A	105	VAL	N-CA-C	-5.52	100.28	108.45
1	D	433	PRO	CA-C-N	-5.52	112.94	119.84
1	D	433	PRO	C-N-CA	-5.52	112.94	119.84
1	D	132	ALA	O-C-N	-5.52	117.10	123.33
1	E	260	LEU	N-CA-C	-5.52	101.55	110.32
1	F	181	GLN	N-CA-C	-5.52	103.25	108.22
1	D	315	ARG	O-C-N	-5.51	115.45	122.78
1	C	307	PHE	CA-C-O	-5.51	115.44	121.89
1	D	10	THR	CA-C-N	5.51	131.62	121.70
1	D	10	THR	C-N-CA	5.51	131.62	121.70
1	D	181	GLN	N-CA-C	-5.50	103.27	108.22
1	B	216	ASN	O-C-N	5.50	129.38	122.23
1	E	185	CYS	CA-C-O	-5.50	114.58	119.75
1	C	354	THR	CA-C-O	-5.50	114.59	120.42
1	B	268	GLY	CA-C-N	5.49	132.03	121.54
1	B	268	GLY	C-N-CA	5.49	132.03	121.54
1	E	194	VAL	CA-C-O	-5.49	115.36	121.23
1	B	92	ASN	CA-C-O	-5.49	114.72	120.70
1	B	139	ALA	N-CA-C	-5.49	105.53	113.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	413	THR	CA-C-N	5.49	132.02	121.54
1	B	413	THR	C-N-CA	5.49	132.02	121.54
1	A	309	LYS	CA-C-N	5.49	125.25	119.76
1	A	309	LYS	C-N-CA	5.49	125.25	119.76
1	C	54	LYS	CA-C-N	5.48	125.10	119.56
1	C	54	LYS	C-N-CA	5.48	125.10	119.56
1	E	181	GLN	CA-C-N	5.48	125.42	119.78
1	E	181	GLN	C-N-CA	5.48	125.42	119.78
1	B	289	SER	CA-C-N	5.47	130.06	121.08
1	B	289	SER	C-N-CA	5.47	130.06	121.08
1	F	310	PRO	O-C-N	5.47	129.67	123.10
1	C	442	LYS	N-CA-C	-5.47	99.81	108.73
1	E	369	GLU	O-C-N	5.47	129.94	123.27
1	E	419	ARG	CA-C-N	5.46	131.54	121.70
1	E	419	ARG	C-N-CA	5.46	131.54	121.70
1	C	167	GLU	CA-C-O	5.46	127.34	121.16
1	D	466	ARG	CA-C-N	5.46	128.61	120.31
1	D	466	ARG	C-N-CA	5.46	128.61	120.31
1	F	424	GLN	CA-C-O	-5.46	116.22	119.55
1	A	415	GLU	N-CA-C	-5.46	105.27	113.89
1	D	473	GLY	CA-C-N	5.46	131.97	121.54
1	D	473	GLY	C-N-CA	5.46	131.97	121.54
1	F	371	ASP	N-CA-C	-5.46	99.78	109.06
1	A	88	THR	CA-C-O	-5.46	113.57	120.28
1	E	340	THR	CA-C-N	5.46	130.68	122.99
1	E	340	THR	C-N-CA	5.46	130.68	122.99
1	C	392	HIS	CA-C-N	5.46	127.59	120.28
1	C	392	HIS	C-N-CA	5.46	127.59	120.28
1	C	273	ASP	CA-C-N	5.46	129.83	120.72
1	C	273	ASP	C-N-CA	5.46	129.83	120.72
1	B	298	SER	CA-C-O	5.45	128.75	121.78
1	D	461	GLN	CA-C-O	5.45	125.87	119.06
1	B	466	ARG	CA-C-N	5.45	128.03	120.29
1	B	466	ARG	C-N-CA	5.45	128.03	120.29
1	D	480	PHE	CA-C-N	5.45	131.50	121.70
1	D	480	PHE	C-N-CA	5.45	131.50	121.70
1	A	464	LEU	CA-C-N	5.45	132.08	121.41
1	A	464	LEU	C-N-CA	5.45	132.08	121.41
1	E	431	HIS	O-C-N	-5.44	116.90	123.27
1	F	401	ASP	CA-C-N	5.44	127.57	120.28
1	F	401	ASP	C-N-CA	5.44	127.57	120.28
1	E	181	GLN	CA-C-O	-5.44	114.48	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	195	ILE	N-CA-C	-5.44	101.71	108.89
1	A	471	GLN	CA-C-O	5.44	126.50	120.63
1	E	407	GLN	CA-C-N	5.44	125.98	120.38
1	E	407	GLN	C-N-CA	5.44	125.98	120.38
1	D	295	PRO	CA-C-O	-5.44	115.12	122.08
1	C	65	VAL	N-CA-C	-5.44	100.23	108.17
1	D	157	CYS	N-CA-C	-5.44	100.45	108.99
1	E	196	GLN	CA-C-N	5.43	129.06	121.02
1	E	196	GLN	C-N-CA	5.43	129.06	121.02
1	E	314	GLN	CA-C-N	5.43	130.67	122.68
1	E	314	GLN	C-N-CA	5.43	130.67	122.68
1	A	357	ASN	N-CA-C	-5.43	105.39	112.23
1	B	34	TYR	CA-C-N	5.43	131.93	122.81
1	B	34	TYR	C-N-CA	5.43	131.93	122.81
1	D	65	VAL	N-CA-C	-5.43	97.79	107.18
1	A	130	GLU	N-CA-C	5.42	117.19	111.28
1	E	125	LYS	CA-C-O	-5.42	114.92	120.99
1	D	173	SER	N-CA-C	-5.42	101.40	109.42
1	E	342	MET	N-CA-C	-5.41	100.58	109.40
1	D	130	GLU	N-CA-C	-5.41	105.46	111.36
1	F	319	HIS	CA-C-N	5.41	133.03	121.45
1	F	319	HIS	C-N-CA	5.41	133.03	121.45
1	A	56	ASN	N-CA-C	-5.41	105.71	114.09
1	A	389	THR	CA-C-N	5.40	127.96	120.29
1	A	389	THR	C-N-CA	5.40	127.96	120.29
1	F	456	SER	CA-C-N	5.40	127.96	120.29
1	F	456	SER	C-N-CA	5.40	127.96	120.29
1	B	338	ARG	N-CA-C	-5.40	104.96	112.30
1	C	82	LYS	CA-C-N	5.40	129.41	120.94
1	C	82	LYS	C-N-CA	5.40	129.41	120.94
1	C	471	GLN	O-C-N	-5.40	115.91	122.22
1	B	272	PRO	CA-C-O	-5.39	115.46	121.23
1	C	176	THR	N-CA-C	-5.39	106.55	113.02
1	C	211	THR	N-CA-C	-5.39	106.20	112.89
1	E	13	LEU	CA-C-N	5.39	125.93	120.38
1	E	13	LEU	C-N-CA	5.39	125.93	120.38
1	C	16	VAL	CA-C-N	5.38	126.57	119.84
1	C	16	VAL	C-N-CA	5.38	126.57	119.84
1	B	68	LEU	O-C-N	-5.38	115.89	122.34
1	D	344	LEU	N-CA-C	-5.38	100.30	107.88
1	B	274	ASP	N-CA-C	-5.38	105.69	113.21
1	B	143	ASN	N-CA-C	-5.37	99.36	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	85	PHE	N-CA-C	-5.37	97.94	109.81
1	B	234	TYR	CA-C-O	5.37	126.24	120.55
1	E	69	GLN	N-CA-C	-5.37	100.27	109.24
1	E	357	ASN	N-CA-C	-5.37	106.23	112.89
1	F	455	PHE	N-CA-C	-5.37	99.57	108.75
1	F	421	VAL	CA-C-N	5.37	131.36	121.70
1	F	421	VAL	C-N-CA	5.37	131.36	121.70
1	F	132	ALA	N-CA-C	-5.36	104.16	111.56
1	B	154	THR	CA-C-N	5.36	130.33	122.77
1	B	154	THR	C-N-CA	5.36	130.33	122.77
1	A	399	LEU	CA-C-N	5.36	128.46	120.31
1	A	399	LEU	C-N-CA	5.36	128.46	120.31
1	C	252	ARG	O-C-N	-5.36	116.82	123.36
1	A	25	ASP	N-CA-C	-5.36	99.36	108.26
1	E	91	TYR	O-C-N	5.35	130.15	123.19
1	A	467	LYS	N-CA-C	-5.35	105.53	111.36
1	F	87	ASP	N-CA-C	-5.34	99.97	109.06
1	A	76	HIS	CA-C-O	5.34	126.12	120.36
1	E	334	VAL	N-CA-C	-5.34	100.51	108.46
1	E	381	ILE	CA-C-N	5.34	129.71	122.19
1	E	381	ILE	C-N-CA	5.34	129.71	122.19
1	D	224	ILE	CA-C-N	5.34	127.43	120.28
1	D	224	ILE	C-N-CA	5.34	127.43	120.28
1	C	376	PHE	CA-C-O	5.33	126.46	120.70
1	D	140	GLY	CA-C-O	-5.33	116.43	121.60
1	C	75	ILE	CA-C-O	5.33	126.74	120.71
1	A	103	VAL	N-CA-C	-5.33	106.66	113.22
1	A	292	PHE	CA-C-O	-5.33	114.27	120.03
1	D	291	TYR	CA-C-O	5.33	127.05	121.19
1	A	129	THR	CA-C-N	5.33	127.42	120.28
1	A	129	THR	C-N-CA	5.33	127.42	120.28
1	B	15	PRO	O-C-N	-5.33	115.45	122.64
1	A	446	PHE	N-CA-C	-5.33	100.34	108.76
1	B	350	THR	N-CA-C	-5.32	105.24	112.26
1	B	299	MET	CA-C-N	5.31	130.50	122.91
1	B	299	MET	C-N-CA	5.31	130.50	122.91
1	B	394	MET	N-CA-C	5.31	116.87	111.14
1	F	185	CYS	N-CA-C	-5.30	103.39	110.07
1	F	94	ASP	N-CA-C	-5.30	106.58	113.16
1	B	388	MET	CA-C-N	5.30	127.33	120.44
1	B	388	MET	C-N-CA	5.30	127.33	120.44
1	E	373	GLN	N-CA-C	-5.30	100.39	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	17	PRO	N-CA-C	5.30	119.53	111.11
1	C	433	PRO	CA-C-O	-5.30	112.88	120.56
1	F	199	ASP	CA-C-O	-5.29	115.73	121.87
1	C	410	PRO	N-CA-C	5.29	123.38	112.47
1	A	331	VAL	O-C-N	-5.29	117.68	123.18
1	E	239	SER	CA-C-N	5.29	127.75	120.67
1	E	239	SER	C-N-CA	5.29	127.75	120.67
1	B	247	PHE	N-CA-C	-5.28	105.11	112.30
1	C	280	SER	O-C-N	-5.28	117.36	123.33
1	D	399	LEU	CA-C-N	5.28	127.62	120.44
1	D	399	LEU	C-N-CA	5.28	127.62	120.44
1	B	77	LEU	CA-C-N	5.28	126.44	119.84
1	B	77	LEU	C-N-CA	5.28	126.44	119.84
1	E	474	LEU	N-CA-C	5.28	117.34	108.73
1	E	264	ALA	CA-C-N	5.28	128.06	121.83
1	E	264	ALA	C-N-CA	5.28	128.06	121.83
1	E	108	GLY	CA-C-O	5.28	126.33	121.58
1	B	250	LEU	N-CA-C	-5.27	100.90	108.60
1	E	199	ASP	N-CA-C	-5.27	102.59	110.23
1	B	386	ASP	N-CA-C	5.27	117.02	111.28
1	A	52	ILE	N-CA-C	-5.27	100.17	108.23
1	C	377	GLN	N-CA-C	-5.27	101.11	109.59
1	B	380	LYS	CA-C-O	-5.26	115.45	121.40
1	A	320	ASN	N-CA-C	-5.26	101.12	109.96
1	F	354	THR	N-CA-C	-5.26	100.73	109.46
1	D	183	GLY	CA-C-O	5.25	124.94	119.06
1	C	145	GLU	CA-C-O	5.25	127.34	121.40
1	A	408	PRO	CA-C-O	-5.25	116.58	120.73
1	B	42	LEU	O-C-N	-5.25	116.87	123.27
1	E	416	ASP	CA-C-O	-5.25	115.80	121.36
1	B	401	ASP	O-C-N	5.25	127.68	122.12
1	D	151	TYR	CA-C-N	5.25	131.56	121.54
1	D	151	TYR	C-N-CA	5.25	131.56	121.54
1	B	63	PRO	O-C-N	5.25	129.72	122.64
1	B	393	SER	CA-C-N	5.25	127.57	120.44
1	B	393	SER	C-N-CA	5.25	127.57	120.44
1	B	477	LYS	O-C-N	-5.25	115.29	121.32
1	C	266	THR	N-CA-C	-5.24	100.63	108.96
1	D	158	LEU	O-C-N	-5.24	116.99	123.33
1	B	135	TYR	O-C-N	-5.24	115.33	122.19
1	A	368	GLU	N-CA-C	-5.23	99.92	108.76
1	C	85	PHE	CA-C-N	5.23	124.74	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	85	PHE	C-N-CA	5.23	124.74	119.19
1	F	408	PRO	CA-C-N	5.23	125.77	120.38
1	F	408	PRO	C-N-CA	5.23	125.77	120.38
1	B	439	ASP	CA-C-O	-5.23	111.91	120.80
1	E	318	GLY	O-C-N	5.23	127.93	122.86
1	E	245	SER	CA-C-O	5.22	126.00	120.10
1	E	475	LYS	N-CA-C	5.22	125.62	111.00
1	D	153	GLN	CA-C-O	-5.22	114.69	120.70
1	D	365	ARG	N-CA-C	-5.22	101.48	109.41
1	B	272	PRO	O-C-N	5.21	129.01	123.01
1	F	72	VAL	CA-C-N	5.21	130.76	122.94
1	F	72	VAL	C-N-CA	5.21	130.76	122.94
1	F	364	LEU	O-C-N	-5.21	116.91	123.27
1	B	171	LYS	CA-C-O	5.21	126.16	120.58
1	B	484	LYS	CA-C-N	5.21	131.08	121.70
1	B	484	LYS	C-N-CA	5.21	131.08	121.70
1	A	277	ILE	CA-C-O	5.21	126.60	120.71
1	A	292	PHE	CA-C-N	5.21	125.62	119.99
1	A	292	PHE	C-N-CA	5.21	125.62	119.99
1	D	93	PRO	CA-C-N	5.21	129.41	120.71
1	D	93	PRO	C-N-CA	5.21	129.41	120.71
1	D	100	TRP	N-CA-C	5.21	117.99	110.28
1	D	109	ARG	N-CA-C	-5.21	105.92	113.21
1	A	321	ASN	CA-C-O	5.21	125.99	119.59
1	C	320	ASN	N-CA-C	-5.21	102.77	110.48
1	B	332	THR	N-CA-C	-5.20	100.42	108.90
1	E	194	VAL	O-C-N	5.20	128.27	122.61
1	D	413	THR	O-C-N	-5.20	116.88	123.17
1	C	186	PRO	CA-C-N	5.20	125.19	119.89
1	C	186	PRO	C-N-CA	5.20	125.19	119.89
1	F	396	SER	CA-C-N	5.20	127.24	120.28
1	F	396	SER	C-N-CA	5.20	127.24	120.28
1	B	122	LEU	CA-C-N	5.19	128.14	120.82
1	B	122	LEU	C-N-CA	5.19	128.14	120.82
1	E	396	SER	CA-C-N	5.19	127.75	120.28
1	E	396	SER	C-N-CA	5.19	127.75	120.28
1	C	58	ASN	CA-C-O	5.19	124.85	119.97
1	B	231	TYR	CA-C-N	5.19	125.43	119.83
1	B	231	TYR	C-N-CA	5.19	125.43	119.83
1	C	228	ILE	N-CA-C	-5.19	101.01	108.48
1	D	29	ALA	CA-C-O	5.18	126.62	120.66
1	F	314	GLN	CA-C-O	-5.18	113.10	120.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	387	VAL	CA-C-O	-5.18	115.56	120.95
1	D	208	MET	CA-C-N	5.17	128.06	120.71
1	D	208	MET	C-N-CA	5.17	128.06	120.71
1	C	434	PRO	N-CA-C	-5.17	103.65	111.41
1	C	440	PRO	N-CA-C	5.17	121.37	114.18
1	F	15	PRO	N-CA-C	5.17	123.12	112.47
1	C	35	TYR	N-CA-C	-5.17	101.44	109.24
1	D	464	LEU	CA-C-N	5.17	125.81	120.03
1	D	464	LEU	C-N-CA	5.17	125.81	120.03
1	B	432	THR	N-CA-C	-5.16	96.56	111.00
1	D	448	GLU	CA-C-N	5.16	130.04	123.13
1	D	448	GLU	C-N-CA	5.16	130.04	123.13
1	D	305	GLN	N-CA-C	-5.15	101.28	108.96
1	B	40	SER	N-CA-C	-5.15	105.46	112.26
1	C	70	TYR	CA-C-O	5.15	126.86	121.19
1	E	167	GLU	CA-C-N	5.15	131.04	121.62
1	E	167	GLU	C-N-CA	5.15	131.04	121.62
1	A	307	PHE	N-CA-C	-5.15	102.57	110.14
1	E	310	PRO	CA-C-N	5.15	130.00	122.85
1	E	310	PRO	C-N-CA	5.15	130.00	122.85
1	B	82	LYS	N-CA-C	-5.14	106.69	113.17
1	E	55	PRO	CA-C-N	5.14	130.29	122.37
1	E	55	PRO	C-N-CA	5.14	130.29	122.37
1	C	246	LEU	N-CA-C	-5.14	101.25	109.07
1	B	352	GLU	N-CA-C	-5.14	100.03	108.41
1	F	28	VAL	N-CA-C	-5.14	99.11	107.28
1	E	111	GLN	CA-C-N	5.14	126.26	119.84
1	E	111	GLN	C-N-CA	5.14	126.26	119.84
1	F	337	THR	CA-C-O	5.13	125.99	120.55
1	E	426	ILE	CA-C-N	5.13	130.94	121.70
1	E	426	ILE	C-N-CA	5.13	130.94	121.70
1	E	449	VAL	CA-C-N	5.13	129.23	122.30
1	E	449	VAL	C-N-CA	5.13	129.23	122.30
1	B	392	HIS	CA-C-N	5.13	127.15	120.28
1	B	392	HIS	C-N-CA	5.13	127.15	120.28
1	F	276	TYR	CA-C-N	5.13	128.44	120.34
1	F	276	TYR	C-N-CA	5.13	128.44	120.34
1	C	234	TYR	CA-C-N	5.13	127.12	120.56
1	C	234	TYR	C-N-CA	5.13	127.12	120.56
1	F	426	ILE	CA-C-N	5.13	130.93	121.70
1	F	426	ILE	C-N-CA	5.13	130.93	121.70
1	B	99	VAL	N-CA-C	-5.12	101.09	108.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	PHE	CA-C-O	5.12	126.52	120.89
1	F	404	PHE	CA-C-N	5.12	128.20	121.85
1	F	404	PHE	C-N-CA	5.12	128.20	121.85
1	A	59	LYS	CA-C-O	-5.12	115.43	121.16
1	C	330	PHE	O-C-N	-5.12	116.37	123.12
1	F	359	ASN	CA-C-O	5.12	127.83	120.51
1	A	215	ALA	CA-C-N	5.11	127.39	120.44
1	A	215	ALA	C-N-CA	5.11	127.39	120.44
1	D	102	CYS	CA-C-O	-5.11	115.60	120.92
1	C	463	PRO	CA-C-N	5.11	127.39	120.44
1	C	463	PRO	C-N-CA	5.11	127.39	120.44
1	D	454	LYS	N-CA-C	-5.10	105.96	113.61
1	C	458	ASP	CA-C-N	5.10	131.28	121.54
1	C	458	ASP	C-N-CA	5.10	131.28	121.54
1	F	439	ASP	CA-C-N	5.10	125.18	119.87
1	F	439	ASP	C-N-CA	5.10	125.18	119.87
1	C	197	ASP	O-C-N	5.10	129.03	123.01
1	E	353	THR	N-CA-C	-5.10	106.31	112.88
1	F	466	ARG	CA-C-N	5.10	128.06	120.31
1	F	466	ARG	C-N-CA	5.10	128.06	120.31
1	E	42	LEU	O-C-N	-5.09	117.42	123.22
1	F	361	LYS	N-CA-C	-5.09	98.98	107.99
1	A	338	ARG	O-C-N	5.09	128.20	122.20
1	B	407	GLN	CA-C-O	-5.09	113.36	119.67
1	F	406	LEU	O-C-N	-5.09	115.83	122.59
1	F	456	SER	O-C-N	-5.09	117.18	123.33
1	F	288	SER	N-CA-C	-5.08	102.95	110.48
1	B	438	GLU	CA-C-N	5.08	130.85	121.70
1	B	438	GLU	C-N-CA	5.08	130.85	121.70
1	D	190	LEU	CA-C-O	-5.08	115.14	120.58
1	A	82	LYS	N-CA-C	-5.08	99.00	107.99
1	B	237	MET	N-CA-C	5.08	117.71	111.82
1	B	441	LEU	N-CA-C	-5.08	101.42	109.59
1	C	444	TYR	CA-C-N	5.08	127.92	120.71
1	C	444	TYR	C-N-CA	5.08	127.92	120.71
1	A	114	GLY	N-CA-C	-5.07	101.16	113.18
1	A	438	GLU	CA-C-O	-5.07	115.61	121.19
1	C	172	GLY	O-C-N	5.07	129.81	122.26
1	F	331	VAL	CA-C-N	-5.07	115.86	123.00
1	F	331	VAL	C-N-CA	-5.07	115.86	123.00
1	E	314	GLN	N-CA-C	-5.07	100.01	110.80
1	C	59	LYS	N-CA-C	-5.06	101.62	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	GLU	O-C-N	-5.06	116.62	123.19
1	D	17	PRO	CA-C-O	-5.05	112.41	119.74
1	A	40	SER	N-CA-C	-5.05	105.24	111.40
1	C	311	TYR	N-CA-C	-5.05	97.12	107.67
1	E	176	THR	CA-C-N	5.05	127.46	120.29
1	E	176	THR	C-N-CA	5.05	127.46	120.29
1	F	159	ILE	N-CA-C	-5.05	100.85	108.12
1	D	51	PRO	CA-C-O	-5.05	115.86	122.12
1	F	355	TYR	N-CA-C	5.05	117.79	110.42
1	D	80	PRO	CA-C-N	5.04	127.98	120.31
1	D	80	PRO	C-N-CA	5.04	127.98	120.31
1	C	417	THR	CA-C-N	5.04	130.78	121.70
1	C	417	THR	C-N-CA	5.04	130.78	121.70
1	F	389	THR	CA-C-O	-5.04	115.08	120.42
1	E	401	ASP	O-C-N	5.04	127.53	122.09
1	E	222	LEU	O-C-N	5.04	127.46	122.12
1	F	258	ARG	N-CA-C	-5.04	105.87	111.36
1	E	369	GLU	CA-C-O	-5.03	114.87	120.66
1	B	81	ASN	N-CA-C	-5.03	106.98	113.02
1	B	244	ASP	N-CA-C	-5.03	106.65	112.89
1	C	53	LYS	O-C-N	-5.03	116.37	123.11
1	C	120	HIS	CA-C-N	5.03	125.10	119.87
1	C	120	HIS	C-N-CA	5.03	125.10	119.87
1	F	321	ASN	N-CA-C	-5.03	106.56	113.30
1	A	65	VAL	N-CA-C	-5.02	100.30	107.78
1	F	426	ILE	CA-C-O	-5.02	114.50	120.78
1	E	461	GLN	O-C-N	-5.02	116.25	122.83
1	C	73	PHE	N-CA-C	-5.02	100.55	108.73
1	E	228	ILE	O-C-N	5.01	128.65	122.83
1	A	200	MET	CA-C-N	5.01	129.31	121.85
1	A	200	MET	C-N-CA	5.01	129.31	121.85
1	E	244	ASP	CA-C-N	5.00	127.49	120.28
1	E	244	ASP	C-N-CA	5.00	127.49	120.28
1	A	177	GLN	N-CA-C	-5.00	106.96	113.16
1	B	474	LEU	CA-C-N	5.00	131.09	121.54
1	B	474	LEU	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (71) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	VAL	Peptide

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Mol	Chain	Res	Type	Group
1	A	13	LEU	Peptide
1	A	16	VAL	Peptide
1	A	405	GLY	Peptide
1	A	407	GLN	Peptide
1	A	408	PRO	Peptide
1	A	409	PRO	Peptide
1	A	415	GLU	Peptide
1	A	433	PRO	Peptide
1	A	434	PRO	Peptide
1	A	436	PRO	Peptide
1	A	437	LYS	Peptide
1	A	477	LYS	Peptide
1	B	13	LEU	Peptide
1	B	14	PRO	Peptide
1	B	181	GLN	Peptide
1	B	408	PRO	Peptide
1	B	409	PRO	Peptide
1	B	414	LEU	Peptide
1	B	424	GLN	Peptide
1	B	433	PRO	Peptide
1	B	443	LYS	Peptide
1	B	481	THR	Peptide
1	C	12	TYR	Peptide
1	C	13	LEU	Peptide
1	C	14	PRO	Peptide
1	C	16	VAL	Peptide
1	C	181	GLN	Peptide
1	C	405	GLY	Peptide
1	C	407	GLN	Peptide
1	C	416	ASP	Peptide
1	C	418	TYR	Peptide
1	C	421	VAL	Peptide
1	C	435	ALA	Peptide
1	C	476	ALA	Peptide
1	C	477	LYS	Peptide
1	D	13	LEU	Peptide
1	D	17	PRO	Peptide
1	D	407	GLN	Peptide
1	D	408	PRO	Peptide
1	D	409	PRO	Peptide
1	D	422	THR	Peptide
1	D	424	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	D	432	THR	Peptide
1	D	433	PRO	Peptide
1	D	435	ALA	Peptide
1	D	438	GLU	Peptide
1	D	473	GLY	Peptide
1	D	477	LYS	Peptide
1	D	481	THR	Peptide
1	D	9	ALA	Peptide
1	E	10	THR	Peptide
1	E	13	LEU	Peptide
1	E	14	PRO	Peptide
1	E	406	LEU	Peptide
1	E	407	GLN	Peptide
1	E	408	PRO	Peptide
1	E	433	PRO	Peptide
1	E	477	LYS	Peptide
1	E	481	THR	Peptide
1	F	10	THR	Peptide
1	F	12	TYR	Peptide
1	F	13	LEU	Peptide
1	F	16	VAL	Peptide
1	F	19	SER	Peptide
1	F	408	PRO	Peptide
1	F	409	PRO	Peptide
1	F	414	LEU	Peptide
1	F	435	ALA	Peptide
1	F	476	ALA	Peptide
1	F	479	LYS	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	A	1911	958	512	1	0
1	B	1911	958	512	1	0
1	C	1911	958	512	0	0
1	D	1911	958	512	0	0
1	E	1911	958	512	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1911	958	512	2	0
All	All	11466	5748	3072	4	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 0.

All (4) 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:F:427:ALA:H	1:F:428:CYS:CA	2.27	0.48
1:A:12:TYR:H	1:A:13:LEU:CA	2.31	0.42
1:F:23:SER:C	1:F:25:ASP:H	2.26	0.42
1:B:242:TYR:O	1:B:318:GLY:HA3	2.20	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	476/478 (100%)	403 (85%)	54 (11%)	19 (4%)	2	18
1	B	476/478 (100%)	395 (83%)	50 (10%)	31 (6%)	1	12
1	C	476/478 (100%)	401 (84%)	53 (11%)	22 (5%)	2	17
1	D	476/478 (100%)	404 (85%)	47 (10%)	25 (5%)	1	15
1	E	476/478 (100%)	417 (88%)	43 (9%)	16 (3%)	3	21
1	F	476/478 (100%)	405 (85%)	52 (11%)	19 (4%)	2	18
All	All	2856/2868 (100%)	2425 (85%)	299 (10%)	132 (5%)	3	17

All (132) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	15	PRO
1	B	87	ASP
1	B	133	SER
1	B	395	ASN
1	B	408	PRO
1	B	409	PRO
1	B	414	LEU
1	B	415	GLU
1	B	439	ASP
1	A	41	ARG
1	A	86	PRO
1	A	340	THR
1	A	427	ALA
1	E	11	VAL
1	E	289	SER
1	E	475	LYS
1	E	480	PHE
1	D	152	LYS
1	D	290	ASN
1	D	476	ALA
1	C	89	SER
1	C	202	ASP
1	C	355	TYR
1	C	395	ASN
1	C	408	PRO
1	C	417	THR
1	C	425	ALA
1	C	478	PRO
1	F	339	SER
1	B	143	ASN
1	B	152	LYS
1	B	410	PRO
1	B	421	VAL
1	A	14	PRO
1	A	15	PRO
1	A	26	GLU
1	A	424	GLN
1	E	425	ALA
1	D	41	ARG
1	D	408	PRO
1	D	409	PRO
1	D	457	ALA
1	D	474	LEU

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Mol	Chain	Res	Type
1	D	482	LEU
1	C	14	PRO
1	C	26	GLU
1	C	41	ARG
1	F	315	ARG
1	F	406	LEU
1	F	415	GLU
1	B	13	LEU
1	B	14	PRO
1	B	132	ALA
1	B	202	ASP
1	B	221	PRO
1	B	326	GLY
1	B	457	ALA
1	A	351	SER
1	A	358	THR
1	E	48	PRO
1	E	110	GLY
1	E	202	ASP
1	E	308	ASN
1	E	423	SER
1	E	479	LYS
1	D	78	PRO
1	D	89	SER
1	D	395	ASN
1	D	427	ALA
1	D	433	PRO
1	D	436	PRO
1	D	453	GLU
1	D	479	LYS
1	C	133	SER
1	C	182	PRO
1	C	459	LEU
1	C	479	LYS
1	F	314	GLN
1	F	395	ASN
1	F	425	ALA
1	F	477	LYS
1	B	435	ALA
1	B	475	LYS
1	B	478	PRO
1	B	479	LYS

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Mol	Chain	Res	Type
1	B	482	LEU
1	A	13	LEU
1	A	185	CYS
1	A	247	PHE
1	A	308	ASN
1	A	437	LYS
1	A	440	PRO
1	A	462	PHE
1	E	314	GLN
1	E	439	ASP
1	D	90	PHE
1	D	139	ALA
1	D	259	HIS
1	D	410	PRO
1	D	434	PRO
1	C	16	VAL
1	C	161	CYS
1	C	173	SER
1	C	436	PRO
1	F	11	VAL
1	F	247	PHE
1	F	259	HIS
1	F	479	LYS
1	B	20	LYS
1	B	173	SER
1	B	403	ASN
1	B	416	ASP
1	B	445	THR
1	E	409	PRO
1	D	484	LYS
1	D	485	ARG
1	C	90	PHE
1	F	41	ARG
1	F	218	SER
1	F	241	PRO
1	F	403	ASN
1	F	420	PHE
1	A	124	ASN
1	A	137	ALA
1	E	41	ARG
1	E	259	HIS
1	D	403	ASN

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Mol	Chain	Res	Type
1	F	417	THR
1	B	434	PRO
1	F	180	VAL
1	C	407	GLN
1	C	164	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

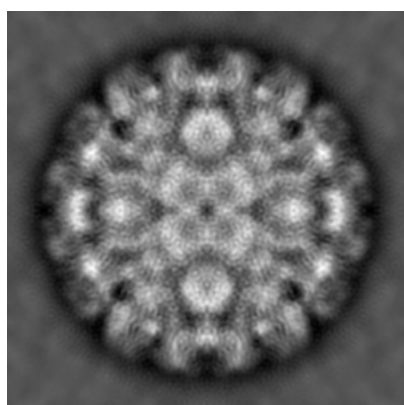
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5932. These allow visual inspection of the internal detail of the map and identification of artifacts.

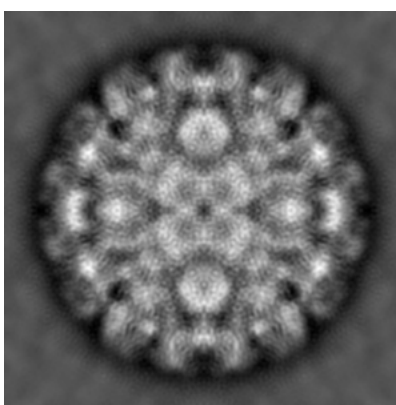
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

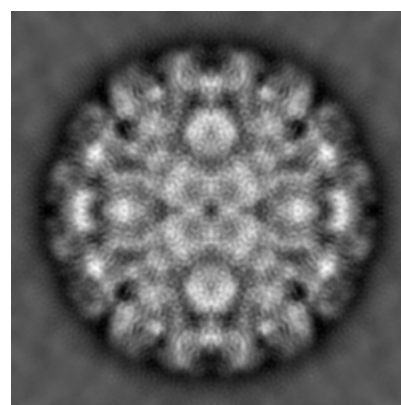
6.1.1 Primary map



X



Y

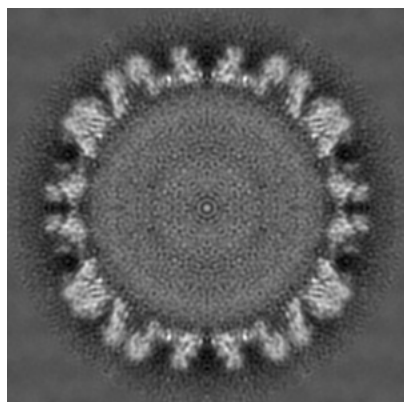


Z

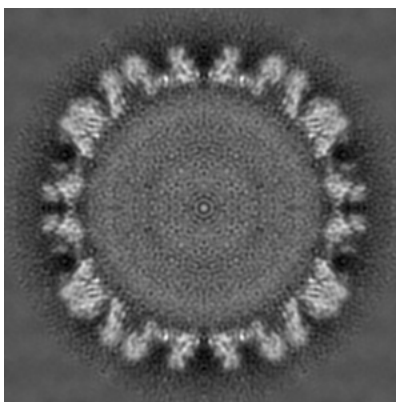
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

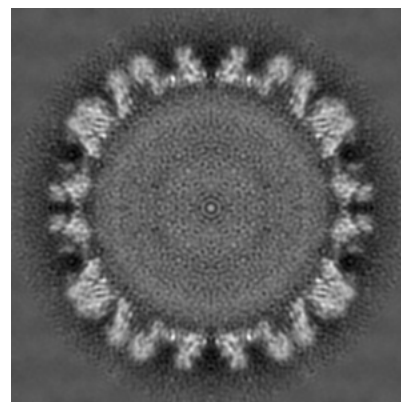
6.2.1 Primary map



X Index: 255



Y Index: 255

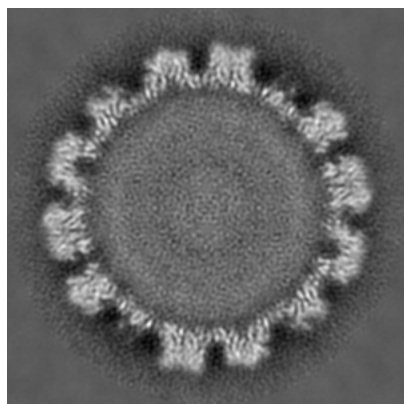


Z Index: 255

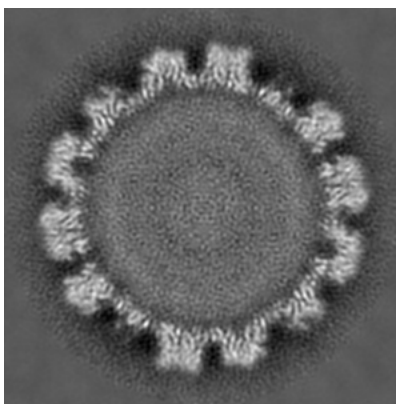
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

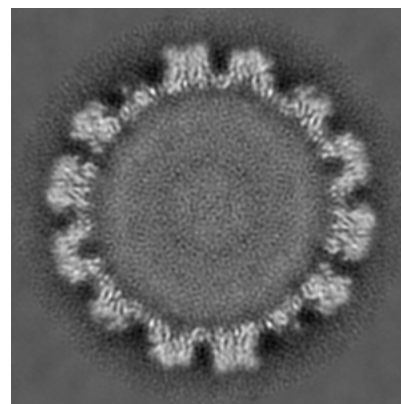
6.3.1 Primary map



X Index: 297



Y Index: 297

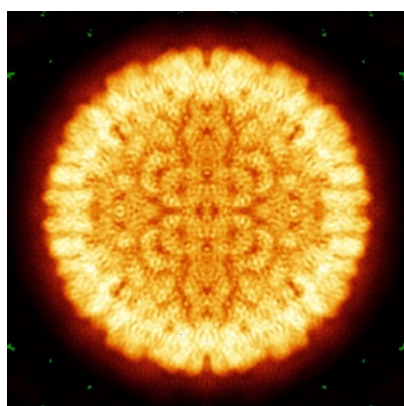


Z Index: 212

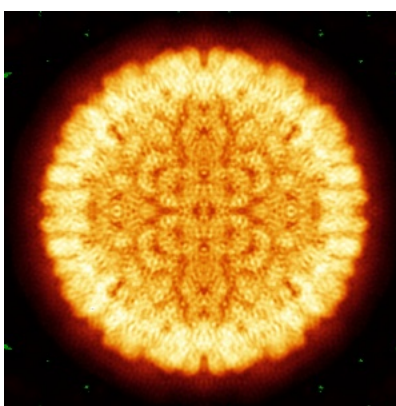
The images above show the largest variance slices of the map in three orthogonal directions.

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

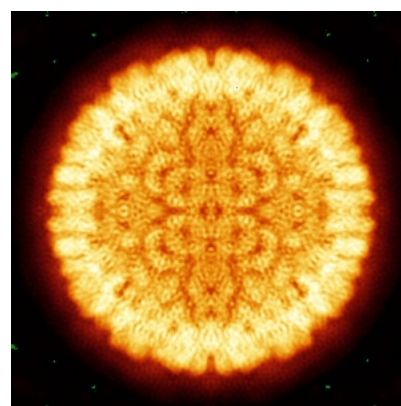
6.4.1 Primary map



X



Y

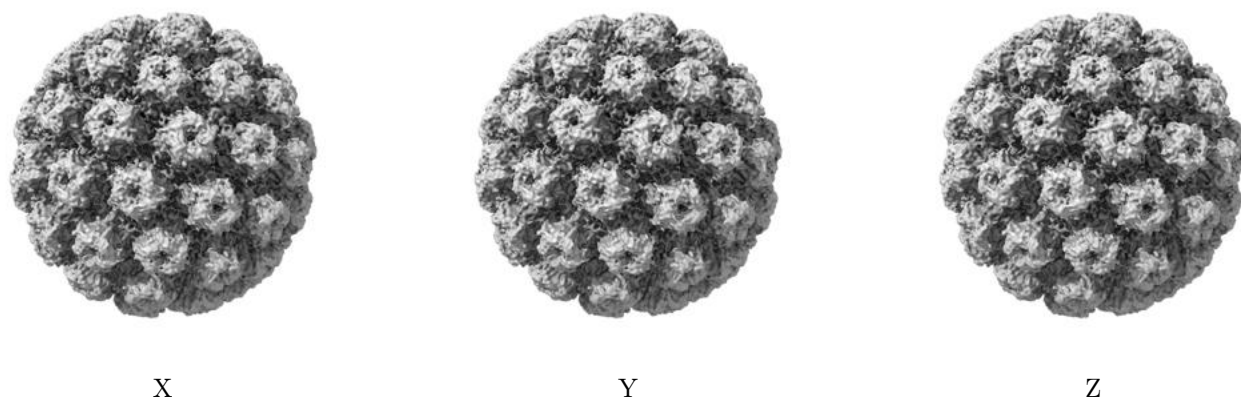


Z

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 800.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

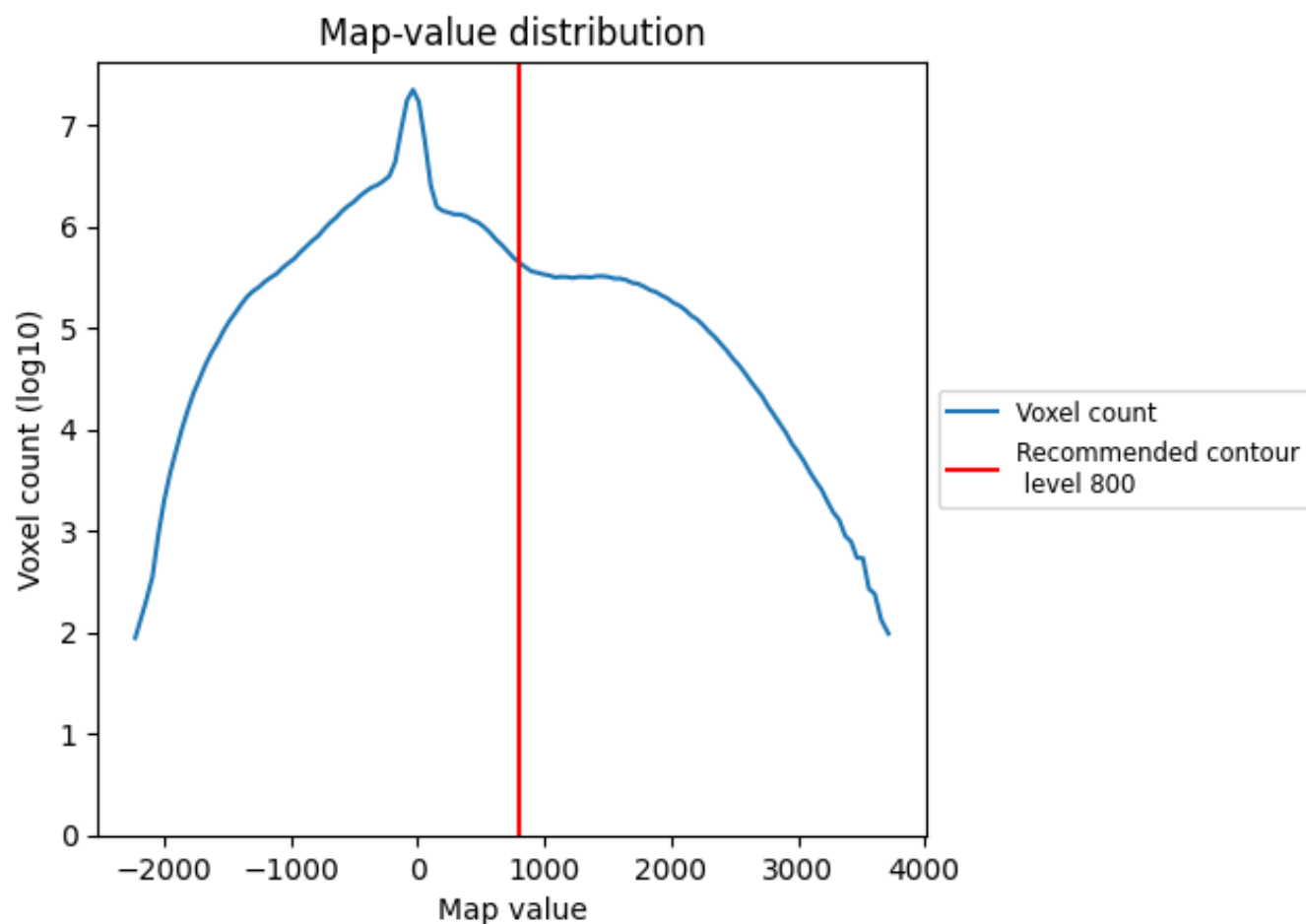
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

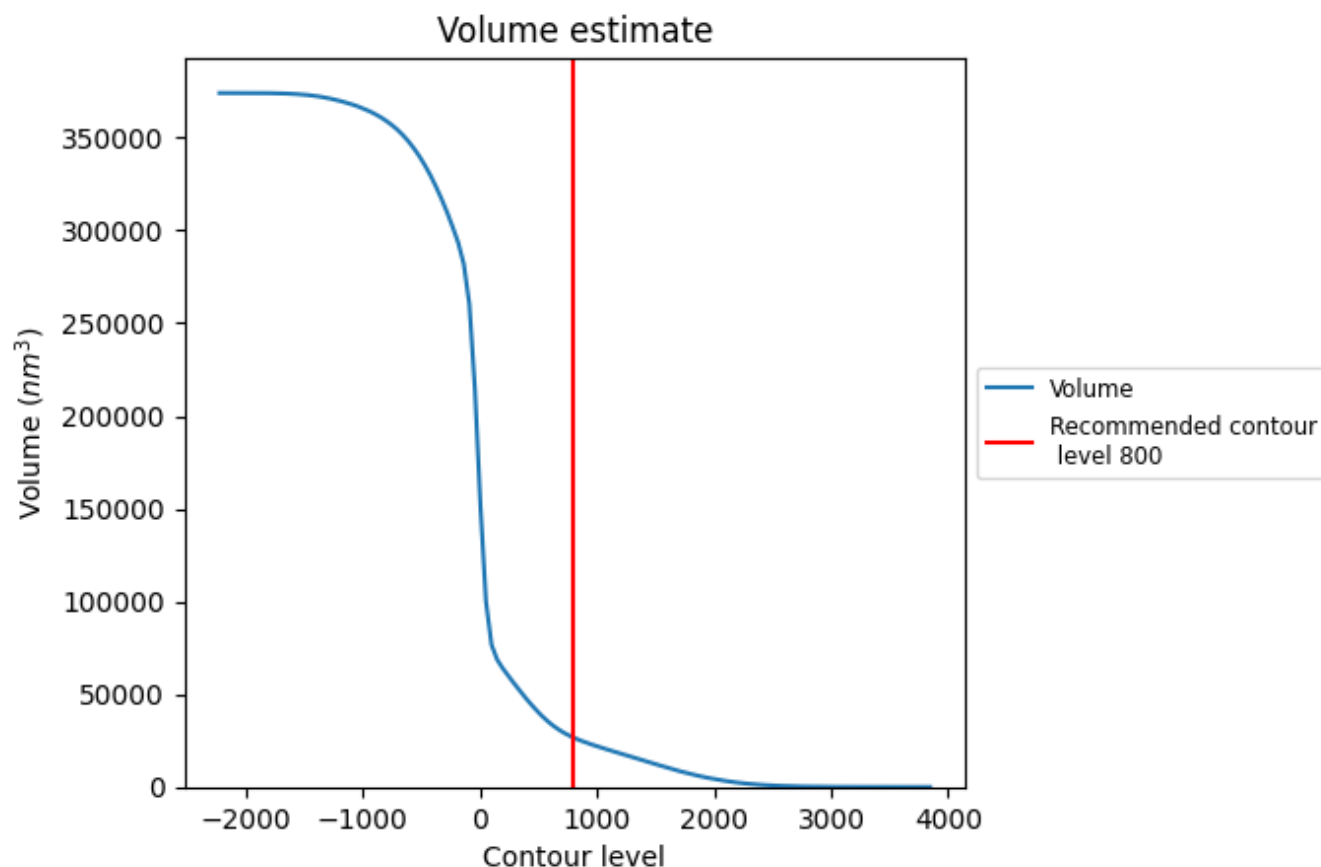
This section contains the results of statistical analysis of the map.

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.

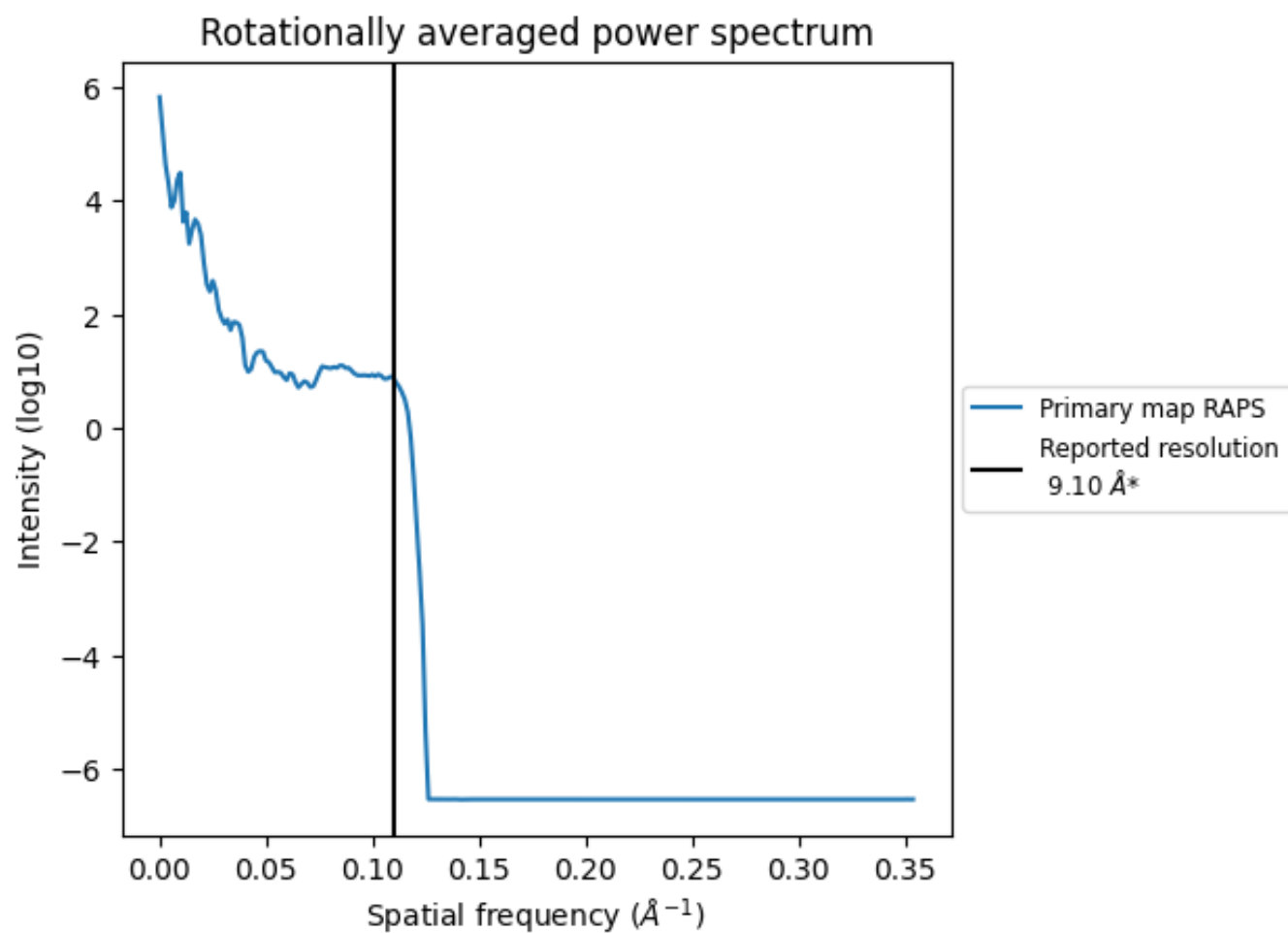
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 26595 nm³; this corresponds to an approximate mass of 24024 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 0.110 Å⁻¹

8 Fourier-Shell correlation ⓘ

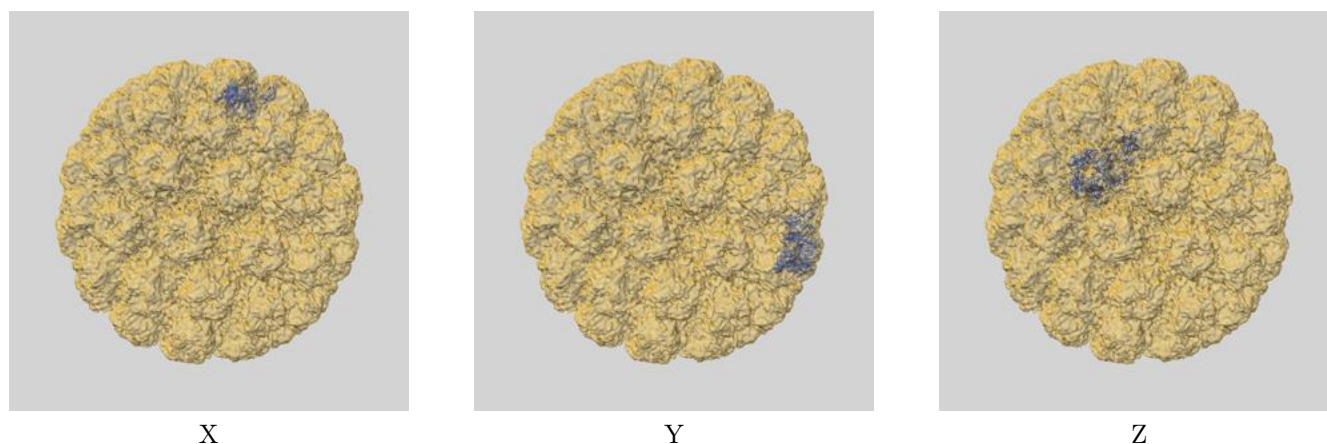
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

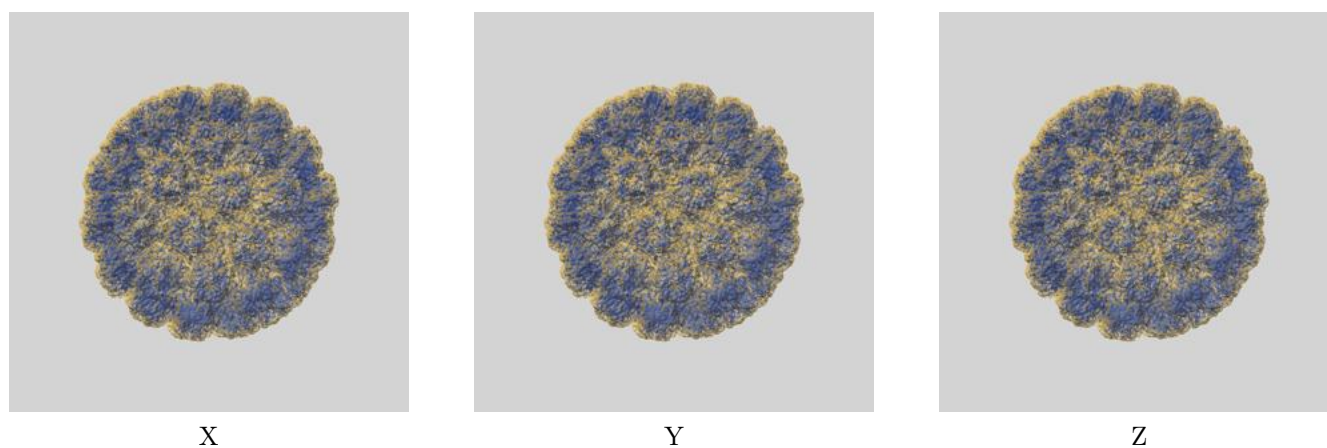
This section contains information regarding the fit between EMDB map EMD-5932 and PDB model 3J6R. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

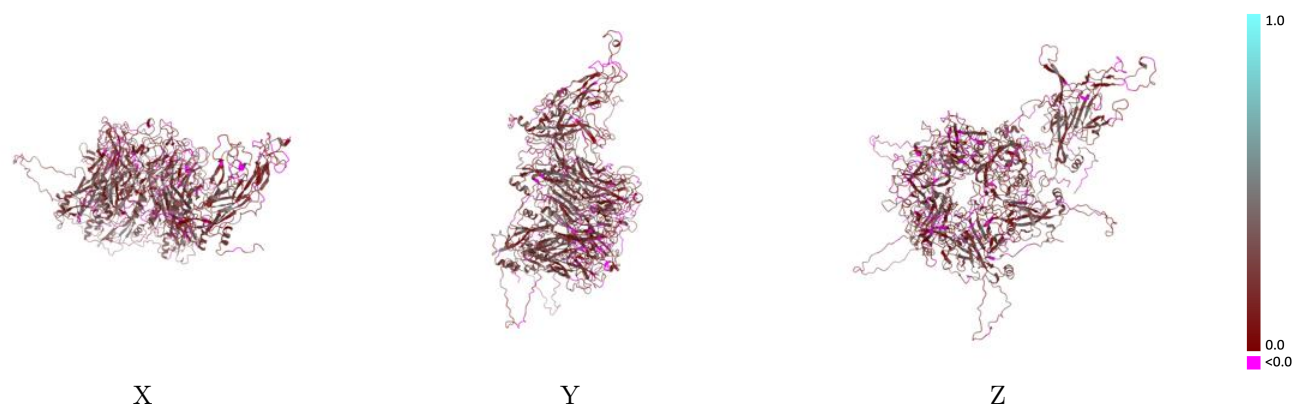


9.1.2 Map-model assembly overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 800.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



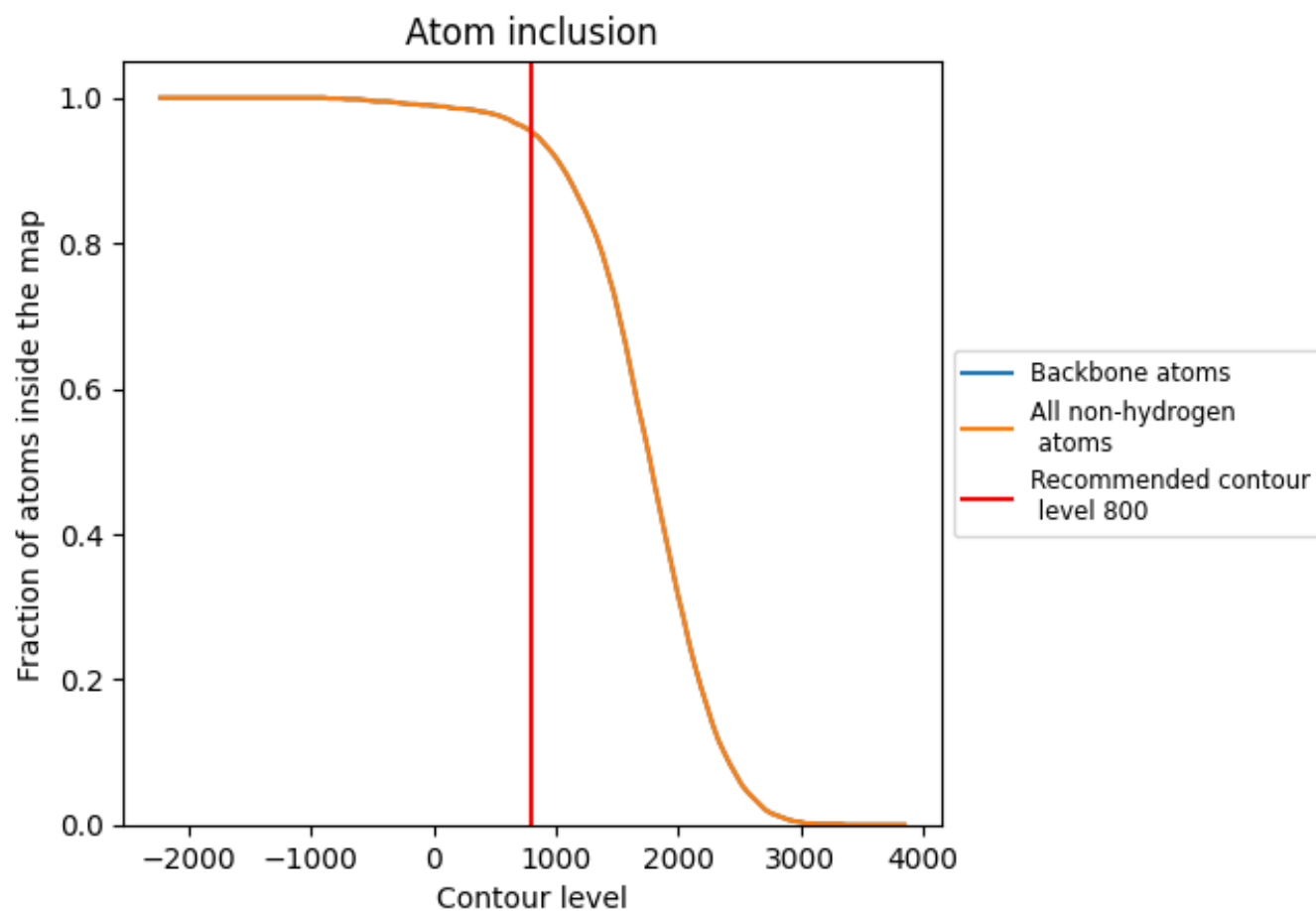
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (800).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (800) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9540	0.1930
A	0.9560	0.1830
B	0.9420	0.1980
C	0.9690	0.2000
D	0.9590	0.2020
E	0.9520	0.1880
F	0.9520	0.1850

1.0

0.0

<0.0