



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:36 PM UTC

PDB ID : 7TNT / pdb_00007tnt
EMDB ID : EMD-26020
Title : The tubulin-based conoid from detergent-extract *Toxoplasma gondii* cells
Authors : Sun, S.Y.; Pintilie, G.D.; Chen, M.; Chiu, W.
Deposited on : 2022-01-21
Resolution : 9.30 Å (reported)
Based on initial model : 7MIZ

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:

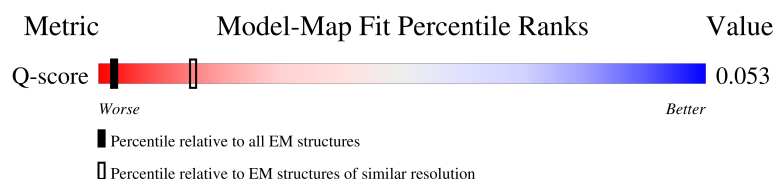
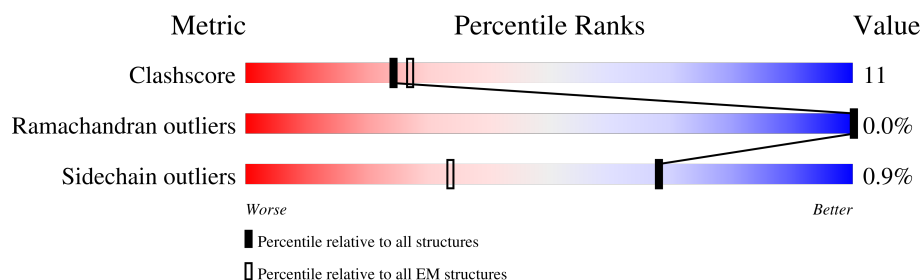
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.30 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	228 (8.80 - 9.80)

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	2A	437	22% 71% 24% ..
1	2B	437	27% 74% 22% ..
1	2C	437	27% 81% 16% ..
1	2D	437	33% 75% 21% ..

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Mol	Chain	Length	Quality of chain
1	2E	437	
1	2F	437	
1	2G	437	
1	2H	437	
1	2I	437	
1	4A	437	
1	4B	437	
1	4C	437	
1	4D	437	
1	4E	437	
1	4F	437	
1	4G	437	
1	4H	437	
1	4I	437	
2	3A	426	
2	3B	426	
2	3C	426	
2	3D	426	
2	3E	426	
2	3F	426	
2	3G	426	
2	3H	426	
2	3I	426	
2	5A	426	
2	5B	426	

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Mol	Chain	Length	Quality of chain
2	5C	426	
2	5D	426	
2	5E	426	
2	5F	426	
2	5G	426	
2	5H	426	
2	5I	426	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 119808 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 Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2A	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2B	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2C	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2D	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2E	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2F	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2G	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2H	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	2I	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4A	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4B	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4C	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4D	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4E	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4F	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4G	428	Total 3325	C 2105	N 569	O 625	S 26	0	0
1	4H	428	Total 3325	C 2105	N 569	O 625	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	4I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

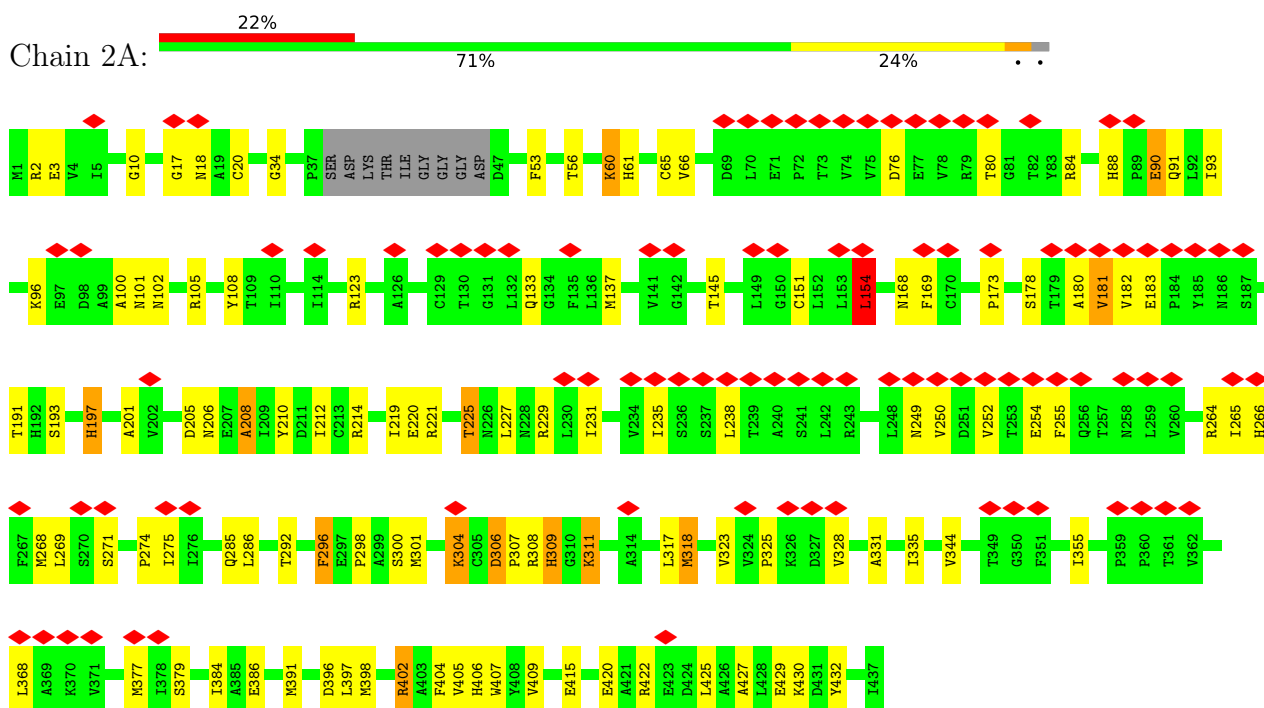
- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3A	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3C	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3E	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3G	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	3I	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5A	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5C	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5E	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5G	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
2	5I	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

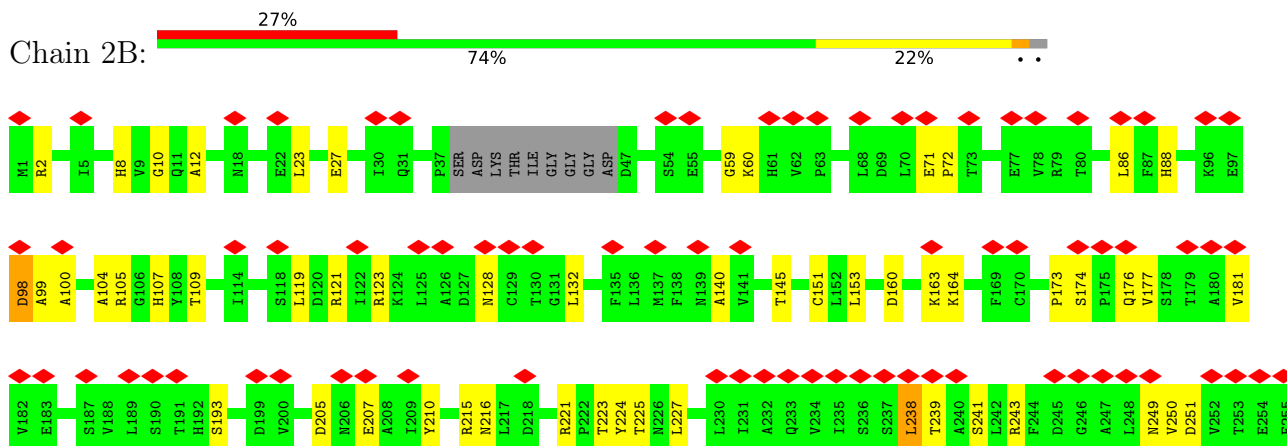
3 Residue-property plots

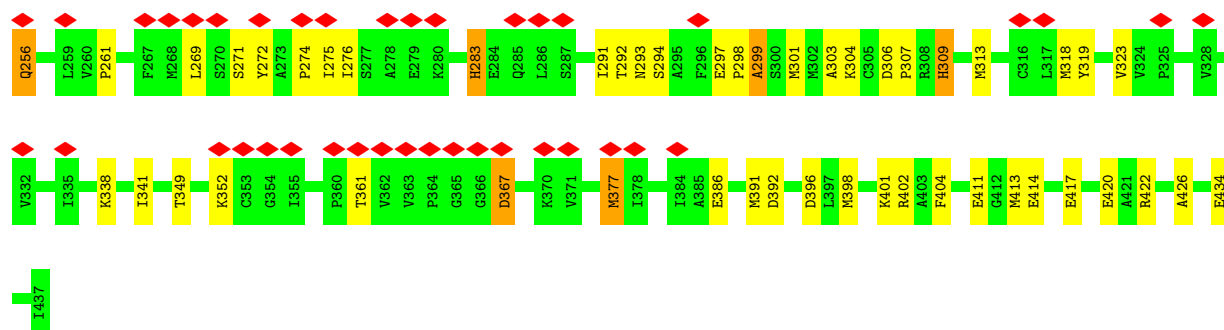
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Tubulin alpha chain

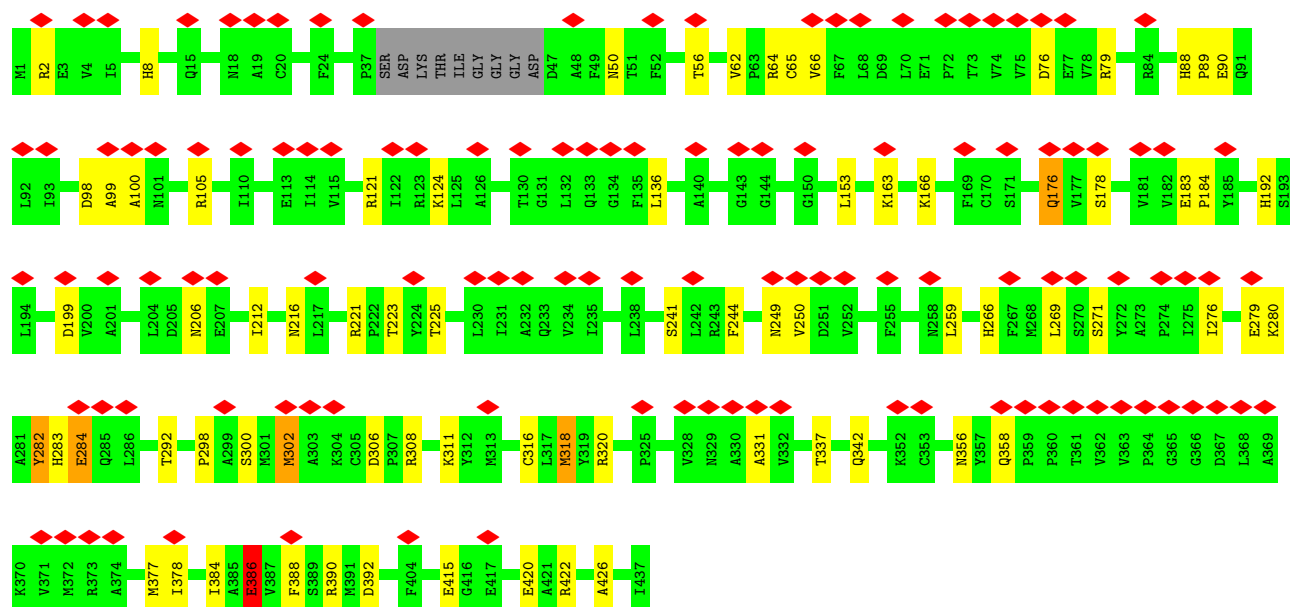
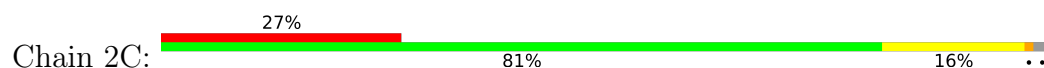


- Molecule 1: Tubulin alpha chain

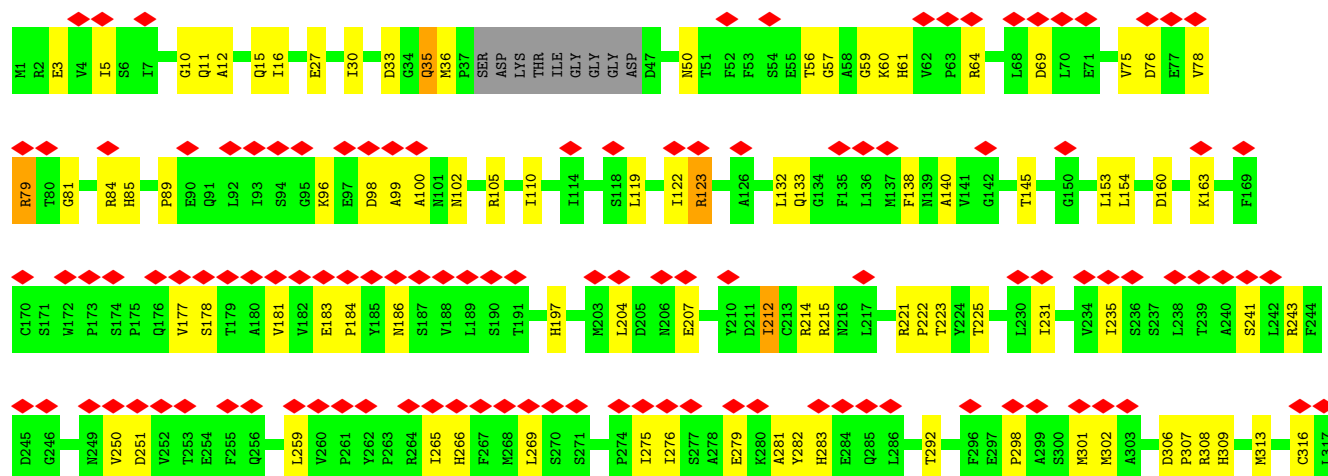
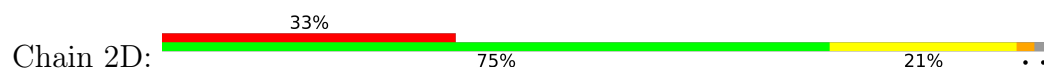


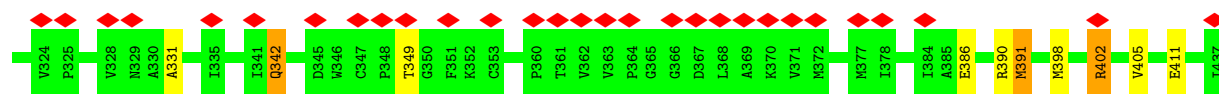


• Molecule 1: Tubulin alpha chain

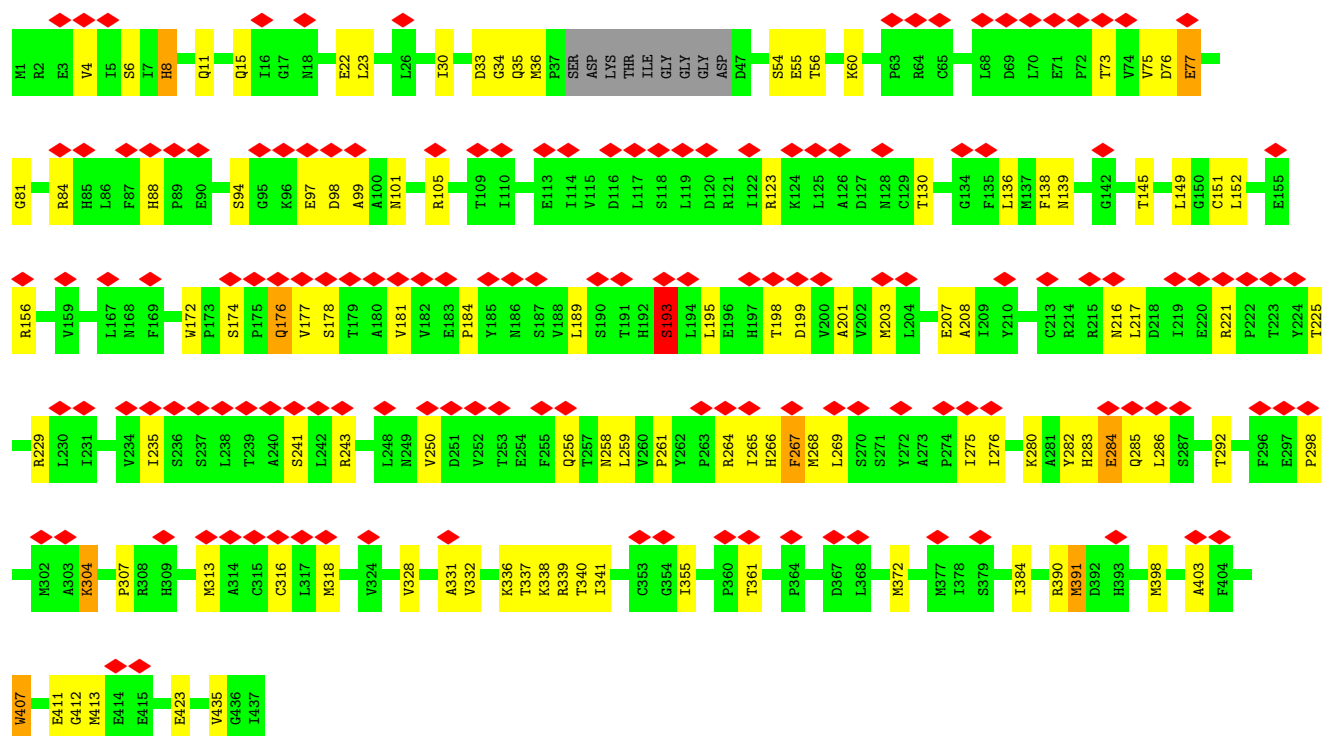
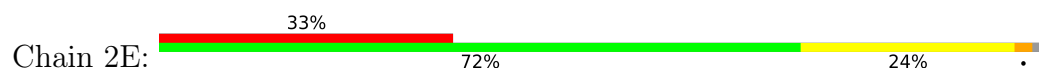


• Molecule 1: Tubulin alpha chain

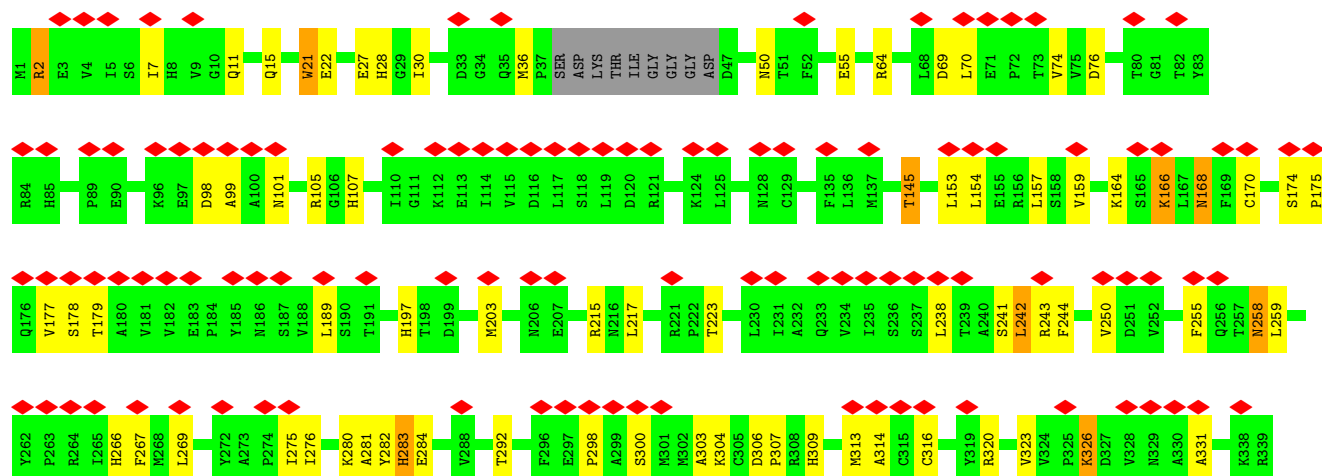
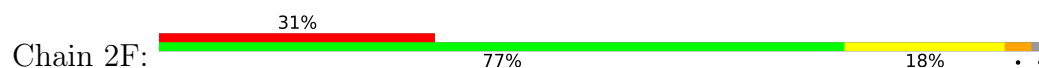




• Molecule 1: Tubulin alpha chain

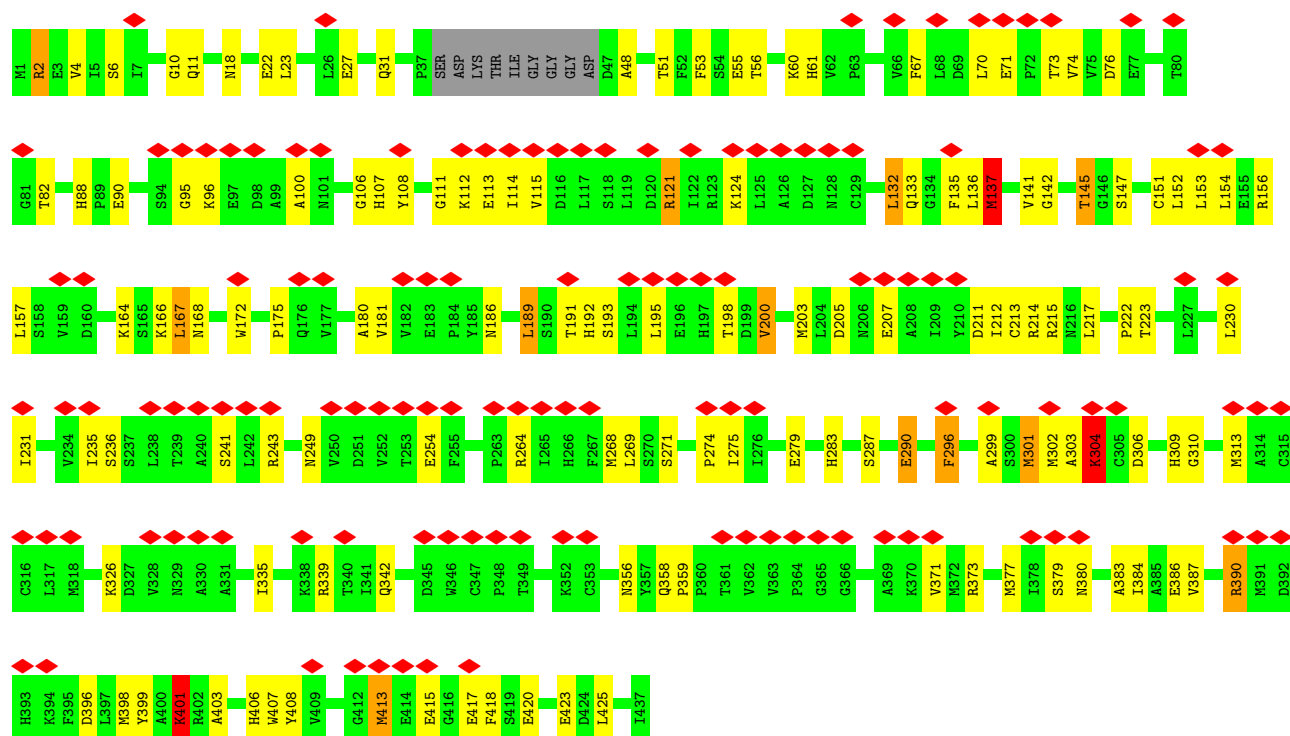


• Molecule 1: Tubulin alpha chain

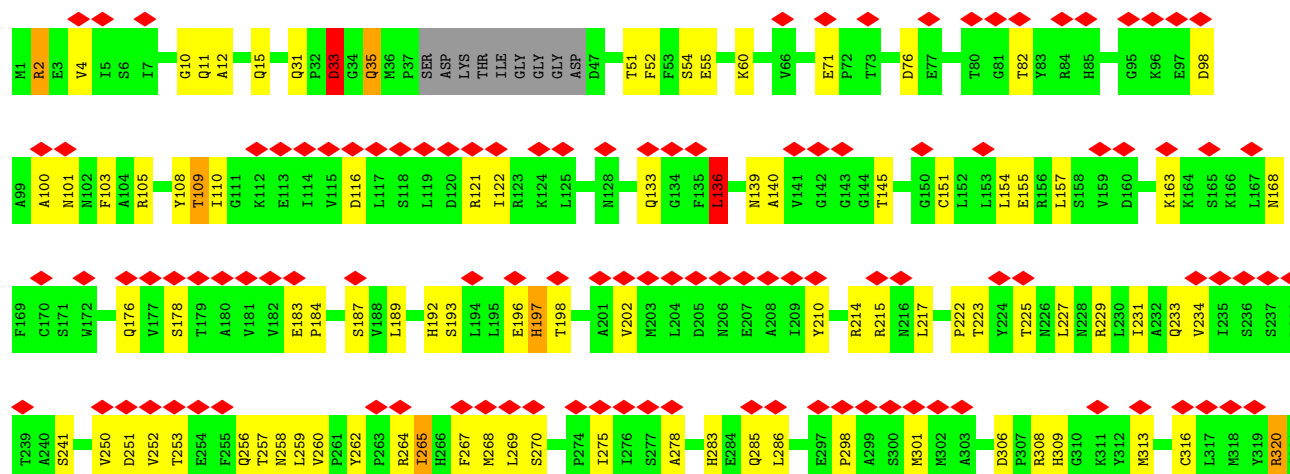


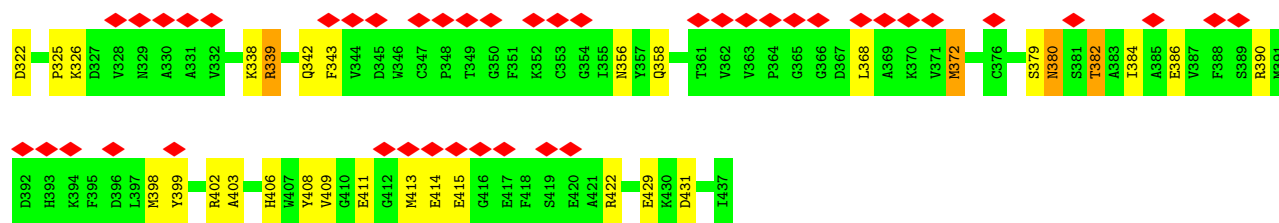


• Molecule 1: Tubulin alpha chain

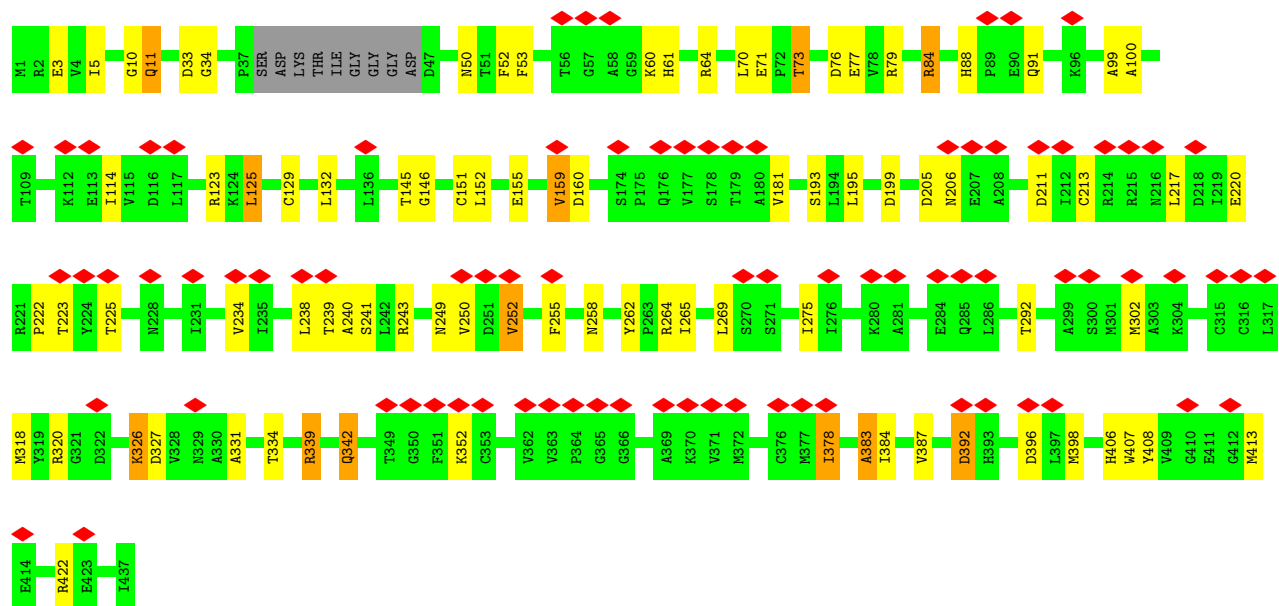
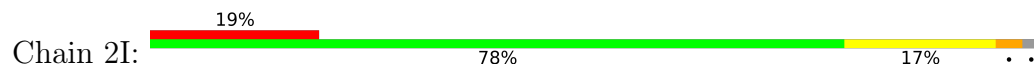


• Molecule 1: Tubulin alpha chain

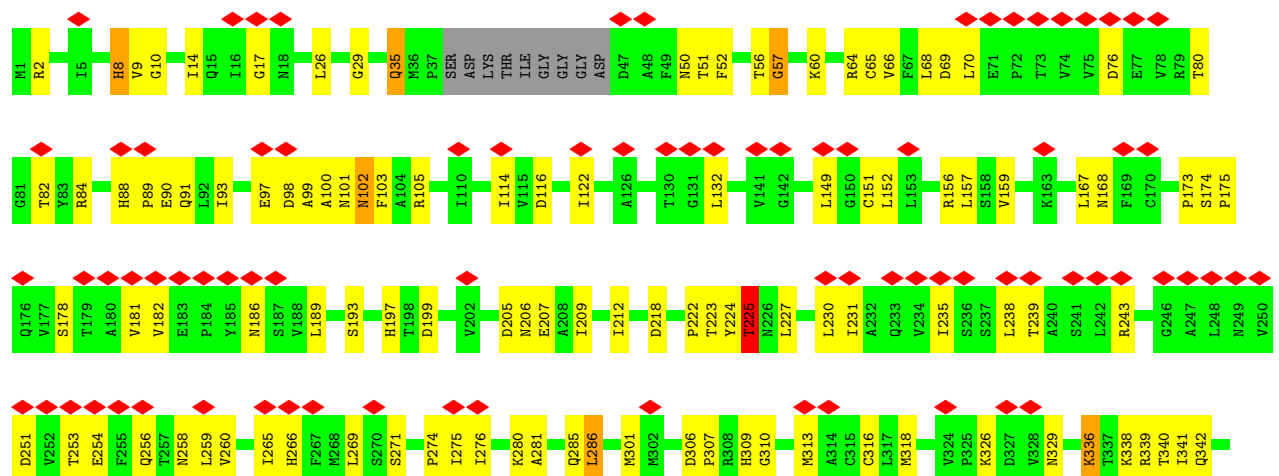


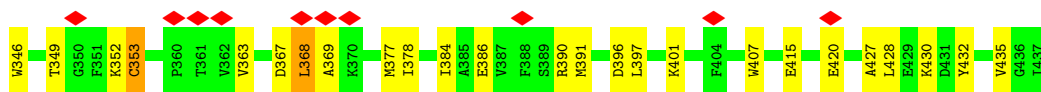


• Molecule 1: Tubulin alpha chain

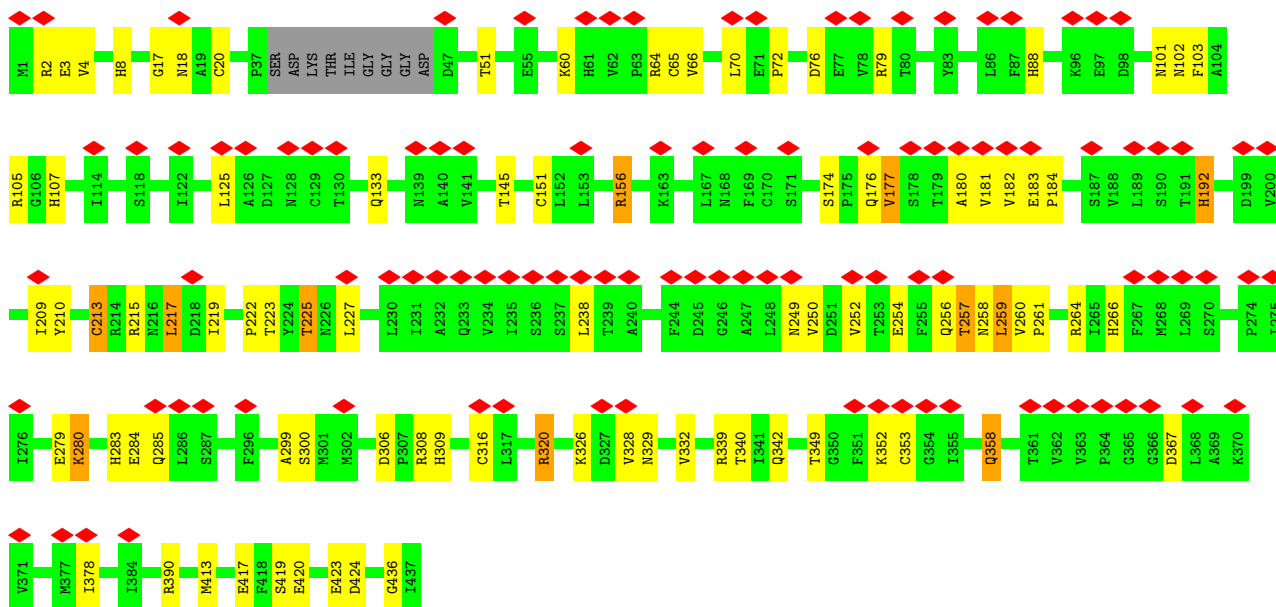
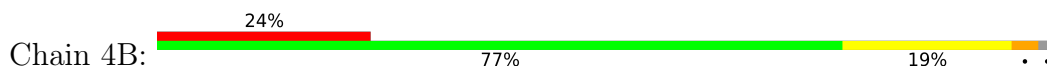


• Molecule 1: Tubulin alpha chain

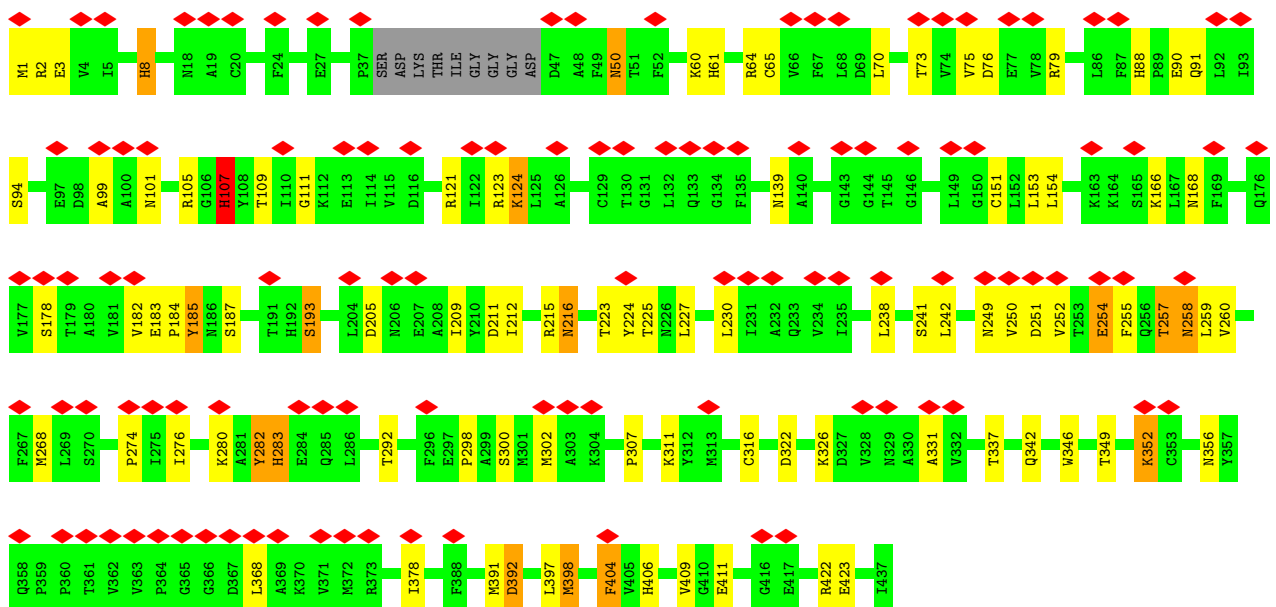
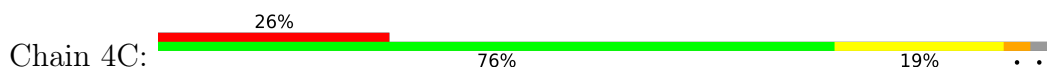




- Molecule 1: Tubulin alpha chain

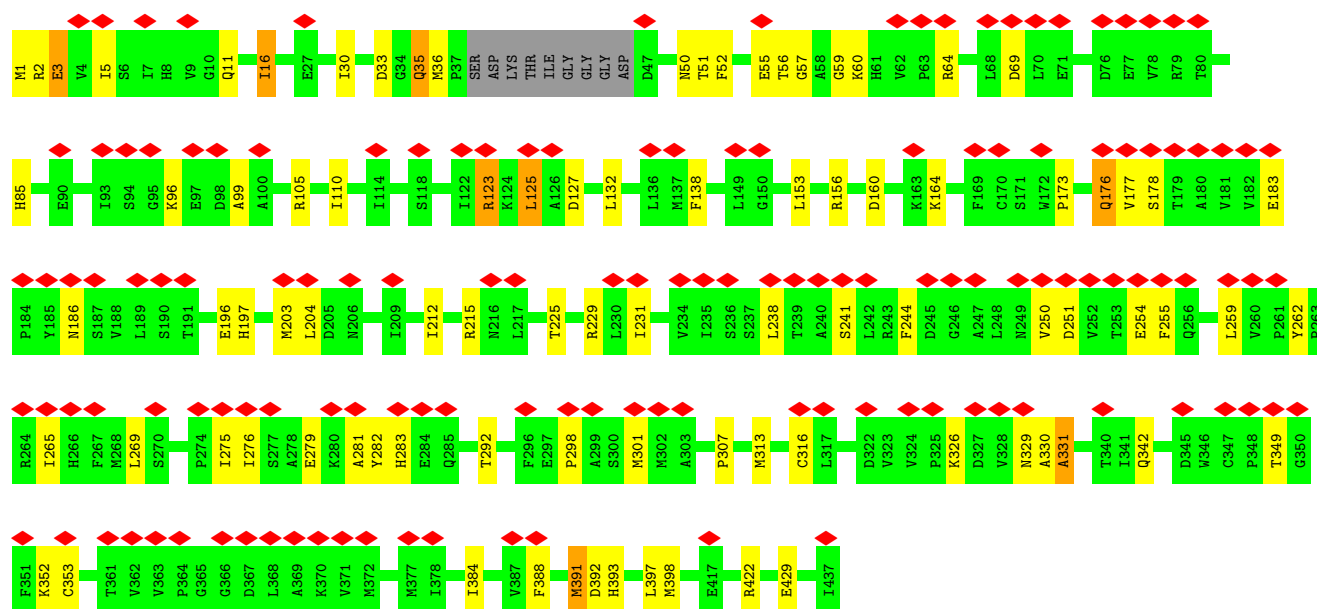


- Molecule 1: Tubulin alpha chain



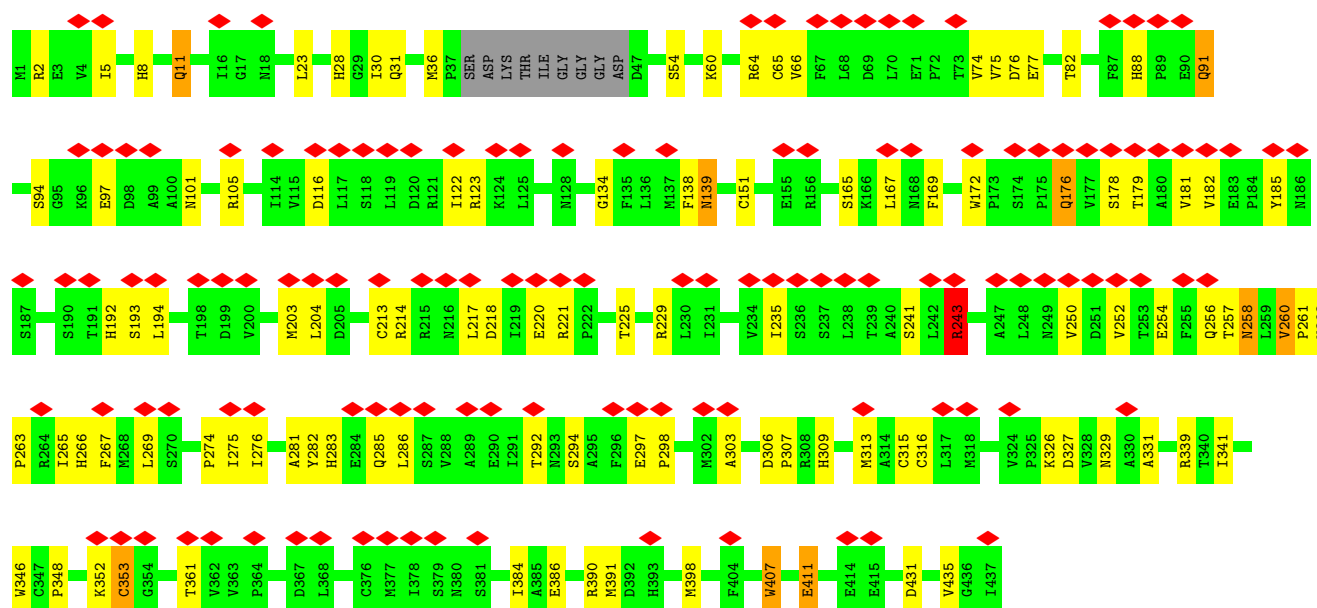
- Molecule 1: Tubulin alpha chain

Chain 4D: 



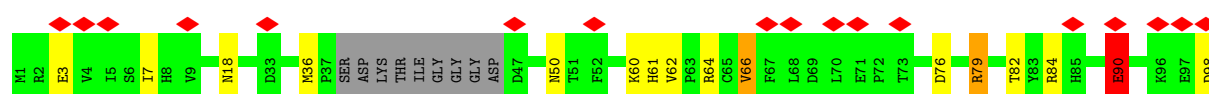
• Molecule 1: Tubulin alpha chain

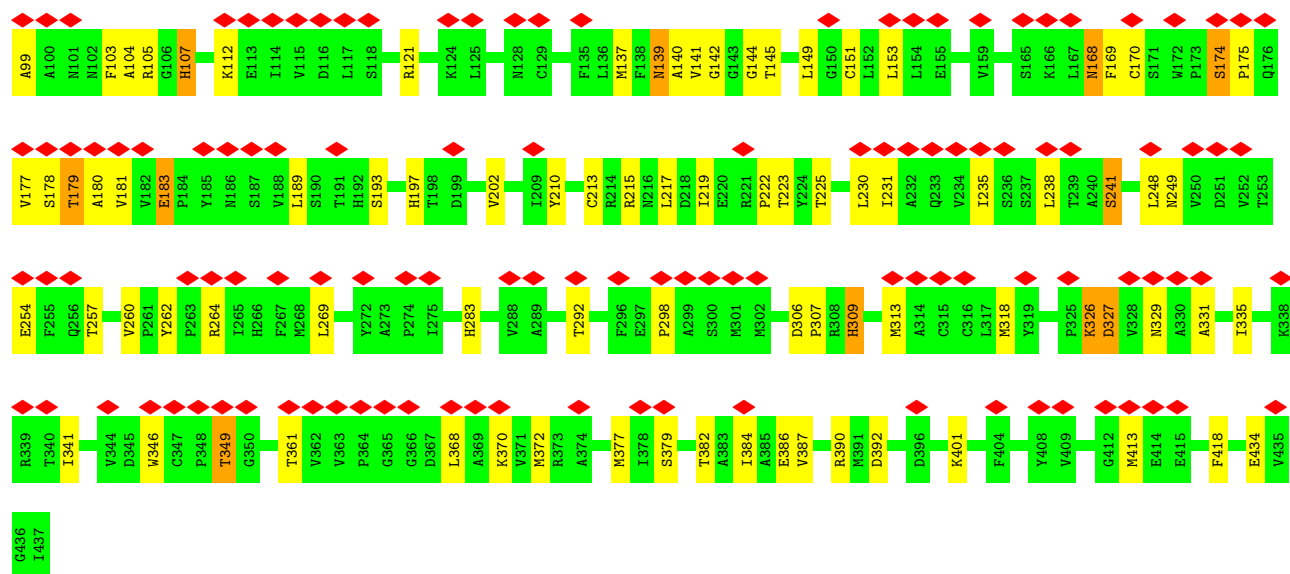
Chain 4E: 



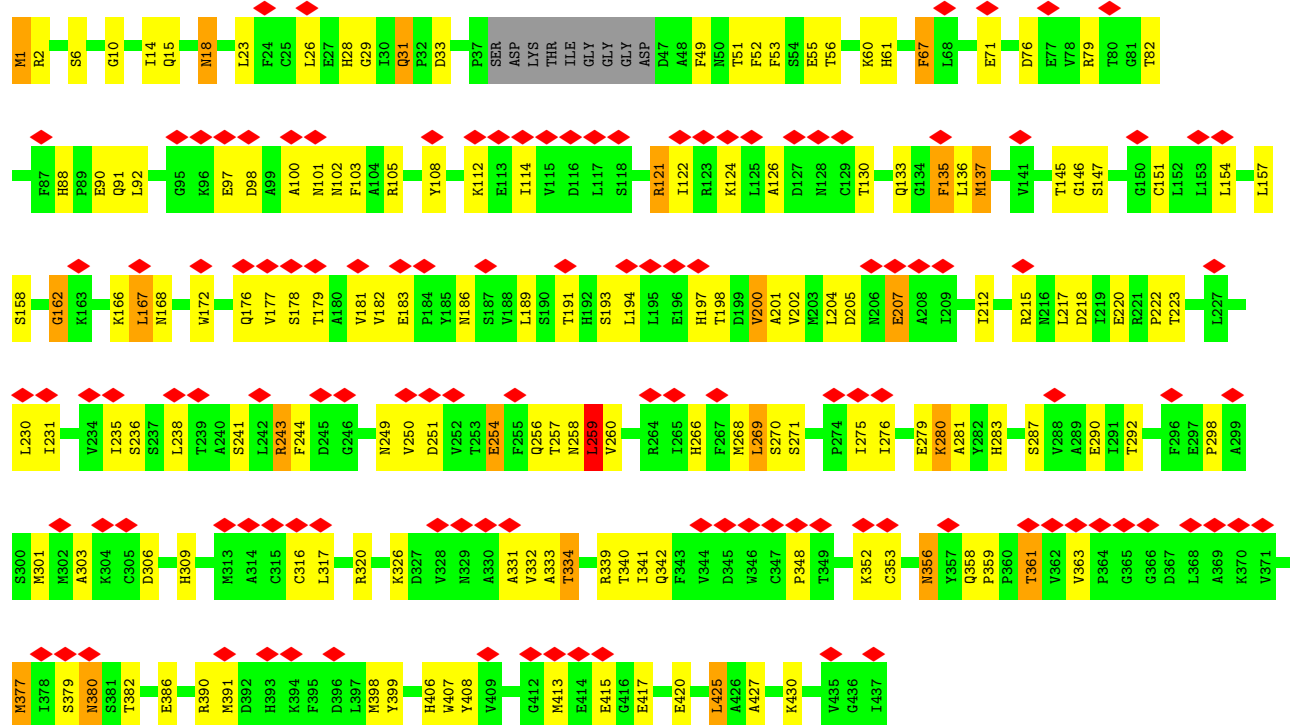
• Molecule 1: Tubulin alpha chain

Chain 4F: 



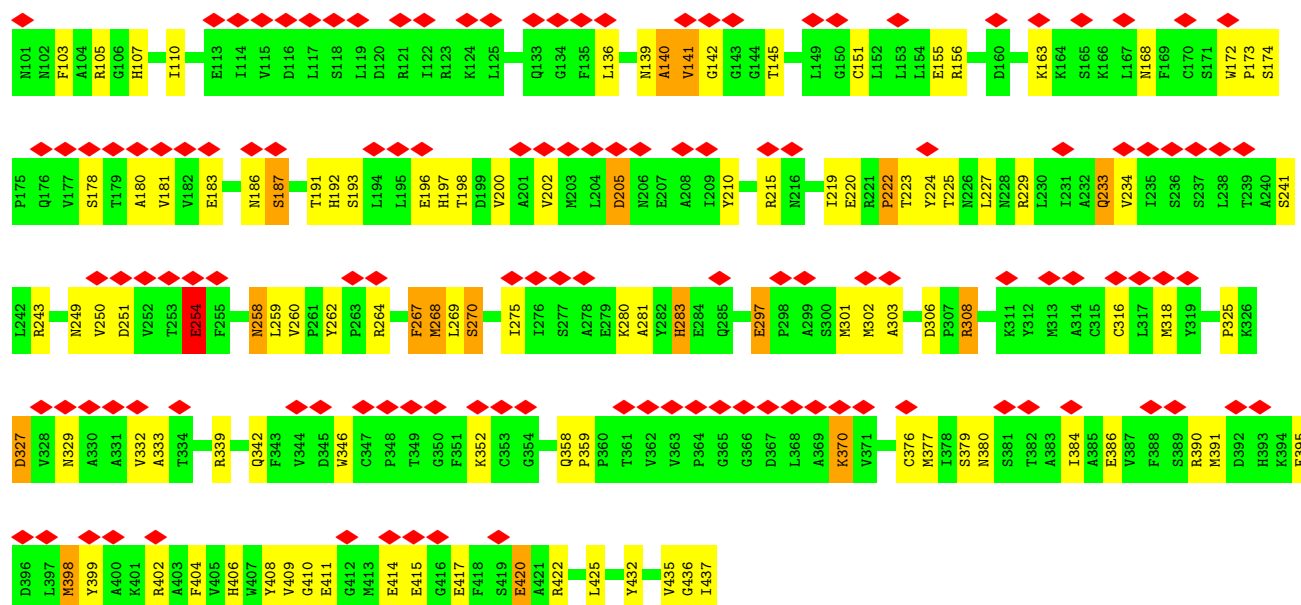


• Molecule 1: Tubulin alpha chain

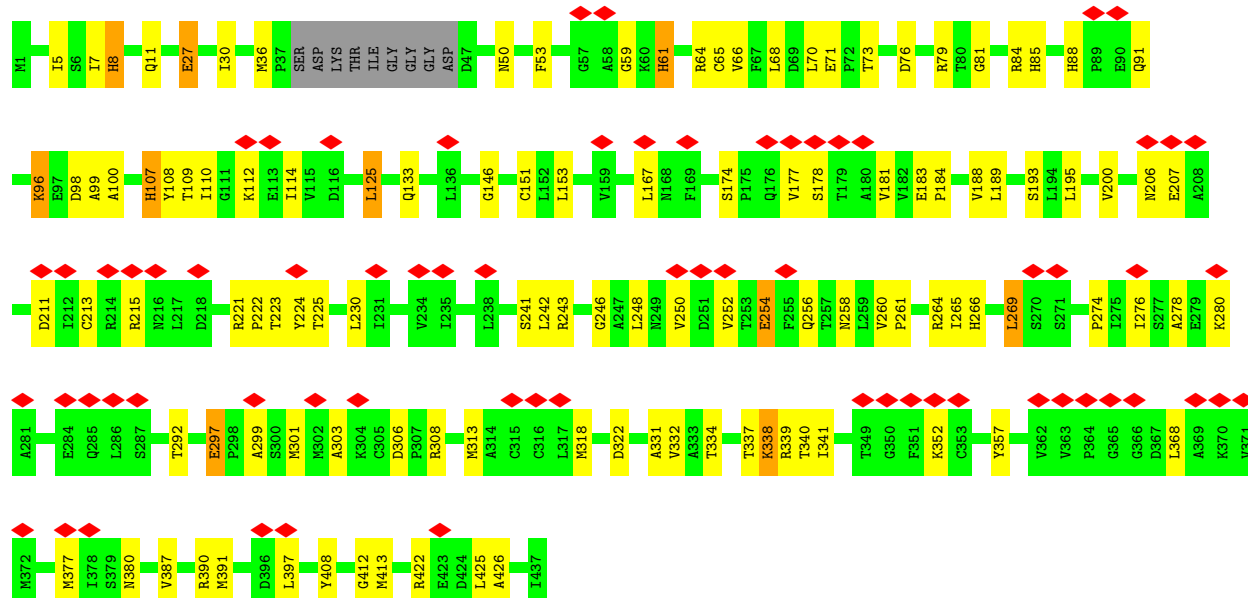
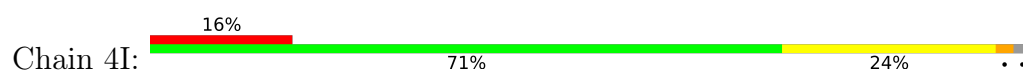


• Molecule 1: Tubulin alpha chain

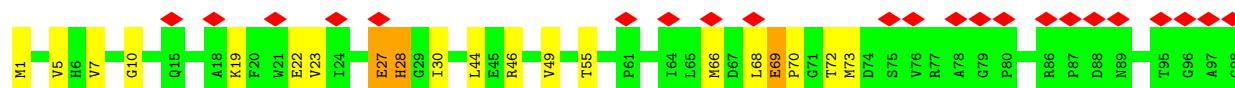
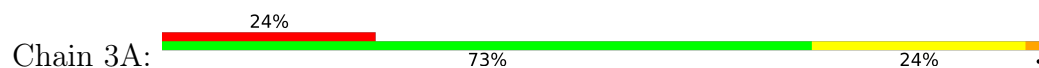


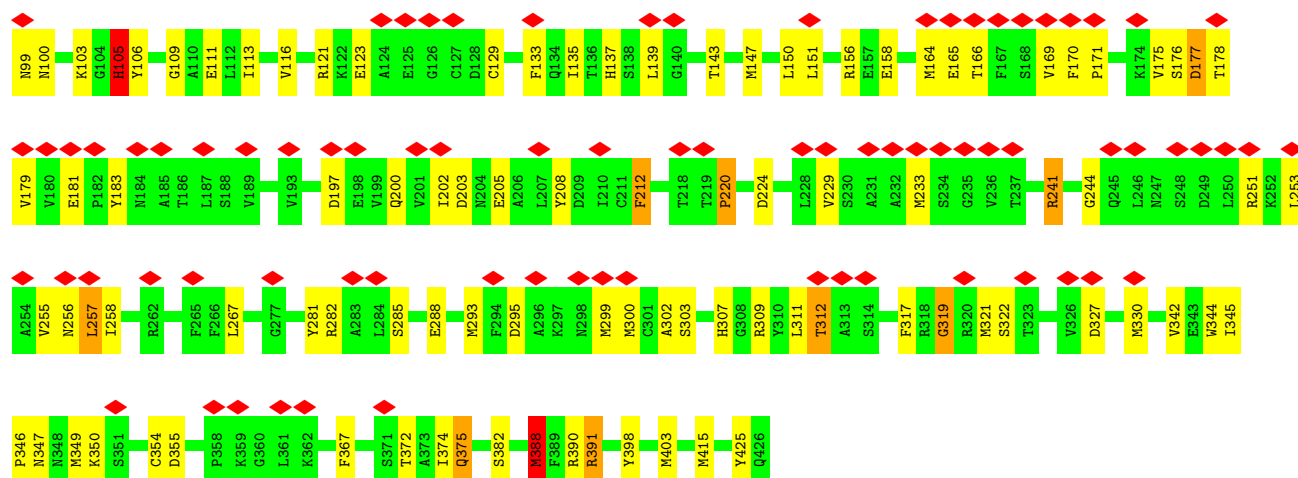


• Molecule 1: Tubulin alpha chain

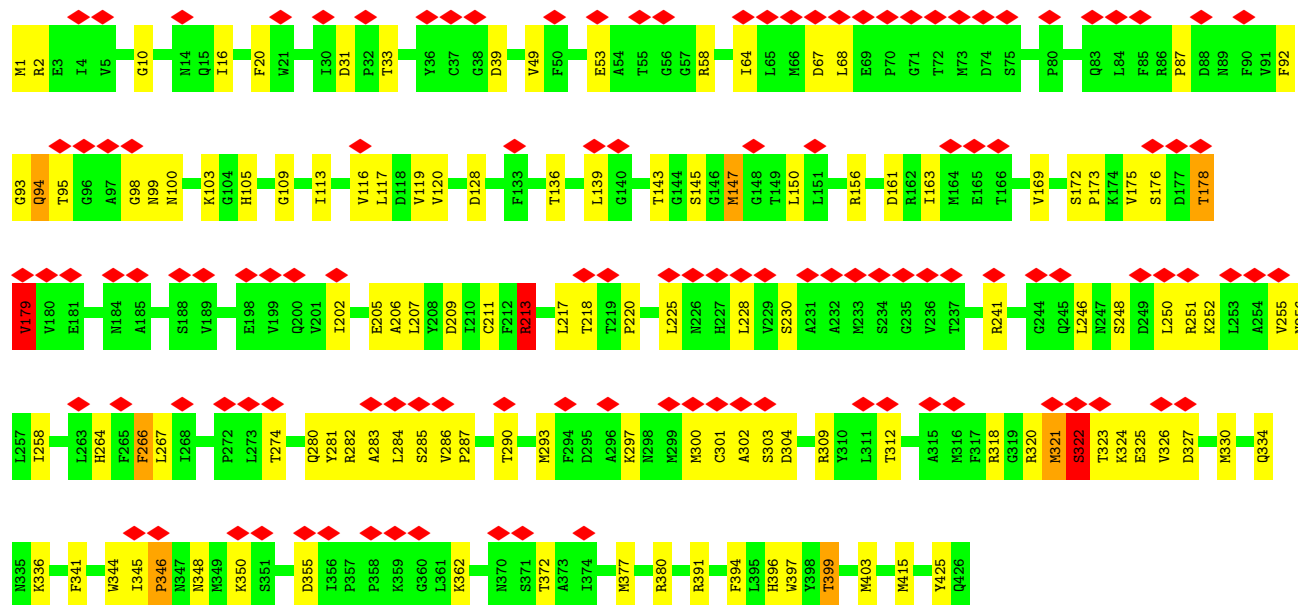


• Molecule 2: Tubulin beta chain

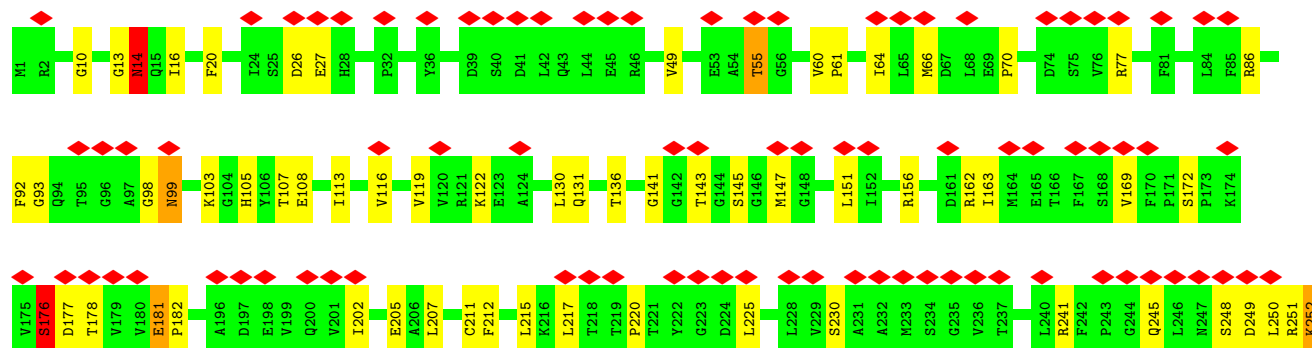
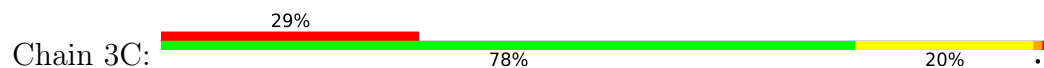


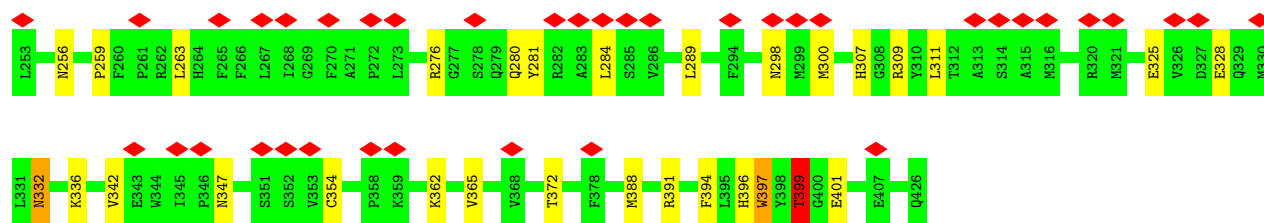


• Molecule 2: Tubulin beta chain

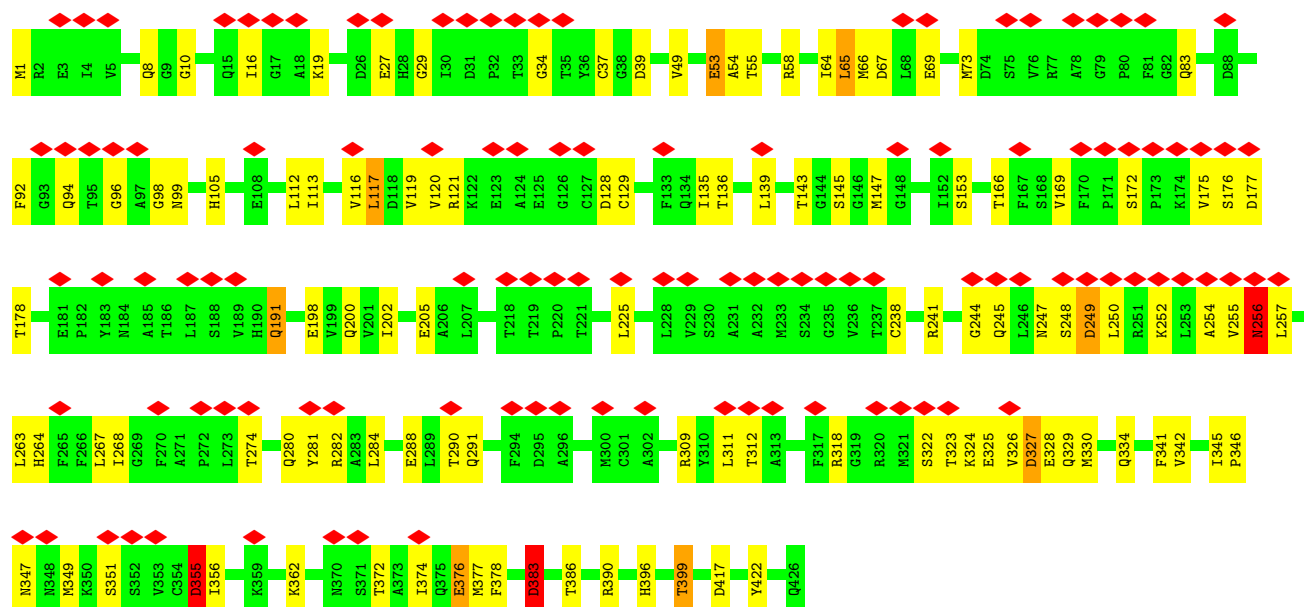
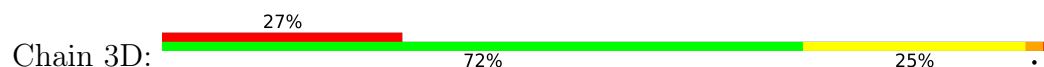


• Molecule 2: Tubulin beta chain

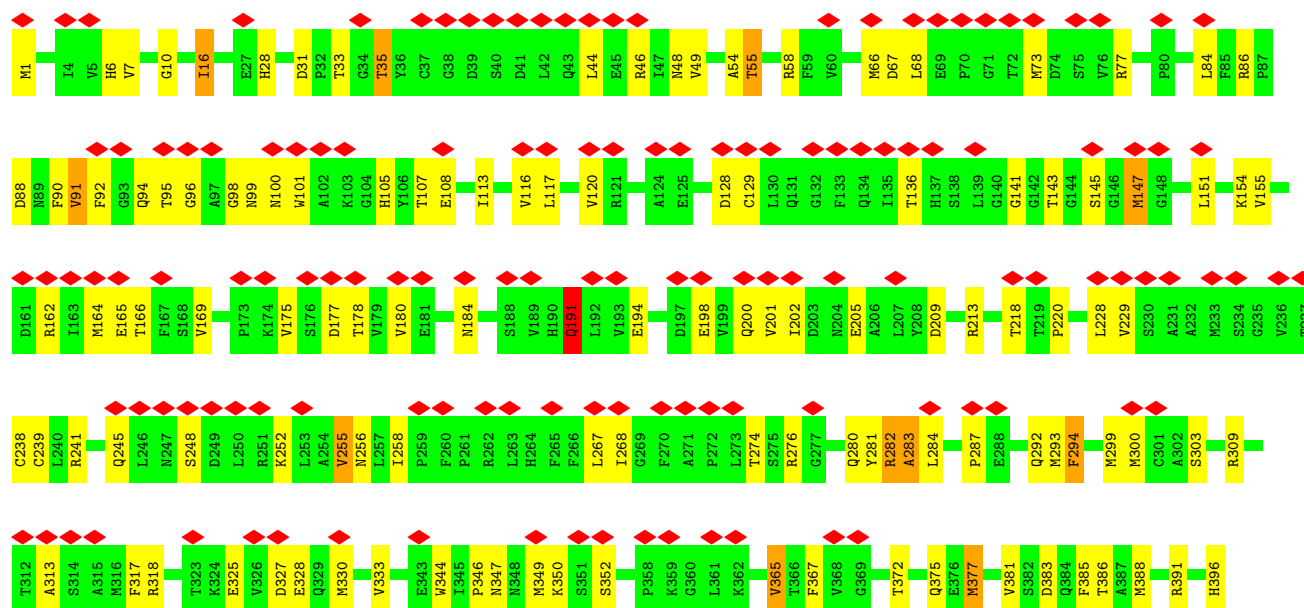


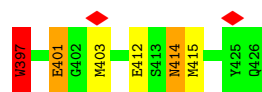


• Molecule 2: Tubulin beta chain

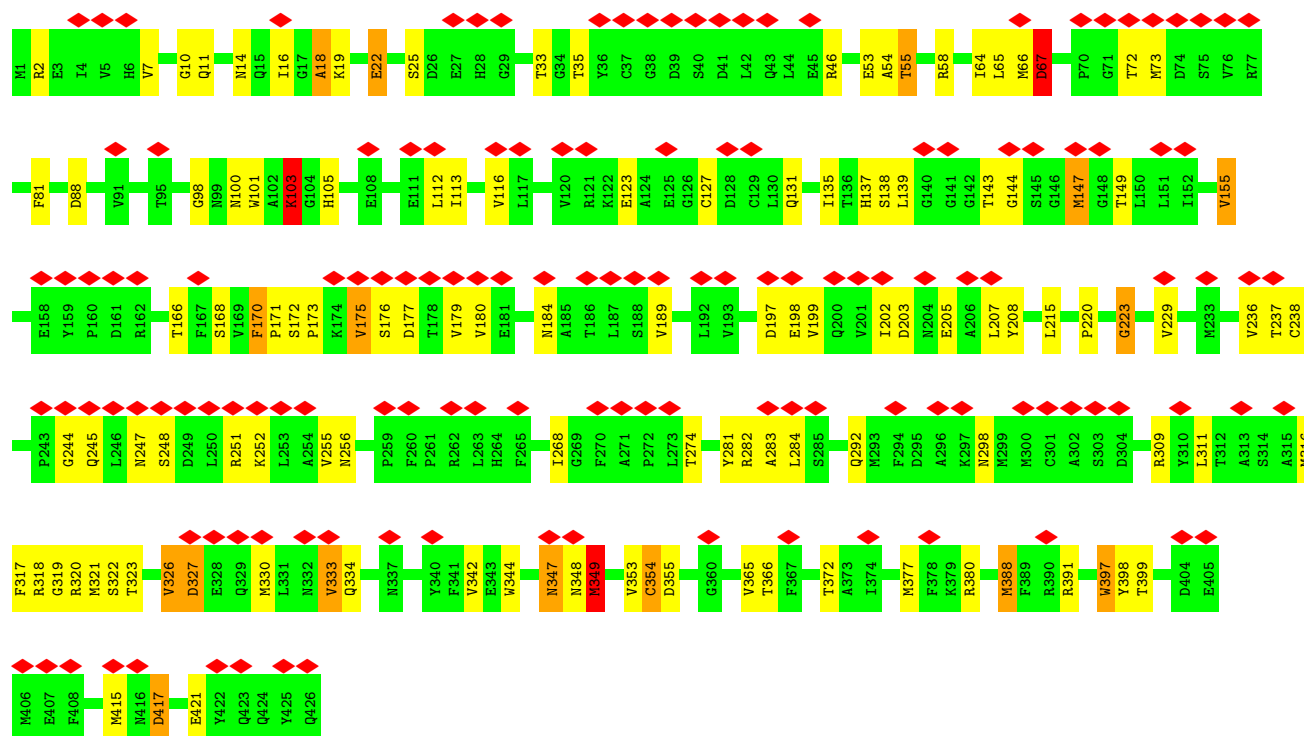
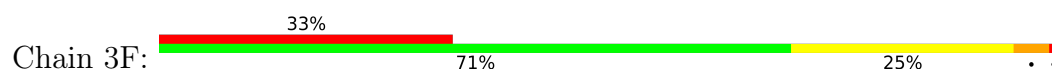


• Molecule 2: Tubulin beta chain

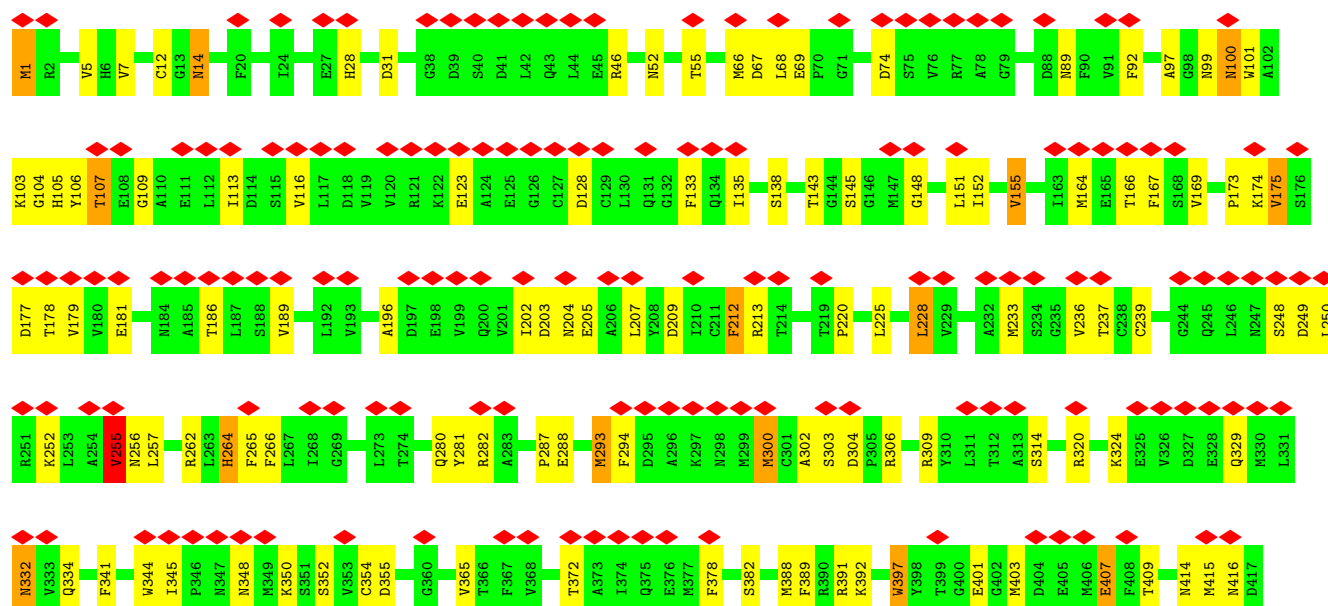
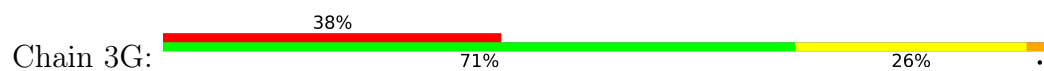


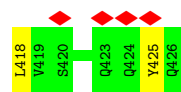


• Molecule 2: Tubulin beta chain

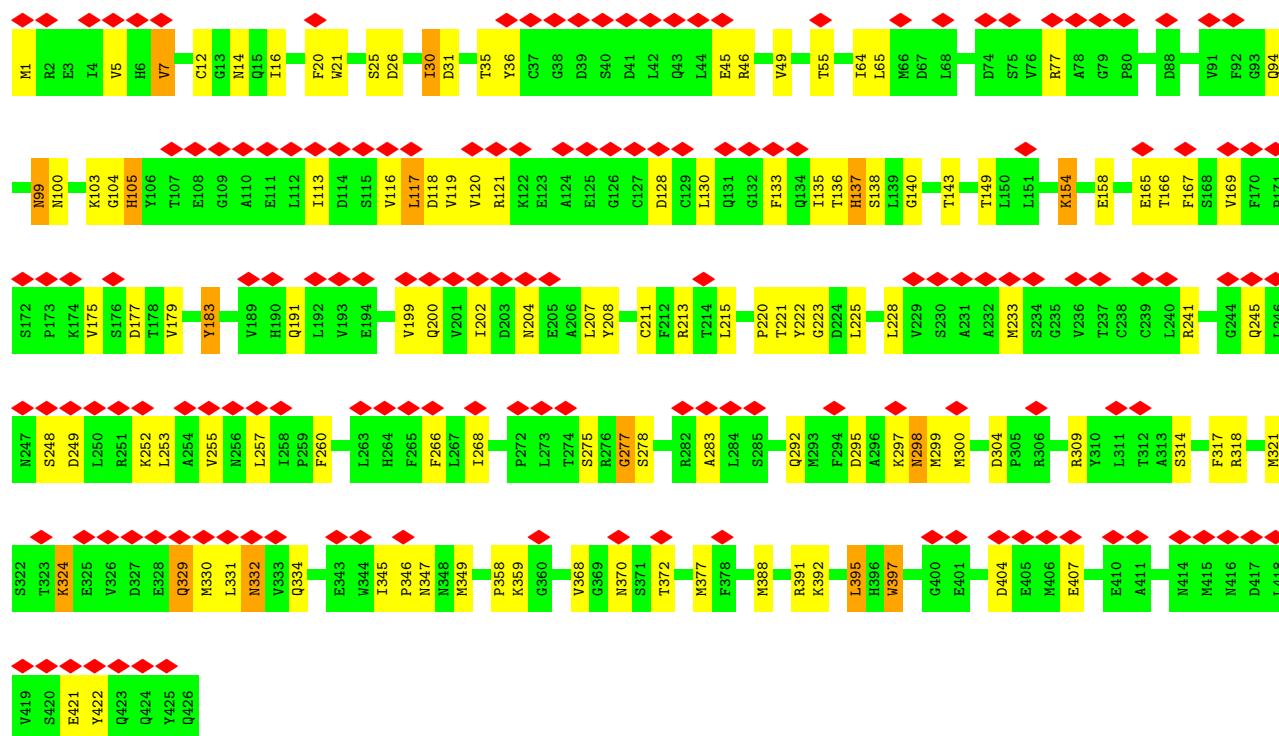
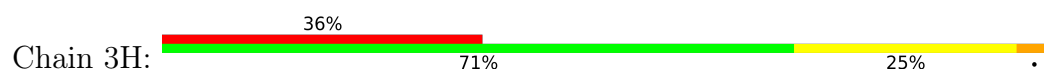


• Molecule 2: Tubulin beta chain

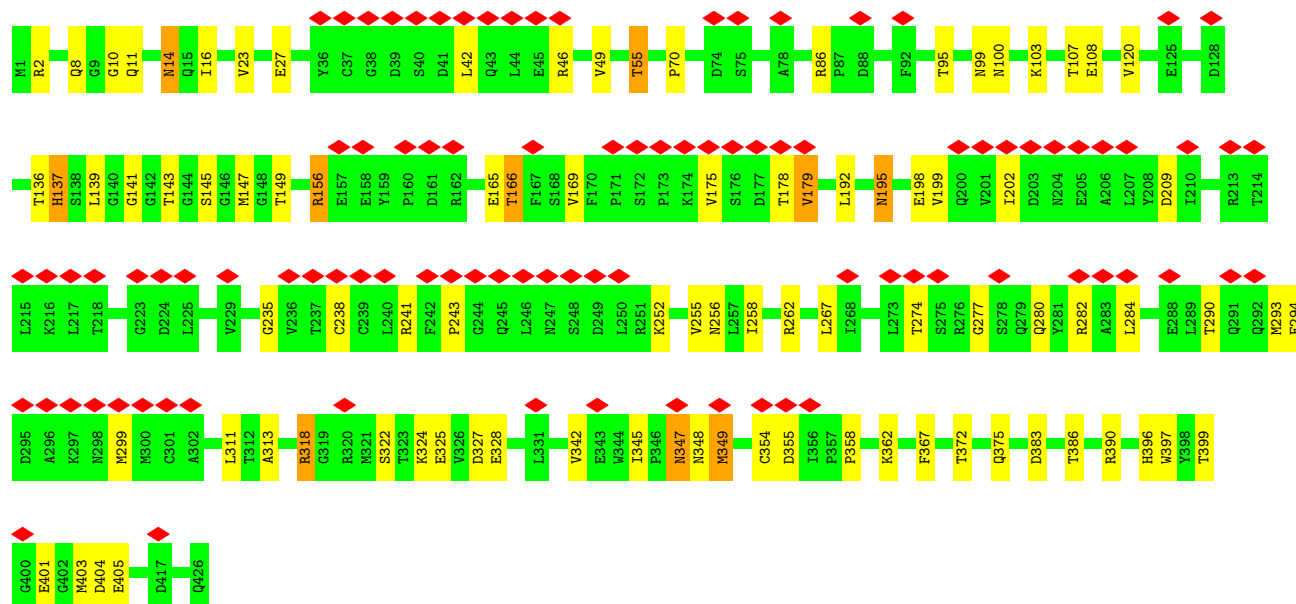
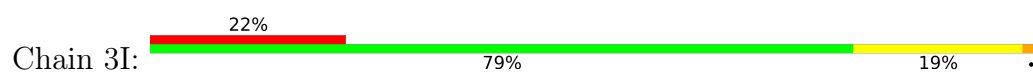




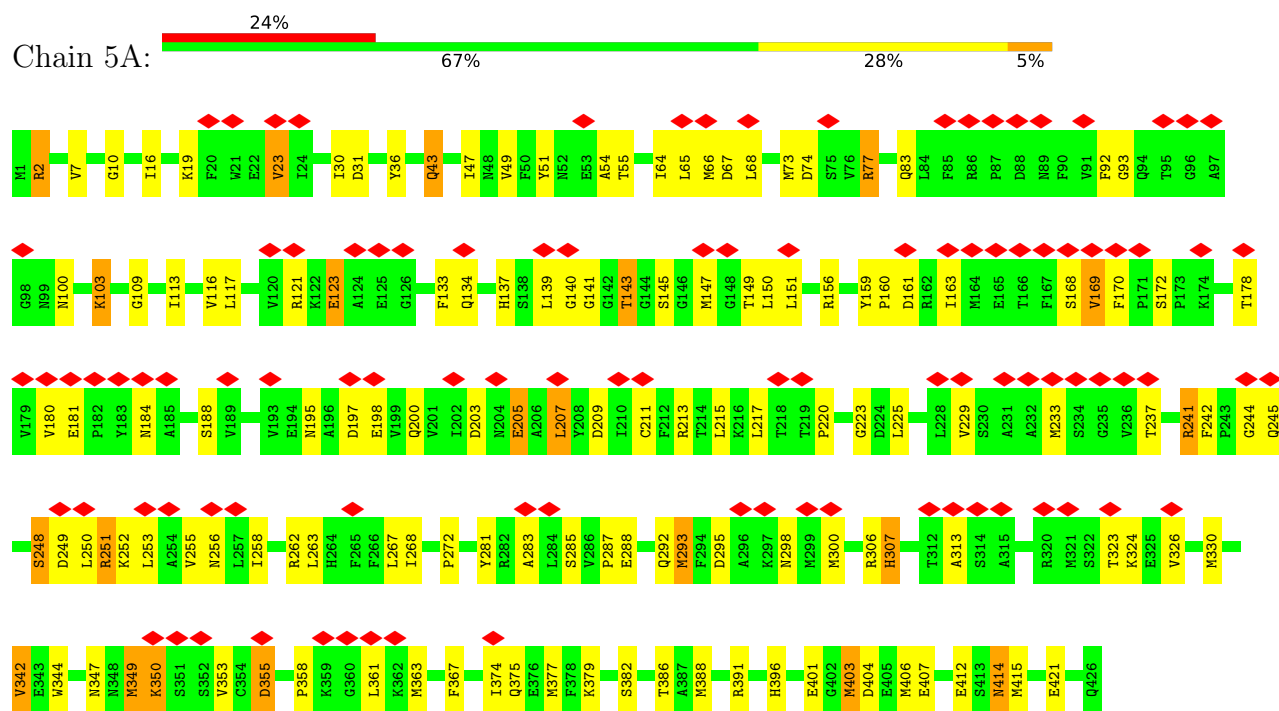
• Molecule 2: Tubulin beta chain



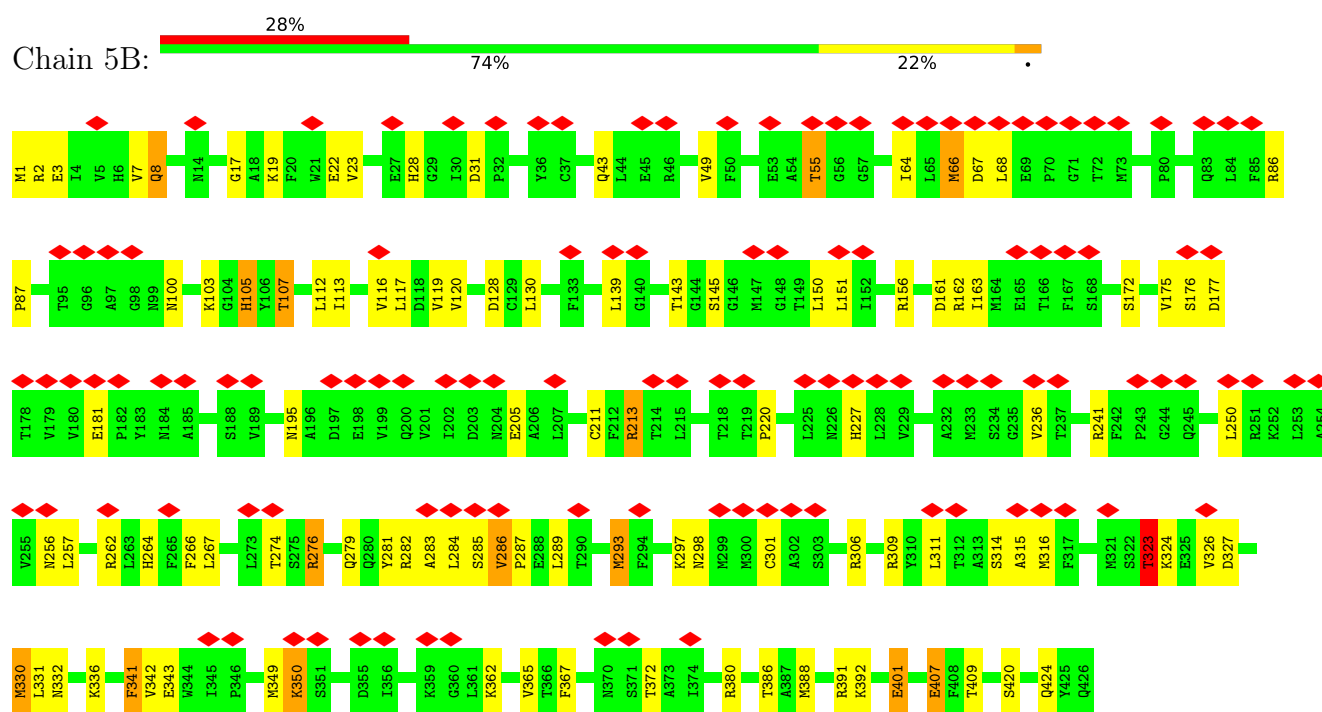
• Molecule 2: Tubulin beta chain



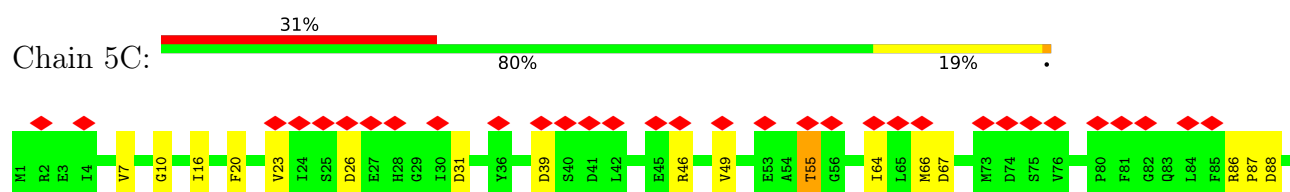
- Molecule 2: Tubulin beta chain

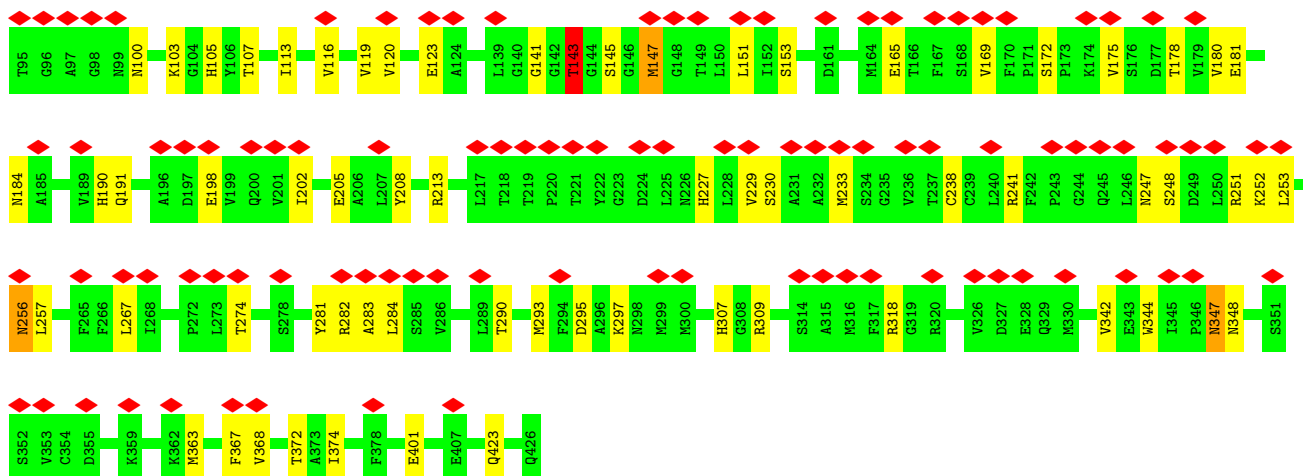


- Molecule 2: Tubulin beta chain

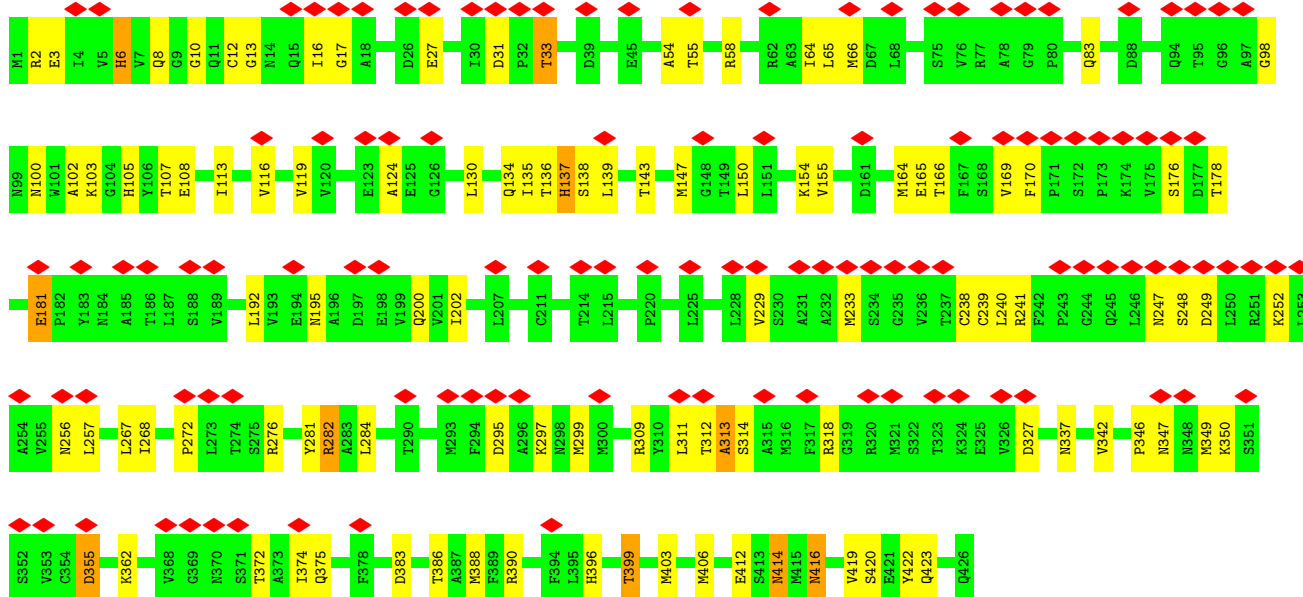
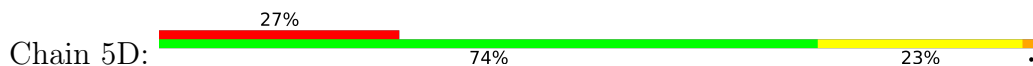


- Molecule 2: Tubulin beta chain

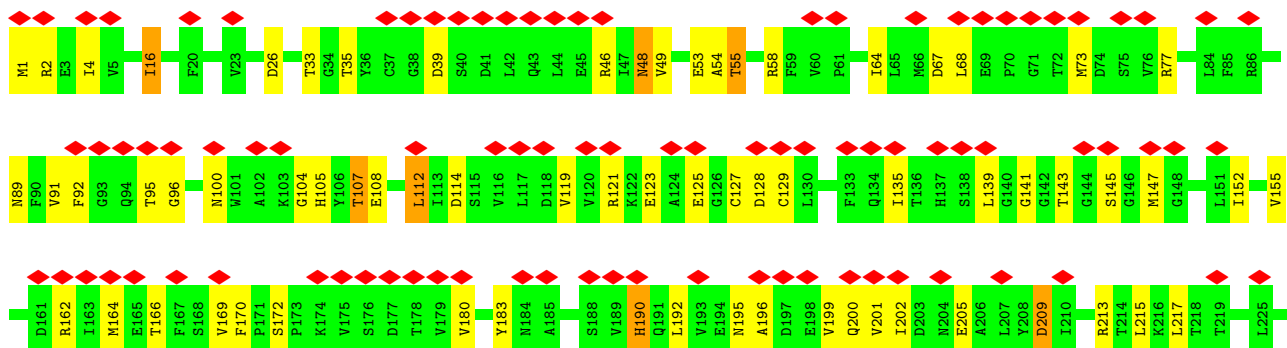
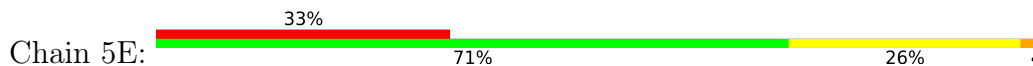


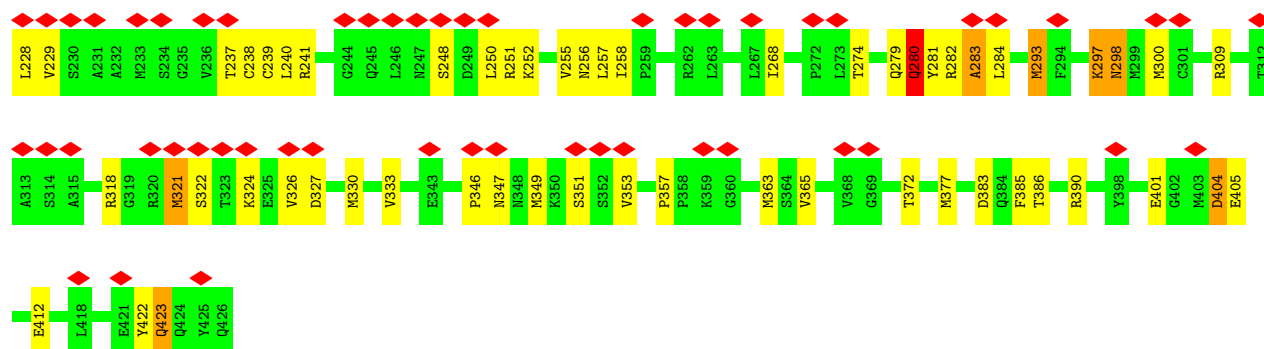


• Molecule 2: Tubulin beta chain

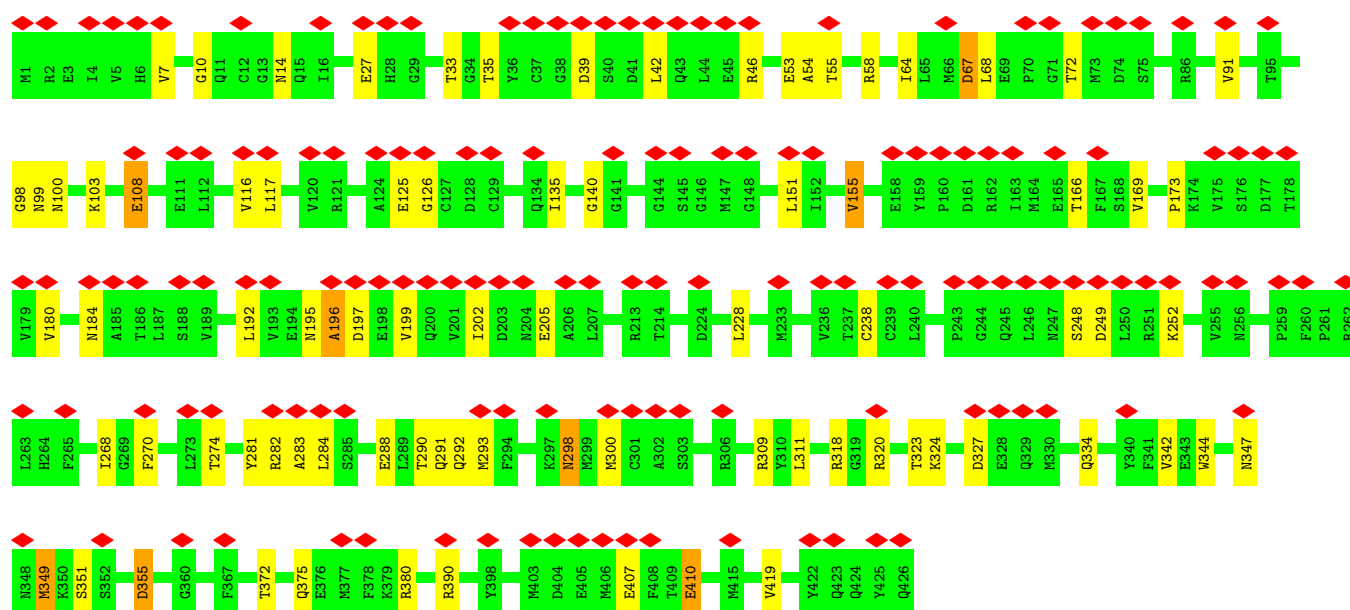
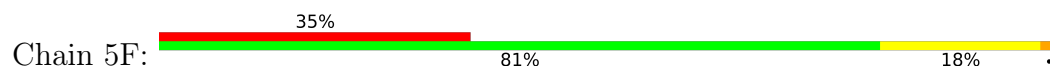


• Molecule 2: Tubulin beta chain

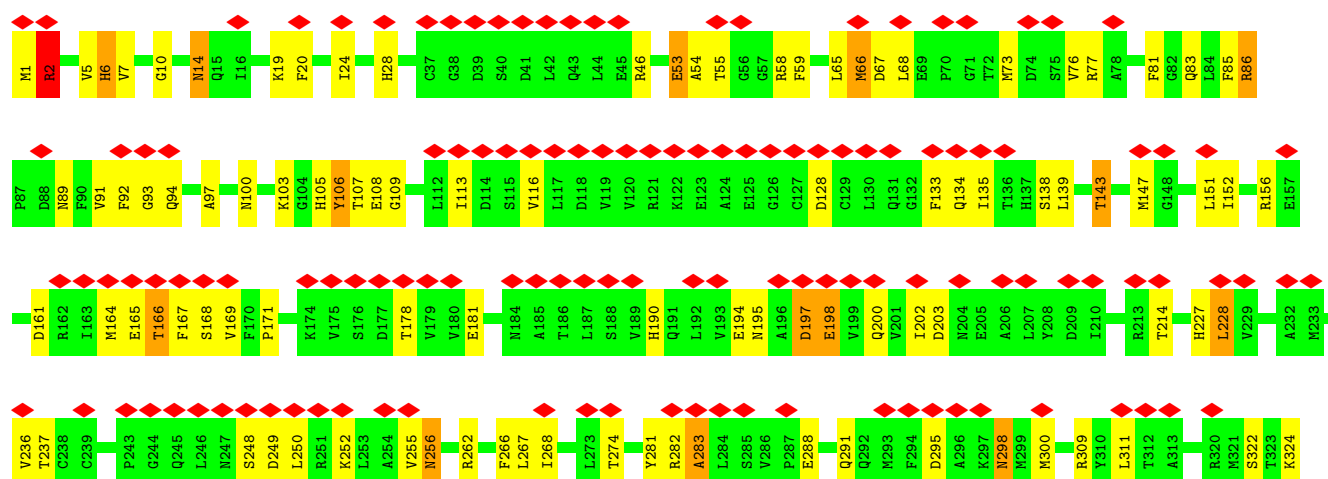


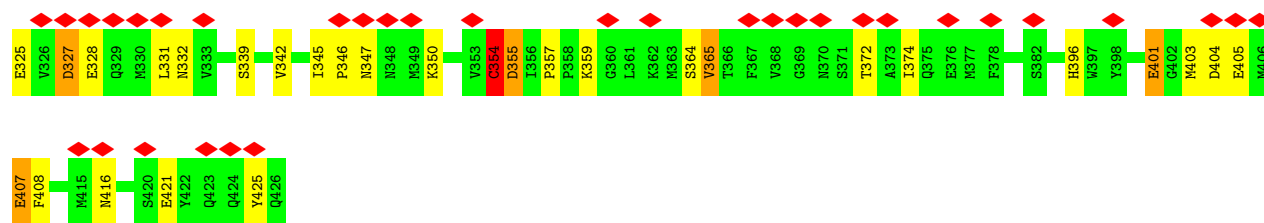


• Molecule 2: Tubulin beta chain

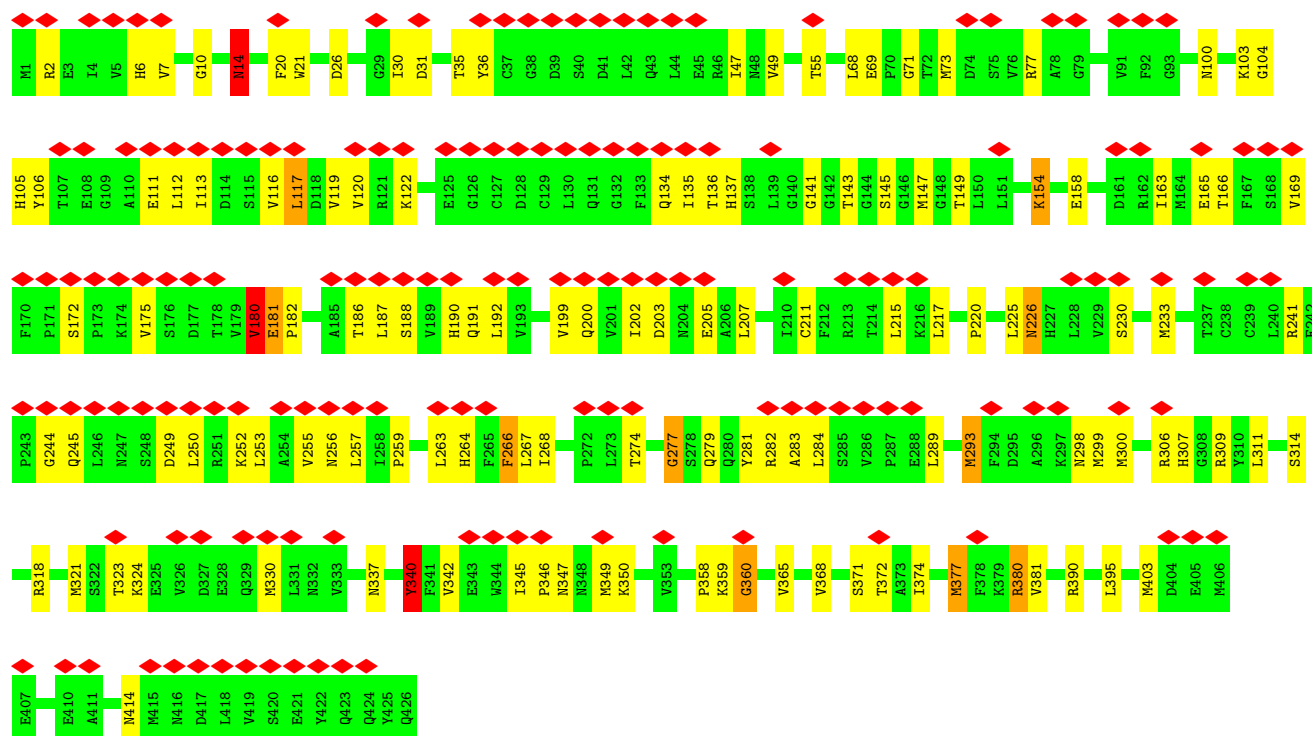
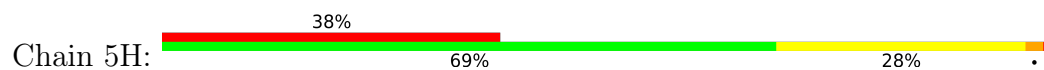


• Molecule 2: Tubulin beta chain

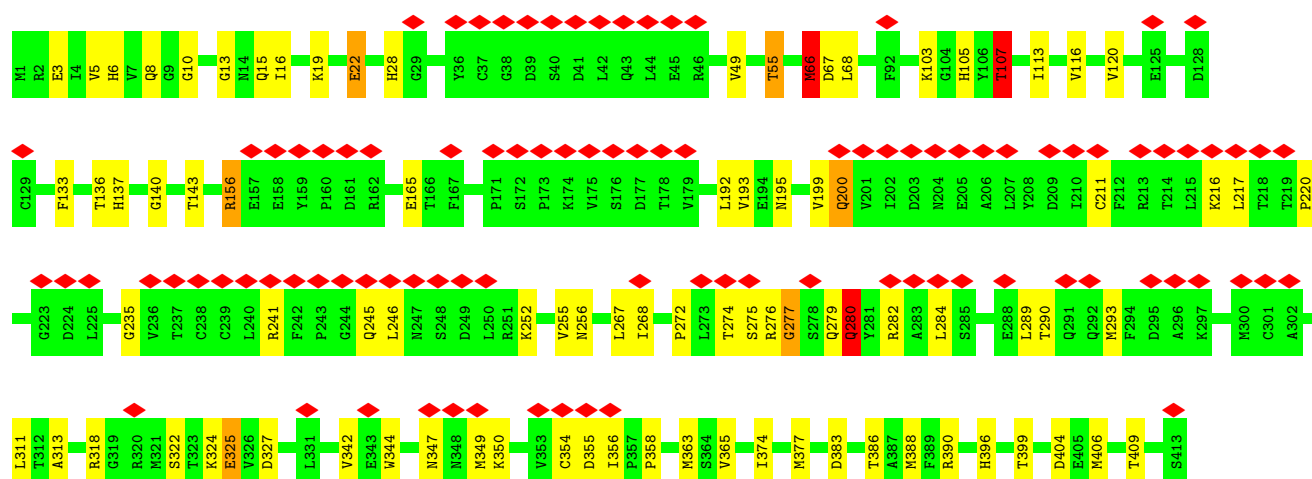
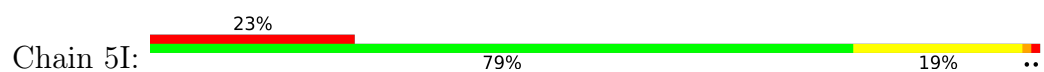




• Molecule 2: Tubulin beta chain



• Molecule 2: Tubulin beta chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	29524	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	96	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.463	Depositor
Minimum map value	-3.203	Depositor
Average map value	0.053	Depositor
Map value standard deviation	0.287	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	452.352, 452.352, 452.352	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.534, 3.534, 3.534	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	2A	1.13	7/3398 (0.2%)	1.42	28/4606 (0.6%)
1	2B	1.08	8/3398 (0.2%)	1.31	21/4606 (0.5%)
1	2C	1.03	6/3398 (0.2%)	1.23	16/4606 (0.3%)
1	2D	1.00	4/3398 (0.1%)	1.26	14/4606 (0.3%)
1	2E	1.07	9/3398 (0.3%)	1.32	24/4606 (0.5%)
1	2F	1.12	3/3398 (0.1%)	1.42	32/4606 (0.7%)
1	2G	1.21	13/3398 (0.4%)	1.49	33/4606 (0.7%)
1	2H	1.19	10/3398 (0.3%)	1.46	29/4606 (0.6%)
1	2I	1.04	3/3398 (0.1%)	1.31	23/4606 (0.5%)
1	4A	1.22	10/3398 (0.3%)	1.47	25/4606 (0.5%)
1	4B	1.09	9/3398 (0.3%)	1.30	20/4606 (0.4%)
1	4C	1.07	7/3398 (0.2%)	1.33	19/4606 (0.4%)
1	4D	1.05	5/3398 (0.1%)	1.31	19/4606 (0.4%)
1	4E	1.08	7/3398 (0.2%)	1.31	19/4606 (0.4%)
1	4F	1.11	10/3398 (0.3%)	1.35	20/4606 (0.4%)
1	4G	1.21	10/3398 (0.3%)	1.54	45/4606 (1.0%)
1	4H	1.20	9/3398 (0.3%)	1.46	30/4606 (0.7%)
1	4I	1.08	11/3398 (0.3%)	1.30	20/4606 (0.4%)
2	3A	1.15	7/3404 (0.2%)	1.42	30/4606 (0.7%)
2	3B	1.07	9/3404 (0.3%)	1.37	20/4606 (0.4%)
2	3C	1.02	4/3404 (0.1%)	1.26	18/4606 (0.4%)
2	3D	1.09	6/3404 (0.2%)	1.32	22/4606 (0.5%)
2	3E	1.04	5/3404 (0.1%)	1.33	24/4606 (0.5%)
2	3F	1.12	6/3404 (0.2%)	1.39	31/4606 (0.7%)
2	3G	1.24	12/3404 (0.4%)	1.49	39/4606 (0.8%)
2	3H	1.13	10/3404 (0.3%)	1.44	23/4606 (0.5%)
2	3I	1.02	1/3404 (0.0%)	1.30	22/4606 (0.5%)
2	5A	1.15	9/3404 (0.3%)	1.47	41/4606 (0.9%)
2	5B	1.07	5/3404 (0.1%)	1.35	28/4606 (0.6%)
2	5C	1.00	3/3404 (0.1%)	1.27	14/4606 (0.3%)
2	5D	1.06	4/3404 (0.1%)	1.31	21/4606 (0.5%)
2	5E	1.07	3/3404 (0.1%)	1.35	23/4606 (0.5%)
2	5F	1.10	4/3404 (0.1%)	1.30	14/4606 (0.3%)
2	5G	1.17	7/3404 (0.2%)	1.51	36/4606 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	5H	1.16	13/3404 (0.4%)	1.43	19/4606 (0.4%)
2	5I	1.05	2/3404 (0.1%)	1.33	23/4606 (0.5%)
All	All	1.10	251/122436 (0.2%)	1.37	885/165816 (0.5%)

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	2A	0	7
1	2B	0	5
1	2C	0	6
1	2D	0	3
1	2E	0	7
1	2F	0	7
1	2G	0	12
1	2H	0	8
1	2I	0	6
1	4A	0	10
1	4B	0	5
1	4C	0	6
1	4D	0	5
1	4E	0	8
1	4F	0	7
1	4G	0	7
1	4H	0	9
1	4I	0	5
2	3A	0	11
2	3B	0	7
2	3C	0	8
2	3D	0	8
2	3E	0	8
2	3F	0	8
2	3G	0	5
2	3H	0	9
2	3I	0	4
2	5A	0	14
2	5B	0	4
2	5C	0	6
2	5D	0	6
2	5E	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	5F	0	4
2	5G	0	12
2	5H	0	8
2	5I	0	5
All	All	0	259

All (251) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2E	8	HIS	CE1-NE2	-11.47	1.21	1.32
1	2F	107	HIS	CE1-NE2	11.16	1.43	1.32
2	3A	137	HIS	CE1-NE2	10.33	1.42	1.32
2	5B	264	HIS	CE1-NE2	-9.29	1.23	1.32
1	4C	8	HIS	CE1-NE2	-9.16	1.23	1.32
1	2B	392	ASP	CG-OD1	-8.73	1.08	1.25
2	3A	105	HIS	CE1-NE2	-8.57	1.24	1.32
1	4F	183	GLU	CD-OE2	-8.38	1.09	1.25
2	3D	264	HIS	ND1-CE1	-8.37	1.24	1.32
2	3H	167	PHE	C-O	-8.36	1.14	1.24
2	3E	28	HIS	CD2-NE2	-8.21	1.28	1.37
1	4F	392	ASP	CG-OD1	-8.13	1.09	1.25
2	3G	104	GLY	C-O	-7.91	1.14	1.23
1	4F	107	HIS	ND1-CE1	7.88	1.40	1.32
2	3G	264	HIS	CG-ND1	-7.83	1.29	1.38
1	4E	266	HIS	CE1-NE2	7.70	1.40	1.32
1	4H	61	HIS	CE1-NE2	7.54	1.40	1.32
1	4H	275	ILE	C-O	-7.53	1.14	1.23
2	3G	266	PHE	C-O	-7.51	1.14	1.24
2	5A	349	MET	C-O	-7.40	1.15	1.23
2	5F	249	ASP	CG-OD1	-7.37	1.11	1.25
1	2C	318	MET	C-O	-7.32	1.15	1.24
1	4I	8	HIS	CE1-NE2	-7.21	1.25	1.32
1	4G	306	ASP	CG-OD1	-7.19	1.11	1.25
2	5D	137	HIS	CE1-NE2	-7.12	1.25	1.32
1	2G	192	HIS	CE1-NE2	7.03	1.39	1.32
1	2G	107	HIS	CE1-NE2	7.01	1.39	1.32
2	5A	141	GLY	C-O	-6.97	1.17	1.23
2	5A	74	ASP	CG-OD1	-6.84	1.12	1.25
2	5E	196	ALA	CA-CB	-6.82	1.42	1.53
2	3G	105	HIS	CG-CD2	-6.80	1.28	1.35
1	2A	264	ARG	NE-CZ	-6.80	1.25	1.33
1	2E	267	PHE	C-O	-6.78	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4B	192	HIS	ND1-CE1	-6.78	1.25	1.32
2	3H	299	MET	C-O	-6.75	1.15	1.23
1	2H	342	GLN	C-O	-6.73	1.15	1.24
1	4E	192	HIS	CE1-NE2	6.66	1.39	1.32
2	5D	6	HIS	CE1-NE2	-6.64	1.25	1.32
1	2C	8	HIS	CG-ND1	-6.63	1.30	1.38
2	3G	304	ASP	CG-OD1	-6.60	1.12	1.25
1	4C	107	HIS	CE1-NE2	6.60	1.39	1.32
2	5H	180	VAL	C-O	-6.59	1.16	1.24
1	2F	266	HIS	CE1-NE2	-6.57	1.25	1.32
2	3A	165	GLU	C-O	-6.54	1.16	1.23
1	2B	309	HIS	CE1-NE2	6.53	1.39	1.32
2	3D	248	SER	C-N	-6.53	1.24	1.33
1	2E	77	GLU	CD-OE2	6.51	1.37	1.25
1	4C	61	HIS	CE1-NE2	-6.45	1.26	1.32
2	3A	288	GLU	CD-OE2	6.42	1.37	1.25
1	4A	98	ASP	CG-OD1	-6.39	1.13	1.25
1	4F	107	HIS	CD2-NE2	-6.36	1.30	1.37
1	4B	266	HIS	CG-ND1	-6.34	1.31	1.38
1	4G	250	VAL	C-O	-6.31	1.17	1.24
2	3D	29	GLY	C-O	-6.30	1.15	1.24
2	3E	31	ASP	CG-OD1	-6.29	1.13	1.25
2	5I	137	HIS	CE1-NE2	6.29	1.38	1.32
1	2E	391	MET	CG-SD	-6.28	1.65	1.80
1	2H	116	ASP	CG-OD2	6.26	1.37	1.25
1	4D	69	ASP	CG-OD2	-6.26	1.13	1.25
2	3A	303	SER	CA-CB	-6.23	1.44	1.53
1	4B	8	HIS	CG-ND1	-6.22	1.31	1.38
1	2I	327	ASP	CG-OD1	6.19	1.37	1.25
2	3B	355	ASP	C-O	-6.17	1.15	1.24
2	3G	148	GLY	C-O	-6.17	1.16	1.23
2	3F	199	VAL	C-O	-6.16	1.17	1.24
2	3G	31	ASP	CG-OD1	-6.13	1.13	1.25
2	5E	104	GLY	C-O	-6.13	1.16	1.24
2	5B	105	HIS	CE1-NE2	-6.13	1.26	1.32
1	2H	192	HIS	CE1-NE2	6.12	1.38	1.32
2	3G	92	PHE	C-N	-6.11	1.26	1.33
1	2G	61	HIS	CG-ND1	-6.10	1.31	1.38
2	5A	248	SER	C-N	-6.10	1.25	1.33
1	4B	192	HIS	CE1-NE2	-6.09	1.26	1.32
1	4D	392	ASP	CG-OD1	-6.09	1.13	1.25
2	5I	28	HIS	CE1-NE2	6.07	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4D	197	HIS	C-O	6.07	1.29	1.24
2	5H	380	ARG	NE-CZ	-6.05	1.26	1.33
1	4A	369	ALA	CA-CB	-6.04	1.44	1.53
1	4C	392	ASP	CG-OD1	-6.01	1.14	1.25
1	2G	4	VAL	C-O	-6.01	1.18	1.24
1	4I	341	ILE	C-O	-6.01	1.17	1.24
1	2A	318	MET	C-O	-5.96	1.17	1.23
2	5H	307	HIS	CG-ND1	-5.95	1.31	1.38
1	2H	278	ALA	C-O	-5.94	1.16	1.24
1	4A	57	GLY	C-O	-5.93	1.16	1.23
1	4E	316	CYS	C-O	-5.92	1.17	1.24
1	4F	174	SER	CB-OG	-5.90	1.30	1.42
1	2D	153	LEU	C-O	-5.89	1.16	1.24
1	2G	55	GLU	CA-CB	-5.89	1.45	1.53
1	2C	8	HIS	CE1-NE2	-5.88	1.26	1.32
1	4H	342	GLN	C-O	-5.88	1.17	1.24
2	3D	383	ASP	CG-OD1	-5.87	1.14	1.25
1	4G	406	HIS	CG-ND1	5.83	1.44	1.38
1	2H	257	THR	C-O	-5.82	1.16	1.24
1	4H	88	HIS	CG-ND1	-5.81	1.31	1.38
1	2A	169	PHE	C-O	-5.79	1.16	1.23
1	4H	205	ASP	CG-OD1	-5.78	1.14	1.25
2	3H	65	LEU	C-O	5.78	1.30	1.24
2	3C	130	LEU	C-O	-5.78	1.16	1.23
1	4E	243	ARG	C-O	-5.78	1.16	1.24
1	4G	167	LEU	C-O	-5.78	1.17	1.24
2	5B	401	GLU	C-O	-5.77	1.16	1.24
1	2B	160	ASP	CG-OD1	-5.77	1.14	1.25
2	3E	282	ARG	C-O	-5.76	1.17	1.24
1	4E	192	HIS	CG-ND1	5.75	1.44	1.38
2	3B	264	HIS	CG-ND1	-5.74	1.31	1.38
1	2B	205	ASP	CG-OD2	-5.72	1.14	1.25
2	3G	28	HIS	CD2-NE2	5.72	1.44	1.37
1	2E	193	SER	CA-CB	-5.71	1.43	1.53
2	3E	92	PHE	C-O	-5.70	1.16	1.23
1	4C	111	GLY	C-O	-5.70	1.17	1.23
1	4A	367	ASP	CG-OD1	-5.69	1.14	1.25
2	3I	137	HIS	CE1-NE2	5.68	1.38	1.32
1	4I	85	HIS	CG-ND1	5.67	1.44	1.38
2	3B	399	THR	C-O	-5.67	1.17	1.24
2	3B	318	ARG	NE-CZ	-5.66	1.26	1.33
2	3F	177	ASP	CG-OD2	-5.65	1.14	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2H	187	SER	C-N	-5.63	1.26	1.33
1	2H	192	HIS	ND1-CE1	-5.63	1.26	1.32
2	3B	304	ASP	CG-OD2	-5.62	1.14	1.25
2	3H	275	SER	C-O	-5.61	1.16	1.23
1	4I	387	VAL	C-O	-5.59	1.16	1.24
2	5H	154	LYS	C-O	-5.58	1.17	1.24
2	5H	244	GLY	C-O	-5.58	1.18	1.23
1	2E	55	GLU	C-O	-5.57	1.17	1.24
1	4H	28	HIS	CG-ND1	5.55	1.44	1.38
1	2H	251	ASP	CG-OD2	-5.55	1.14	1.25
1	4A	266	HIS	ND1-CE1	5.54	1.38	1.32
2	3F	144	GLY	C-O	-5.53	1.17	1.24
2	5H	6	HIS	CE1-NE2	-5.53	1.27	1.32
1	4I	254	GLU	C-O	-5.48	1.17	1.24
1	2E	201	ALA	C-O	-5.48	1.17	1.24
1	2G	290	GLU	CD-OE1	5.46	1.35	1.25
1	4A	396	ASP	CG-OD2	-5.44	1.15	1.25
1	2G	396	ASP	CG-OD2	-5.44	1.15	1.25
2	3H	177	ASP	CG-OD2	-5.43	1.15	1.25
1	4A	428	LEU	C-O	-5.43	1.17	1.24
1	2G	406	HIS	CG-ND1	5.43	1.44	1.38
2	5B	293	MET	CB-CG	-5.43	1.36	1.52
1	2H	285	GLN	C-O	-5.42	1.17	1.24
2	3F	127	CYS	C-O	-5.42	1.17	1.24
1	4A	8	HIS	CG-CD2	-5.41	1.29	1.35
2	5C	67	ASP	CG-OD1	-5.41	1.15	1.25
2	5E	209	ASP	CG-OD1	-5.40	1.15	1.25
1	4I	266	HIS	C-O	-5.40	1.17	1.24
1	2A	250	VAL	C-N	-5.40	1.26	1.33
1	4G	202	VAL	C-O	-5.39	1.18	1.24
1	2G	413	MET	C-O	-5.39	1.17	1.24
2	5H	134	GLN	C-O	-5.39	1.17	1.24
1	2G	167	LEU	C-O	-5.39	1.17	1.23
2	5F	249	ASP	C-O	-5.39	1.17	1.23
2	5G	288	GLU	CD-OE1	5.38	1.35	1.25
2	3C	176	SER	CA-CB	-5.37	1.44	1.53
1	2D	61	HIS	CE1-NE2	5.37	1.38	1.32
1	4H	422	ARG	CD-NE	-5.36	1.38	1.46
2	5A	401	GLU	CD-OE1	5.36	1.35	1.25
1	2D	69	ASP	CG-OD2	-5.35	1.15	1.25
2	5H	104	GLY	C-O	-5.34	1.17	1.23
2	3G	303	SER	CA-CB	-5.34	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	3H	104	GLY	C-O	-5.34	1.17	1.23
2	3A	44	LEU	CA-CB	5.33	1.60	1.53
1	4E	116	ASP	CG-OD1	5.32	1.35	1.25
1	2B	163	LYS	C-O	-5.32	1.17	1.24
2	3C	61	PRO	C-O	-5.32	1.17	1.23
1	4I	339	ARG	NE-CZ	5.32	1.38	1.33
1	4A	266	HIS	CG-ND1	-5.30	1.32	1.38
1	4F	309	HIS	ND1-CE1	-5.30	1.27	1.32
2	3F	319	GLY	C-O	-5.30	1.18	1.23
1	2G	2	ARG	C-O	-5.30	1.17	1.23
2	3B	320	ARG	C-O	-5.30	1.17	1.23
1	4F	326	LYS	C-O	-5.30	1.17	1.24
2	5H	264	HIS	CG-ND1	-5.30	1.32	1.38
2	5H	264	HIS	CE1-NE2	-5.30	1.27	1.32
2	3B	93	GLY	C-O	-5.28	1.16	1.23
1	2B	251	ASP	CG-OD2	-5.28	1.15	1.25
1	4F	197	HIS	CG-ND1	5.28	1.44	1.38
1	2E	284	GLU	C-O	-5.28	1.17	1.24
1	4C	193	SER	CA-CB	-5.27	1.44	1.53
2	5C	175	VAL	C-O	-5.26	1.18	1.24
2	5G	92	PHE	C-N	-5.26	1.26	1.33
2	3A	300	MET	C-O	-5.25	1.17	1.24
2	5G	28	HIS	CD2-NE2	5.25	1.43	1.37
2	5G	401	GLU	CD-OE1	-5.25	1.15	1.25
1	4H	192	HIS	CG-ND1	-5.23	1.32	1.38
2	5G	6	HIS	CG-ND1	-5.23	1.32	1.38
2	3G	1	MET	N-CA	-5.23	1.36	1.46
2	3B	264	HIS	CE1-NE2	-5.23	1.27	1.32
2	5A	163	ILE	C-O	-5.23	1.17	1.24
2	3C	399	THR	C-O	-5.21	1.17	1.24
1	4H	420	GLU	CD-OE1	-5.21	1.15	1.25
1	4F	349	THR	C-O	-5.20	1.17	1.23
1	4C	283	HIS	ND1-CE1	-5.20	1.27	1.32
1	4I	61	HIS	CG-ND1	-5.20	1.32	1.38
2	5G	203	ASP	CG-OD2	5.20	1.35	1.25
1	2C	153	LEU	C-O	-5.19	1.17	1.24
1	2C	266	HIS	CG-ND1	5.19	1.44	1.38
2	3H	7	VAL	C-O	-5.19	1.18	1.24
2	5F	195	ASN	C-O	-5.19	1.17	1.24
1	2A	304	LYS	C-O	-5.18	1.17	1.24
1	2F	69	ASP	CG-OD2	5.18	1.35	1.25
2	3F	138	SER	C-O	-5.18	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4D	16	ILE	C-O	-5.17	1.18	1.24
1	4I	242	LEU	C-O	-5.17	1.17	1.24
2	5A	355	ASP	C-O	-5.17	1.17	1.24
1	4B	177	VAL	C-O	-5.17	1.18	1.24
1	4G	147	SER	CA-CB	-5.17	1.45	1.53
1	2B	8	HIS	CE1-NE2	-5.16	1.27	1.32
2	5A	342	VAL	C-O	-5.15	1.17	1.24
1	2D	266	HIS	CG-ND1	5.15	1.44	1.38
1	4B	284	GLU	CD-OE2	5.14	1.35	1.25
2	3E	209	ASP	CG-OD2	5.14	1.35	1.25
1	4F	168	ASN	C-O	-5.14	1.17	1.24
1	2A	34	GLY	C-O	-5.14	1.18	1.24
1	2G	147	SER	CA-CB	-5.14	1.45	1.53
2	5B	177	ASP	CG-OD2	5.14	1.35	1.25
1	4D	127	ASP	CG-OD2	-5.14	1.15	1.25
1	2G	283	HIS	CG-ND1	-5.14	1.32	1.38
2	3G	105	HIS	CG-ND1	-5.12	1.32	1.38
1	4A	225	THR	C-O	-5.12	1.17	1.24
2	5A	160	PRO	C-O	-5.12	1.17	1.24
2	3D	264	HIS	CG-CD2	-5.11	1.30	1.35
1	2A	309	HIS	C-O	-5.10	1.17	1.24
2	3H	154	LYS	C-O	-5.10	1.18	1.24
1	2E	8	HIS	CG-ND1	-5.08	1.32	1.38
1	4I	7	ILE	CG1-CD1	-5.08	1.31	1.51
1	4G	29	GLY	C-O	-5.08	1.16	1.24
2	5D	420	SER	C-O	-5.07	1.17	1.24
2	5H	299	MET	C-O	-5.07	1.17	1.23
1	2C	136	LEU	C-O	-5.06	1.17	1.24
2	5C	190	HIS	CG-ND1	-5.06	1.32	1.38
1	2I	129	CYS	C-O	-5.06	1.17	1.23
1	4G	49	PHE	C-O	-5.06	1.17	1.24
1	4G	135	PHE	C-O	-5.05	1.17	1.23
2	5H	371	SER	C-O	-5.05	1.17	1.23
2	5H	377	MET	CG-SD	5.05	1.93	1.80
1	2H	197	HIS	CD2-NE2	-5.05	1.32	1.37
1	4I	27	GLU	CD-OE1	5.05	1.34	1.25
1	2I	383	ALA	C-N	-5.05	1.28	1.34
2	3H	137	HIS	CE1-NE2	5.05	1.37	1.32
1	2B	276	ILE	C-O	5.04	1.29	1.23
1	4G	377	MET	CG-SD	-5.04	1.68	1.80
2	5G	161	ASP	C-O	-5.03	1.17	1.24
2	3D	327	ASP	CG-OD1	-5.03	1.15	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4B	300	SER	CA-CB	-5.03	1.45	1.53
2	5D	181	GLU	CD-OE1	-5.03	1.15	1.25
2	3H	105	HIS	ND1-CE1	-5.03	1.27	1.32
1	4B	192	HIS	CG-ND1	5.02	1.43	1.38
2	5F	410	GLU	CD-OE1	-5.01	1.15	1.25
1	4B	192	HIS	CG-CD2	-5.01	1.30	1.35
1	4E	194	LEU	C-O	-5.00	1.17	1.24
2	3B	322	SER	CA-CB	-5.00	1.45	1.53

All (885) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3I	375	GLN	CB-CG-CD	-13.58	89.52	112.60
1	2F	386	GLU	CB-CG-CD	10.86	131.06	112.60
1	2F	358	GLN	CB-CA-C	10.83	126.84	109.51
2	3F	298	ASN	OD1-CG-ND2	-10.40	112.20	122.60
2	5I	325	GLU	N-CA-CB	10.17	126.00	110.44
1	4D	392	ASP	CA-CB-CG	10.03	122.63	112.60
1	4D	215	ARG	CG-CD-NE	9.92	133.82	112.00
1	2G	142	GLY	CA-C-N	-9.85	113.66	122.43
1	2G	142	GLY	C-N-CA	-9.85	113.66	122.43
2	3H	298	ASN	CA-CB-CG	9.81	122.41	112.60
2	5E	121	ARG	CB-CA-C	-9.79	94.21	110.85
2	3A	391	ARG	CB-CG-CD	9.75	133.73	111.30
2	5A	123	GLU	CB-CG-CD	9.39	128.56	112.60
1	4G	130	THR	OG1-CB-CG2	9.29	127.88	109.30
1	2A	181	VAL	CA-CB-CG2	9.26	126.14	110.40
1	2F	22	GLU	N-CA-CB	9.22	123.94	110.20
1	4E	134	GLY	CA-C-O	-9.21	114.56	120.91
2	5E	121	ARG	CA-CB-CG	9.16	132.42	114.10
1	4A	420	GLU	N-CA-CB	9.15	124.40	110.30
1	2F	390	ARG	CG-CD-NE	9.12	132.06	112.00
1	2D	215	ARG	CG-CD-NE	9.06	131.93	112.00
2	3H	298	ASN	OD1-CG-ND2	-9.04	113.56	122.60
1	4E	11	GLN	OE1-CD-NE2	8.96	131.56	122.60
1	2G	88	HIS	CA-CB-CG	8.82	122.62	113.80
1	2H	339	ARG	O-C-N	-8.79	111.45	122.26
1	2I	392	ASP	CA-CB-CG	8.75	121.35	112.60
2	5G	214	THR	CA-CB-OG1	8.72	122.68	109.60
1	4I	391	MET	CB-CG-SD	-8.70	86.61	112.70
2	3H	14	ASN	CB-CG-ND2	8.63	129.34	116.40
2	3F	327	ASP	CA-CB-CG	-8.53	104.07	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3H	370	ASN	OD1-CG-ND2	-8.45	114.15	122.60
2	5H	31	ASP	CA-CB-CG	8.43	121.03	112.60
1	2B	402	ARG	CG-CD-NE	8.39	130.46	112.00
2	3A	69	GLU	CB-CG-CD	8.35	126.79	112.60
1	4G	218	ASP	CA-CB-CG	8.34	120.94	112.60
1	2A	208	ALA	CA-C-O	-8.32	111.73	120.55
1	4F	3	GLU	CB-CG-CD	8.32	126.74	112.60
2	3G	302	ALA	CA-C-O	-8.31	110.42	119.97
1	4G	162	GLY	CA-C-O	-8.26	111.21	120.30
1	2H	415	GLU	CA-C-O	8.26	130.31	121.55
2	3F	223	GLY	CA-C-O	-8.25	111.92	120.66
2	3G	107	THR	CA-CB-OG1	8.25	121.97	109.60
1	2I	383	ALA	O-C-N	-8.22	111.11	122.46
2	5I	200	GLN	CB-CA-C	8.21	123.80	110.16
1	2H	214	ARG	CA-C-O	8.17	129.30	120.55
2	5A	241	ARG	CG-CD-NE	8.17	129.98	112.00
1	4E	176	GLN	CA-C-O	-8.13	110.32	119.67
1	4G	279	GLU	CB-CA-C	-8.08	97.11	110.85
1	4D	16	ILE	CB-CA-C	8.07	123.35	112.22
1	4A	102	ASN	OD1-CG-ND2	8.06	130.66	122.60
2	3A	354	CYS	O-C-N	-8.05	113.79	123.29
1	2E	423	GLU	CB-CG-CD	8.01	126.22	112.60
2	5I	3	GLU	CB-CG-CD	8.01	126.22	112.60
1	4G	137	MET	O-C-N	-8.01	113.87	123.16
1	4F	139	ASN	OD1-CG-ND2	-8.00	114.60	122.60
2	5A	295	ASP	CA-CB-CG	7.99	120.58	112.60
1	2C	216	ASN	OD1-CG-ND2	7.93	130.53	122.60
1	2A	3	GLU	CB-CG-CD	7.88	125.99	112.60
2	3A	285	SER	CA-C-N	7.83	125.17	120.24
2	3A	285	SER	C-N-CA	7.83	125.17	120.24
2	5B	107	THR	OG1-CB-CG2	-7.83	93.64	109.30
2	3E	77	ARG	CG-CD-NE	7.82	129.19	112.00
2	5E	48	ASN	CA-CB-CG	7.81	120.41	112.60
2	3B	285	SER	CA-C-N	7.78	125.14	120.24
2	3B	285	SER	C-N-CA	7.78	125.14	120.24
2	5G	396	HIS	CB-CG-CD2	-7.77	121.10	131.20
2	3C	354	CYS	O-C-N	-7.76	114.11	123.27
2	3F	22	GLU	N-CA-CB	7.75	122.24	110.30
1	2H	233	GLN	CG-CD-NE2	7.75	128.03	116.40
1	2I	206	ASN	CB-CG-ND2	7.75	128.02	116.40
2	5G	407	GLU	CB-CG-CD	-7.73	99.45	112.60
1	2B	123	ARG	CG-CD-NE	7.72	128.98	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5D	166	THR	CA-CB-OG1	-7.71	98.04	109.60
1	4H	156	ARG	CG-CD-NE	-7.70	95.07	112.00
2	3H	277	GLY	CA-C-O	-7.67	111.86	120.30
2	3B	53	GLU	CB-CG-CD	7.67	125.64	112.60
1	4H	283	HIS	N-CA-CB	-7.66	99.37	110.47
2	5B	293	MET	N-CA-CB	7.65	122.08	110.30
1	2A	402	ARG	CG-CD-NE	7.64	128.80	112.00
2	3B	147	MET	CG-SD-CE	-7.63	84.12	100.90
1	2B	367	ASP	CB-CA-C	7.61	121.14	109.34
2	5B	323	THR	CA-CB-OG1	7.61	121.01	109.60
2	3E	48	ASN	CA-CB-CG	7.60	120.20	112.60
2	3B	218	THR	CA-CB-OG1	7.59	120.98	109.60
1	2I	11	GLN	CB-CA-C	7.55	125.77	109.99
1	4C	211	ASP	CA-CB-CG	7.54	120.14	112.60
2	5G	396	HIS	CB-CG-ND1	7.52	133.98	122.70
2	3B	179	VAL	CA-CB-CG1	7.51	123.17	110.40
2	5B	3	GLU	CB-CG-CD	7.51	125.36	112.60
1	2I	342	GLN	CB-CG-CD	7.47	125.30	112.60
1	4G	179	THR	CA-CB-OG1	-7.47	98.40	109.60
1	2D	212	ILE	CB-CA-C	7.46	122.52	112.22
2	5B	407	GLU	CB-CG-CD	-7.43	99.96	112.60
1	4B	340	THR	OG1-CB-CG2	7.43	124.16	109.30
1	4G	102	ASN	OD1-CG-ND2	-7.42	115.18	122.60
1	2I	326	LYS	CB-CA-C	7.42	123.46	110.85
1	2B	121	ARG	CG-CD-NE	7.41	128.31	112.00
1	4D	197	HIS	N-CA-CB	7.41	120.69	111.79
1	2G	137	MET	O-C-N	-7.41	114.57	123.16
2	3G	92	PHE	CA-C-N	7.41	127.95	121.58
2	3G	92	PHE	C-N-CA	7.41	127.95	121.58
2	3D	53	GLU	CB-CG-CD	7.40	125.18	112.60
2	3F	197	ASP	CA-CB-CG	-7.40	105.20	112.60
1	4E	353	CYS	N-CA-CB	7.39	123.09	110.68
1	4H	233	GLN	OE1-CD-NE2	-7.38	115.22	122.60
2	3F	326	VAL	CA-C-O	-7.38	112.50	120.47
2	5G	365	VAL	CA-CB-CG2	7.37	122.92	110.40
2	5I	277	GLY	CA-C-O	-7.37	112.20	120.30
1	2H	339	ARG	CG-CD-NE	7.35	128.17	112.00
2	3A	241	ARG	CG-CD-NE	7.35	128.17	112.00
2	3F	365	VAL	CA-CB-CG2	7.35	122.89	110.40
2	3I	14	ASN	CB-CG-ND2	7.33	127.40	116.40
2	3G	293	MET	CB-CA-C	-7.33	99.37	110.88
1	4I	211	ASP	CA-CB-CG	7.31	119.91	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4I	206	ASN	CB-CG-ND2	7.31	127.36	116.40
1	2I	211	ASP	CA-CB-CG	7.27	119.87	112.60
2	5C	143	THR	O-C-N	-7.26	112.52	122.46
2	5F	355	ASP	CA-CB-CG	7.25	119.84	112.60
2	3D	256	ASN	CA-CB-CG	-7.24	105.36	112.60
1	2E	123	ARG	CB-CG-CD	7.24	127.95	111.30
1	4C	139	ASN	OD1-CG-ND2	-7.23	115.37	122.60
2	3D	355	ASP	N-CA-CB	7.23	121.72	110.44
2	5E	298	ASN	O-C-N	-7.22	112.95	122.20
2	5F	323	THR	CA-CB-OG1	7.21	120.42	109.60
1	2F	179	THR	CA-CB-OG1	-7.21	98.79	109.60
1	4C	423	GLU	CG-CD-OE1	-7.20	101.85	118.40
2	3B	31	ASP	CA-CB-CG	7.19	119.79	112.60
2	5I	274	THR	CA-CB-OG1	-7.17	98.85	109.60
1	4D	176	GLN	CA-C-O	-7.16	111.44	119.67
1	4B	249	ASN	CA-CB-CG	7.12	119.72	112.60
1	2D	16	ILE	CB-CA-C	7.10	122.02	112.22
1	4A	102	ASN	CA-CB-CG	7.09	119.69	112.60
1	2E	390	ARG	CG-CD-NE	7.09	127.59	112.00
2	3F	67	ASP	CA-CB-CG	7.08	119.69	112.60
2	3F	274	THR	OG1-CB-CG2	-7.08	95.13	109.30
2	5D	31	ASP	CA-CB-CG	7.08	119.68	112.60
2	3G	392	LYS	CB-CG-CD	7.06	127.54	111.30
2	5H	226	ASN	OD1-CG-ND2	-7.06	115.54	122.60
2	5B	285	SER	CA-C-N	7.05	124.68	120.24
2	5B	285	SER	C-N-CA	7.05	124.68	120.24
2	5E	365	VAL	CA-CB-CG2	7.03	122.35	110.40
1	4A	186	ASN	OD1-CG-ND2	-7.02	115.58	122.60
1	4G	306	ASP	CA-CB-CG	7.01	119.61	112.60
1	4G	130	THR	CA-CB-OG1	-7.01	99.09	109.60
2	5B	409	THR	OG1-CB-CG2	-7.00	95.30	109.30
1	4F	79	ARG	CG-CD-NE	6.98	127.36	112.00
1	2H	286	LEU	CA-C-O	-6.96	113.60	121.39
1	2G	223	THR	CA-CB-CG2	6.95	122.31	110.50
2	5A	414	ASN	CA-C-O	-6.94	111.98	119.97
2	3G	14	ASN	OD1-CG-ND2	-6.94	115.66	122.60
2	3C	298	ASN	CA-CB-CG	6.93	119.53	112.60
2	5G	354	CYS	CA-C-O	-6.92	113.22	121.66
1	2H	109	THR	OG1-CB-CG2	-6.90	95.49	109.30
1	4H	339	ARG	CG-CD-NE	6.90	127.17	112.00
1	4G	207	GLU	CB-CG-CD	6.89	124.32	112.60
1	4I	322	ASP	CA-CB-CG	6.89	119.49	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3D	225	LEU	CB-CA-C	6.85	123.82	110.67
2	3C	14	ASN	OD1-CG-ND2	-6.85	115.75	122.60
2	3H	183	TYR	O-C-N	-6.85	114.34	122.15
2	5H	298	ASN	CA-CB-CG	6.83	119.44	112.60
2	3A	105	HIS	ND1-CG-CD2	-6.82	99.28	106.10
2	3A	354	CYS	CA-C-O	6.82	127.82	120.38
1	2G	356	ASN	OD1-CG-ND2	-6.82	115.78	122.60
2	5G	108	GLU	CB-CG-CD	6.80	124.16	112.60
2	3I	27	GLU	N-CA-CB	6.78	121.45	110.40
2	3G	414	ASN	CA-CB-CG	6.75	119.35	112.60
1	2H	267	PHE	CA-C-O	6.74	127.86	120.71
1	4F	66	VAL	CA-CB-CG1	6.72	121.83	110.40
1	2G	207	GLU	CB-CG-CD	6.72	124.02	112.60
2	5E	53	GLU	CB-CG-CD	6.72	124.02	112.60
1	2I	11	GLN	CA-C-O	-6.72	110.98	119.31
2	3G	100	ASN	OD1-CG-ND2	-6.72	115.88	122.60
2	5H	360	GLY	O-C-N	-6.71	115.06	122.65
1	4G	356	ASN	OD1-CG-ND2	-6.71	115.89	122.60
2	3G	212	PHE	CA-CB-CG	6.71	120.51	113.80
2	3B	321	MET	O-C-N	-6.68	114.11	122.73
2	5H	14	ASN	OD1-CG-ND2	-6.67	115.93	122.60
1	2I	199	ASP	CA-CB-CG	-6.66	105.94	112.60
1	4C	216	ASN	OD1-CG-ND2	6.66	129.26	122.60
1	4D	35	GLN	CA-CB-CG	6.64	127.38	114.10
1	2E	198	THR	CA-CB-OG1	-6.63	99.66	109.60
1	4G	320	ARG	NE-CZ-NH1	-6.63	114.87	121.50
2	5I	280	GLN	CA-CB-CG	6.62	127.33	114.10
1	2E	339	ARG	CG-CD-NE	6.61	126.54	112.00
2	3I	14	ASN	CB-CG-OD1	-6.60	107.59	120.80
2	3H	329	GLN	OE1-CD-NE2	-6.60	116.00	122.60
2	5A	31	ASP	CA-CB-CG	6.60	119.20	112.60
1	2A	56	THR	N-CA-CB	-6.58	100.22	110.55
1	4H	339	ARG	O-C-N	-6.58	114.45	122.34
1	2F	422	ARG	NE-CZ-NH2	6.57	125.11	119.20
1	4G	259	LEU	N-CA-C	6.55	121.41	113.41
1	2D	123	ARG	CG-CD-NE	6.55	126.41	112.00
1	2F	358	GLN	N-CA-CB	6.55	120.11	109.90
1	4C	250	VAL	CA-CB-CG1	6.54	121.52	110.40
1	4E	218	ASP	CA-CB-CG	6.54	119.14	112.60
1	4A	116	ASP	CA-CB-CG	-6.53	106.07	112.60
1	4E	214	ARG	CB-CG-CD	6.53	126.32	111.30
1	2B	205	ASP	CA-CB-CG	6.53	119.13	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5A	195	ASN	OD1-CG-ND2	-6.52	116.08	122.60
2	3H	324	LYS	CB-CA-C	-6.52	100.60	110.90
2	5B	213	ARG	N-CA-CB	6.52	119.99	110.47
1	2E	176	GLN	CA-C-O	-6.51	112.18	119.67
2	5C	227	HIS	CB-CG-CD2	6.51	139.66	131.20
1	4F	179	THR	CA-CB-OG1	-6.50	99.85	109.60
2	5F	67	ASP	CA-CB-CG	6.49	119.09	112.60
1	4D	342	GLN	CA-C-O	6.49	128.70	121.11
2	5H	321	MET	N-CA-CB	6.49	122.74	111.39
2	3C	212	PHE	CA-CB-CG	6.48	120.28	113.80
1	4I	146	GLY	CA-C-O	6.48	127.53	120.66
1	2A	168	ASN	CB-CA-C	6.47	122.36	111.22
2	3E	213	ARG	CG-CD-NE	6.47	126.24	112.00
2	5G	416	ASN	CA-CB-CG	6.46	119.06	112.60
2	3D	249	ASP	CA-CB-CG	6.46	119.06	112.60
1	4H	141	VAL	CB-CA-C	6.45	116.74	111.06
2	3I	166	THR	OG1-CB-CG2	6.45	122.20	109.30
1	2E	258	ASN	CA-CB-CG	-6.44	106.16	112.60
1	2E	123	ARG	CG-CD-NE	-6.44	97.84	112.00
1	2H	265	ILE	CA-CB-CG2	6.43	121.43	110.50
1	4C	50	ASN	CA-CB-CG	6.42	119.02	112.60
1	4E	77	GLU	N-CA-CB	6.42	120.23	110.28
2	3E	92	PHE	CA-C-N	6.41	127.09	121.58
2	3E	92	PHE	C-N-CA	6.41	127.09	121.58
1	4F	179	THR	CA-CB-CG2	6.41	121.39	110.50
1	2H	35	GLN	CG-CD-NE2	6.41	126.01	116.40
2	3B	94	GLN	N-CA-CB	-6.40	100.46	110.44
1	2A	429	GLU	CB-CA-C	6.39	121.72	110.85
2	5A	149	THR	OG1-CB-CG2	-6.39	96.52	109.30
2	5I	107	THR	CA-C-O	-6.39	112.32	119.67
2	5A	161	ASP	O-C-N	-6.38	114.68	122.34
2	5G	228	LEU	CB-CA-C	6.38	122.37	110.70
1	2G	390	ARG	CG-CD-NE	-6.37	97.99	112.00
2	5D	414	ASN	CA-CB-CG	6.37	118.97	112.60
2	3A	391	ARG	N-CA-CB	6.36	120.93	111.51
1	4G	361	THR	CA-CB-OG1	-6.36	100.06	109.60
2	3C	212	PHE	CB-CA-C	-6.36	100.36	110.86
1	4B	390	ARG	CG-CD-NE	6.36	125.98	112.00
2	5E	321	MET	CG-SD-CE	-6.35	86.92	100.90
1	2F	313	MET	N-CA-CB	6.35	119.61	110.40
2	3I	277	GLY	CA-C-O	-6.35	113.93	120.66
2	5I	409	THR	CA-CB-OG1	6.35	119.13	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4G	320	ARG	NH1-CZ-NH2	6.35	127.55	119.30
2	5H	359	LYS	CB-CA-C	6.34	120.04	109.89
2	5H	181	GLU	CA-CB-CG	6.34	126.78	114.10
2	3A	319	GLY	CA-C-O	-6.33	116.25	121.76
2	5F	108	GLU	CB-CA-C	6.33	120.66	110.09
1	2E	258	ASN	OD1-CG-ND2	-6.33	116.27	122.60
2	5A	77	ARG	NE-CZ-NH1	-6.33	115.17	121.50
2	5G	166	THR	OG1-CB-CG2	6.33	121.95	109.30
2	5G	365	VAL	CA-CB-CG1	6.32	121.14	110.40
1	4F	84	ARG	CG-CD-NE	6.32	125.90	112.00
1	2H	322	ASP	CA-CB-CG	6.31	118.91	112.60
1	2G	279	GLU	CB-CA-C	-6.31	100.12	110.85
1	2B	283	HIS	N-CA-CB	-6.30	100.81	110.44
1	2D	342	GLN	CA-C-O	6.29	128.47	121.11
2	5G	332	ASN	CA-CB-CG	6.28	118.88	112.60
2	3E	365	VAL	CA-CB-CG2	6.26	121.05	110.40
2	5H	340	TYR	N-CA-CB	-6.26	100.87	110.44
1	4H	82	THR	OG1-CB-CG2	6.25	121.81	109.30
2	3E	414	ASN	O-C-N	-6.25	113.84	122.46
2	5A	23	VAL	CA-CB-CG1	6.25	121.02	110.40
2	3B	391	ARG	CB-CG-CD	6.25	125.67	111.30
2	3H	377	MET	CG-SD-CE	-6.24	87.17	100.90
1	4C	352	LYS	CA-CB-CG	-6.24	101.63	114.10
2	3F	333	VAL	CA-CB-CG1	6.23	120.99	110.40
2	3C	99	ASN	N-CA-CB	6.22	121.11	111.84
2	3I	327	ASP	CA-CB-CG	6.22	118.82	112.60
2	5G	58	ARG	CB-CG-CD	-6.21	97.00	111.30
1	2F	392	ASP	CA-CB-CG	-6.21	106.39	112.60
1	2F	21	TRP	CA-C-O	-6.21	111.16	119.11
1	4A	310	GLY	CA-C-O	-6.20	116.18	121.57
1	2A	169	PHE	CA-CB-CG	6.19	119.99	113.80
1	2B	434	GLU	CB-CG-CD	6.18	123.11	112.60
1	2I	205	ASP	CA-CB-CG	6.17	118.77	112.60
2	3E	147	MET	N-CA-CB	6.17	120.06	110.44
2	3E	276	ARG	CB-CG-CD	6.17	125.48	111.30
1	2A	60	LYS	O-C-N	-6.17	115.69	122.84
2	5A	251	ARG	CB-CG-CD	6.17	125.48	111.30
1	2A	102	ASN	CA-CB-CG	6.16	118.76	112.60
1	2H	105	ARG	NE-CZ-NH2	6.16	124.74	119.20
2	5E	89	ASN	OD1-CG-ND2	-6.16	116.44	122.60
2	5I	137	HIS	CB-CG-CD2	-6.15	123.20	131.20
2	5I	22	GLU	CA-CB-CG	6.15	126.41	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2D	391	MET	CB-CG-SD	-6.15	94.25	112.70
2	5C	208	TYR	CB-CG-CD1	-6.15	111.57	120.80
1	2E	88	HIS	CB-CG-ND1	-6.15	113.48	122.70
1	4C	205	ASP	CA-CB-CG	6.15	118.75	112.60
1	2E	372	MET	CG-SD-CE	6.14	114.42	100.90
2	5H	342	VAL	CA-CB-CG2	6.14	120.83	110.40
1	4D	123	ARG	CG-CD-NE	6.13	125.50	112.00
1	4C	187	SER	CB-CA-C	6.13	121.92	110.70
1	2E	88	HIS	CB-CG-CD2	6.13	139.17	131.20
2	3F	298	ASN	CA-CB-CG	-6.13	106.47	112.60
2	5G	58	ARG	CG-CD-NE	-6.13	98.52	112.00
1	4F	361	THR	CA-CB-OG1	-6.11	100.44	109.60
2	3F	349	MET	N-CA-CB	-6.11	101.00	109.97
2	3A	388	MET	O-C-N	-6.10	113.95	122.37
2	5G	77	ARG	NH1-CZ-NH2	6.10	127.23	119.30
2	3E	166	THR	OG1-CB-CG2	-6.10	97.10	109.30
1	4E	123	ARG	CB-CG-CD	6.10	125.33	111.30
1	2D	349	THR	CA-C-O	6.10	127.43	120.84
1	2F	244	PHE	CB-CG-CD2	-6.10	110.33	120.70
1	4G	380	ASN	O-C-N	-6.10	116.27	123.22
2	3G	213	ARG	CG-CD-NE	6.10	125.41	112.00
2	3G	67	ASP	CA-CB-CG	-6.09	106.51	112.60
2	5F	197	ASP	CA-CB-CG	-6.09	106.51	112.60
1	2A	225	THR	CA-CB-CG2	6.08	120.84	110.50
1	4I	337	THR	CA-CB-OG1	-6.08	100.47	109.60
2	5H	26	ASP	CA-CB-CG	6.08	118.68	112.60
1	4H	140	ALA	O-C-N	-6.08	116.25	123.06
2	5G	256	ASN	OD1-CG-ND2	6.08	128.68	122.60
2	5F	320	ARG	CG-CD-NE	6.07	125.36	112.00
1	2H	356	ASN	OD1-CG-ND2	-6.07	116.53	122.60
2	3F	147	MET	CG-SD-CE	-6.06	87.56	100.90
2	5I	15	GLN	N-CA-CB	6.06	119.98	110.46
1	4G	317	LEU	CA-C-N	-6.06	114.51	123.11
1	4G	317	LEU	C-N-CA	-6.06	114.51	123.11
1	2C	358	GLN	OE1-CD-NE2	6.06	128.66	122.60
1	2H	82	THR	OG1-CB-CG2	6.06	121.41	109.30
2	5D	65	LEU	N-CA-CB	-6.06	100.17	110.16
1	2E	138	PHE	CB-CG-CD1	6.04	130.97	120.70
1	2F	166	LYS	O-C-N	-6.04	115.99	123.36
1	4C	423	GLU	CB-CG-CD	6.04	122.87	112.60
2	5D	249	ASP	CA-CB-CG	6.04	118.64	112.60
1	2A	415	GLU	CB-CG-CD	6.03	122.85	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3G	212	PHE	CA-C-N	-6.03	111.26	122.60
2	3G	212	PHE	C-N-CA	-6.03	111.26	122.60
2	3F	88	ASP	CA-CB-CG	6.03	118.63	112.60
2	5G	355	ASP	CB-CA-C	6.02	121.00	110.64
1	2C	386	GLU	CB-CG-CD	6.02	122.84	112.60
1	2I	146	GLY	CA-C-O	6.02	127.04	120.66
1	2A	18	ASN	CB-CA-C	6.02	121.08	110.85
1	4F	327	ASP	O-C-N	-6.01	114.38	122.43
2	3G	181	GLU	CB-CG-CD	6.00	122.80	112.60
1	4E	139	ASN	OD1-CG-ND2	-6.00	116.60	122.60
1	2A	304	LYS	N-CA-CB	-5.99	100.36	110.49
1	4A	29	GLY	CA-C-O	5.99	126.65	119.82
2	3G	407	GLU	CB-CG-CD	-5.98	102.43	112.60
2	5B	8	GLN	CB-CG-CD	5.98	122.77	112.60
2	5D	165	GLU	CB-CA-C	5.98	120.32	109.37
1	2D	79	ARG	CB-CA-C	5.98	122.81	110.31
2	5A	350	LYS	CB-CG-CD	5.98	125.05	111.30
1	4G	270	SER	N-CA-CB	-5.98	102.08	111.05
1	2D	207	GLU	CA-CB-CG	5.97	126.04	114.10
2	3D	65	LEU	N-CA-CB	-5.97	100.31	110.16
1	2A	311	LYS	CB-CA-C	5.97	119.33	110.62
1	2F	244	PHE	CB-CG-CD1	5.97	130.85	120.70
2	3I	100	ASN	OD1-CG-ND2	-5.97	116.63	122.60
1	4G	55	GLU	CA-C-O	5.96	126.66	120.40
2	3E	377	MET	CA-CB-CG	-5.96	102.17	114.10
2	3C	181	GLU	CA-CB-CG	5.96	126.02	114.10
1	2C	2	ARG	CB-CG-CD	-5.95	97.62	111.30
1	2I	339	ARG	CG-CD-NE	5.95	125.09	112.00
2	5A	245	GLN	CB-CG-CD	5.95	122.71	112.60
1	4G	269	LEU	CA-C-O	-5.95	114.22	121.36
2	5A	253	LEU	CB-CA-C	5.94	122.41	109.99
1	4B	308	ARG	NE-CZ-NH1	-5.94	115.56	121.50
1	4F	144	GLY	N-CA-C	5.93	119.38	112.50
1	4D	391	MET	CB-CG-SD	-5.93	94.91	112.70
1	2D	214	ARG	CB-CG-CD	5.93	124.94	111.30
2	3C	300	MET	CG-SD-CE	-5.93	87.86	100.90
1	2G	10	GLY	CA-C-O	-5.92	117.49	122.29
1	4G	258	ASN	CA-CB-CG	5.92	118.52	112.60
2	5A	287	PRO	N-CA-C	5.92	123.37	113.78
2	3F	103	LYS	O-C-N	-5.92	113.79	122.43
1	2C	279	GLU	CB-CA-C	-5.91	100.80	110.85
1	2E	22	GLU	CB-CG-CD	5.91	122.65	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5E	333	VAL	CA-CB-CG1	5.91	120.45	110.40
2	3C	332	ASN	OD1-CG-ND2	5.91	128.51	122.60
1	4B	18	ASN	OD1-CG-ND2	5.91	128.51	122.60
1	4C	254	GLU	CB-CG-CD	5.91	122.64	112.60
1	2H	136	LEU	CA-C-O	-5.91	113.86	120.54
2	5G	327	ASP	CA-CB-CG	-5.90	106.70	112.60
2	5E	293	MET	CB-CA-C	-5.90	100.82	110.85
1	2G	137	MET	CB-CA-C	-5.90	99.80	109.53
2	3A	72	THR	CA-C-N	-5.89	112.81	122.54
2	3A	72	THR	C-N-CA	-5.89	112.81	122.54
2	3H	278	SER	CA-C-O	-5.89	112.77	119.78
1	2C	320	ARG	CG-CD-NE	5.89	124.96	112.00
1	4F	66	VAL	CG1-CB-CG2	5.89	123.76	110.80
2	3G	287	PRO	CB-CA-C	5.89	121.39	112.21
2	5B	31	ASP	CA-CB-CG	5.88	118.48	112.60
1	2F	145	THR	OG1-CB-CG2	-5.88	97.55	109.30
1	2I	327	ASP	CA-CB-CG	-5.88	106.72	112.60
1	4I	107	HIS	CB-CA-C	-5.87	99.87	109.56
2	5B	66	MET	CA-CB-CG	5.87	125.84	114.10
2	5I	390	ARG	CB-CG-CD	5.87	124.80	111.30
1	2D	3	GLU	CB-CG-CD	5.86	122.57	112.60
1	4B	51	THR	OG1-CB-CG2	-5.86	97.58	109.30
1	2F	281	ALA	CA-C-N	5.85	128.71	120.28
1	2F	281	ALA	C-N-CA	5.85	128.71	120.28
2	5E	423	GLN	CG-CD-OE1	5.85	132.50	120.80
1	2I	73	THR	CA-CB-OG1	-5.85	100.82	109.60
1	4G	179	THR	CA-CB-CG2	5.84	120.43	110.50
1	4C	398	MET	CB-CA-C	5.83	118.87	109.07
1	4G	382	THR	OG1-CB-CG2	-5.83	97.63	109.30
2	5A	353	VAL	O-C-N	-5.83	116.75	122.99
2	5A	306	ARG	CB-CG-CD	5.83	124.70	111.30
2	5G	198	GLU	N-CA-CB	5.83	120.27	110.77
1	2A	123	ARG	NH1-CZ-NH2	5.82	126.87	119.30
2	5A	207	LEU	CB-CG-CD2	-5.82	93.23	110.70
2	5C	26	ASP	CA-CB-CG	5.82	118.42	112.60
2	3G	228	LEU	CB-CA-C	5.82	120.75	110.85
1	2A	308	ARG	CB-CG-CD	5.82	124.68	111.30
1	4G	130	THR	CB-CA-C	5.82	119.45	109.51
2	3H	26	ASP	CA-CB-CG	5.81	118.41	112.60
2	5C	123	GLU	CB-CG-CD	-5.81	102.73	112.60
2	5B	22	GLU	CA-CB-CG	5.80	125.71	114.10
1	4G	18	ASN	CB-CA-C	5.80	121.81	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5G	86	ARG	CB-CA-C	5.80	116.74	108.68
1	4H	297	GLU	CB-CA-C	5.79	119.22	109.67
1	2C	378	ILE	CA-CB-CG2	5.79	120.34	110.50
2	5D	313	ALA	N-CA-CB	-5.79	102.25	111.62
2	5D	295	ASP	CA-CB-CG	-5.78	106.82	112.60
1	2C	56	THR	CA-C-O	-5.78	114.09	120.33
1	4B	436	GLY	O-C-N	-5.78	115.19	122.70
2	5F	155	VAL	CA-CB-CG1	5.78	120.22	110.40
1	2F	179	THR	CA-CB-CG2	5.77	120.31	110.50
1	4D	156	ARG	CB-CG-CD	5.77	124.57	111.30
1	4H	270	SER	N-CA-CB	-5.77	102.11	110.70
1	4A	116	ASP	CA-C-O	-5.76	114.44	120.55
1	2G	31	GLN	CA-CB-CG	5.76	125.61	114.10
2	3B	178	THR	OG1-CB-CG2	-5.76	97.79	109.30
1	2F	166	LYS	CA-C-O	5.75	127.36	120.28
1	4A	386	GLU	CB-CG-CD	5.75	122.38	112.60
1	4H	398	MET	N-CA-CB	-5.75	100.77	110.49
1	2E	216	ASN	CA-C-O	-5.75	112.99	120.00
2	3G	262	ARG	CA-C-O	5.74	127.01	120.00
2	3B	415	MET	CB-CG-SD	5.74	129.93	112.70
1	4G	268	MET	O-C-N	5.74	130.66	123.19
2	5D	276	ARG	CB-CG-CD	5.74	124.51	111.30
1	4H	233	GLN	CB-CG-CD	-5.74	102.84	112.60
2	5I	140	GLY	CA-C-N	-5.74	116.72	122.69
2	5I	140	GLY	C-N-CA	-5.74	116.72	122.69
2	5G	14	ASN	OD1-CG-ND2	-5.73	116.87	122.60
2	5H	277	GLY	O-C-N	-5.73	115.25	122.70
2	3C	177	ASP	N-CA-CB	5.73	120.01	110.85
1	4G	243	ARG	NE-CZ-NH2	5.72	124.35	119.20
2	5F	64	ILE	CB-CG1-CD1	5.72	125.82	113.80
1	4H	281	ALA	N-CA-CB	5.72	119.11	110.30
1	2B	98	ASP	CA-CB-CG	5.72	118.32	112.60
1	4E	431	ASP	CA-CB-CG	5.72	118.32	112.60
1	2G	90	GLU	CA-C-O	-5.71	113.11	119.34
2	3D	417	ASP	CA-CB-CG	5.71	118.31	112.60
2	3G	155	VAL	CA-CB-CG1	5.71	120.10	110.40
1	4F	18	ASN	OD1-CG-ND2	5.71	128.31	122.60
1	4G	250	VAL	CA-CB-CG1	5.71	120.10	110.40
1	4D	69	ASP	CA-CB-CG	5.71	118.31	112.60
1	2G	61	HIS	CB-CG-ND1	5.70	131.25	122.70
2	5C	55	THR	CA-CB-OG1	-5.70	101.05	109.60
2	3H	99	ASN	CA-CB-CG	-5.70	106.90	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4G	250	VAL	CA-CB-CG2	5.70	120.08	110.40
1	2H	33	ASP	CB-CA-C	5.70	121.60	110.67
1	4I	71	GLU	CB-CA-C	5.70	117.63	109.26
2	5F	390	ARG	CG-CD-NE	5.70	124.53	112.00
1	2I	84	ARG	CB-CA-C	5.69	121.12	110.70
2	3A	111	GLU	CB-CG-CD	-5.69	102.92	112.60
1	2I	252	VAL	O-C-N	-5.68	115.46	122.57
1	2A	102	ASN	OD1-CG-ND2	5.68	128.28	122.60
1	4G	90	GLU	CB-CA-C	5.68	120.63	109.72
1	2D	402	ARG	CG-CD-NE	5.68	124.50	112.00
2	3E	88	ASP	CA-CB-CG	5.68	118.28	112.60
2	5E	100	ASN	CA-CB-CG	5.68	118.28	112.60
2	3I	209	ASP	CA-CB-CG	5.68	118.28	112.60
1	2B	298	PRO	CB-CA-C	-5.67	103.79	111.85
1	4F	90	GLU	CG-CD-OE1	-5.67	105.37	118.40
1	4G	1	MET	CA-C-O	-5.66	111.17	120.80
1	2B	294	SER	O-C-N	-5.66	115.12	122.37
1	4A	396	ASP	CA-CB-CG	5.66	118.26	112.60
2	5B	330	MET	CB-CG-SD	5.66	129.68	112.70
2	3H	31	ASP	CA-CB-CG	5.66	118.26	112.60
1	4A	415	GLU	CA-C-N	-5.66	116.74	123.08
1	4A	415	GLU	C-N-CA	-5.66	116.74	123.08
1	4G	121	ARG	CG-CD-NE	5.66	124.45	112.00
1	2F	145	THR	CB-CA-C	-5.66	99.81	110.67
2	5D	33	THR	CA-CB-OG1	5.66	118.08	109.60
2	5A	396	HIS	CB-CG-CD2	5.65	138.55	131.20
1	2I	3	GLU	CB-CG-CD	5.64	122.19	112.60
2	3D	37	CYS	O-C-N	-5.64	116.72	123.27
1	4G	82	THR	CA-CB-OG1	-5.64	101.13	109.60
1	4H	410	GLY	CA-C-N	-5.64	112.50	122.26
1	4H	410	GLY	C-N-CA	-5.64	112.50	122.26
2	3A	295	ASP	CA-CB-CG	5.64	118.24	112.60
2	3C	401	GLU	O-C-N	-5.64	115.32	122.26
2	3H	77	ARG	CB-CA-C	5.64	121.88	110.38
2	3C	397	TRP	N-CA-CB	5.63	118.98	110.30
1	2I	406	HIS	CB-CG-CD2	-5.63	123.88	131.20
2	3F	417	ASP	CA-CB-CG	5.63	118.23	112.60
1	2E	54	SER	CA-C-O	-5.63	114.55	120.80
2	5G	190	HIS	CA-C-N	-5.63	113.31	122.26
2	5G	190	HIS	C-N-CA	-5.63	113.31	122.26
1	4E	258	ASN	CA-CB-CG	-5.63	106.97	112.60
2	3I	390	ARG	CB-CG-CD	5.62	124.24	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3B	251	ARG	CG-CD-NE	-5.62	99.63	112.00
1	4B	156	ARG	CA-C-O	-5.62	113.16	119.79
1	2F	168	ASN	OD1-CG-ND2	-5.62	116.98	122.60
2	5I	325	GLU	CB-CA-C	-5.62	99.89	110.01
2	5H	120	VAL	CA-CB-CG1	5.62	119.95	110.40
2	5F	33	THR	O-C-N	-5.61	114.08	122.39
2	3D	327	ASP	CA-CB-CG	5.61	118.21	112.60
1	2H	431	ASP	CA-CB-CG	5.61	118.21	112.60
2	3G	348	ASN	CB-CG-ND2	5.61	124.81	116.40
2	5G	77	ARG	NE-CZ-NH1	-5.61	115.89	121.50
1	2I	11	GLN	CA-CB-CG	-5.60	102.89	114.10
1	4B	279	GLU	N-CA-CB	5.60	118.54	110.20
1	4H	249	ASN	CA-CB-CG	5.60	118.20	112.60
2	3C	276	ARG	CG-CD-NE	5.59	124.30	112.00
2	3E	91	VAL	CA-C-O	5.59	126.63	120.48
1	4E	339	ARG	CG-CD-NE	5.59	124.30	112.00
1	4H	222	PRO	O-C-N	-5.59	117.03	123.23
2	3F	18	ALA	CA-C-O	-5.59	113.55	119.97
1	2H	264	ARG	CA-CB-CG	5.58	125.26	114.10
1	4A	29	GLY	O-C-N	-5.58	116.85	122.54
1	4H	267	PHE	CA-C-O	5.58	127.47	121.16
1	4I	352	LYS	CB-CG-CD	5.58	124.13	111.30
2	3I	348	ASN	CB-CG-ND2	-5.57	108.04	116.40
2	3D	376	GLU	CA-C-O	-5.57	113.56	119.97
1	2F	314	ALA	N-CA-CB	-5.57	101.17	111.53
2	3F	155	VAL	CA-CB-CG1	5.57	119.86	110.40
1	4G	137	MET	CB-CA-C	-5.57	100.35	109.53
2	3E	375	GLN	N-CA-CB	5.56	119.62	110.39
1	4A	82	THR	CA-CB-OG1	-5.56	101.26	109.60
2	5I	324	LYS	CA-C-N	-5.56	112.32	122.38
2	5I	324	LYS	C-N-CA	-5.56	112.32	122.38
2	3D	291	GLN	OE1-CD-NE2	-5.56	117.04	122.60
1	2F	304	LYS	CB-CG-CD	5.55	124.07	111.30
1	4I	96	LYS	N-CA-CB	5.55	118.45	110.40
1	2C	320	ARG	CB-CG-CD	-5.55	98.54	111.30
1	4H	187	SER	CB-CA-C	5.55	120.86	110.70
1	2G	423	GLU	N-CA-CB	5.55	119.60	110.39
1	2A	420	GLU	N-CA-CB	5.54	118.36	110.16
1	2G	326	LYS	CB-CA-C	5.54	120.27	110.85
1	2F	55	GLU	N-CA-CB	-5.54	101.60	109.85
1	2F	258	ASN	CA-CB-CG	5.53	118.13	112.60
2	5I	66	MET	N-CA-CB	-5.53	101.23	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5C	347	ASN	CA-CB-CG	5.53	118.13	112.60
2	5D	195	ASN	CA-CB-CG	5.52	118.12	112.60
2	3F	149	THR	OG1-CB-CG2	-5.52	98.25	109.30
2	5I	140	GLY	CA-C-O	-5.52	111.60	119.28
2	5B	55	THR	CA-CB-OG1	-5.52	101.32	109.60
1	2H	415	GLU	O-C-N	-5.52	116.02	122.81
1	4D	422	ARG	CB-CG-CD	-5.52	98.61	111.30
1	2E	138	PHE	CB-CG-CD2	-5.52	111.32	120.70
2	3B	213	ARG	N-CA-CB	5.51	118.63	110.53
2	3G	179	VAL	CA-CB-CG2	5.51	119.77	110.40
2	5F	298	ASN	CB-CG-ND2	5.51	124.66	116.40
2	3F	103	LYS	CB-CA-C	5.51	120.91	109.95
1	4B	259	LEU	CA-C-N	-5.51	117.19	123.25
1	4B	259	LEU	C-N-CA	-5.51	117.19	123.25
2	3I	23	VAL	CA-CB-CG1	5.50	119.76	110.40
2	3G	416	ASN	CA-CB-CG	5.50	118.10	112.60
2	5B	23	VAL	CA-CB-CG1	5.50	119.76	110.40
2	5B	380	ARG	CG-CD-NE	-5.50	99.89	112.00
2	3H	332	ASN	CA-CB-CG	5.50	118.10	112.60
1	4I	254	GLU	CB-CG-CD	5.50	121.95	112.60
2	3G	204	ASN	CB-CG-ND2	5.50	124.65	116.40
2	5G	143	THR	OG1-CB-CG2	-5.49	98.31	109.30
1	2B	119	LEU	CB-CA-C	5.49	121.79	110.31
1	4A	76	ASP	CA-CB-CG	5.49	118.09	112.60
1	4A	116	ASP	O-C-N	5.49	127.94	122.12
1	4B	192	HIS	CB-CG-ND1	5.49	130.94	122.70
2	5H	263	LEU	CD1-CG-CD2	-5.49	98.73	110.80
2	3G	255	VAL	CA-C-N	-5.48	113.99	122.49
2	3G	255	VAL	C-N-CA	-5.48	113.99	122.49
2	3E	401	GLU	N-CA-CB	5.48	120.16	111.17
1	4I	278	ALA	N-CA-CB	5.48	118.78	110.28
2	5B	350	LYS	CD-CE-NZ	-5.48	94.36	111.90
2	5G	274	THR	OG1-CB-CG2	-5.48	98.34	109.30
2	3G	378	PHE	CA-C-O	-5.48	113.67	119.97
1	4I	391	MET	CA-CB-CG	5.47	125.05	114.10
1	2F	326	LYS	CB-CA-C	5.47	120.15	110.85
1	2G	61	HIS	CB-CG-CD2	-5.47	124.09	131.20
2	3G	181	GLU	CA-CB-CG	-5.47	103.16	114.10
1	4I	146	GLY	O-C-N	-5.47	116.88	122.19
1	4D	3	GLU	CB-CG-CD	5.46	121.88	112.60
1	4D	330	ALA	CA-C-O	-5.46	113.69	119.97
2	5B	175	VAL	CA-CB-CG1	5.45	119.67	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3H	31	ASP	CB-CA-C	5.45	117.97	109.42
1	2H	382	THR	OG1-CB-CG2	5.45	120.19	109.30
1	4G	254	GLU	N-CA-CB	5.43	118.52	110.53
2	5D	390	ARG	CG-CD-NE	5.43	123.95	112.00
1	2F	283	HIS	N-CA-CB	5.43	117.81	110.59
1	2H	380	ASN	OD1-CG-ND2	5.43	128.03	122.60
1	4A	206	ASN	N-CA-CB	5.43	118.60	110.19
2	5A	137	HIS	CB-CG-ND1	5.43	130.84	122.70
2	5A	233	MET	CB-CA-C	5.42	121.09	110.67
2	3D	121	ARG	CG-CD-NE	5.42	123.93	112.00
2	3I	147	MET	CG-SD-CE	-5.42	88.97	100.90
1	4H	220	GLU	N-CA-CB	5.42	118.28	110.20
1	4F	387	VAL	CA-CB-CG1	5.42	119.61	110.40
1	4I	338	LYS	CB-CA-C	5.42	118.56	109.89
1	2F	159	VAL	CA-CB-CG1	5.42	119.61	110.40
2	5C	23	VAL	CA-CB-CG1	5.42	119.61	110.40
2	3D	356	ILE	CB-CG1-CD1	5.41	125.17	113.80
2	3F	347	ASN	CA-CB-CG	5.41	118.01	112.60
2	3E	35	THR	OG1-CB-CG2	-5.41	98.48	109.30
1	4C	337	THR	CA-CB-OG1	5.41	117.72	109.60
2	5E	298	ASN	CA-C-O	5.41	127.10	120.55
1	2A	108	TYR	CB-CG-CD1	5.41	128.91	120.80
2	3A	27	GLU	CA-CB-CG	5.41	124.91	114.10
1	2G	396	ASP	CA-CB-CG	5.40	118.00	112.60
2	5A	181	GLU	CA-CB-CG	5.40	124.89	114.10
2	5E	77	ARG	NE-CZ-NH1	-5.40	116.10	121.50
1	4H	254	GLU	N-CA-C	5.40	117.92	111.71
1	2B	128	ASN	CA-CB-CG	5.39	117.99	112.60
2	3D	247	ASN	CB-CG-OD1	5.39	131.59	120.80
2	3G	255	VAL	CA-CB-CG1	5.39	119.56	110.40
1	4D	52	PHE	CA-CB-CG	5.39	119.19	113.80
2	5G	14	ASN	CB-CG-ND2	-5.38	108.32	116.40
2	3G	409	THR	CA-CB-OG1	5.38	117.67	109.60
2	5B	213	ARG	CG-CD-NE	5.38	123.84	112.00
2	5G	359	LYS	CA-CB-CG	5.38	124.87	114.10
1	4G	133	GLN	N-CA-CB	5.38	121.07	110.63
2	5A	160	PRO	CA-C-N	5.38	131.26	122.65
2	5A	160	PRO	C-N-CA	5.38	131.26	122.65
1	2A	90	GLU	CB-CG-CD	5.38	121.74	112.60
1	4H	233	GLN	CG-CD-NE2	5.38	124.47	116.40
1	2A	254	GLU	CB-CG-CD	5.38	121.74	112.60
2	3E	86	ARG	CB-CG-CD	5.38	123.66	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3E	375	GLN	OE1-CD-NE2	5.37	127.97	122.60
1	4A	285	GLN	N-CA-CB	5.37	119.20	110.17
1	2B	297	GLU	CB-CG-CD	-5.37	103.47	112.60
1	4C	187	SER	CA-CB-OG	-5.37	100.36	111.10
1	2E	391	MET	CA-CB-CG	-5.37	103.36	114.10
2	3G	332	ASN	CA-CB-CG	5.37	117.97	112.60
2	5I	282	ARG	CG-CD-NE	5.37	123.81	112.00
1	4H	327	ASP	CA-CB-CG	5.37	117.97	112.60
1	2C	206	ASN	CA-CB-CG	5.36	117.96	112.60
2	5A	134	GLN	OE1-CD-NE2	5.36	127.96	122.60
2	3C	55	THR	CA-CB-OG1	-5.36	101.57	109.60
2	5D	414	ASN	OD1-CG-ND2	5.35	127.95	122.60
2	3E	191	GLN	N-CA-C	-5.35	106.13	113.30
2	3E	255	VAL	CA-CB-CG1	5.35	119.50	110.40
1	2B	349	THR	CA-C-O	5.35	128.17	122.13
1	2B	377	MET	N-CA-CB	-5.35	102.18	110.57
1	4H	13	GLY	CA-C-O	-5.34	115.25	120.75
1	2H	320	ARG	CA-CB-CG	5.34	124.78	114.10
2	5D	350	LYS	CB-CG-CD	5.34	123.59	111.30
2	5E	390	ARG	CG-CD-NE	5.34	123.75	112.00
1	2F	145	THR	CA-C-O	-5.34	113.83	119.97
1	2F	358	GLN	CG-CD-NE2	5.34	124.41	116.40
1	2E	411	GLU	N-CA-CB	-5.33	102.78	110.56
2	5I	324	LYS	O-C-N	5.33	127.85	122.09
1	4B	256	GLN	CB-CG-CD	5.33	121.66	112.60
1	4H	370	LYS	N-CA-CB	5.33	118.03	110.46
2	3A	375	GLN	CB-CG-CD	-5.33	103.54	112.60
1	4B	358	GLN	OE1-CD-NE2	-5.33	117.27	122.60
2	3A	391	ARG	CB-CA-C	5.33	120.61	111.45
1	4B	280	LYS	CA-CB-CG	5.33	124.75	114.10
2	3H	334	GLN	OE1-CD-NE2	-5.33	117.27	122.60
1	4E	8	HIS	CG-CD2-NE2	5.33	112.53	107.20
1	2H	325	PRO	CB-CA-C	5.32	120.31	111.21
1	4F	82	THR	CA-CB-OG1	-5.32	101.61	109.60
2	3F	147	MET	CB-CG-SD	5.32	128.67	112.70
2	5G	357	PRO	N-CA-CB	5.32	108.24	103.08
1	2A	197	HIS	CA-CB-CG	5.32	119.12	113.80
1	4C	168	ASN	CA-CB-CG	-5.32	107.28	112.60
1	4H	268	MET	O-C-N	-5.32	116.24	123.15
2	5D	337	ASN	CA-CB-CG	-5.32	107.28	112.60
2	5G	66	MET	N-CA-CB	5.32	119.36	110.59
1	2D	35	GLN	CA-CB-CG	5.32	124.73	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5E	423	GLN	CG-CD-NE2	-5.32	108.43	116.40
2	5A	178	THR	CA-CB-OG1	5.31	117.57	109.60
2	3A	105	HIS	CG-CD2-NE2	5.31	112.51	107.20
1	4H	308	ARG	CA-CB-CG	5.31	124.72	114.10
1	2G	113	GLU	CB-CG-CD	5.31	121.62	112.60
2	5B	177	ASP	CA-CB-CG	-5.31	107.29	112.60
2	3B	425	TYR	CB-CG-CD1	5.31	128.76	120.80
1	4A	336	LYS	CG-CD-CE	5.31	123.50	111.30
2	3E	377	MET	CG-SD-CE	-5.30	89.23	100.90
1	4A	353	CYS	N-CA-CB	5.30	119.23	110.69
1	4G	146	GLY	CA-C-O	5.30	126.13	120.30
2	3I	86	ARG	CB-CG-CD	5.30	123.48	111.30
1	2G	90	GLU	CB-CA-C	5.30	119.34	110.44
1	4A	35	GLN	CA-CB-CG	5.30	124.69	114.10
1	4C	123	ARG	CG-CD-NE	5.30	123.65	112.00
1	2E	35	GLN	CA-CB-CG	5.29	124.69	114.10
1	4F	168	ASN	CA-CB-CG	5.29	117.89	112.60
2	5D	3	GLU	CB-CG-CD	5.29	121.60	112.60
2	3B	39	ASP	CA-CB-CG	5.29	117.89	112.60
1	4B	3	GLU	N-CA-CB	5.29	121.00	111.37
1	4G	280	LYS	N-CA-CB	5.29	118.93	110.73
1	4B	156	ARG	CB-CA-C	5.29	121.16	110.38
1	4G	126	ALA	CA-C-O	-5.28	113.42	119.60
2	3I	55	THR	CA-CB-OG1	-5.28	101.68	109.60
2	5G	85	PHE	O-C-N	-5.28	116.21	122.65
1	2B	176	GLN	CA-C-N	5.28	128.94	121.66
1	2B	176	GLN	C-N-CA	5.28	128.94	121.66
1	4C	216	ASN	CA-CB-CG	5.27	117.87	112.60
1	2G	106	GLY	CA-C-O	5.27	126.10	120.30
1	2A	154	LEU	CB-CG-CD2	-5.27	94.89	110.70
2	3F	170	PHE	CA-CB-CG	-5.27	108.53	113.80
2	3I	318	ARG	CB-CG-CD	-5.27	99.19	111.30
1	4F	434	GLU	CB-CG-CD	5.27	121.56	112.60
2	5A	103	LYS	CG-CD-CE	5.27	123.41	111.30
1	2G	132	LEU	CA-C-O	5.26	127.06	121.16
1	4A	199	ASP	CA-CB-CG	-5.26	107.34	112.60
2	5B	286	VAL	O-C-N	-5.26	116.33	120.07
1	2G	279	GLU	CA-C-N	-5.26	114.34	122.49
1	2G	279	GLU	C-N-CA	-5.26	114.34	122.49
1	2F	349	THR	CA-C-O	5.26	128.07	122.13
2	3A	312	THR	OG1-CB-CG2	5.26	119.81	109.30
1	2I	159	VAL	CA-CB-CG1	5.25	119.33	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5B	306	ARG	CB-CG-CD	5.25	123.38	111.30
2	5F	355	ASP	CB-CA-C	5.25	119.43	110.56
2	5H	186	THR	CA-CB-OG1	-5.25	101.72	109.60
2	3D	39	ASP	CA-CB-CG	5.25	117.85	112.60
1	4H	420	GLU	CB-CG-CD	5.25	121.52	112.60
2	3D	37	CYS	CA-C-O	5.25	127.14	121.06
1	4D	244	PHE	N-CA-CB	-5.24	103.19	111.05
1	2I	342	GLN	N-CA-CB	-5.24	101.87	110.52
2	3G	106	TYR	O-C-N	-5.24	114.90	122.03
2	3G	397	TRP	CB-CA-C	5.24	120.38	109.95
1	4E	91	GLN	CA-CB-CG	5.24	124.58	114.10
2	3A	425	TYR	CA-C-O	5.23	127.99	120.51
2	5I	55	THR	CA-CB-OG1	-5.23	101.75	109.60
1	2C	216	ASN	CA-CB-CG	5.23	117.83	112.60
2	5E	107	THR	OG1-CB-CG2	-5.23	98.85	109.30
2	3F	319	GLY	CA-C-O	-5.22	116.94	122.01
2	5D	388	MET	N-CA-CB	5.22	118.59	110.44
1	4C	356	ASN	OD1-CG-ND2	-5.22	117.38	122.60
2	3A	253	LEU	CB-CA-C	5.22	121.03	110.38
2	5D	282	ARG	CB-CG-CD	5.22	123.30	111.30
2	3F	55	THR	CA-CB-OG1	-5.21	101.78	109.60
2	5B	391	ARG	CB-CG-CD	5.21	123.29	111.30
2	3F	388	MET	CG-SD-CE	-5.21	89.43	100.90
2	5C	348	ASN	OD1-CG-ND2	-5.21	117.39	122.60
1	2I	84	ARG	CA-C-O	-5.21	114.45	120.24
2	5A	401	GLU	O-C-N	-5.21	115.53	122.20
1	4F	141	VAL	N-CA-C	-5.21	107.08	111.56
2	5C	120	VAL	CA-CB-CG1	5.21	119.26	110.40
2	3E	55	THR	CA-CB-OG1	-5.20	101.80	109.60
2	5E	195	ASN	CA-CB-CG	5.20	117.80	112.60
1	2H	215	ARG	CB-CG-CD	5.20	123.26	111.30
2	3F	198	GLU	CA-C-N	-5.20	116.19	123.10
2	3F	198	GLU	C-N-CA	-5.20	116.19	123.10
2	3I	195	ASN	CB-CG-ND2	-5.20	108.61	116.40
2	3A	73	MET	CB-CG-SD	-5.20	97.11	112.70
2	3H	397	TRP	N-CA-CB	5.20	118.30	110.30
1	4G	259	LEU	N-CA-CB	-5.19	102.89	110.47
2	3D	390	ARG	CG-CD-NE	5.19	123.42	112.00
1	4G	380	ASN	CB-CG-ND2	5.19	124.19	116.40
2	5F	196	ALA	N-CA-CB	-5.19	102.55	110.85
2	3H	213	ARG	CG-CD-NE	5.19	123.42	112.00
2	5A	168	SER	CA-C-N	-5.18	115.50	122.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5A	168	SER	C-N-CA	-5.18	115.50	122.91
1	4B	320	ARG	NE-CZ-NH2	5.18	123.86	119.20
2	5B	298	ASN	OD1-CG-ND2	5.18	127.78	122.60
1	2B	414	GLU	CB-CA-C	5.18	118.08	109.53
2	3I	70	PRO	CA-C-N	5.18	125.69	119.94
2	3I	70	PRO	C-N-CA	5.18	125.69	119.94
1	4H	411	GLU	N-CA-CB	5.18	118.25	110.53
1	4E	407	TRP	CA-CB-CG	-5.18	103.76	113.60
2	3E	397	TRP	O-C-N	-5.18	114.09	122.42
2	5G	85	PHE	CA-C-O	5.18	127.89	121.99
2	3A	347	ASN	CA-CB-CG	5.17	117.77	112.60
1	4D	244	PHE	CB-CG-CD1	5.17	129.49	120.70
1	2E	139	ASN	OD1-CG-ND2	-5.17	117.43	122.60
2	3G	89	ASN	OD1-CG-ND2	-5.16	117.44	122.60
2	3G	213	ARG	CA-C-O	5.16	127.35	120.13
2	3H	120	VAL	CA-CB-CG1	5.16	119.17	110.40
1	4G	268	MET	CA-C-O	-5.16	115.28	121.11
2	5A	140	GLY	CA-C-N	-5.16	116.88	122.55
2	5A	140	GLY	C-N-CA	-5.16	116.88	122.55
2	5C	208	TYR	CB-CG-CD2	5.16	128.54	120.80
2	5I	120	VAL	CA-CB-CG1	5.16	119.17	110.40
1	2C	176	GLN	CA-C-O	-5.16	113.54	119.78
2	5A	403	MET	CB-CG-SD	5.16	128.17	112.70
2	3H	204	ASN	OD1-CG-ND2	-5.15	117.45	122.60
2	5B	386	THR	CA-CB-OG1	5.15	117.33	109.60
2	3H	143	THR	CA-CB-CG2	5.15	119.25	110.50
1	2A	60	LYS	CA-C-O	5.14	128.42	121.89
1	2C	337	THR	CA-CB-OG1	5.14	117.31	109.60
1	2E	266	HIS	CB-CG-ND1	5.14	130.41	122.70
2	3A	212	PHE	CA-CB-CG	5.14	118.94	113.80
2	5D	355	ASP	O-C-N	-5.14	115.42	122.46
1	2H	372	MET	CB-CG-SD	5.14	128.11	112.70
2	3I	179	VAL	CA-CB-CG2	5.13	119.12	110.40
1	4B	219	ILE	CB-CG1-CD1	5.13	124.58	113.80
2	3D	34	GLY	CA-C-N	-5.13	113.40	122.74
2	3D	34	GLY	C-N-CA	-5.13	113.40	122.74
2	3F	366	THR	OG1-CB-CG2	5.13	119.55	109.30
1	2F	2	ARG	N-CA-C	5.12	117.09	109.25
1	2H	33	ASP	O-C-N	-5.12	115.97	122.27
2	3G	66	MET	N-CA-CB	5.12	119.12	110.77
1	2C	415	GLU	CB-CG-CD	5.12	121.31	112.60
2	3C	252	LYS	CB-CG-CD	5.12	123.08	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5D	416	ASN	CB-CG-ND2	-5.12	108.72	116.40
2	5E	190	HIS	CA-C-O	5.12	125.86	119.97
2	3G	212	PHE	CB-CA-C	-5.12	102.20	110.79
2	3B	178	THR	CA-CB-CG2	5.11	119.19	110.50
2	5B	392	LYS	CB-CG-CD	5.11	123.05	111.30
2	5C	401	GLU	O-C-N	-5.11	115.98	122.26
1	2H	214	ARG	O-C-N	-5.11	115.99	122.17
2	3G	67	ASP	N-CA-CB	5.11	119.32	111.56
2	5B	276	ARG	CG-CD-NE	5.11	123.24	112.00
1	2G	121	ARG	CG-CD-NE	5.11	123.23	112.00
1	2B	396	ASP	CA-CB-CG	5.10	117.70	112.60
1	4B	192	HIS	ND1-CG-CD2	-5.10	101.00	106.10
2	5E	55	THR	CA-CB-OG1	-5.10	101.95	109.60
2	5H	136	THR	N-CA-CB	5.10	118.77	110.77
2	5E	404	ASP	CA-CB-CG	5.09	117.69	112.60
1	4E	82	THR	CA-CB-OG1	-5.09	101.96	109.60
2	3F	397	TRP	N-CA-CB	5.09	118.14	110.30
1	4E	260	VAL	N-CA-CB	5.09	116.60	111.36
1	4E	390	ARG	CB-CG-CD	-5.09	99.59	111.30
1	2G	145	THR	CA-C-N	5.09	125.60	120.00
1	2G	145	THR	C-N-CA	5.09	125.60	120.00
1	4D	197	HIS	O-C-N	-5.09	117.14	122.18
1	4G	380	ASN	CA-CB-CG	5.09	117.69	112.60
2	3G	303	SER	CA-CB-OG	5.08	121.27	111.10
1	4I	297	GLU	CA-CB-CG	5.08	124.27	114.10
1	2D	186	ASN	OD1-CG-ND2	5.08	127.68	122.60
2	3D	34	GLY	O-C-N	5.08	128.28	122.33
1	2H	429	GLU	N-CA-CB	5.08	117.68	110.16
2	3A	390	ARG	CA-C-N	-5.08	113.53	123.13
2	3A	390	ARG	C-N-CA	-5.08	113.53	123.13
1	2I	378	ILE	CB-CG1-CD1	-5.08	103.14	113.80
1	2G	82	THR	CA-CB-OG1	-5.08	101.98	109.60
2	3F	399	THR	CA-CB-CG2	5.08	119.13	110.50
2	3D	191	GLN	OE1-CD-NE2	5.08	127.68	122.60
1	4F	168	ASN	CB-CA-C	5.08	118.50	109.72
1	2F	242	LEU	CB-CA-C	5.07	120.41	110.67
2	3A	200	GLN	OE1-CD-NE2	5.07	127.67	122.60
2	3E	201	VAL	CA-CB-CG2	5.07	119.02	110.40
2	3H	21	TRP	O-C-N	-5.07	114.88	122.39
2	5A	207	LEU	N-CA-CB	-5.07	102.42	110.28
2	5G	197	ASP	CB-CG-OD1	-5.07	106.74	118.40
1	2G	145	THR	O-C-N	-5.07	115.54	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5G	106	TYR	N-CA-CB	5.06	119.33	110.27
1	4C	258	ASN	CA-CB-CG	-5.06	107.54	112.60
2	5A	287	PRO	CB-CA-C	-5.06	104.65	113.20
1	2G	115	VAL	CA-CB-CG1	5.06	119.00	110.40
2	3I	347	ASN	CA-CB-CG	5.06	117.66	112.60
2	5A	169	VAL	CA-CB-CG1	5.06	119.00	110.40
1	4G	334	THR	CA-CB-OG1	5.06	117.19	109.60
2	5H	390	ARG	CG-CD-NE	5.06	123.13	112.00
1	2E	337	THR	CA-CB-OG1	5.05	117.18	109.60
2	3A	220	PRO	N-CA-C	5.05	119.25	111.57
2	3D	191	GLN	CG-CD-NE2	-5.05	108.82	116.40
1	2A	266	HIS	CB-CG-CD2	-5.05	124.63	131.20
1	4A	56	THR	N-CA-CB	-5.05	102.67	110.65
1	4F	264	ARG	CA-CB-CG	-5.05	104.00	114.10
1	2G	215	ARG	CG-CD-NE	5.05	123.10	112.00
2	3I	120	VAL	CA-CB-CG1	5.04	118.98	110.40
1	4I	73	THR	N-CA-C	5.04	116.47	111.07
2	5G	190	HIS	CA-C-O	-5.04	113.18	119.38
1	2C	358	GLN	CB-CG-CD	5.04	121.17	112.60
1	2A	311	LYS	N-CA-CB	-5.04	103.04	110.90
1	2G	301	MET	N-CA-CB	5.04	117.28	110.38
2	3B	92	PHE	CA-C-N	-5.04	118.65	122.33
2	3B	92	PHE	C-N-CA	-5.04	118.65	122.33
2	3C	107	THR	CA-CB-OG1	-5.04	102.04	109.60
1	2H	101	ASN	CB-CG-OD1	-5.04	110.73	120.80
1	4A	251	ASP	N-CA-CB	5.04	120.31	111.55
1	4H	174	SER	CA-CB-OG	-5.03	101.03	111.10
2	5H	111	GLU	CA-C-O	5.03	125.72	119.79
1	2B	297	GLU	CB-CA-C	5.03	117.31	109.42
2	3C	176	SER	CA-C-N	-5.03	114.78	122.87
2	3C	176	SER	C-N-CA	-5.03	114.78	122.87
2	5C	401	GLU	CA-C-O	5.03	125.88	119.95
2	5H	293	MET	CB-CA-C	-5.03	102.96	110.90
2	3A	105	HIS	CB-CG-CD2	5.03	137.73	131.20
1	4I	261	PRO	N-CA-CB	-5.03	97.97	103.25
1	2B	292	THR	OG1-CB-CG2	-5.02	99.25	109.30
1	4A	98	ASP	CA-CB-CG	5.02	117.62	112.60
2	3B	346	PRO	N-CA-CB	-5.02	98.66	103.33
1	4D	186	ASN	OD1-CG-ND2	5.02	127.62	122.60
1	4I	390	ARG	CG-CD-NE	-5.02	100.95	112.00
1	2G	304	LYS	CA-C-O	-5.02	113.33	120.51
2	5A	93	GLY	CA-C-O	-5.02	116.59	121.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5A	391	ARG	CA-C-N	5.02	129.25	122.07
2	5A	391	ARG	C-N-CA	5.02	129.25	122.07
2	5C	31	ASP	CA-CB-CG	5.02	117.62	112.60
2	5E	39	ASP	CA-CB-CG	5.02	117.62	112.60
2	5E	26	ASP	CA-CB-CG	5.02	117.62	112.60
1	2E	304	LYS	CG-CD-CE	5.01	122.83	111.30
1	4E	411	GLU	CB-CG-CD	5.01	121.12	112.60
1	2A	206	ASN	N-CA-CB	5.01	117.95	110.19
1	2C	284	GLU	O-C-N	-5.01	117.46	123.27
2	5A	188	SER	CA-CB-OG	-5.01	101.09	111.10
2	5G	2	ARG	CB-CG-CD	-5.01	99.78	111.30
2	5A	307	HIS	CB-CG-CD2	-5.00	124.69	131.20
2	5F	39	ASP	CA-CB-CG	5.00	117.61	112.60
1	4I	73	THR	CA-CB-CG2	5.00	119.00	110.50
2	5D	406	MET	CB-CG-SD	5.00	127.71	112.70

There are no chirality outliers.

All (259) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2A	201	ALA	Mainchain
1	2A	205	ASP	Mainchain
1	2A	208	ALA	Mainchain
1	2A	249	ASN	Sidechain
1	2A	285	GLN	Mainchain
1	2A	296	PHE	Sidechain
1	2A	306	ASP	Sidechain
1	2B	2	ARG	Mainchain
1	2B	293	ASN	Sidechain
1	2B	299	ALA	Mainchain
1	2B	367	ASP	Sidechain
1	2B	59	GLY	Mainchain
1	2C	163	LYS	Mainchain
1	2C	176	GLN	Mainchain
1	2C	282	TYR	Peptide
1	2C	284	GLU	Peptide
1	2C	388	PHE	Sidechain
1	2C	392	ASP	Sidechain
1	2D	163	LYS	Mainchain
1	2D	279	GLU	Mainchain
1	2D	59	GLY	Mainchain
1	2E	130	THR	Mainchain

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Mol	Chain	Res	Type	Group
1	2E	176	GLN	Mainchain
1	2E	193	SER	Mainchain
1	2E	284	GLU	Peptide
1	2E	341	ILE	Mainchain
1	2E	407	TRP	Mainchain
1	2E	412	GLY	Mainchain
1	2F	2	ARG	Mainchain
1	2F	21	TRP	Mainchain
1	2F	242	LEU	Mainchain
1	2F	258	ASN	Mainchain
1	2F	284	GLU	Peptide
1	2F	326	LYS	Mainchain
1	2F	436	GLY	Mainchain
1	2G	111	GLY	Peptide
1	2G	137	MET	Mainchain
1	2G	145	THR	Mainchain
1	2G	189	LEU	Mainchain
1	2G	203	MET	Mainchain
1	2G	296	PHE	Sidechain
1	2G	299	ALA	Mainchain
1	2G	304	LYS	Peptide
1	2G	401	LYS	Peptide
1	2G	413	MET	Mainchain
1	2G	53	PHE	Mainchain
1	2G	67	PHE	Sidechain
1	2H	136	LEU	Mainchain
1	2H	139	ASN	Sidechain
1	2H	163	LYS	Mainchain
1	2H	2	ARG	Mainchain
1	2H	33	ASP	Mainchain
1	2H	343	PHE	Mainchain
1	2H	379	SER	Peptide
1	2H	422	ARG	Sidechain
1	2I	11	GLN	Mainchain
1	2I	225	THR	Mainchain
1	2I	326	LYS	Mainchain
1	2I	383	ALA	Mainchain
1	2I	387	VAL	Mainchain
1	2I	84	ARG	Mainchain
2	3A	105	HIS	Mainchain
2	3A	175	VAL	Mainchain
2	3A	177	ASP	Peptide

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Mol	Chain	Res	Type	Group
2	3A	257	LEU	Mainchain
2	3A	28	HIS	Sidechain
2	3A	281	TYR	Mainchain
2	3A	282	ARG	Mainchain
2	3A	302	ALA	Mainchain
2	3A	307	HIS	Mainchain
2	3A	319	GLY	Mainchain
2	3A	388	MET	Mainchain
2	3B	161	ASP	Mainchain
2	3B	213	ARG	Mainchain
2	3B	266	PHE	Mainchain
2	3B	321	MET	Peptide
2	3B	322	SER	Peptide
2	3B	323	THR	Mainchain
2	3B	33	THR	Mainchain
2	3C	105	HIS	Mainchain
2	3C	14	ASN	Sidechain
2	3C	176	SER	Mainchain
2	3C	256	ASN	Mainchain
2	3C	26	ASP	Sidechain
2	3C	307	HIS	Mainchain
2	3C	399	THR	Mainchain
2	3C	93	GLY	Mainchain
2	3D	105	HIS	Mainchain
2	3D	256	ASN	Mainchain
2	3D	263	LEU	Mainchain
2	3D	355	ASP	Mainchain
2	3D	376	GLU	Mainchain
2	3D	378	PHE	Sidechain
2	3D	383	ASP	Sidechain
2	3D	399	THR	Mainchain
2	3E	105	HIS	Mainchain
2	3E	16	ILE	Mainchain
2	3E	283	ALA	Mainchain
2	3E	294	PHE	Sidechain
2	3E	33	THR	Mainchain
2	3E	35	THR	Mainchain
2	3E	397	TRP	Mainchain
2	3E	414	ASN	Mainchain
2	3F	103	LYS	Mainchain
2	3F	105	HIS	Mainchain
2	3F	223	GLY	Mainchain

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Mol	Chain	Res	Type	Group
2	3F	33	THR	Mainchain
2	3F	349	MET	Mainchain
2	3F	35	THR	Mainchain
2	3F	354	CYS	Mainchain
2	3F	67	ASP	Mainchain
2	3G	14	ASN	Sidechain
2	3G	175	VAL	Mainchain
2	3G	300	MET	Mainchain
2	3G	389	PHE	Sidechain
2	3G	74	ASP	Sidechain
2	3H	105	HIS	Mainchain
2	3H	118	ASP	Sidechain
2	3H	140	GLY	Mainchain
2	3H	183	TYR	Mainchain
2	3H	277	GLY	Mainchain
2	3H	30	ILE	Mainchain
2	3H	304	ASP	Sidechain
2	3H	388	MET	Mainchain
2	3H	421	GLU	Mainchain
2	3I	149	THR	Mainchain
2	3I	156	ARG	Mainchain
2	3I	262	ARG	Mainchain
2	3I	372	THR	Mainchain
1	4A	168	ASN	Mainchain
1	4A	197	HIS	Mainchain
1	4A	205	ASP	Mainchain
1	4A	225	THR	Mainchain
1	4A	253	THR	Mainchain
1	4A	286	LEU	Mainchain
1	4A	35	GLN	Mainchain
1	4A	368	LEU	Mainchain
1	4A	69	ASP	Sidechain
1	4A	89	PRO	Mainchain
1	4B	156	ARG	Mainchain
1	4B	213	CYS	Mainchain
1	4B	225	THR	Mainchain
1	4B	257	THR	Mainchain
1	4B	264	ARG	Mainchain
1	4C	185	TYR	Sidechain
1	4C	257	THR	Mainchain
1	4C	282	TYR	Sidechain
1	4C	322	ASP	Mainchain

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Mol	Chain	Res	Type	Group
1	4C	404	PHE	Mainchain
1	4C	411	GLU	Mainchain
1	4D	176	GLN	Mainchain
1	4D	196	GLU	Mainchain
1	4D	279	GLU	Mainchain
1	4D	331	ALA	Mainchain
1	4D	59	GLY	Mainchain
1	4E	139	ASN	Sidechain
1	4E	165	SER	Mainchain
1	4E	169	PHE	Sidechain
1	4E	176	GLN	Mainchain
1	4E	243	ARG	Mainchain
1	4E	341	ILE	Mainchain
1	4E	411	GLU	Mainchain
1	4E	54	SER	Mainchain
1	4F	140	ALA	Mainchain
1	4F	202	VAL	Mainchain
1	4F	215	ARG	Mainchain
1	4F	217	LEU	Mainchain
1	4F	241	SER	Mainchain
1	4F	327	ASP	Mainchain
1	4F	90	GLU	Mainchain
1	4G	1	MET	Mainchain
1	4G	137	MET	Mainchain
1	4G	162	GLY	Mainchain
1	4G	217	LEU	Mainchain
1	4G	259	LEU	Mainchain
1	4G	380	ASN	Mainchain
1	4G	67	PHE	Sidechain
1	4H	136	LEU	Mainchain
1	4H	139	ASN	Sidechain
1	4H	140	ALA	Mainchain
1	4H	163	LYS	Mainchain
1	4H	233	GLN	Sidechain
1	4H	254	GLU	Mainchain
1	4H	258	ASN	Mainchain
1	4H	264	ARG	Mainchain
1	4H	327	ASP	Sidechain
1	4I	225	THR	Mainchain
1	4I	269	LEU	Mainchain
1	4I	412	GLY	Mainchain
1	4I	59	GLY	Mainchain

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Mol	Chain	Res	Type	Group
1	4I	96	LYS	Mainchain
2	5A	143	THR	Mainchain
2	5A	170	PHE	Sidechain
2	5A	205	GLU	Mainchain
2	5A	281	TYR	Sidechain
2	5A	283	ALA	Mainchain
2	5A	293	MET	Mainchain
2	5A	307	HIS	Mainchain
2	5A	342	VAL	Mainchain
2	5A	349	MET	Mainchain
2	5A	36	TYR	Sidechain
2	5A	388	MET	Mainchain
2	5A	414	ASN	Mainchain
2	5A	43	GLN	Mainchain
2	5A	83	GLN	Sidechain
2	5B	195	ASN	Mainchain
2	5B	266	PHE	Mainchain
2	5B	341	PHE	Mainchain
2	5B	388	MET	Mainchain
2	5C	105	HIS	Mainchain
2	5C	143	THR	Mainchain
2	5C	256	ASN	Mainchain
2	5C	283	ALA	Mainchain
2	5C	307	HIS	Mainchain
2	5C	423	GLN	Sidechain
2	5D	105	HIS	Mainchain
2	5D	297	LYS	Mainchain
2	5D	33	THR	Mainchain
2	5D	355	ASP	Mainchain
2	5D	399	THR	Mainchain
2	5D	414	ASN	Mainchain
2	5E	105	HIS	Mainchain
2	5E	16	ILE	Mainchain
2	5E	257	LEU	Mainchain
2	5E	280	GLN	Mainchain
2	5E	283	ALA	Mainchain
2	5E	293	MET	Mainchain
2	5E	298	ASN	Mainchain
2	5E	33	THR	Mainchain
2	5E	35	THR	Mainchain
2	5F	126	GLY	Mainchain
2	5F	196	ALA	Mainchain

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Mol	Chain	Res	Type	Group
2	5F	349	MET	Mainchain
2	5F	35	THR	Mainchain
2	5G	105	HIS	Mainchain
2	5G	106	TYR	Mainchain
2	5G	14	ASN	Sidechain
2	5G	194	GLU	Mainchain
2	5G	283	ALA	Mainchain
2	5G	298	ASN	Mainchain
2	5G	354	CYS	Mainchain
2	5G	425	TYR	Mainchain
2	5G	53	GLU	Sidechain
2	5G	59	PHE	Mainchain
2	5G	81	PHE	Sidechain
2	5G	94	GLN	Mainchain
2	5H	14	ASN	Sidechain
2	5H	180	VAL	Mainchain
2	5H	21	TRP	Mainchain
2	5H	226	ASN	Sidechain
2	5H	266	PHE	Mainchain
2	5H	277	GLY	Mainchain
2	5H	340	TYR	Mainchain
2	5H	360	GLY	Mainchain
2	5I	105	HIS	Mainchain
2	5I	107	THR	Mainchain
2	5I	156	ARG	Mainchain
2	5I	277	GLY	Mainchain
2	5I	388	MET	Mainchain

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	2A	3325	0	3252	84	0
1	2B	3325	0	3252	79	0
1	2C	3325	0	3252	61	0
1	2D	3325	0	3252	105	0
1	2E	3325	0	3252	98	0
1	2F	3325	0	3252	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2G	3325	0	3252	95	0
1	2H	3325	0	3252	86	0
1	2I	3325	0	3252	57	0
1	4A	3325	0	3252	94	0
1	4B	3325	0	3252	96	0
1	4C	3325	0	3252	84	0
1	4D	3325	0	3251	87	0
1	4E	3325	0	3252	124	0
1	4F	3325	0	3252	89	0
1	4G	3325	0	3252	107	0
1	4H	3325	0	3252	104	0
1	4I	3325	0	3252	74	0
2	3A	3331	0	3207	104	0
2	3B	3331	0	3207	118	0
2	3C	3331	0	3207	75	0
2	3D	3331	0	3207	106	0
2	3E	3331	0	3207	143	0
2	3F	3331	0	3209	116	0
2	3G	3331	0	3209	102	0
2	3H	3331	0	3209	98	0
2	3I	3331	0	3209	60	0
2	5A	3331	0	3207	89	0
2	5B	3331	0	3207	84	0
2	5C	3331	0	3208	65	0
2	5D	3331	0	3206	116	0
2	5E	3331	0	3207	128	0
2	5F	3331	0	3209	74	0
2	5G	3331	0	3209	104	0
2	5H	3331	0	3209	88	0
2	5I	3331	0	3209	57	0
All	All	119808	0	116277	2526	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 11.

All (2526) 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)
1:4E:60:LYS:HZ2	1:4F:283:HIS:CD2	1.09	1.60
2:3E:58:ARG:NH1	2:3F:281:TYR:HE1	0.98	1.44
1:4C:121:ARG:HH12	1:4D:283:HIS:CE1	1.35	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4E:60:LYS:NZ	1:4F:283:HIS:HD2	0.94	1.40
2:3E:58:ARG:NH1	2:3F:281:TYR:CE1	1.89	1.39
2:5C:88:ASP:N	2:5D:281:TYR:OH	1.56	1.34
2:3A:220:PRO:HD2	1:4A:326:LYS:CE	1.58	1.33
1:2C:121:ARG:HH12	1:2D:283:HIS:CE1	1.51	1.25
2:5D:55:THR:OG1	2:5E:284:LEU:N	1.71	1.23
2:3D:55:THR:OG1	2:3E:284:LEU:N	1.72	1.23
1:4G:178:SER:OG	2:5G:347:ASN:ND2	1.70	1.21
1:2E:60:LYS:NZ	1:2F:282:TYR:CE2	2.12	1.18
2:5E:55:THR:HB	2:5F:283:ALA:HA	1.22	1.17
2:3G:55:THR:HG21	2:3H:283:ALA:HA	1.22	1.16
2:3D:58:ARG:HD3	2:3E:281:TYR:CA	1.76	1.16
2:3D:58:ARG:CD	2:3E:281:TYR:HA	1.75	1.16
1:4B:181:VAL:HG13	2:5B:350:LYS:NZ	1.60	1.16
1:2H:210:TYR:CD1	2:3H:324:LYS:HE3	1.81	1.15
1:2F:178:SER:HB2	2:3F:347:ASN:ND2	1.60	1.15
2:5A:55:THR:HG21	2:5B:283:ALA:HA	1.26	1.15
1:4E:60:LYS:NZ	1:4F:283:HIS:CD2	1.83	1.14
2:5G:55:THR:HG21	2:5H:283:ALA:HA	1.30	1.14
1:4G:398:MET:HE1	2:5G:345:ILE:HG23	1.30	1.12
2:5D:54:ALA:O	2:5E:283:ALA:HA	1.46	1.12
1:4C:121:ARG:NH1	1:4D:283:HIS:CE1	2.17	1.11
2:3E:58:ARG:HD3	2:3F:281:TYR:HD1	1.14	1.11
2:5D:58:ARG:HD3	2:5E:281:TYR:CA	1.79	1.11
1:4F:178:SER:HB2	2:5F:347:ASN:ND2	1.65	1.11
2:3A:220:PRO:CD	1:4A:326:LYS:HE2	1.79	1.11
2:5D:58:ARG:CD	2:5E:281:TYR:HA	1.81	1.11
1:2E:398:MET:HE2	2:3E:346:PRO:HD2	1.28	1.10
1:4D:57:GLY:H	1:4E:285:GLN:HB3	1.14	1.09
2:5D:54:ALA:C	2:5E:283:ALA:HA	1.74	1.09
2:5E:55:THR:HG22	2:5F:282:ARG:O	1.51	1.09
2:5E:54:ALA:HB1	2:5F:281:TYR:O	1.54	1.07
1:2D:60:LYS:HD3	1:2E:282:TYR:O	1.52	1.06
1:4B:181:VAL:HG13	2:5B:350:LYS:HZ2	1.05	1.06
1:4D:60:LYS:HD3	1:4E:282:TYR:O	1.53	1.06
2:5D:58:ARG:NH2	2:5E:281:TYR:CE1	2.24	1.06
2:3B:179:VAL:H	1:4B:352:LYS:NZ	1.54	1.05
1:2E:60:LYS:HE2	1:2F:283:HIS:HD2	1.22	1.05
1:4E:221:ARG:HG2	2:5E:322:SER:CB	1.87	1.04
1:2H:222:PRO:HG2	2:3H:324:LYS:HZ3	1.21	1.03
2:3H:99:ASN:HD22	1:4H:254:GLU:CD	1.66	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2C:62:VAL:HG12	1:2D:282:TYR:OH	1.59	1.02
2:3E:397:TRP:CH2	1:4E:260:VAL:HG23	1.93	1.02
2:3E:55:THR:HG22	2:3F:282:ARG:O	1.60	1.01
2:5E:55:THR:CB	2:5F:283:ALA:HA	1.91	1.01
2:3A:55:THR:HG21	2:3B:283:ALA:CB	1.89	1.01
2:3B:175:VAL:HG11	1:4B:332:VAL:HG13	1.40	1.01
1:2C:121:ARG:NH1	1:2D:283:HIS:CE1	2.27	1.01
1:2C:88:HIS:HA	1:2D:282:TYR:HE2	1.22	1.00
1:4I:181:VAL:HG22	2:5I:256:ASN:OD1	1.59	1.00
1:4D:55:GLU:O	1:4E:285:GLN:HG2	1.61	1.00
2:3D:54:ALA:O	2:3E:283:ALA:HA	1.60	1.00
2:5A:267:LEU:HD21	2:5A:374:ILE:HD11	1.44	1.00
2:3A:55:THR:CG2	2:3B:283:ALA:HB2	1.92	0.99
1:4D:60:LYS:CE	1:4E:283:HIS:CD2	2.46	0.99
1:4E:151:CYS:HG	1:4E:193:SER:HG	1.05	0.99
1:2H:259:LEU:O	1:2H:380:ASN:ND2	1.96	0.98
2:5F:54:ALA:HB1	2:5G:281:TYR:C	1.88	0.98
1:2D:60:LYS:CE	1:2E:283:HIS:CD2	2.46	0.98
2:3C:86:ARG:HD3	2:3D:281:TYR:HD1	1.26	0.98
2:5F:125:GLU:OE1	2:5G:291:GLN:NE2	1.95	0.97
2:5F:54:ALA:HB1	2:5G:281:TYR:O	1.62	0.97
2:3E:58:ARG:CD	2:3F:281:TYR:HD1	1.77	0.97
1:2C:88:HIS:HA	1:2D:282:TYR:CE2	1.98	0.97
2:5A:55:THR:CG2	2:5B:283:ALA:HA	1.93	0.97
1:2C:62:VAL:CG1	1:2D:282:TYR:OH	2.12	0.97
1:2A:181:VAL:HG22	2:3A:350:LYS:HZ1	1.27	0.96
1:2E:60:LYS:HE2	1:2F:283:HIS:CD2	2.00	0.96
2:3C:60:VAL:HG11	2:3D:280:GLN:HE22	1.25	0.96
2:3F:208:TYR:HD1	1:4F:326:LYS:HE2	1.27	0.95
1:2H:222:PRO:HG2	2:3H:324:LYS:NZ	1.82	0.95
1:4B:60:LYS:NZ	1:4C:282:TYR:CE2	2.35	0.95
2:5H:259:PRO:HG2	2:5H:311:LEU:HD21	1.49	0.95
1:4D:60:LYS:NZ	1:4E:283:HIS:CD2	2.35	0.94
1:4F:213:CYS:SG	1:4F:219:ILE:HD11	2.08	0.94
2:5D:55:THR:HG1	2:5E:284:LEU:H	0.98	0.94
1:4A:151:CYS:HG	1:4A:193:SER:HG	1.12	0.93
1:4B:60:LYS:HE3	1:4C:282:TYR:CZ	2.02	0.93
2:3E:54:ALA:HB1	2:3F:281:TYR:O	1.66	0.93
2:3I:175:VAL:HG21	1:4I:332:VAL:HG13	1.49	0.93
2:3D:54:ALA:C	2:3E:283:ALA:HA	1.94	0.93
1:2D:56:THR:CB	1:2E:283:HIS:O	2.17	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2G:60:LYS:CD	1:2H:283:HIS:HD2	1.82	0.92
2:3C:60:VAL:HG11	2:3D:280:GLN:NE2	1.84	0.92
2:3C:220:PRO:HD2	1:4C:326:LYS:HD2	1.48	0.92
2:3E:58:ARG:HD3	2:3F:281:TYR:CD1	2.04	0.92
2:3A:267:LEU:HD21	2:3A:374:ILE:HD11	1.51	0.92
2:3F:208:TYR:CD1	1:4F:326:LYS:HE2	2.04	0.92
1:4C:151:CYS:HG	1:4C:193:SER:HG	0.95	0.92
2:3E:55:THR:CG2	2:3F:283:ALA:HA	1.97	0.92
2:5G:55:THR:CG2	2:5H:283:ALA:HA	2.00	0.92
2:5E:201:VAL:HG11	2:5E:377:MET:HE1	1.52	0.91
1:2B:151:CYS:HG	1:2B:193:SER:HG	1.13	0.91
1:2C:124:LYS:HD2	1:2D:283:HIS:NE2	1.84	0.91
1:4H:151:CYS:HG	1:4H:193:SER:HG	0.92	0.91
1:2D:222:PRO:O	2:3D:324:LYS:NZ	2.03	0.91
1:4A:222:PRO:HD2	2:5A:324:LYS:NZ	1.85	0.91
1:4E:398:MET:HE3	2:5E:346:PRO:HD2	1.51	0.91
2:3A:212:PHE:HE1	1:4A:326:LYS:HZ2	0.91	0.90
1:2D:60:LYS:HE3	1:2E:283:HIS:CD2	2.06	0.90
2:3D:55:THR:HG1	2:3E:284:LEU:H	1.17	0.90
1:4F:222:PRO:HD2	2:5F:324:LYS:HD3	1.52	0.90
2:5D:54:ALA:O	2:5E:283:ALA:CA	2.17	0.90
2:3E:58:ARG:HH11	2:3F:281:TYR:HE1	0.98	0.90
1:4A:57:GLY:H	1:4B:285:GLN:HG2	1.35	0.90
1:2D:85:HIS:O	1:2E:283:HIS:NE2	2.04	0.90
2:5B:87:PRO:HD2	2:5C:281:TYR:CE2	2.06	0.90
2:5D:58:ARG:HD2	2:5E:280:GLN:O	1.70	0.90
2:5G:54:ALA:HB1	2:5H:281:TYR:O	1.70	0.90
1:2A:407:TRP:HZ2	2:3A:258:ILE:HD11	1.37	0.89
2:3D:153:SER:HB2	2:3D:191:GLN:HE22	1.36	0.89
2:3B:179:VAL:H	1:4B:352:LYS:HZ1	1.04	0.89
2:5D:58:ARG:CD	2:5E:280:GLN:O	2.20	0.89
2:3A:55:THR:HG23	2:3B:283:ALA:HB2	1.53	0.89
1:2D:56:THR:HA	1:2E:285:GLN:HB3	1.54	0.89
2:5C:88:ASP:HB2	2:5D:281:TYR:CE1	2.07	0.89
1:4F:178:SER:HB2	2:5F:347:ASN:HD22	1.26	0.89
2:3E:55:THR:HB	2:3F:283:ALA:HA	1.55	0.88
2:3G:55:THR:CG2	2:3H:283:ALA:HA	2.01	0.88
1:2D:33:ASP:HB3	1:2E:282:TYR:OH	1.71	0.88
1:2A:96:LYS:HE3	2:3A:129:CYS:SG	2.14	0.88
1:4G:168:ASN:HD21	1:4G:194:LEU:HD11	1.38	0.88
1:4D:33:ASP:OD1	1:4E:282:TYR:CE2	2.26	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4C:184:PRO:HA	1:4C:391:MET:HE1	1.57	0.87
2:3E:58:ARG:CZ	2:3F:281:TYR:CE1	2.57	0.87
2:3D:54:ALA:O	2:3E:283:ALA:CA	2.23	0.86
2:3E:218:THR:O	1:4E:326:LYS:HE2	1.74	0.86
2:5F:54:ALA:CB	2:5G:281:TYR:O	2.24	0.86
2:5H:200:GLN:HB3	2:5H:266:PHE:HB2	1.58	0.86
1:4D:85:HIS:O	1:4E:283:HIS:NE2	2.08	0.85
1:4H:222:PRO:HD2	2:5H:324:LYS:NZ	1.91	0.85
1:2F:178:SER:HB2	2:3F:347:ASN:HD22	1.37	0.85
1:2A:407:TRP:CZ2	2:3A:258:ILE:HD11	2.11	0.85
2:3A:220:PRO:HD2	1:4A:326:LYS:HE2	0.88	0.85
2:3A:212:PHE:HE1	1:4A:326:LYS:NZ	1.75	0.85
2:5A:55:THR:HG21	2:5B:283:ALA:CA	2.05	0.85
2:5D:54:ALA:C	2:5E:283:ALA:CA	2.50	0.85
2:3E:202:ILE:HD11	2:3E:268:ILE:HD12	1.60	0.84
1:4B:258:ASN:HB3	1:4B:352:LYS:HE3	1.57	0.84
2:3I:99:ASN:ND2	1:4I:254:GLU:OE1	2.09	0.84
2:5E:135:ILE:HG13	2:5E:152:ILE:HD11	1.59	0.84
1:2G:60:LYS:NZ	1:2H:283:HIS:CD2	2.45	0.84
2:3F:220:PRO:HG2	1:4F:326:LYS:HE3	1.57	0.84
2:5E:55:THR:HB	2:5F:283:ALA:CA	2.08	0.84
1:4D:85:HIS:O	1:4E:283:HIS:CD2	2.31	0.84
2:5A:207:LEU:HD21	2:5A:225:LEU:HB3	1.57	0.84
1:4C:121:ARG:HH12	1:4D:283:HIS:HE1	1.24	0.84
2:3C:176:SER:HB2	1:4C:349:THR:OG1	1.78	0.83
1:4D:57:GLY:H	1:4E:285:GLN:CB	1.89	0.83
2:3B:98:GLY:O	1:4B:257:THR:HG21	1.79	0.83
2:3B:286:VAL:HG23	2:3B:287:PRO:HD3	1.61	0.83
1:4B:60:LYS:HE3	1:4C:282:TYR:OH	1.79	0.82
1:2A:96:LYS:NZ	2:3A:1:MET:O	2.12	0.82
1:4D:60:LYS:HE3	1:4E:283:HIS:HA	1.61	0.82
2:3F:139:LEU:HD13	2:3F:168:SER:HB2	1.59	0.82
2:5B:87:PRO:CD	2:5C:281:TYR:CE2	2.62	0.82
2:5F:58:ARG:HD3	2:5G:281:TYR:CD1	2.14	0.82
2:3A:55:THR:HG21	2:3B:283:ALA:HA	1.61	0.82
2:3D:55:THR:OG1	2:3E:283:ALA:HA	1.79	0.82
2:5F:54:ALA:HB1	2:5G:281:TYR:CA	2.09	0.82
1:4D:57:GLY:N	1:4E:285:GLN:HB3	1.94	0.81
2:3A:55:THR:CG2	2:3B:283:ALA:CB	2.54	0.81
2:3E:55:THR:CB	2:3F:283:ALA:HA	2.09	0.81
2:3E:58:ARG:CD	2:3F:281:TYR:CD1	2.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2C:124:LYS:HD2	1:2D:283:HIS:CE1	2.16	0.81
2:3B:179:VAL:N	1:4B:352:LYS:HZ1	1.77	0.81
1:4D:60:LYS:HE3	1:4E:283:HIS:CD2	2.15	0.81
2:5F:55:THR:CG2	2:5G:283:ALA:HA	2.11	0.81
1:4A:212:ILE:HG23	1:4A:275:ILE:HD12	1.61	0.81
2:3A:55:THR:HG21	2:3B:283:ALA:CA	2.11	0.81
1:2E:60:LYS:NZ	1:2F:282:TYR:HE2	1.72	0.81
1:2I:292:THR:HG21	1:2I:331:ALA:HB1	1.63	0.81
2:3H:99:ASN:ND2	1:4H:254:GLU:OE1	2.13	0.80
2:5E:55:THR:CG2	2:5F:283:ALA:HA	2.11	0.80
1:2G:407:TRP:CE3	2:3G:255:VAL:HG22	2.15	0.80
1:4D:178:SER:HB2	2:5D:347:ASN:ND2	1.96	0.80
1:2D:221:ARG:HA	2:3D:324:LYS:HE3	1.63	0.80
2:5D:58:ARG:CZ	2:5E:281:TYR:CD1	2.64	0.80
2:5D:54:ALA:HA	2:5E:283:ALA:HB2	1.64	0.79
1:2C:100:ALA:HA	2:3C:252:LYS:HD2	1.63	0.79
1:2B:338:LYS:HZ1	1:2B:341:ILE:HG12	1.47	0.79
2:3D:178:THR:HG22	1:4D:352:LYS:HZ3	1.47	0.79
1:4H:191:THR:HG21	1:4H:425:LEU:HD21	1.65	0.79
2:3F:179:VAL:HG23	1:4F:349:THR:O	1.82	0.79
1:4G:407:TRP:HE3	2:5G:255:VAL:HG12	1.47	0.79
1:2F:177:VAL:HG13	2:3F:327:ASP:OD2	1.83	0.79
1:4D:178:SER:HB2	2:5D:347:ASN:HD22	1.46	0.79
2:5B:286:VAL:HG23	2:5B:287:PRO:HD3	1.62	0.79
1:2G:2:ARG:HB3	1:2G:133:GLN:HE21	1.48	0.79
1:2E:398:MET:HE2	2:3E:346:PRO:CD	2.12	0.78
1:2G:181:VAL:HG12	2:3G:256:ASN:HB2	1.65	0.78
2:3D:54:ALA:O	2:3E:283:ALA:N	2.16	0.78
1:4E:221:ARG:HG2	2:5E:322:SER:HB2	1.65	0.78
2:3C:176:SER:CB	1:4C:349:THR:OG1	2.30	0.78
1:4F:213:CYS:SG	1:4F:219:ILE:CG1	2.71	0.78
1:2F:178:SER:HB2	2:3F:347:ASN:HD21	1.41	0.78
2:5E:202:ILE:HD11	2:5E:268:ILE:HD12	1.63	0.78
1:2G:287:SER:OG	1:2G:290:GLU:OE1	2.00	0.78
2:3B:205:GLU:CD	1:4B:329:ASN:HD21	1.91	0.78
1:2E:181:VAL:HG22	2:3E:256:ASN:HD22	1.46	0.78
2:5C:87:PRO:N	2:5D:281:TYR:OH	2.16	0.78
1:2B:221:ARG:CZ	2:3B:325:GLU:H	1.96	0.78
1:4G:108:TYR:O	1:4G:112:LYS:NZ	2.16	0.78
1:2C:292:THR:HG21	1:2C:331:ALA:HB1	1.64	0.78
1:2E:60:LYS:CE	1:2F:283:HIS:CD2	2.67	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4E:221:ARG:HG2	2:5E:322:SER:HB3	1.66	0.78
2:3C:98:GLY:O	1:4C:257:THR:HG21	1.83	0.78
1:2E:60:LYS:CE	1:2F:283:HIS:HD2	1.95	0.77
1:2H:399:TYR:O	1:2H:402:ARG:NH2	2.17	0.77
2:5C:88:ASP:HB2	2:5D:281:TYR:CZ	2.19	0.77
2:5C:86:ARG:HG2	2:5D:281:TYR:OH	1.55	0.77
1:2G:387:VAL:HA	1:2G:390:ARG:HH21	1.48	0.77
1:2D:89:PRO:HG2	1:2E:280:LYS:HE3	1.66	0.77
1:2H:151:CYS:HG	1:2H:193:SER:HG	1.25	0.77
2:3H:391:ARG:O	1:4H:262:TYR:OH	2.03	0.77
1:4F:213:CYS:SG	1:4F:219:ILE:CD1	2.73	0.77
2:5C:49:VAL:HG21	2:5C:241:ARG:HG2	1.66	0.77
2:3A:178:THR:HA	1:4A:352:LYS:HE3	1.66	0.77
1:2G:60:LYS:HD3	1:2H:283:HIS:HD2	1.47	0.77
1:4G:151:CYS:SG	1:4G:193:SER:OG	2.42	0.77
1:2I:238:LEU:HD11	1:2I:378:ILE:HD11	1.67	0.76
1:4H:399:TYR:O	1:4H:402:ARG:NH2	2.18	0.76
2:5E:49:VAL:HG21	2:5E:241:ARG:HG2	1.67	0.76
1:4C:121:ARG:NH1	1:4D:283:HIS:HE1	1.79	0.76
1:2D:27:GLU:OE1	1:2D:243:ARG:NH1	2.18	0.76
2:5A:49:VAL:HG11	2:5A:241:ARG:HG2	1.65	0.76
1:4C:60:LYS:HE2	1:4D:282:TYR:OH	1.86	0.76
1:4H:222:PRO:HD2	2:5H:324:LYS:HZ1	1.50	0.76
2:5C:88:ASP:N	2:5D:281:TYR:CZ	2.53	0.76
2:3B:178:THR:HA	1:4B:352:LYS:NZ	2.00	0.76
2:3B:175:VAL:CG1	1:4B:332:VAL:HG13	2.16	0.76
1:4H:202:VAL:HG22	1:4H:268:MET:HG3	1.68	0.76
1:2E:407:TRP:HZ2	2:3E:258:ILE:HD11	1.51	0.76
2:3D:49:VAL:HG21	2:3D:241:ARG:HG2	1.67	0.76
2:3D:177:ASP:CG	1:4D:353:CYS:SG	2.69	0.76
1:4I:292:THR:HG21	1:4I:331:ALA:HB1	1.68	0.76
2:3C:49:VAL:HG21	2:3C:241:ARG:HG2	1.69	0.75
2:3C:86:ARG:HD3	2:3D:281:TYR:CD1	2.17	0.75
1:4G:181:VAL:HG22	2:5G:347:ASN:O	1.86	0.75
2:3B:179:VAL:N	1:4B:352:LYS:NZ	2.32	0.75
1:4D:35:GLN:OE1	1:4E:282:TYR:OH	2.00	0.75
1:2G:151:CYS:SG	1:2G:193:SER:OG	2.41	0.75
1:2E:56:THR:CB	1:2F:283:HIS:O	2.35	0.75
2:3H:179:VAL:HG12	1:4H:258:ASN:OD1	1.87	0.74
2:3G:55:THR:HG21	2:3H:283:ALA:CA	2.11	0.74
2:3A:49:VAL:HG21	2:3A:241:ARG:HG2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4A:57:GLY:N	1:4B:285:GLN:HG2	2.03	0.74
1:4F:292:THR:HG21	1:4F:331:ALA:HB1	1.69	0.74
2:5B:332:ASN:OD1	2:5B:336:LYS:NZ	2.20	0.74
2:3B:205:GLU:OE1	1:4B:329:ASN:ND2	2.19	0.74
2:3E:49:VAL:HG21	2:3E:241:ARG:HG2	1.67	0.74
2:3H:7:VAL:HB	2:3H:135:ILE:HD13	1.69	0.74
1:4G:407:TRP:CE3	2:5G:255:VAL:HG12	2.23	0.74
1:2A:151:CYS:SG	1:2A:193:SER:OG	2.41	0.74
1:4B:88:HIS:ND1	1:4C:283:HIS:CG	2.55	0.74
1:4G:6:SER:HA	1:4G:136:LEU:HB2	1.69	0.74
2:3E:391:ARG:O	1:4E:262:TYR:OH	2.05	0.74
2:3E:313:ALA:HB1	2:3E:367:PHE:HE1	1.53	0.74
1:4D:33:ASP:OD1	1:4E:282:TYR:HE2	1.67	0.74
2:5A:55:THR:HG23	2:5B:283:ALA:HB2	1.70	0.74
2:3E:248:SER:HA	2:3E:252:LYS:HD3	1.68	0.73
1:4F:189:LEU:HD11	1:4F:418:PHE:HD1	1.53	0.73
1:2E:217:LEU:HD11	1:2E:275:ILE:HG22	1.68	0.73
2:3H:221:THR:HG22	2:3H:223:GLY:H	1.52	0.73
1:4G:121:ARG:HH12	1:4G:124:LYS:HE3	1.53	0.73
1:4H:223:THR:OG1	2:5H:245:GLN:OE1	2.04	0.73
2:5F:55:THR:HG21	2:5G:283:ALA:HA	1.70	0.73
1:4I:11:GLN:NE2	2:5I:245:GLN:O	2.21	0.73
1:2G:212:ILE:HG23	1:2G:275:ILE:HD12	1.70	0.73
1:4D:212:ILE:CG2	1:4D:275:ILE:HD11	2.19	0.73
2:5D:58:ARG:HD3	2:5E:281:TYR:HA	0.87	0.73
1:2B:221:ARG:NH2	2:3B:322:SER:O	2.22	0.73
1:2H:176:GLN:HB3	2:3H:331:LEU:HD11	1.69	0.73
1:2I:151:CYS:SG	1:2I:193:SER:OG	2.46	0.73
2:3A:256:ASN:HD21	2:3A:350:LYS:HG2	1.52	0.73
1:4D:60:LYS:HE3	1:4E:283:HIS:CG	2.23	0.73
1:4F:213:CYS:SG	1:4F:219:ILE:HG13	2.28	0.73
2:5I:318:ARG:HD2	2:5I:358:PRO:HD3	1.69	0.73
2:3D:58:ARG:NH1	2:3E:280:GLN:HG3	2.03	0.73
1:4B:176:GLN:HB3	2:5B:331:LEU:HD11	1.70	0.73
2:5D:58:ARG:CZ	2:5E:281:TYR:CE1	2.72	0.73
2:5H:55:THR:OG1	2:5I:280:GLN:O	2.06	0.73
2:3A:176:SER:OG	1:4A:349:THR:OG1	2.04	0.73
1:4F:174:SER:OG	1:4F:177:VAL:O	2.06	0.73
2:5B:274:THR:HG21	2:5B:282:ARG:HD2	1.71	0.73
2:3D:58:ARG:HD2	2:3E:280:GLN:O	1.89	0.72
2:3E:397:TRP:CZ3	1:4E:260:VAL:O	2.42	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5F:54:ALA:HB1	2:5G:281:TYR:HA	1.69	0.72
1:2E:60:LYS:HZ1	1:2F:282:TYR:HE2	1.32	0.72
2:3D:55:THR:OG1	2:3E:283:ALA:C	2.31	0.72
1:4C:292:THR:HG21	1:4C:331:ALA:HB1	1.71	0.72
1:2B:221:ARG:NH1	2:3B:325:GLU:H	1.86	0.72
2:3H:49:VAL:HG11	2:3H:241:ARG:HG2	1.71	0.72
1:4A:222:PRO:HD2	2:5A:324:LYS:HZ3	1.54	0.72
1:4B:60:LYS:CE	1:4C:282:TYR:CZ	2.73	0.72
1:4D:388:PHE:HB2	1:4D:429:GLU:OE2	1.90	0.72
1:2B:72:PRO:HD2	2:3B:2:ARG:HH22	1.54	0.72
1:2D:212:ILE:HG12	1:2D:275:ILE:HD11	1.72	0.72
2:5E:200:GLN:HB3	2:5E:268:ILE:HD11	1.72	0.72
2:3B:267:LEU:HD12	2:3B:301:CYS:HB3	1.71	0.72
1:4G:76:ASP:OD2	2:5G:46:ARG:NH1	2.23	0.72
1:4G:151:CYS:HG	1:4G:193:SER:HG	1.29	0.72
1:2G:56:THR:CB	1:2H:283:HIS:O	2.37	0.72
1:4C:88:HIS:HB3	1:4C:91:GLN:HG2	1.70	0.72
2:3E:55:THR:CG2	2:3F:282:ARG:O	2.37	0.72
1:2D:56:THR:HA	1:2E:285:GLN:H	1.55	0.71
2:3G:135:ILE:HD11	2:3G:152:ILE:HD11	1.72	0.71
2:5E:55:THR:HG21	2:5F:284:LEU:H	1.55	0.71
2:5A:7:VAL:HG22	2:5A:64:ILE:CG2	2.18	0.71
1:2E:60:LYS:NZ	1:2F:282:TYR:CD2	2.58	0.71
1:2A:191:THR:HG23	1:2A:425:LEU:HD21	1.71	0.71
1:2B:88:HIS:CD2	1:2C:283:HIS:HB3	2.26	0.71
1:4E:292:THR:HG21	1:4E:331:ALA:HB1	1.70	0.71
2:5I:313:ALA:HB3	2:5I:349:MET:HE1	1.71	0.71
1:2F:401:LYS:HZ1	2:3F:344:TRP:CG	2.09	0.71
1:2G:6:SER:HA	1:2G:136:LEU:HB2	1.73	0.71
2:5F:55:THR:HG23	2:5G:283:ALA:CB	2.21	0.71
1:2A:96:LYS:CE	2:3A:129:CYS:SG	2.78	0.71
1:2G:398:MET:HE1	2:3G:345:ILE:HG23	1.71	0.71
2:3F:248:SER:OG	2:3F:316:MET:HE1	1.91	0.71
1:4A:222:PRO:HD2	2:5A:324:LYS:HZ1	1.55	0.71
2:3E:129:CYS:SG	2:3E:162:ARG:NH2	2.64	0.71
1:4F:137:MET:HE3	1:4F:139:ASN:HD22	1.56	0.71
2:5G:91:VAL:HG21	2:5G:116:VAL:HG12	1.73	0.71
1:4H:181:VAL:HG22	2:5H:256:ASN:OD1	1.89	0.71
1:4G:292:THR:HG21	1:4G:331:ALA:HB1	1.72	0.71
2:3B:220:PRO:HD2	1:4B:326:LYS:HD2	1.73	0.70
2:3F:66:MET:HE2	2:3F:116:VAL:HG21	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2B:60:LYS:HE2	1:2C:282:TYR:CD2	2.26	0.70
1:2F:223:THR:HG22	2:3F:322:SER:HA	1.72	0.70
1:2H:76:ASP:OD2	2:3H:46:ARG:NH1	2.24	0.70
2:5H:306:ARG:HA	2:5H:340:TYR:HE1	1.55	0.70
2:3B:49:VAL:HG11	2:3B:241:ARG:HG2	1.72	0.70
2:3E:220:PRO:HD2	1:4E:326:LYS:HD3	1.72	0.70
2:5B:163:ILE:HD13	2:5B:250:LEU:HB3	1.73	0.70
2:5F:55:THR:HG23	2:5G:283:ALA:HB2	1.72	0.70
2:3B:87:PRO:HD2	2:3C:281:TYR:CE2	2.26	0.70
2:3B:172:SER:OG	2:3B:175:VAL:O	2.10	0.70
2:3D:54:ALA:C	2:3E:283:ALA:CA	2.63	0.70
1:4I:27:GLU:OE2	1:4I:243:ARG:NH1	2.24	0.70
2:5A:55:THR:CG2	2:5B:283:ALA:CA	2.67	0.70
2:3D:396:HIS:HA	2:3D:399:THR:HG22	1.71	0.70
2:5F:274:THR:HG21	2:5F:282:ARG:HD2	1.71	0.70
2:3F:208:TYR:HD1	1:4F:326:LYS:CE	2.04	0.70
1:4A:397:LEU:HD21	2:5A:344:TRP:HA	1.73	0.69
1:4C:182:VAL:HG12	2:5C:256:ASN:HD21	1.56	0.69
1:2E:221:ARG:HD3	2:3E:325:GLU:OE2	1.92	0.69
1:4E:407:TRP:HH2	2:5E:258:ILE:HB	1.57	0.69
2:5B:49:VAL:HG11	2:5B:241:ARG:HG2	1.73	0.69
1:4B:181:VAL:H	2:5B:350:LYS:HE3	1.56	0.69
1:4C:209:ILE:HD11	1:4C:302:MET:HG3	1.74	0.69
2:5H:49:VAL:HG11	2:5H:241:ARG:HG2	1.75	0.69
2:5A:55:THR:CG2	2:5B:283:ALA:CB	2.70	0.69
1:2C:88:HIS:CA	1:2D:282:TYR:HE2	2.00	0.69
1:2D:269:LEU:HD23	1:2D:301:MET:HG2	1.73	0.69
1:2H:298:PRO:HG3	1:2H:308:ARG:HH12	1.58	0.69
2:5I:49:VAL:HG11	2:5I:241:ARG:HG2	1.75	0.69
2:5B:213:ARG:HH22	2:5B:297:LYS:HB2	1.58	0.69
2:5G:55:THR:CG2	2:5H:283:ALA:CA	2.71	0.69
1:2H:217:LEU:HD21	1:2H:275:ILE:HG13	1.74	0.68
1:2G:230:LEU:CD2	1:2G:302:MET:HE2	2.23	0.68
1:2B:151:CYS:SG	1:2B:193:SER:OG	2.40	0.68
1:2C:62:VAL:HG11	1:2D:282:TYR:CZ	2.29	0.68
1:2C:62:VAL:HG11	1:2D:282:TYR:OH	1.93	0.68
1:2G:60:LYS:CD	1:2H:283:HIS:CD2	2.73	0.68
1:4G:56:THR:CB	1:4H:283:HIS:O	2.42	0.68
2:3C:176:SER:OG	1:4C:349:THR:OG1	2.11	0.68
1:4I:397:LEU:HD21	2:5I:344:TRP:HA	1.75	0.68
1:4B:133:GLN:HG3	1:4B:252:VAL:HG22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2D:57:GLY:H	1:2E:285:GLN:CB	2.07	0.68
2:3D:54:ALA:HB1	2:3E:281:TYR:O	1.94	0.68
1:2F:292:THR:HG21	1:2F:331:ALA:HB1	1.73	0.68
2:3D:54:ALA:O	2:3E:282:ARG:C	2.37	0.68
2:3H:397:TRP:HH2	1:4H:260:VAL:O	1.77	0.68
2:5A:113:ILE:HG13	2:5A:150:LEU:HD22	1.76	0.67
1:4A:212:ILE:CG2	1:4A:275:ILE:HD12	2.24	0.67
2:5A:374:ILE:O	2:5A:374:ILE:HG22	1.94	0.67
2:5G:68:LEU:HD23	2:5G:147:MET:HE2	1.75	0.67
2:3B:274:THR:HG21	2:3B:282:ARG:HD2	1.77	0.67
2:3B:396:HIS:HA	2:3B:399:THR:HG22	1.77	0.67
2:3F:220:PRO:HG2	1:4F:326:LYS:CE	2.24	0.67
1:4A:173:PRO:HG2	1:4A:391:MET:HE1	1.76	0.67
1:4D:60:LYS:CD	1:4E:282:TYR:O	2.36	0.67
1:4H:269:LEU:HB3	1:4H:301:MET:HE2	1.75	0.67
2:3A:113:ILE:HG13	2:3A:150:LEU:HD22	1.76	0.67
1:4G:60:LYS:HD2	1:4H:283:HIS:CD2	2.30	0.67
2:5A:203:ASP:OD1	2:5A:377:MET:HE1	1.94	0.67
2:3B:175:VAL:HG11	1:4B:332:VAL:CG1	2.20	0.67
2:3F:208:TYR:CD1	1:4F:326:LYS:CE	2.78	0.67
2:3H:208:TYR:HE2	1:4H:329:ASN:HD22	1.42	0.67
1:2A:181:VAL:HG22	2:3A:350:LYS:NZ	2.07	0.67
2:3I:175:VAL:HG21	1:4I:332:VAL:CG1	2.24	0.67
1:4F:151:CYS:SG	1:4F:193:SER:OG	2.47	0.67
2:5H:203:ASP:OD1	2:5H:377:MET:HE1	1.94	0.67
1:2A:268:MET:N	1:2A:268:MET:SD	2.67	0.67
1:4I:5:ILE:HD12	1:4I:125:LEU:CD2	2.24	0.67
2:3F:317:PHE:HB3	2:3F:321:MET:HE1	1.76	0.66
1:4B:181:VAL:CG1	2:5B:350:LYS:NZ	2.49	0.66
1:4H:234:VAL:HG21	1:4H:302:MET:HE1	1.76	0.66
2:5D:396:HIS:HA	2:5D:399:THR:HG22	1.77	0.66
2:3D:58:ARG:HD3	2:3E:281:TYR:HA	0.82	0.66
2:5E:55:THR:CG2	2:5F:282:ARG:O	2.37	0.66
1:4E:181:VAL:HG22	2:5E:256:ASN:HD22	1.60	0.66
1:2D:60:LYS:CD	1:2E:282:TYR:O	2.36	0.66
1:4C:397:LEU:HD21	2:5C:344:TRP:HA	1.78	0.66
1:4F:179:THR:OG1	2:5F:351:SER:OG	2.06	0.66
1:4G:97:GLU:OE2	1:4G:105:ARG:NH2	2.25	0.66
2:5H:117:LEU:HD13	2:5H:154:LYS:HG3	1.77	0.66
1:2C:221:ARG:HG3	2:3C:325:GLU:CD	2.20	0.66
2:5G:178:THR:OG1	2:5G:181:GLU:OE2	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2D:138:PHE:HZ	1:2D:235:ILE:HD12	1.60	0.66
1:2G:60:LYS:HZ3	1:2H:283:HIS:CD2	2.12	0.66
2:3I:49:VAL:HG11	2:3I:241:ARG:HG2	1.77	0.66
2:5I:289:LEU:HD12	2:5I:365:VAL:HG12	1.77	0.66
1:2D:292:THR:HG21	1:2D:331:ALA:HB1	1.78	0.66
2:3A:212:PHE:CE1	1:4A:326:LYS:NZ	2.58	0.66
2:3F:54:ALA:HB1	2:3G:281:TYR:HA	1.77	0.66
1:2A:2:ARG:HE	1:2A:133:GLN:HE21	1.44	0.66
1:2D:33:ASP:O	1:2D:60:LYS:NZ	2.28	0.66
1:2E:151:CYS:SG	1:2E:193:SER:OG	2.46	0.66
1:4G:31:GLN:NE2	1:4G:33:ASP:OD2	2.29	0.66
1:2H:133:GLN:HG3	1:2H:252:VAL:HG22	1.76	0.65
2:3D:55:THR:OG1	2:3E:283:ALA:CA	2.44	0.65
2:3F:330:MET:HB3	2:3F:349:MET:SD	2.35	0.65
1:4I:8:HIS:HD2	1:4I:65:CYS:SG	2.18	0.65
2:5G:139:LEU:HD13	2:5G:168:SER:HB2	1.79	0.65
2:3F:377:MET:HG3	2:3F:380:ARG:NH1	2.11	0.65
1:4D:33:ASP:OD2	1:4E:282:TYR:OH	2.14	0.65
1:4G:177:VAL:HG13	2:5G:327:ASP:OD2	1.96	0.65
1:2A:178:SER:HB3	1:2A:183:GLU:HG3	1.79	0.65
1:2A:301:MET:HE1	1:2A:307:PRO:HG3	1.78	0.65
2:3D:274:THR:HG21	2:3D:282:ARG:HD2	1.78	0.65
2:5D:412:GLU:O	2:5D:416:ASN:ND2	2.29	0.65
1:4E:407:TRP:CH2	2:5E:258:ILE:HB	2.32	0.65
1:4G:122:ILE:HD13	1:4G:157:LEU:HD11	1.78	0.65
2:3F:98:GLY:O	1:4F:257:THR:HG21	1.97	0.65
2:3F:220:PRO:HG2	1:4F:326:LYS:HG3	1.78	0.65
2:5A:207:LEU:HD23	2:5A:225:LEU:HD22	1.79	0.65
2:5E:129:CYS:SG	2:5E:162:ARG:NH2	2.70	0.65
2:3E:396:HIS:CE1	1:4E:263:PRO:HD3	2.32	0.65
2:3H:391:ARG:HD2	1:4H:346:TRP:CE2	2.32	0.65
1:4A:178:SER:HB2	2:5A:347:ASN:CG	2.22	0.65
1:4B:181:VAL:CG1	2:5B:350:LYS:HZ2	1.96	0.65
1:4H:398:MET:HE3	2:5H:346:PRO:HD2	1.78	0.65
2:5C:88:ASP:OD2	2:5D:281:TYR:CD2	2.50	0.65
1:2D:60:LYS:NZ	1:2E:283:HIS:CD2	2.65	0.65
1:4G:88:HIS:CE1	1:4H:280:LYS:HD2	2.32	0.65
2:5H:163:ILE:HD13	2:5H:250:LEU:HB3	1.79	0.65
2:5I:396:HIS:HA	2:5I:399:THR:HG22	1.78	0.64
1:2C:178:SER:HB2	2:3C:347:ASN:ND2	2.12	0.64
2:3D:249:ASP:OD1	2:3D:250:LEU:N	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4A:60:LYS:CE	1:4B:283:HIS:HD2	2.10	0.64
1:4D:60:LYS:CE	1:4E:283:HIS:CG	2.79	0.64
2:5C:88:ASP:CB	2:5D:281:TYR:CZ	2.80	0.64
2:5E:95:THR:OG1	2:5E:108:GLU:OE2	2.14	0.64
1:2B:23:LEU:HD11	1:2B:361:THR:HG23	1.78	0.64
1:2B:221:ARG:NH2	2:3B:325:GLU:H	1.95	0.64
1:2C:298:PRO:HG3	1:2C:308:ARG:HH22	1.62	0.64
1:2G:401:LYS:HD2	2:3G:344:TRP:CH2	2.33	0.64
1:4D:30:ILE:HG22	1:4D:36:MET:HB3	1.78	0.64
2:5A:55:THR:HG23	2:5B:283:ALA:CB	2.27	0.64
2:5A:248:SER:OG	2:5A:350:LYS:NZ	2.31	0.64
1:2A:101:ASN:HB3	1:2A:182:VAL:HG21	1.78	0.64
1:2I:5:ILE:HD12	1:2I:125:LEU:CD2	2.26	0.64
2:3G:257:LEU:HD11	2:3G:314:SER:HB3	1.80	0.64
1:2E:250:VAL:HG11	1:2E:318:MET:HE1	1.78	0.64
1:2H:210:TYR:HD1	2:3H:324:LYS:HE3	1.56	0.64
1:4G:339:ARG:O	1:4G:342:GLN:NE2	2.30	0.64
2:5B:87:PRO:HD3	2:5C:281:TYR:CZ	2.32	0.64
1:2A:311:LYS:HE2	1:2A:344:VAL:HA	1.80	0.64
1:2D:100:ALA:HA	2:3D:252:LYS:HG3	1.77	0.64
1:2E:292:THR:HG21	1:2E:331:ALA:HB1	1.80	0.64
2:3H:166:THR:HB	2:3H:199:VAL:HG12	1.80	0.64
2:3B:178:THR:CA	1:4B:352:LYS:HZ3	2.11	0.63
2:3E:175:VAL:HG23	1:4E:329:ASN:OD1	1.97	0.63
1:4D:55:GLU:O	1:4E:285:GLN:CG	2.43	0.63
2:5D:54:ALA:O	2:5E:283:ALA:N	2.30	0.63
1:2A:96:LYS:HG2	2:3A:129:CYS:SG	2.38	0.63
1:2E:73:THR:HA	2:3E:46:ARG:HH11	1.64	0.63
2:5G:165:GLU:OE2	2:5G:200:GLN:NE2	2.30	0.63
1:2B:398:MET:SD	2:3B:346:PRO:HD2	2.38	0.63
1:2E:328:VAL:HG21	1:2E:355:ILE:HD11	1.80	0.63
1:2A:377:MET:HE2	1:2A:379:SER:HB3	1.79	0.63
2:3E:313:ALA:HB1	2:3E:367:PHE:CE1	2.33	0.63
2:3E:397:TRP:CH2	1:4E:260:VAL:CG2	2.77	0.63
1:2A:191:THR:CG2	1:2A:425:LEU:HD21	2.28	0.63
1:2D:398:MET:HE2	2:3D:346:PRO:HD2	1.81	0.63
1:4I:5:ILE:HD12	1:4I:125:LEU:HD23	1.79	0.63
2:5D:83:GLN:O	2:5E:281:TYR:OH	2.14	0.62
2:5D:83:GLN:O	2:5E:281:TYR:CE1	2.52	0.62
1:2E:208:ALA:HB2	1:2E:304:LYS:HG2	1.81	0.62
1:2G:407:TRP:HE3	2:3G:255:VAL:HG22	1.60	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3F:208:TYR:CD1	1:4F:326:LYS:HD3	2.34	0.62
2:5E:58:ARG:HD3	2:5F:281:TYR:CD1	2.34	0.62
1:2B:181:VAL:HG12	2:3B:256:ASN:OD1	1.99	0.62
2:3B:87:PRO:CD	2:3C:281:TYR:CE2	2.83	0.62
1:2E:101:ASN:ND2	2:3E:252:LYS:HZ2	1.97	0.62
1:2E:407:TRP:CZ2	2:3E:258:ILE:HD11	2.34	0.62
2:3H:175:VAL:HG11	1:4H:332:VAL:HG13	1.81	0.62
2:5A:249:ASP:OD1	2:5A:250:LEU:N	2.32	0.62
2:3I:318:ARG:HD3	2:3I:358:PRO:HD3	1.81	0.62
1:4E:60:LYS:HZ1	1:4F:283:HIS:CD2	2.11	0.62
2:5A:7:VAL:HG22	2:5A:64:ILE:HG22	1.82	0.62
1:4B:103:PHE:HD2	1:4B:413:MET:HE1	1.63	0.62
2:5A:326:VAL:HG13	2:5A:330:MET:HE1	1.82	0.62
2:5H:20:PHE:HD2	2:5H:233:MET:HE3	1.65	0.62
1:2D:56:THR:HA	1:2E:285:GLN:N	2.15	0.62
1:2G:151:CYS:HG	1:2G:193:SER:HG	1.35	0.62
2:3A:391:ARG:NH2	1:4A:346:TRP:CD1	2.68	0.62
2:3D:54:ALA:HA	2:3E:283:ALA:HB2	1.80	0.62
2:3F:180:VAL:O	2:3F:184:ASN:ND2	2.32	0.62
2:3I:95:THR:OG1	2:3I:108:GLU:OE2	2.09	0.62
1:4I:109:THR:HG22	1:4I:110:ILE:HG23	1.82	0.62
2:5H:68:LEU:HD12	2:5H:143:THR:HG22	1.81	0.62
1:2A:105:ARG:HH12	2:3A:251:ARG:HD2	1.65	0.62
1:2G:212:ILE:CG2	1:2G:275:ILE:HD12	2.29	0.62
1:2H:176:GLN:HB3	2:3H:331:LEU:CD1	2.28	0.62
1:4A:66:VAL:HG12	1:4A:91:GLN:HB2	1.81	0.62
1:4D:265:ILE:HG21	1:4D:313:MET:HE1	1.80	0.62
1:4E:221:ARG:CG	2:5E:322:SER:HB3	2.29	0.62
2:5D:267:LEU:HB3	2:5D:299:MET:HE2	1.81	0.62
2:3B:334:GLN:OE1	2:3B:348:ASN:ND2	2.32	0.61
2:3C:64:ILE:HD12	2:3C:119:VAL:HG12	1.82	0.61
1:2I:100:ALA:HA	2:3I:252:LYS:HE3	1.82	0.61
1:2I:392:ASP:OD1	1:2I:422:ARG:NH2	2.20	0.61
1:2G:417:GLU:HA	1:2G:420:GLU:HG3	1.81	0.61
2:3F:54:ALA:HB1	2:3G:281:TYR:CA	2.30	0.61
1:4E:167:LEU:HD21	1:4E:252:VAL:HG13	1.80	0.61
1:4G:178:SER:CB	2:5G:347:ASN:ND2	2.62	0.61
1:4I:68:LEU:CD1	1:4I:153:LEU:HD11	2.30	0.61
1:4I:241:SER:OG	1:4I:250:VAL:O	2.17	0.61
2:5B:161:ASP:OD1	2:5B:162:ARG:NH1	2.32	0.61
2:5D:155:VAL:HG13	2:5D:164:MET:HE1	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5I:211:CYS:SG	2:5I:217:LEU:HB2	2.40	0.61
2:5I:404:ASP:HB3	2:5I:406:MET:SD	2.41	0.61
1:2G:200:VAL:HG23	1:2G:268:MET:CE	2.30	0.61
2:3B:99:ASN:OD1	1:4B:254:GLU:OE1	2.18	0.61
2:3E:381:VAL:CG2	2:3E:415:MET:HE1	2.30	0.61
1:4B:316:CYS:HA	1:4B:352:LYS:HB2	1.81	0.61
2:3E:99:ASN:ND2	1:4E:254:GLU:OE1	2.33	0.61
2:3H:20:PHE:HD2	2:3H:233:MET:HE3	1.64	0.61
1:4I:195:LEU:HD21	1:4I:264:ARG:HE	1.65	0.61
1:2D:85:HIS:O	1:2E:283:HIS:CD2	2.52	0.61
1:2H:241:SER:OG	1:2H:250:VAL:O	2.18	0.61
2:3E:58:ARG:HH12	2:3F:281:TYR:HE1	1.33	0.61
1:4E:398:MET:HE3	2:5E:346:PRO:CD	2.28	0.61
2:5E:321:MET:HE3	2:5E:326:VAL:HG21	1.82	0.61
2:5F:55:THR:CG2	2:5G:283:ALA:CB	2.79	0.61
1:2A:60:LYS:HE2	1:2B:283:HIS:HD2	1.66	0.61
1:2D:30:ILE:HG22	1:2D:36:MET:HB3	1.83	0.61
2:3B:220:PRO:CD	1:4B:326:LYS:HD2	2.30	0.61
2:3C:70:PRO:HD2	1:4C:2:ARG:HH22	1.65	0.61
1:2B:221:ARG:HH12	2:3B:324:LYS:HB3	1.66	0.61
2:3F:391:ARG:O	1:4F:262:TYR:OH	2.14	0.61
1:4E:23:LEU:HD11	1:4E:361:THR:HG23	1.82	0.61
1:4E:274:PRO:HG3	1:4E:286:LEU:HD23	1.83	0.61
2:3E:294:PHE:CD2	2:3E:333:VAL:HG21	2.36	0.61
1:2B:27:GLU:HB3	1:2B:361:THR:HG21	1.82	0.61
2:3C:66:MET:HE1	2:3C:151:LEU:HD22	1.82	0.61
1:4D:292:THR:HG21	1:4D:331:ALA:HB1	1.81	0.61
1:4E:88:HIS:HB3	1:4E:91:GLN:HG2	1.83	0.61
1:4F:103:PHE:HD2	1:4F:413:MET:HE1	1.66	0.61
1:4H:223:THR:HG23	1:4H:225:THR:HG22	1.83	0.61
1:4I:8:HIS:CD2	1:4I:65:CYS:SG	2.94	0.61
1:2E:398:MET:CE	2:3E:346:PRO:HD2	2.18	0.60
2:3G:69:GLU:HG2	1:4G:2:ARG:HH22	1.65	0.60
2:3H:175:VAL:HG21	1:4H:333:ALA:HA	1.82	0.60
1:4B:328:VAL:CG1	1:4B:353:CYS:SG	2.89	0.60
1:4D:177:VAL:HG11	2:5D:327:ASP:HB3	1.83	0.60
1:4E:407:TRP:HZ3	2:5E:258:ILE:O	1.84	0.60
2:5B:8:GLN:OE1	2:5B:17:GLY:HA3	2.01	0.60
2:5H:68:LEU:HD21	2:5H:147:MET:SD	2.41	0.60
1:2B:238:LEU:HD13	1:2B:318:MET:HE3	1.82	0.60
2:3C:122:LYS:HE2	2:3D:281:TYR:OH	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4C:154:LEU:HD13	1:4C:166:LYS:HE3	1.82	0.60
1:4H:202:VAL:HA	1:4H:268:MET:HB2	1.82	0.60
1:2D:56:THR:CA	1:2E:285:GLN:HB3	2.28	0.60
2:3G:249:ASP:OD1	2:3G:250:LEU:N	2.34	0.60
1:4B:223:THR:HG23	1:4B:225:THR:HG22	1.82	0.60
1:4H:51:THR:HG23	1:4H:52:PHE:HD1	1.66	0.60
1:2E:177:VAL:HG11	2:3E:327:ASP:HB3	1.83	0.60
2:3G:55:THR:HG23	2:3H:283:ALA:HB2	1.84	0.60
1:4F:178:SER:HB2	2:5F:347:ASN:HD21	1.63	0.60
1:4H:318:MET:HE2	1:4H:376:CYS:SG	2.41	0.60
2:5B:87:PRO:HD3	2:5C:281:TYR:OH	2.02	0.60
1:2H:262:TYR:HB2	1:2H:265:ILE:HG22	1.84	0.60
2:3A:349:MET:C	2:3A:350:LYS:HD2	2.27	0.60
2:3I:325:GLU:HA	2:3I:328:GLU:HG3	1.82	0.60
2:5C:64:ILE:HD12	2:5C:119:VAL:HG12	1.83	0.60
2:5F:58:ARG:HD3	2:5G:281:TYR:CE1	2.37	0.60
2:5H:105:HIS:HE1	2:5H:191:GLN:HE22	1.49	0.60
2:3C:396:HIS:HA	2:3C:399:THR:HG22	1.84	0.60
1:4A:390:ARG:NH2	1:4A:390:ARG:HB3	2.17	0.60
2:5D:6:HIS:HD2	2:5D:134:GLN:HE21	1.48	0.60
2:5H:166:THR:HB	2:5H:199:VAL:HG22	1.84	0.60
1:2I:238:LEU:CD1	1:2I:378:ILE:HD11	2.31	0.60
2:5A:54:ALA:HB1	2:5B:281:TYR:O	2.02	0.60
2:5D:55:THR:OG1	2:5E:283:ALA:C	2.42	0.60
1:2G:60:LYS:HZ2	1:2H:283:HIS:CD2	2.18	0.60
2:3C:178:THR:HA	1:4C:352:LYS:HD3	1.83	0.60
1:2B:239:THR:OG1	1:2B:243:ARG:NH1	2.34	0.60
2:5A:2:ARG:NH2	2:5A:249:ASP:OD2	2.35	0.60
2:3E:66:MET:HE3	2:3E:147:MET:HE2	1.84	0.59
1:4D:57:GLY:N	1:4E:285:GLN:HA	2.17	0.59
1:4H:168:ASN:HD22	1:4H:198:THR:HG21	1.67	0.59
1:4D:60:LYS:HE3	1:4E:283:HIS:CA	2.30	0.59
1:4I:178:SER:HB3	2:5I:347:ASN:ND2	2.16	0.59
1:2G:18:ASN:O	1:2G:22:GLU:HG2	2.01	0.59
2:3F:16:ILE:HD11	2:3F:229:VAL:HG21	1.84	0.59
1:4G:222:PRO:HD2	2:5G:324:LYS:HG2	1.82	0.59
1:2F:276:ILE:HG23	1:2F:280:LYS:HB2	1.84	0.59
1:2G:339:ARG:O	1:2G:342:GLN:NE2	2.34	0.59
1:2G:403:ALA:HB2	2:3G:344:TRP:CZ3	2.38	0.59
2:3E:381:VAL:HG23	2:3E:415:MET:HE1	1.84	0.59
1:4H:215:ARG:NH2	1:4H:297:GLU:OE2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5I:290:THR:HA	2:5I:293:MET:HE3	1.85	0.59
1:2A:60:LYS:CE	1:2B:283:HIS:HD2	2.14	0.59
1:2D:105:ARG:HG2	1:2D:110:ILE:HG12	1.84	0.59
1:4G:178:SER:CB	2:5G:347:ASN:HD21	2.10	0.59
2:5A:10:GLY:HA2	2:5A:143:THR:HG23	1.85	0.59
2:5B:87:PRO:HD3	2:5C:281:TYR:CE2	2.38	0.59
2:5E:91:VAL:HG12	2:5E:112:LEU:HD21	1.83	0.59
1:2C:241:SER:OG	1:2C:249:ASN:HB2	2.02	0.59
2:3A:267:LEU:HB3	2:3A:299:MET:SD	2.43	0.59
2:3F:176:SER:OG	1:4F:349:THR:HB	2.03	0.59
1:4D:60:LYS:HZ1	1:4E:283:HIS:CD2	2.11	0.59
2:5D:64:ILE:HD12	2:5D:119:VAL:HG12	1.84	0.59
1:2D:60:LYS:HE3	1:2E:283:HIS:CG	2.38	0.59
1:4D:259:LEU:HD11	1:4D:316:CYS:HB2	1.84	0.59
1:4E:105:ARG:HH12	2:5E:251:ARG:HD3	1.68	0.59
1:4G:51:THR:HG23	1:4G:52:PHE:HD1	1.66	0.59
2:3D:83:GLN:O	2:3E:281:TYR:HE2	1.86	0.59
1:4C:124:LYS:HD2	1:4D:283:HIS:CE1	2.38	0.59
1:4I:177:VAL:HB	2:5I:327:ASP:OD2	2.02	0.59
1:2I:5:ILE:HD12	1:2I:125:LEU:HD23	1.83	0.59
2:3I:175:VAL:CG2	1:4I:332:VAL:HG13	2.30	0.59
2:5B:172:SER:HB3	2:5B:205:GLU:OE1	2.03	0.59
1:2H:151:CYS:SG	1:2H:193:SER:OG	2.47	0.58
2:3I:235:GLY:HA2	2:3I:238:CYS:SG	2.42	0.58
1:4D:241:SER:OG	1:4D:250:VAL:O	2.19	0.58
1:4G:191:THR:OG1	1:4G:425:LEU:HD21	2.03	0.58
2:5I:103:LYS:HA	2:5I:107:THR:HG22	1.84	0.58
2:5I:267:LEU:CD2	2:5I:374:ILE:HD11	2.33	0.58
2:3D:172:SER:HB3	2:3D:205:GLU:OE1	2.03	0.58
2:3G:100:ASN:HB2	1:4G:257:THR:HG21	1.86	0.58
2:3H:397:TRP:CH2	1:4H:260:VAL:O	2.55	0.58
1:4B:60:LYS:CE	1:4C:282:TYR:CE2	2.86	0.58
1:4F:142:GLY:HA3	1:4F:183:GLU:HG2	1.85	0.58
1:4F:189:LEU:HD11	1:4F:418:PHE:CD1	2.37	0.58
2:5D:55:THR:HG1	2:5E:284:LEU:N	1.73	0.58
2:3E:55:THR:HG21	2:3F:283:ALA:HA	1.84	0.58
1:2C:276:ILE:HG23	1:2C:280:LYS:HB2	1.85	0.58
1:2F:323:VAL:HG13	1:2F:355:ILE:HG23	1.84	0.58
2:3B:209:ASP:CG	2:3B:213:ARG:HH21	2.10	0.58
2:3D:322:SER:OG	2:3D:325:GLU:OE2	2.22	0.58
1:4H:241:SER:OG	1:4H:250:VAL:O	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2B:401:LYS:HE2	2:3B:344:TRP:CD2	2.39	0.58
2:3B:176:SER:HB2	1:4B:349:THR:HB	1.84	0.58
2:3E:165:GLU:OE2	2:3E:200:GLN:NE2	2.36	0.58
2:3E:178:THR:HA	1:4E:352:LYS:HD2	1.84	0.58
2:3H:55:THR:OG1	2:3I:280:GLN:O	2.21	0.58
1:4A:390:ARG:HB3	1:4A:390:ARG:HH21	1.67	0.58
1:4E:217:LEU:HD11	1:4E:275:ILE:HG22	1.85	0.58
2:5F:91:VAL:HG11	2:5F:116:VAL:HG22	1.86	0.58
1:2E:23:LEU:HD11	1:2E:361:THR:HG23	1.84	0.58
2:3A:220:PRO:HB3	2:3A:224:ASP:OD2	2.04	0.58
2:5G:228:LEU:HD12	2:5G:300:MET:HE2	1.85	0.58
2:5G:237:THR:HG22	2:5G:250:LEU:HD11	1.86	0.58
1:2F:174:SER:OG	1:2F:177:VAL:O	2.19	0.58
2:3B:256:ASN:HD21	2:3B:350:LYS:HD3	1.68	0.58
2:3D:58:ARG:HH11	2:3E:280:GLN:HG3	1.67	0.58
1:4E:65:CYS:O	1:4E:91:GLN:NE2	2.34	0.58
1:2B:60:LYS:HE2	1:2C:282:TYR:HD2	1.65	0.58
1:2F:175:PRO:HB3	1:2F:390:ARG:HD3	1.84	0.58
2:5C:87:PRO:C	2:5D:281:TYR:OH	2.42	0.58
2:5G:156:ARG:HG2	2:5G:195:ASN:HB2	1.85	0.58
2:5H:165:GLU:OE2	2:5H:200:GLN:NE2	2.35	0.58
1:2C:89:PRO:HD2	1:2D:282:TYR:HD2	1.69	0.58
2:3H:179:VAL:CG1	1:4H:258:ASN:OD1	2.50	0.58
2:5E:248:SER:HA	2:5E:252:LYS:HG2	1.85	0.58
2:5I:267:LEU:HD21	2:5I:374:ILE:HD11	1.86	0.58
1:2D:57:GLY:H	1:2E:285:GLN:HB3	1.68	0.58
2:3D:98:GLY:HA2	1:4D:254:GLU:OE2	2.04	0.58
1:4A:60:LYS:HE2	1:4B:283:HIS:HD2	1.69	0.58
1:4C:76:ASP:HA	1:4C:79:ARG:HD2	1.85	0.58
1:4I:221:ARG:HG2	2:5I:325:GLU:OE1	2.04	0.58
2:5C:257:LEU:HD11	2:5C:368:VAL:HG23	1.85	0.58
2:3A:139:LEU:HD12	2:3A:170:PHE:HE1	1.68	0.57
2:3G:167:PHE:CD2	2:3G:233:MET:HG2	2.39	0.57
1:4A:301:MET:HE1	1:4A:307:PRO:HG3	1.86	0.57
1:4F:309:HIS:NE2	1:4F:386:GLU:OE1	2.29	0.57
1:4H:417:GLU:HA	1:4H:420:GLU:HG3	1.86	0.57
1:2A:181:VAL:HG11	1:2A:404:PHE:CE1	2.39	0.57
2:3B:178:THR:CA	1:4B:352:LYS:NZ	2.67	0.57
2:3C:248:SER:HA	2:3C:252:LYS:HG3	1.86	0.57
1:4G:60:LYS:HD2	1:4H:283:HIS:HD2	1.68	0.57
2:5A:285:SER:N	2:5A:288:GLU:OE2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2D:96:LYS:HE2	2:3D:129:CYS:HB2	1.87	0.57
1:2F:101:ASN:HD22	2:3F:256:ASN:HD21	1.52	0.57
1:2H:33:ASP:O	1:2H:60:LYS:NZ	2.37	0.57
2:3B:286:VAL:CG2	2:3B:287:PRO:HD3	2.34	0.57
2:5H:149:THR:HG21	2:5H:188:SER:OG	2.04	0.57
1:2B:274:PRO:HD3	1:2B:291:ILE:HD11	1.87	0.57
2:3E:397:TRP:CZ2	1:4E:260:VAL:HG23	2.39	0.57
2:5D:12:CYS:SG	2:5D:138:SER:HB2	2.44	0.57
2:5D:54:ALA:O	2:5E:282:ARG:O	2.22	0.57
2:5D:54:ALA:HA	2:5E:283:ALA:CB	2.34	0.57
2:3H:165:GLU:OE2	2:3H:200:GLN:NE2	2.38	0.57
1:4A:57:GLY:H	1:4B:285:GLN:CG	2.13	0.57
2:5D:58:ARG:NE	2:5E:281:TYR:CD1	2.72	0.57
2:3A:66:MET:HG3	2:3A:116:VAL:HG21	1.87	0.57
1:4H:318:MET:HB2	1:4H:376:CYS:SG	2.45	0.57
2:5C:253:LEU:HD11	2:5C:368:VAL:HG21	1.85	0.57
1:2H:256:GLN:O	1:2H:260:VAL:HG22	2.04	0.57
1:4B:101:ASN:HB3	1:4B:182:VAL:HG11	1.85	0.57
1:2B:398:MET:HE1	2:3B:345:ILE:HG12	1.87	0.57
1:2B:422:ARG:HH12	1:2B:426:ALA:HB2	1.70	0.57
1:2F:70:LEU:HD12	1:2F:145:THR:HG22	1.86	0.57
1:4A:178:SER:HB2	2:5A:347:ASN:OD1	2.05	0.57
2:5H:172:SER:OG	2:5H:205:GLU:OE2	2.23	0.57
2:3E:117:LEU:HD11	2:3E:154:LYS:HD3	1.86	0.57
1:4A:174:SER:HB2	1:4A:207:GLU:OE1	2.04	0.57
1:4A:223:THR:HG23	1:4A:225:THR:HG22	1.86	0.57
1:2D:178:SER:HB3	2:3D:347:ASN:ND2	2.20	0.56
1:2H:313:MET:HE3	1:2H:382:THR:HG23	1.86	0.56
1:2H:403:ALA:HA	2:3H:260:PHE:CE1	2.40	0.56
2:3F:175:VAL:HB	1:4F:329:ASN:OD1	2.04	0.56
1:4B:88:HIS:CE1	1:4C:283:HIS:HB2	2.39	0.56
2:5D:27:GLU:OE2	2:5D:241:ARG:NH1	2.35	0.56
2:3C:70:PRO:HD2	1:4C:2:ARG:NH2	2.19	0.56
1:4B:176:GLN:HB3	2:5B:331:LEU:CD1	2.35	0.56
1:4D:212:ILE:HG21	1:4D:275:ILE:HD11	1.87	0.56
1:4G:352:LYS:NZ	1:4G:353:CYS:O	2.37	0.56
2:5F:55:THR:HG23	2:5G:283:ALA:HA	1.87	0.56
1:2I:53:PHE:HB3	1:2I:61:HIS:HB3	1.87	0.56
1:2I:269:LEU:HD21	1:2I:384:ILE:HD11	1.87	0.56
2:3A:105:HIS:HD2	2:3A:150:LEU:HD12	1.69	0.56
2:3A:220:PRO:CD	1:4A:326:LYS:CE	2.55	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3D:374:ILE:HD11	2:3D:422:TYR:CZ	2.39	0.56
2:3E:391:ARG:HD2	1:4E:346:TRP:CD1	2.40	0.56
1:4B:60:LYS:NZ	1:4C:282:TYR:HE2	1.96	0.56
1:4B:417:GLU:HA	1:4B:420:GLU:HG3	1.86	0.56
1:4E:30:ILE:HG22	1:4E:36:MET:HB3	1.86	0.56
1:4G:220:GLU:O	2:5G:324:LYS:HD3	2.04	0.56
1:4G:309:HIS:NE2	1:4G:386:GLU:OE1	2.39	0.56
1:4G:407:TRP:CE3	2:5G:255:VAL:HA	2.41	0.56
1:4H:398:MET:HE1	2:5H:345:ILE:CD1	2.35	0.56
2:5C:88:ASP:CG	2:5D:281:TYR:CE2	2.83	0.56
2:5C:248:SER:HA	2:5C:252:LYS:HG2	1.87	0.56
2:5F:228:LEU:HG	2:5F:300:MET:HE2	1.87	0.56
2:5I:276:ARG:NH2	2:5I:279:GLN:OE1	2.38	0.56
2:3B:284:LEU:HD23	2:3B:362:LYS:HG2	1.88	0.56
2:3D:54:ALA:O	2:3E:282:ARG:O	2.22	0.56
2:3D:54:ALA:CB	2:3E:281:TYR:O	2.53	0.56
2:3G:282:ARG:NH1	2:3G:288:GLU:OE2	2.38	0.56
1:4D:56:THR:CB	1:4E:283:HIS:O	2.53	0.56
1:4I:68:LEU:HD12	1:4I:153:LEU:HD11	1.88	0.56
2:5C:153:SER:HB2	2:5C:191:GLN:NE2	2.20	0.56
2:5D:55:THR:OG1	2:5E:283:ALA:HA	2.05	0.56
2:5D:169:VAL:HG12	2:5D:202:ILE:HB	1.88	0.56
2:5H:380:ARG:HH11	2:5H:381:VAL:HG23	1.70	0.56
1:4E:298:PRO:HB3	1:4E:307:PRO:HD2	1.86	0.56
1:4H:210:TYR:CE1	2:5H:324:LYS:HG2	2.40	0.56
2:5E:321:MET:HE2	2:5E:353:VAL:HG13	1.88	0.56
2:5I:383:ASP:HA	2:5I:386:THR:HG22	1.88	0.56
1:2A:298:PRO:HA	1:2A:301:MET:HE3	1.87	0.56
1:2H:202:VAL:HA	1:2H:268:MET:HB2	1.88	0.56
2:3H:200:GLN:HB3	2:3H:266:PHE:HB2	1.86	0.56
2:5D:54:ALA:O	2:5E:282:ARG:C	2.48	0.56
1:2G:287:SER:HA	1:2G:373:ARG:HH21	1.70	0.56
2:3G:167:PHE:HD2	2:3G:233:MET:HE3	1.70	0.56
2:3H:397:TRP:HH2	1:4H:260:VAL:HG23	1.71	0.56
1:2E:207:GLU:HG3	1:2E:304:LYS:HG3	1.88	0.56
1:2I:33:ASP:O	1:2I:60:LYS:NZ	2.39	0.56
2:3B:397:TRP:HZ2	1:4B:260:VAL:CG2	2.19	0.56
2:3C:86:ARG:CD	2:3D:281:TYR:HD1	2.09	0.56
1:4A:60:LYS:HD2	1:4B:283:HIS:CD2	2.40	0.56
1:4B:180:ALA:HA	2:5B:350:LYS:HE3	1.86	0.56
1:4G:158:SER:OG	1:4G:166:LYS:NZ	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3G:220:PRO:HD2	1:4G:326:LYS:HD3	1.87	0.56
2:3H:391:ARG:HD2	1:4H:346:TRP:CD2	2.40	0.56
1:4H:103:PHE:H	1:4H:408:TYR:HE1	1.54	0.56
2:5B:1:MET:N	2:5B:128:ASP:OD2	2.36	0.56
2:5D:66:MET:HG2	2:5D:147:MET:HE1	1.88	0.56
2:5F:14:ASN:ND2	2:5F:67:ASP:OD1	2.39	0.56
1:2C:212:ILE:HD11	1:2C:300:SER:HA	1.88	0.56
1:2G:309:HIS:NE2	1:2G:386:GLU:OE1	2.39	0.56
2:3B:64:ILE:HD12	2:3B:119:VAL:HG12	1.88	0.56
2:3G:1:MET:N	2:3G:128:ASP:OD2	2.38	0.56
1:4C:1:MET:N	1:4C:3:GLU:OE2	2.34	0.56
2:5A:262:ARG:HH21	2:5A:421:GLU:CD	2.14	0.56
2:5C:213:ARG:HA	2:5C:213:ARG:HE	1.71	0.56
1:2C:269:LEU:HD22	1:2C:384:ILE:HD11	1.87	0.55
2:3D:83:GLN:O	2:3E:281:TYR:CE2	2.59	0.55
2:5C:66:MET:HG2	2:5C:147:MET:HE1	1.88	0.55
1:2B:215:ARG:NH1	1:2B:216:ASN:OD1	2.39	0.55
1:2H:10:GLY:HA2	1:2H:145:THR:HG23	1.87	0.55
2:3G:177:ASP:OD2	2:3G:178:THR:HG23	2.06	0.55
1:4H:10:GLY:HA2	1:4H:145:THR:HG23	1.87	0.55
2:5D:267:LEU:HD11	2:5D:374:ILE:HG23	1.89	0.55
2:5G:256:ASN:HD21	2:5G:350:LYS:HD3	1.71	0.55
1:2E:241:SER:OG	1:2E:250:VAL:O	2.17	0.55
2:3E:55:THR:HB	2:3F:283:ALA:CA	2.32	0.55
1:4B:258:ASN:CB	1:4B:352:LYS:HE3	2.34	0.55
1:4D:298:PRO:HB3	1:4D:307:PRO:HD2	1.88	0.55
2:5C:284:LEU:HD21	2:5C:363:MET:HB2	1.88	0.55
2:5G:55:THR:HG23	2:5H:283:ALA:HB2	1.89	0.55
1:2A:181:VAL:CG2	2:3A:350:LYS:HZ1	2.10	0.55
1:2B:417:GLU:HA	1:2B:420:GLU:HG3	1.87	0.55
1:2D:222:PRO:HD2	2:3D:324:LYS:CE	2.37	0.55
1:2H:2:ARG:NH2	1:2H:133:GLN:OE1	2.40	0.55
2:3H:208:TYR:HE2	1:4H:329:ASN:ND2	2.03	0.55
1:4A:151:CYS:SG	1:4A:193:SER:OG	2.44	0.55
1:4A:209:ILE:HB	1:4A:227:LEU:HD13	1.89	0.55
1:4A:339:ARG:O	1:4A:342:GLN:NE2	2.39	0.55
2:5C:267:LEU:HD21	2:5C:374:ILE:HG12	1.88	0.55
1:2B:221:ARG:NE	2:3B:322:SER:OG	2.40	0.55
1:2C:121:ARG:HH22	1:2D:283:HIS:CE1	2.24	0.55
1:2G:230:LEU:CD2	1:2G:302:MET:CE	2.85	0.55
1:2H:103:PHE:H	1:2H:408:TYR:HE1	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2I:73:THR:HG22	2:3I:46:ARG:HE	1.70	0.55
1:4D:398:MET:HE2	2:5D:346:PRO:HD2	1.88	0.55
2:5H:282:ARG:NH2	2:5H:284:LEU:HD13	2.21	0.55
1:2A:80:THR:HA	1:2A:84:ARG:HE	1.71	0.55
1:2D:60:LYS:CE	1:2E:283:HIS:CG	2.90	0.55
1:2E:276:ILE:HD11	1:2E:286:LEU:HD11	1.89	0.55
2:3D:169:VAL:HG12	2:3D:202:ILE:HB	1.88	0.55
1:4G:186:ASN:OD1	1:4G:408:TYR:OH	2.23	0.55
2:5G:249:ASP:H	2:5G:252:LYS:HG2	1.70	0.55
1:2E:101:ASN:CG	2:3E:252:LYS:NZ	2.65	0.55
2:3A:317:PHE:HB3	2:3A:321:MET:HE3	1.87	0.55
2:3E:303:SER:HB3	2:3E:377:MET:HE3	1.88	0.55
2:3I:313:ALA:HB3	2:3I:349:MET:HE2	1.88	0.55
1:4E:60:LYS:HZ3	1:4F:283:HIS:CD2	2.11	0.55
1:4H:51:THR:HG21	1:4H:243:ARG:HG2	1.88	0.55
1:4H:219:ILE:HG22	1:4H:222:PRO:HD3	1.88	0.55
1:4I:301:MET:HE1	1:4I:377:MET:HE1	1.89	0.55
1:2B:221:ARG:NH1	2:3B:324:LYS:HB3	2.21	0.55
1:2D:223:THR:HG23	1:2D:225:THR:HG22	1.88	0.55
2:3A:100:ASN:HB3	2:3A:103:LYS:HG2	1.88	0.55
2:3C:215:LEU:HB3	2:3C:217:LEU:HD13	1.89	0.55
2:3I:11:GLN:NE2	1:4I:248:LEU:HD12	2.21	0.55
1:4I:177:VAL:HB	2:5I:327:ASP:CG	2.32	0.55
1:2B:223:THR:HG23	1:2B:225:THR:HG22	1.88	0.55
1:2C:88:HIS:CE1	1:2D:283:HIS:HB2	2.42	0.55
1:2D:402:ARG:HG3	1:2D:405:VAL:HG21	1.88	0.55
1:2H:231:ILE:O	1:2H:234:VAL:HG12	2.07	0.55
2:3E:55:THR:HG22	2:3F:282:ARG:C	2.29	0.55
2:3G:55:THR:CG2	2:3H:283:ALA:CA	2.78	0.55
2:5E:372:THR:HA	2:5E:422:TYR:CD2	2.42	0.55
1:2D:298:PRO:HB3	1:2D:307:PRO:HD2	1.89	0.55
1:2G:60:LYS:HD3	1:2H:283:HIS:CD2	2.35	0.55
2:3A:293:MET:SD	2:3A:367:PHE:HB2	2.47	0.55
2:3B:172:SER:HB2	2:3B:205:GLU:HG2	1.89	0.55
1:4C:73:THR:HA	2:5C:46:ARG:NH1	2.22	0.55
1:4C:242:LEU:HD11	1:4C:252:VAL:HG23	1.89	0.55
1:2C:259:LEU:HD21	1:2C:316:CYS:HB2	1.90	0.54
2:3D:58:ARG:CD	2:3E:280:GLN:O	2.56	0.54
1:4B:339:ARG:NH2	1:4B:342:GLN:OE1	2.40	0.54
1:4E:261:PRO:HG3	1:4E:313:MET:HE2	1.90	0.54
1:4H:187:SER:HB3	1:4H:391:MET:HE3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2I:213:CYS:SG	1:2I:222:PRO:HG3	2.48	0.54
2:3D:67:ASP:HB3	2:3D:73:MET:HE2	1.88	0.54
1:4A:8:HIS:CD2	1:4A:17:GLY:HA3	2.42	0.54
1:4I:250:VAL:HG11	1:4I:318:MET:CE	2.38	0.54
2:5H:207:LEU:HB3	2:5H:225:LEU:HD12	1.89	0.54
1:2B:174:SER:OG	1:2B:177:VAL:O	2.21	0.54
1:2C:250:VAL:HG22	1:2C:318:MET:HE1	1.88	0.54
1:2E:101:ASN:OD1	2:3E:252:LYS:NZ	2.40	0.54
1:2E:199:ASP:OD2	1:2E:256:GLN:NE2	2.40	0.54
1:2H:386:GLU:O	1:2H:390:ARG:HG2	2.07	0.54
2:3A:374:ILE:O	2:3A:374:ILE:HG22	2.07	0.54
2:3H:317:PHE:HB3	2:3H:321:MET:HE1	1.89	0.54
2:5B:236:VAL:O	2:5B:316:MET:HE1	2.07	0.54
2:5D:12:CYS:SG	2:5D:13:GLY:N	2.80	0.54
1:2G:200:VAL:HG23	1:2G:268:MET:HE1	1.90	0.54
2:3E:107:THR:HG21	2:3E:401:GLU:HB2	1.89	0.54
2:3F:172:SER:HB3	2:3F:205:GLU:OE1	2.07	0.54
1:4C:311:LYS:NZ	1:4C:342:GLN:OE1	2.41	0.54
1:4D:60:LYS:HZ2	1:4E:283:HIS:CD2	2.24	0.54
1:4D:105:ARG:O	1:4D:110:ILE:HG22	2.07	0.54
1:4I:422:ARG:HH12	1:4I:426:ALA:HB2	1.72	0.54
2:5E:372:THR:HA	2:5E:422:TYR:HD2	1.72	0.54
2:5H:256:ASN:HD22	2:5H:350:LYS:HD2	1.73	0.54
1:2B:241:SER:HB2	1:2B:249:ASN:HB2	1.89	0.54
2:3D:244:GLY:HA2	2:3D:355:ASP:OD1	2.08	0.54
2:3F:55:THR:CG2	2:3G:282:ARG:O	2.56	0.54
2:3I:383:ASP:HA	2:3I:386:THR:HG22	1.90	0.54
1:4C:178:SER:OG	2:5C:347:ASN:ND2	2.40	0.54
2:3H:179:VAL:HG12	1:4H:258:ASN:CG	2.32	0.54
1:4B:181:VAL:H	2:5B:350:LYS:CE	2.19	0.54
2:5A:262:ARG:NH2	2:5A:421:GLU:OE1	2.40	0.54
1:2A:96:LYS:NZ	2:3A:129:CYS:SG	2.80	0.54
1:2A:221:ARG:HB2	2:3A:322:SER:CB	2.37	0.54
1:2C:89:PRO:HD2	1:2D:282:TYR:CD2	2.43	0.54
2:3G:135:ILE:HG12	2:3G:166:THR:HG22	1.89	0.54
2:5H:192:LEU:HD21	2:5H:199:VAL:HG21	1.89	0.54
1:2G:141:VAL:HG11	1:2G:172:TRP:CE3	2.42	0.54
2:3E:91:VAL:HG21	2:3E:116:VAL:HG22	1.90	0.54
2:5A:43:GLN:HA	2:5A:242:PHE:HE1	1.73	0.54
2:3B:1:MET:N	2:3B:128:ASP:OD2	2.38	0.54
2:3F:67:ASP:OD2	2:3F:72:THR:OG1	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4E:220:GLU:O	2:5E:324:LYS:HE2	2.08	0.54
1:2H:338:LYS:HZ3	1:2H:339:ARG:H	1.56	0.54
1:2I:392:ASP:CG	1:2I:422:ARG:HH22	2.12	0.54
2:3A:156:ARG:HH22	2:3A:197:ASP:HB2	1.73	0.54
2:3F:11:GLN:HE22	1:4F:248:LEU:HA	1.73	0.54
2:5D:107:THR:OG1	2:5D:108:GLU:OE1	2.26	0.54
1:2I:50:ASN:O	1:2I:64:ARG:NH2	2.41	0.53
2:5F:282:ARG:NH1	2:5F:288:GLU:OE2	2.41	0.53
1:2A:301:MET:CE	1:2A:307:PRO:HG3	2.38	0.53
1:2E:178:SER:OG	2:3E:347:ASN:ND2	2.32	0.53
1:4D:85:HIS:HB3	1:4E:283:HIS:NE2	2.22	0.53
1:4G:189:LEU:HD11	1:4G:413:MET:HE2	1.91	0.53
1:2A:137:MET:HE3	1:2A:154:LEU:HD12	1.90	0.53
1:2A:252:VAL:HA	1:2A:255:PHE:HD2	1.72	0.53
1:2G:181:VAL:CG1	2:3G:256:ASN:HB2	2.38	0.53
2:3F:282:ARG:NH1	2:3F:292:GLN:OE1	2.41	0.53
1:4B:60:LYS:HZ2	1:4C:282:TYR:HE2	1.46	0.53
1:4C:223:THR:HG23	1:4C:225:THR:HG22	1.90	0.53
1:4G:390:ARG:HH22	1:4G:391:MET:HE2	1.74	0.53
2:5A:326:VAL:CG1	2:5A:330:MET:HE1	2.38	0.53
1:2B:177:VAL:HG13	2:3B:327:ASP:OD1	2.08	0.53
1:2C:121:ARG:CZ	1:2D:283:HIS:CE1	2.91	0.53
1:2E:217:LEU:HD11	1:2E:275:ILE:CG2	2.38	0.53
2:3B:87:PRO:HD3	2:3C:281:TYR:OH	2.09	0.53
2:3H:20:PHE:CD2	2:3H:233:MET:HE3	2.44	0.53
1:4E:398:MET:CE	2:5E:346:PRO:HD2	2.31	0.53
1:4G:101:ASN:HB3	1:4G:182:VAL:HG21	1.90	0.53
1:2I:258:ASN:HB3	1:2I:352:LYS:HG3	1.91	0.53
1:4C:259:LEU:HD21	1:4C:316:CYS:HB2	1.90	0.53
2:5D:8:GLN:NE2	2:5D:17:GLY:HA3	2.24	0.53
1:2D:177:VAL:HG13	2:3D:327:ASP:HB2	1.91	0.53
1:2E:250:VAL:CG1	1:2E:318:MET:HE1	2.39	0.53
2:3I:284:LEU:HD23	2:3I:362:LYS:HG2	1.91	0.53
1:4F:178:SER:CB	2:5F:347:ASN:ND2	2.57	0.53
1:4H:254:GLU:HG2	1:4H:352:LYS:HZ2	1.73	0.53
2:5F:67:ASP:OD2	2:5F:72:THR:OG1	2.27	0.53
2:5F:282:ARG:NH1	2:5F:292:GLN:OE1	2.41	0.53
1:2G:76:ASP:OD2	2:3G:46:ARG:NH2	2.42	0.53
2:3A:244:GLY:HA2	2:3A:355:ASP:HB2	1.90	0.53
2:5E:127:CYS:SG	2:5E:128:ASP:N	2.75	0.53
2:5G:135:ILE:HB	2:5G:166:THR:HG22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2C:178:SER:HB2	2:3C:347:ASN:HD22	1.74	0.53
1:2D:241:SER:OG	1:2D:250:VAL:O	2.20	0.53
1:2F:203:MET:HE3	1:2F:267:PHE:HD2	1.73	0.53
2:3A:10:GLY:HA2	2:3A:143:THR:HG23	1.91	0.53
2:3G:248:SER:HA	2:3G:252:LYS:HE3	1.91	0.53
2:3H:1:MET:N	2:3H:128:ASP:OD2	2.40	0.53
2:3H:253:LEU:HD11	2:3H:368:VAL:HG21	1.91	0.53
2:3I:396:HIS:HA	2:3I:399:THR:HG22	1.91	0.53
1:4I:178:SER:HB3	2:5I:347:ASN:HD22	1.74	0.53
2:5A:113:ILE:HA	2:5A:116:VAL:HG12	1.91	0.53
2:5H:20:PHE:HB2	2:5H:233:MET:HE3	1.91	0.53
1:2B:413:MET:HE3	1:2B:417:GLU:HB3	1.90	0.53
1:2C:89:PRO:CD	1:2D:282:TYR:CD2	2.92	0.53
2:3A:113:ILE:HA	2:3A:116:VAL:HG12	1.91	0.53
1:4A:181:VAL:HG22	2:5A:347:ASN:O	2.09	0.53
1:4A:276:ILE:HD12	1:4A:281:ALA:HA	1.89	0.53
2:5B:100:ASN:HB3	2:5B:103:LYS:HG2	1.89	0.53
2:5D:12:CYS:SG	2:5D:138:SER:CB	2.97	0.53
2:3A:68:LEU:HG	2:3A:147:MET:HE2	1.91	0.53
1:4B:177:VAL:HG11	2:5B:327:ASP:HB3	1.91	0.53
1:4D:5:ILE:HD12	1:4D:125:LEU:HG	1.91	0.53
1:4F:137:MET:HE3	1:4F:139:ASN:ND2	2.24	0.53
2:5A:403:MET:HE1	2:5A:407:GLU:HG2	1.89	0.53
2:5B:286:VAL:CG2	2:5B:287:PRO:HD3	2.35	0.53
2:5D:313:ALA:HB3	2:5D:349:MET:HG2	1.90	0.53
1:2A:396:ASP:OD1	1:2A:422:ARG:NH1	2.42	0.52
1:2H:258:ASN:O	1:2H:258:ASN:ND2	2.36	0.52
2:3D:66:MET:HE2	2:3D:116:VAL:HG21	1.91	0.52
2:3G:7:VAL:HB	2:3G:135:ILE:HG22	1.89	0.52
2:3I:267:LEU:HB3	2:3I:299:MET:CE	2.39	0.52
1:4B:181:VAL:HG13	2:5B:350:LYS:HZ1	1.67	0.52
2:5B:293:MET:HE2	2:5B:367:PHE:HB2	1.89	0.52
2:5E:274:THR:OG1	2:5E:279:GLN:OE1	2.27	0.52
2:5F:238:CYS:SG	2:5F:318:ARG:NE	2.82	0.52
1:2A:180:ALA:HB3	1:2A:183:GLU:HG2	1.90	0.52
1:2B:207:GLU:OE1	1:2B:304:LYS:HG2	2.09	0.52
1:2G:23:LEU:HD23	1:2G:27:GLU:HG3	1.89	0.52
1:2G:152:LEU:O	1:2G:156:ARG:HG2	2.10	0.52
2:3A:330:MET:SD	2:3A:349:MET:HG3	2.49	0.52
2:3B:113:ILE:HA	2:3B:116:VAL:HG12	1.91	0.52
2:3D:334:GLN:HE21	2:3D:349:MET:HG2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3G:55:THR:CG2	2:3H:283:ALA:CB	2.87	0.52
1:4A:65:CYS:O	1:4A:91:GLN:HG3	2.10	0.52
1:4A:102:ASN:OD1	2:5A:255:VAL:HG21	2.09	0.52
1:4D:57:GLY:N	1:4E:285:GLN:CA	2.73	0.52
1:4E:97:GLU:OE2	2:5E:2:ARG:HG2	2.09	0.52
2:5I:66:MET:SD	2:5I:116:VAL:HG11	2.49	0.52
1:2G:407:TRP:CZ3	2:3G:255:VAL:HG22	2.44	0.52
2:3F:139:LEU:CD1	2:3F:168:SER:HB2	2.36	0.52
1:4B:328:VAL:HG11	1:4B:353:CYS:SG	2.49	0.52
1:4C:184:PRO:HB2	1:4C:398:MET:HE1	1.92	0.52
1:4F:168:ASN:ND2	1:4F:170:CYS:SG	2.82	0.52
1:4G:23:LEU:HD11	1:4G:361:THR:HG23	1.90	0.52
2:5D:10:GLY:HA2	2:5D:143:THR:HG23	1.90	0.52
2:5D:257:LEU:HD21	2:5D:314:SER:HB2	1.90	0.52
2:5D:311:LEU:HD12	2:5D:342:VAL:HG11	1.92	0.52
2:5F:248:SER:HA	2:5F:252:LYS:HG3	1.91	0.52
2:5I:10:GLY:HA2	2:5I:143:THR:HG23	1.91	0.52
1:2B:88:HIS:CD2	1:2C:283:HIS:CB	2.92	0.52
1:2B:422:ARG:NH1	1:2B:426:ALA:HB2	2.24	0.52
1:2E:75:VAL:HG11	1:2E:94:SER:HB3	1.92	0.52
1:2I:407:TRP:CZ2	2:3I:258:ILE:HD11	2.45	0.52
2:3B:207:LEU:HB3	2:3B:225:LEU:HD22	1.91	0.52
2:3H:211:CYS:SG	2:3H:220:PRO:HB3	2.50	0.52
1:4I:100:ALA:HA	2:5I:252:LYS:HE3	1.92	0.52
1:2C:223:THR:HG23	1:2C:225:THR:HG22	1.90	0.52
1:2D:56:THR:HA	1:2E:285:GLN:CB	2.35	0.52
1:2G:60:LYS:CE	1:2H:283:HIS:HD2	2.23	0.52
2:3E:55:THR:HG23	2:3E:55:THR:O	2.10	0.52
2:3I:311:LEU:HD12	2:3I:342:VAL:HG11	1.91	0.52
1:4A:101:ASN:HB3	1:4A:182:VAL:HG21	1.92	0.52
1:4H:250:VAL:HG23	1:4H:352:LYS:HZ2	1.74	0.52
2:5C:86:ARG:C	2:5D:281:TYR:OH	2.53	0.52
2:5D:98:GLY:H	2:5D:103:LYS:HE2	1.73	0.52
2:5I:165:GLU:OE2	2:5I:200:GLN:NE2	2.41	0.52
2:5I:311:LEU:HD12	2:5I:342:VAL:HG11	1.92	0.52
1:2F:392:ASP:OD1	1:2F:422:ARG:NE	2.43	0.52
1:2G:241:SER:HB2	1:2G:249:ASN:HB2	1.92	0.52
2:3A:55:THR:OG1	2:3B:282:ARG:O	2.28	0.52
2:3G:12:CYS:HB3	2:3G:138:SER:HB3	1.92	0.52
1:4B:76:ASP:OD1	1:4B:79:ARG:NH2	2.42	0.52
1:4G:204:LEU:HD13	1:4G:231:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4H:370:LYS:HG3	1:4H:370:LYS:O	2.10	0.52
2:5A:207:LEU:CD2	2:5A:225:LEU:HD22	2.39	0.52
2:5D:58:ARG:NH2	2:5E:281:TYR:HE1	2.00	0.52
1:2B:261:PRO:HG3	1:2B:313:MET:HE2	1.91	0.52
1:2E:30:ILE:HG22	1:2E:36:MET:HB3	1.92	0.52
1:2H:398:MET:HE1	2:3H:345:ILE:HA	1.92	0.52
2:3A:257:LEU:O	2:3A:312:THR:HG21	2.09	0.52
2:3H:248:SER:HA	2:3H:252:LYS:HG3	1.92	0.52
2:3H:249:ASP:H	2:3H:252:LYS:HB2	1.75	0.52
2:3I:397:TRP:CZ2	1:4I:256:GLN:HB2	2.44	0.52
1:4B:209:ILE:HG22	1:4B:227:LEU:HD22	1.92	0.52
1:4B:217:LEU:HD23	1:4B:217:LEU:O	2.08	0.52
1:4E:138:PHE:CZ	1:4E:235:ILE:HD13	2.44	0.52
2:5H:181:GLU:HG3	2:5H:182:PRO:HD3	1.91	0.52
1:2B:132:LEU:O	1:2B:164:LYS:NZ	2.43	0.52
1:2D:85:HIS:HB3	1:2E:283:HIS:HE2	1.74	0.52
1:2I:123:ARG:HH12	1:2I:160:ASP:CG	2.18	0.52
2:3E:330:MET:HE3	2:3E:349:MET:HB3	1.92	0.52
1:4B:192:HIS:ND1	1:4B:424:ASP:OD2	2.43	0.52
1:4E:221:ARG:CG	2:5E:322:SER:CB	2.75	0.52
2:5A:16:ILE:HD11	2:5A:229:VAL:HG11	1.92	0.52
1:2E:298:PRO:HB3	1:2E:307:PRO:HD2	1.90	0.52
2:3A:203:ASP:OD2	2:3A:205:GLU:HG3	2.10	0.52
2:3G:354:CYS:SG	2:3G:355:ASP:N	2.83	0.52
1:4F:223:THR:HG23	1:4F:225:THR:HG22	1.90	0.52
2:5D:374:ILE:HD11	2:5D:422:TYR:CZ	2.45	0.52
2:5E:125:GLU:OE1	2:5F:291:GLN:NE2	2.42	0.52
1:2D:309:HIS:NE2	1:2D:386:GLU:OE1	2.43	0.52
1:2E:11:GLN:NE2	2:3E:245:GLN:O	2.42	0.52
1:2E:98:ASP:O	1:2E:105:ARG:NH2	2.32	0.52
1:2G:236:SER:O	1:2G:243:ARG:NH2	2.42	0.52
1:2H:398:MET:CE	2:3H:346:PRO:HD2	2.40	0.52
2:3E:397:TRP:CH2	1:4E:260:VAL:O	2.63	0.52
2:3F:354:CYS:SG	2:3F:355:ASP:N	2.83	0.52
2:3H:222:TYR:HD1	2:3H:225:LEU:HD12	1.74	0.52
1:4H:306:ASP:OD1	1:4H:308:ARG:NH1	2.43	0.52
2:5E:16:ILE:HD11	2:5E:229:VAL:HG11	1.92	0.52
2:5G:55:THR:HG23	2:5H:283:ALA:CA	2.40	0.52
2:5H:230:SER:HA	2:5H:233:MET:HE2	1.92	0.52
1:2B:215:ARG:HH21	1:2B:299:ALA:C	2.18	0.51
2:3D:200:GLN:HG2	2:3D:268:ILE:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5B:309:ARG:H	2:5B:372:THR:HG22	1.75	0.51
1:2I:73:THR:HG22	2:3I:46:ARG:NE	2.26	0.51
1:4A:260:VAL:HG23	1:4A:260:VAL:O	2.10	0.51
2:5B:267:LEU:CD1	2:5B:301:CYS:HB3	2.40	0.51
2:5D:58:ARG:CD	2:5E:280:GLN:C	2.83	0.51
2:5G:109:GLY:O	2:5G:113:ILE:HG12	2.09	0.51
2:5H:158:GLU:N	2:5H:158:GLU:OE1	2.43	0.51
1:2C:269:LEU:CD2	1:2C:384:ILE:HD11	2.41	0.51
1:2H:223:THR:HG23	1:2H:225:THR:HG22	1.92	0.51
2:3B:68:LEU:HD11	2:3B:147:MET:HE3	1.93	0.51
2:3B:109:GLY:O	2:3B:113:ILE:HG12	2.09	0.51
2:3H:16:ILE:CG2	2:3H:136:THR:HG21	2.41	0.51
2:5A:258:ILE:O	2:5A:258:ILE:HG13	2.10	0.51
2:5D:135:ILE:HG22	2:5D:137:HIS:HD2	1.74	0.51
2:5G:354:CYS:SG	2:5G:355:ASP:N	2.84	0.51
2:5I:284:LEU:CD2	2:5I:363:MET:HG2	2.40	0.51
1:2A:398:MET:HE2	2:3A:345:ILE:HG23	1.92	0.51
1:2E:261:PRO:HG3	1:2E:313:MET:HE2	1.91	0.51
1:2F:98:ASP:O	1:2F:105:ARG:NH2	2.43	0.51
1:2H:189:LEU:HD21	1:2H:413:MET:HE1	1.91	0.51
2:3E:205:GLU:CD	1:4E:329:ASN:HD21	2.17	0.51
2:3F:248:SER:HG	2:3F:316:MET:HE1	1.74	0.51
1:4A:407:TRP:HZ2	2:5A:258:ILE:HD11	1.74	0.51
2:5B:66:MET:HG2	2:5B:116:VAL:HG21	1.92	0.51
2:5B:276:ARG:NH2	2:5B:279:GLN:OE1	2.35	0.51
2:5C:309:ARG:H	2:5C:372:THR:HG22	1.76	0.51
1:2F:28:HIS:HE1	1:2F:243:ARG:HH11	1.58	0.51
1:2I:76:ASP:HA	1:2I:79:ARG:HD2	1.92	0.51
2:3C:289:LEU:HD12	2:3C:365:VAL:HG12	1.92	0.51
2:3E:267:LEU:HB3	2:3E:299:MET:HE2	1.93	0.51
2:3G:350:LYS:NZ	2:3G:352:SER:OG	2.43	0.51
1:4F:177:VAL:HB	2:5F:327:ASP:OD2	2.11	0.51
1:4H:222:PRO:HD2	2:5H:324:LYS:HZ3	1.74	0.51
2:5D:83:GLN:O	2:5E:281:TYR:CZ	2.63	0.51
2:5D:102:ALA:HB2	2:5D:403:MET:HE2	1.92	0.51
2:5F:100:ASN:HB3	2:5F:103:LYS:HG2	1.92	0.51
2:5G:164:MET:N	2:5G:197:ASP:OD2	2.39	0.51
1:2C:250:VAL:CG2	1:2C:318:MET:HE1	2.41	0.51
1:2G:254:GLU:N	1:2G:254:GLU:OE2	2.44	0.51
2:3A:382:SER:HB2	2:3A:415:MET:HE1	1.93	0.51
2:3D:135:ILE:HB	2:3D:166:THR:HG22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4F:107:HIS:HE2	1:4F:151:CYS:HG	1.58	0.51
2:5A:100:ASN:HB3	2:5A:103:LYS:HG2	1.92	0.51
1:2F:76:ASP:OD2	2:3F:46:ARG:NH2	2.44	0.51
1:2G:70:LEU:HD13	1:2G:95:GLY:HA3	1.92	0.51
2:3B:336:LYS:HE2	2:3B:336:LYS:HA	1.93	0.51
2:3I:404:ASP:OD1	2:3I:405:GLU:N	2.43	0.51
1:4E:105:ARG:HH12	2:5E:251:ARG:CD	2.23	0.51
1:4I:178:SER:CB	2:5I:347:ASN:ND2	2.73	0.51
2:5A:313:ALA:HB1	2:5A:367:PHE:CE1	2.46	0.51
2:5B:55:THR:O	2:5B:55:THR:HG23	2.10	0.51
2:5E:96:GLY:N	2:5E:108:GLU:OE2	2.44	0.51
2:5H:100:ASN:HB3	2:5H:103:LYS:HG2	1.91	0.51
2:5I:55:THR:HG23	2:5I:55:THR:O	2.11	0.51
1:2A:275:ILE:HD12	1:2A:275:ILE:N	2.26	0.51
1:2G:71:GLU:HG2	1:2G:73:THR:HG22	1.93	0.51
1:2G:230:LEU:HD23	1:2G:302:MET:CE	2.40	0.51
2:3A:55:THR:CG2	2:3B:283:ALA:HA	2.38	0.51
2:3C:55:THR:HG23	2:3C:55:THR:O	2.11	0.51
2:3I:55:THR:HG23	2:3I:55:THR:O	2.11	0.51
1:4A:239:THR:OG1	1:4A:243:ARG:NH1	2.44	0.51
1:4E:309:HIS:NE2	1:4E:386:GLU:OE1	2.44	0.51
1:4I:250:VAL:HG21	1:4I:318:MET:HE1	1.91	0.51
2:5B:28:HIS:HA	2:5B:43:GLN:HG2	1.91	0.51
2:5C:87:PRO:HG2	2:5D:281:TYR:HE2	1.76	0.51
2:5H:211:CYS:SG	2:5H:220:PRO:HB3	2.51	0.51
1:2C:100:ALA:HA	2:3C:252:LYS:CD	2.39	0.51
1:2H:260:VAL:HG23	1:2H:260:VAL:O	2.09	0.51
2:3E:95:THR:OG1	2:3E:108:GLU:OE1	2.28	0.51
2:3F:208:TYR:CD1	1:4F:326:LYS:CD	2.93	0.51
1:4F:241:SER:HB2	1:4F:249:ASN:HB2	1.92	0.51
1:4G:236:SER:O	1:4G:243:ARG:NH2	2.44	0.51
1:4H:173:PRO:HG3	1:4H:183:GLU:OE2	2.11	0.51
2:5G:248:SER:HA	2:5G:252:LYS:HD3	1.92	0.51
1:2A:105:ARG:HH12	2:3A:251:ARG:CD	2.24	0.51
1:2H:176:GLN:CB	2:3H:331:LEU:HD11	2.37	0.51
2:3A:208:TYR:CE1	1:4A:326:LYS:HB3	2.46	0.51
2:3C:10:GLY:O	2:3C:14:ASN:ND2	2.44	0.51
2:5A:55:THR:OG1	2:5B:282:ARG:O	2.29	0.51
2:5F:53:GLU:OE2	2:5F:54:ALA:N	2.43	0.51
1:2D:181:VAL:H	2:3D:256:ASN:ND2	2.09	0.50
1:2E:4:VAL:HG21	1:2E:136:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3A:55:THR:CG2	2:3B:283:ALA:CA	2.87	0.50
1:4A:93:ILE:HG21	1:4A:114:ILE:HG23	1.93	0.50
1:4E:265:ILE:HD11	1:4E:435:VAL:HG21	1.93	0.50
2:5A:19:LYS:NZ	2:5A:223:GLY:O	2.44	0.50
2:5H:253:LEU:HD11	2:5H:368:VAL:HG21	1.92	0.50
1:2A:181:VAL:HG11	1:2A:404:PHE:CZ	2.47	0.50
2:3C:122:LYS:HG2	2:3D:281:TYR:OH	2.11	0.50
2:3G:207:LEU:HB3	2:3G:225:LEU:HD12	1.93	0.50
2:3H:329:GLN:OE1	2:3H:332:ASN:ND2	2.43	0.50
1:4D:173:PRO:HB3	1:4D:183:GLU:OE2	2.11	0.50
1:4E:203:MET:HE2	1:4E:267:PHE:HB3	1.93	0.50
2:5A:180:VAL:O	2:5A:184:ASN:ND2	2.45	0.50
2:5E:55:THR:O	2:5E:55:THR:HG23	2.11	0.50
2:5F:311:LEU:HD12	2:5F:342:VAL:HG11	1.93	0.50
1:2B:221:ARG:HH12	2:3B:324:LYS:H	1.57	0.50
2:3D:198:GLU:OE1	2:3D:254:ALA:HB2	2.12	0.50
2:3H:135:ILE:HG22	2:3H:137:HIS:HD2	1.76	0.50
1:4B:174:SER:OG	1:4B:177:VAL:O	2.23	0.50
1:4C:241:SER:OG	1:4C:249:ASN:HB2	2.11	0.50
1:4H:398:MET:HE1	2:5H:345:ILE:HD13	1.92	0.50
2:5A:55:THR:HG21	2:5B:283:ALA:CB	2.35	0.50
2:5C:87:PRO:HG2	2:5D:281:TYR:CE2	2.46	0.50
2:5D:248:SER:HA	2:5D:252:LYS:HD2	1.93	0.50
2:5E:64:ILE:HD12	2:5E:119:VAL:HG12	1.92	0.50
1:2A:53:PHE:HB3	1:2A:61:HIS:HB3	1.92	0.50
1:2B:100:ALA:O	2:3B:255:VAL:HG11	2.12	0.50
1:2C:105:ARG:HH12	2:3C:251:ARG:HD3	1.77	0.50
1:2I:222:PRO:HD2	2:3I:324:LYS:HG2	1.92	0.50
2:3C:172:SER:HB3	2:3C:205:GLU:HG2	1.93	0.50
2:3D:255:VAL:HG23	2:3D:256:ASN:OD1	2.11	0.50
2:3E:175:VAL:CG2	1:4E:329:ASN:OD1	2.58	0.50
2:3G:207:LEU:HG	2:3G:228:LEU:HD11	1.92	0.50
1:4D:56:THR:HA	1:4E:285:GLN:N	2.26	0.50
1:4F:370:LYS:NZ	1:4F:372:MET:CE	2.74	0.50
1:4G:53:PHE:HB3	1:4G:61:HIS:HB3	1.94	0.50
2:5D:383:ASP:HA	2:5D:386:THR:HG22	1.92	0.50
2:5H:175:VAL:HG12	2:5H:205:GLU:OE2	2.11	0.50
1:2G:401:LYS:HD2	2:3G:344:TRP:CZ3	2.47	0.50
1:2H:398:MET:HE3	2:3H:346:PRO:HD2	1.94	0.50
2:3A:403:MET:HA	2:3A:403:MET:HE2	1.92	0.50
2:3B:94:GLN:C	1:4B:2:ARG:NH2	2.70	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3F:100:ASN:HB3	2:3F:103:LYS:HG2	1.93	0.50
2:3G:109:GLY:O	2:3G:113:ILE:HG12	2.11	0.50
1:4B:320:ARG:HG3	1:4B:358:GLN:O	2.11	0.50
1:4F:309:HIS:HE2	1:4F:386:GLU:CD	2.17	0.50
2:5A:203:ASP:CG	2:5A:377:MET:HE1	2.36	0.50
2:5B:86:ARG:HA	2:5C:281:TYR:CZ	2.46	0.50
2:5C:55:THR:HG23	2:5C:55:THR:O	2.10	0.50
2:5F:334:GLN:OE1	2:5F:349:MET:HB3	2.12	0.50
2:5H:337:ASN:HB3	2:5H:340:TYR:HB2	1.93	0.50
1:2G:175:PRO:HG3	1:2G:304:LYS:HG2	1.93	0.50
2:5C:374:ILE:O	2:5C:374:ILE:HG22	2.11	0.50
2:5E:67:ASP:HB3	2:5E:73:MET:HE2	1.94	0.50
2:5G:262:ARG:NH1	2:5G:421:GLU:OE2	2.45	0.50
1:2A:275:ILE:HG23	1:2A:368:LEU:HD21	1.93	0.50
1:2D:123:ARG:NH1	1:2D:160:ASP:OD2	2.32	0.50
1:2G:377:MET:SD	1:2G:379:SER:HB3	2.52	0.50
1:4B:17:GLY:HA2	1:4B:20:CYS:SG	2.52	0.50
1:4G:10:GLY:HA2	1:4G:145:THR:HG23	1.93	0.50
1:4G:223:THR:HG22	2:5G:322:SER:HA	1.93	0.50
2:5A:244:GLY:HA2	2:5A:355:ASP:HB2	1.94	0.50
2:5B:257:LEU:HD21	2:5B:314:SER:HB3	1.94	0.50
1:2A:325:PRO:HA	1:2A:328:VAL:HG12	1.94	0.50
1:2B:88:HIS:CD2	1:2C:283:HIS:CG	2.99	0.50
1:4A:271:SER:HB2	1:4A:377:MET:HB3	1.94	0.50
1:4C:8:HIS:HD2	1:4C:65:CYS:SG	2.35	0.50
1:4F:7:ILE:HD13	1:4F:153:LEU:HD21	1.94	0.50
2:5H:141:GLY:O	2:5H:145:SER:OG	2.27	0.50
1:2I:71:GLU:OE2	2:3I:2:ARG:NH2	2.44	0.50
2:3B:87:PRO:HD3	2:3C:281:TYR:CZ	2.47	0.50
2:3H:404:ASP:OD1	2:3H:407:GLU:HG3	2.11	0.50
1:4I:100:ALA:O	2:5I:255:VAL:HG11	2.11	0.50
1:4I:151:CYS:SG	1:4I:193:SER:OG	2.45	0.50
2:5I:216:LYS:HE2	2:5I:275:SER:HB3	1.93	0.50
1:2B:319:TYR:HB3	1:2B:323:VAL:HG21	1.94	0.49
1:2C:121:ARG:NH2	1:2D:283:HIS:CE1	2.80	0.49
1:2G:274:PRO:HG2	1:2G:371:VAL:HG11	1.94	0.49
2:3F:220:PRO:HG2	1:4F:326:LYS:CG	2.41	0.49
2:3F:334:GLN:HE22	2:3F:348:ASN:N	2.10	0.49
1:4B:260:VAL:O	1:4B:260:VAL:HG23	2.11	0.49
1:4H:224:TYR:HD1	2:5H:323:THR:HG1	1.55	0.49
2:5E:135:ILE:HB	2:5E:166:THR:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5G:68:LEU:CD2	2:5G:147:MET:HE2	2.40	0.49
2:5H:30:ILE:HD11	2:5H:47:ILE:HD11	1.94	0.49
2:5H:257:LEU:HD21	2:5H:314:SER:HB2	1.94	0.49
2:5I:235:GLY:HA2	2:5I:318:ARG:HH21	1.77	0.49
1:2I:76:ASP:OD2	2:3I:46:ARG:NH1	2.40	0.49
1:2I:217:LEU:HD11	1:2I:275:ILE:HG22	1.93	0.49
2:3F:397:TRP:CD1	1:4F:257:THR:HG1	2.30	0.49
2:3G:167:PHE:HZ	2:3G:236:VAL:HG11	1.77	0.49
1:2B:107:HIS:NE2	1:2B:151:CYS:SG	2.84	0.49
2:3C:169:VAL:HG12	2:3C:202:ILE:HB	1.93	0.49
1:4I:50:ASN:O	1:4I:64:ARG:NH2	2.45	0.49
2:5A:139:LEU:HA	2:5A:145:SER:HB2	1.93	0.49
2:5E:228:LEU:HG	2:5E:300:MET:HE2	1.93	0.49
1:2A:105:ARG:HH22	2:3A:251:ARG:NE	2.10	0.49
1:2G:180:ALA:HA	2:3G:350:LYS:HD3	1.94	0.49
2:3C:27:GLU:OE2	2:3C:241:ARG:NH1	2.42	0.49
2:3G:397:TRP:CH2	1:4G:260:VAL:HB	2.47	0.49
1:4C:60:LYS:HE2	1:4D:282:TYR:CZ	2.47	0.49
1:4C:251:ASP:OD1	1:4C:254:GLU:HG2	2.12	0.49
1:4H:76:ASP:HA	1:4H:79:ARG:HD2	1.94	0.49
1:4I:30:ILE:HG22	1:4I:36:MET:HB3	1.94	0.49
1:2A:407:TRP:HE1	2:3A:258:ILE:HG13	1.76	0.49
1:2D:56:THR:CA	1:2E:285:GLN:N	2.76	0.49
1:2G:121:ARG:HH22	1:2G:124:LYS:HE3	1.77	0.49
2:3F:55:THR:HG23	2:3F:55:THR:O	2.12	0.49
2:3H:100:ASN:HB3	2:3H:103:LYS:HG2	1.94	0.49
1:4B:4:VAL:HG12	1:4B:133:GLN:HB3	1.93	0.49
1:4F:90:GLU:HG3	1:4F:121:ARG:HD3	1.94	0.49
1:4F:313:MET:HE2	1:4F:382:THR:HG22	1.93	0.49
1:4G:377:MET:SD	1:4G:379:SER:HB3	2.52	0.49
2:5C:238:CYS:SG	2:5C:318:ARG:NE	2.85	0.49
2:5G:407:GLU:N	2:5G:407:GLU:OE2	2.44	0.49
2:5H:73:MET:HB3	2:5H:77:ARG:HH22	1.78	0.49
1:2G:11:GLN:HB2	1:2G:74:VAL:HG21	1.93	0.49
1:2G:358:GLN:OE1	1:2G:359:PRO:HD2	2.13	0.49
1:2I:217:LEU:HD11	1:2I:275:ILE:CG2	2.42	0.49
2:3A:99:ASN:HD22	1:4A:352:LYS:HZ1	1.59	0.49
2:3B:94:GLN:O	1:4B:2:ARG:NH2	2.46	0.49
2:3D:175:VAL:HG11	1:4D:329:ASN:HA	1.93	0.49
2:3D:311:LEU:HD12	2:3D:342:VAL:HG11	1.93	0.49
2:3F:55:THR:HG21	2:3G:282:ARG:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3F:220:PRO:HD2	1:4F:326:LYS:HG3	1.95	0.49
1:4C:105:ARG:HD2	1:4C:109:THR:HB	1.93	0.49
2:5C:20:PHE:CD1	2:5C:233:MET:HG3	2.47	0.49
2:5D:256:ASN:O	2:5D:312:THR:HG21	2.11	0.49
2:5G:2:ARG:NH1	2:5G:249:ASP:OD2	2.46	0.49
1:2F:250:VAL:HG13	1:2F:255:PHE:HE1	1.77	0.49
1:2F:323:VAL:CG1	1:2F:355:ILE:HG23	2.43	0.49
1:2I:398:MET:HG2	2:3I:345:ILE:HD13	1.94	0.49
2:3A:19:LYS:HD2	2:3A:22:GLU:HG3	1.94	0.49
2:3B:58:ARG:NH1	2:3C:280:GLN:OE1	2.46	0.49
2:3E:287:PRO:HD3	2:3E:325:GLU:OE1	2.12	0.49
2:3F:252:LYS:O	2:3F:256:ASN:ND2	2.28	0.49
1:4A:238:LEU:HD12	1:4A:318:MET:HE3	1.94	0.49
1:4B:215:ARG:NH2	1:4B:299:ALA:O	2.43	0.49
1:4G:417:GLU:HA	1:4G:420:GLU:HG3	1.94	0.49
1:4H:267:PHE:O	1:4H:380:ASN:ND2	2.46	0.49
2:5A:211:CYS:SG	2:5A:220:PRO:HG3	2.53	0.49
2:5B:172:SER:HB3	2:5B:205:GLU:CD	2.37	0.49
2:5C:100:ASN:HB3	2:5C:103:LYS:HG2	1.94	0.49
1:2A:66:VAL:HG12	1:2A:91:GLN:HB2	1.93	0.49
2:3B:10:GLY:HA2	2:3B:143:THR:HG23	1.93	0.49
2:3E:330:MET:HE1	2:3E:349:MET:HE2	1.94	0.49
1:4A:122:ILE:HG21	1:4A:157:LEU:HD21	1.95	0.49
1:4C:73:THR:HA	2:5C:46:ARG:HH12	1.76	0.49
1:4E:179:THR:HB	2:5E:351:SER:OG	2.12	0.49
1:4I:260:VAL:HG23	1:4I:260:VAL:O	2.13	0.49
2:5A:198:GLU:OE2	2:5A:200:GLN:NE2	2.44	0.49
2:5F:55:THR:OG1	2:5G:282:ARG:O	2.29	0.49
2:5H:137:HIS:HE1	2:5H:166:THR:HG21	1.77	0.49
1:2G:271:SER:HB3	1:2G:377:MET:HB3	1.95	0.49
2:3C:397:TRP:CH2	1:4C:260:VAL:O	2.66	0.49
1:4C:76:ASP:OD1	1:4C:79:ARG:NH2	2.41	0.49
1:4C:184:PRO:HA	1:4C:391:MET:CE	2.35	0.49
1:4H:404:PHE:CD1	2:5H:259:PRO:HA	2.48	0.49
1:4I:276:ILE:HG23	1:4I:280:LYS:HG3	1.94	0.49
1:4I:422:ARG:NH1	1:4I:426:ALA:HB2	2.28	0.49
2:5E:180:VAL:HG22	2:5E:183:TYR:HB2	1.93	0.49
2:5F:180:VAL:O	2:5F:184:ASN:ND2	2.45	0.49
1:2D:60:LYS:HE3	1:2E:283:HIS:HA	1.95	0.49
1:2H:320:ARG:NH2	1:2H:358:GLN:OE1	2.46	0.49
1:2I:262:TYR:HB2	1:2I:265:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3A:7:VAL:HG11	2:3A:151:LEU:HD23	1.95	0.49
2:3A:23:VAL:O	2:3A:27:GLU:HG2	2.13	0.49
1:4E:213:CYS:HA	1:4E:217:LEU:HD13	1.95	0.49
2:5B:64:ILE:HD13	2:5B:119:VAL:HG13	1.95	0.49
2:5B:256:ASN:HB3	2:5B:350:LYS:HE2	1.94	0.49
2:5C:180:VAL:O	2:5C:184:ASN:ND2	2.46	0.49
1:2A:80:THR:HG22	1:2A:84:ARG:HH21	1.78	0.48
1:2E:73:THR:O	1:2E:77:GLU:OE1	2.31	0.48
2:3A:70:PRO:HD2	1:4A:2:ARG:HH11	1.77	0.48
2:3D:66:MET:HG2	2:3D:147:MET:HE1	1.94	0.48
2:3G:220:PRO:HB2	2:3G:225:LEU:CD2	2.42	0.48
1:4E:101:ASN:HB3	1:4E:182:VAL:HG21	1.95	0.48
1:4E:204:LEU:N	1:4E:204:LEU:HD12	2.28	0.48
1:4H:186:ASN:OD1	1:4H:408:TYR:OH	2.31	0.48
1:4I:174:SER:HB3	1:4I:207:GLU:HG2	1.94	0.48
2:5B:68:LEU:HD12	2:5B:143:THR:HG22	1.95	0.48
2:5H:190:HIS:HB2	2:5H:414:ASN:HD21	1.78	0.48
2:5H:403:MET:HE2	2:5H:403:MET:HA	1.93	0.48
1:2A:238:LEU:HD12	1:2A:318:MET:HE3	1.94	0.48
1:2B:104:ALA:HB1	1:2B:411:GLU:OE2	2.13	0.48
1:2F:269:LEU:HD23	1:2F:303:ALA:HB3	1.95	0.48
2:3H:292:GLN:HG2	2:3H:298:ASN:HD22	1.78	0.48
1:4G:298:PRO:HA	1:4G:301:MET:HE1	1.95	0.48
1:4I:76:ASP:HA	1:4I:79:ARG:HD2	1.95	0.48
2:5B:282:ARG:HB2	2:5B:282:ARG:NH2	2.28	0.48
2:5E:107:THR:HG21	2:5E:401:GLU:HB2	1.93	0.48
2:5E:112:LEU:HD22	2:5E:147:MET:HE1	1.95	0.48
2:5G:404:ASP:OD1	2:5G:405:GLU:N	2.45	0.48
1:2A:269:LEU:HD21	1:2A:384:ILE:HD11	1.96	0.48
1:2H:306:ASP:N	1:2H:386:GLU:OE2	2.45	0.48
1:2H:414:GLU:N	1:2H:414:GLU:OE2	2.46	0.48
1:2I:240:ALA:HB2	1:2I:320:ARG:HH11	1.78	0.48
2:3E:228:LEU:HG	2:3E:300:MET:HE2	1.94	0.48
2:3H:207:LEU:HB3	2:3H:225:LEU:HD22	1.95	0.48
1:4B:217:LEU:HD21	1:4B:367:ASP:HB3	1.95	0.48
1:4C:209:ILE:HB	1:4C:227:LEU:HD22	1.95	0.48
1:4G:271:SER:HB3	1:4G:377:MET:HB3	1.95	0.48
1:4H:28:HIS:CE1	1:4H:243:ARG:HE	2.31	0.48
2:5C:165:GLU:HG2	2:5C:198:GLU:HG3	1.93	0.48
2:5D:100:ASN:HB3	2:5D:103:LYS:HG2	1.95	0.48
2:5G:202:ILE:CD1	2:5G:268:ILE:HG21	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:173:PRO:HG2	1:2A:391:MET:HE3	1.96	0.48
1:2A:427:ALA:O	1:2A:430:LYS:HG3	2.12	0.48
1:2D:221:ARG:HA	2:3D:324:LYS:CE	2.40	0.48
1:2F:238:LEU:HD11	1:2F:255:PHE:HE2	1.79	0.48
1:2G:407:TRP:CZ3	2:3G:255:VAL:CG2	2.96	0.48
2:3B:100:ASN:HB3	2:3B:103:LYS:HG2	1.94	0.48
2:3G:237:THR:HG22	2:3G:237:THR:O	2.14	0.48
2:3I:103:LYS:HA	2:3I:107:THR:HG22	1.94	0.48
2:3I:258:ILE:O	2:3I:258:ILE:HG13	2.12	0.48
1:4C:230:LEU:HD21	1:4C:368:LEU:HD21	1.95	0.48
1:4D:123:ARG:NH1	1:4D:160:ASP:OD2	2.40	0.48
1:4D:398:MET:CE	2:5D:346:PRO:HD2	2.44	0.48
1:4E:76:ASP:OD2	2:5E:46:ARG:NH1	2.31	0.48
1:4G:269:LEU:HD23	1:4G:303:ALA:HB3	1.95	0.48
2:5C:230:SER:HA	2:5C:233:MET:HG2	1.95	0.48
2:5E:209:ASP:OD1	2:5E:213:ARG:NH1	2.46	0.48
2:5E:309:ARG:H	2:5E:372:THR:HG22	1.78	0.48
2:5H:330:MET:SD	2:5H:349:MET:HG2	2.53	0.48
1:2G:167:LEU:HA	1:2G:200:VAL:HG13	1.95	0.48
1:2G:387:VAL:HA	1:2G:390:ARG:NH2	2.23	0.48
2:3B:211:CYS:SG	2:3B:217:LEU:HB2	2.53	0.48
2:3D:1:MET:N	2:3D:128:ASP:OD2	2.39	0.48
2:5A:375:GLN:HE21	2:5A:379:LYS:HD3	1.78	0.48
1:2B:271:SER:HB2	1:2B:377:MET:HB3	1.94	0.48
1:2E:136:LEU:HD23	1:2E:235:ILE:HD11	1.94	0.48
1:2E:152:LEU:O	1:2E:156:ARG:HG2	2.14	0.48
2:3A:293:MET:HA	2:3A:293:MET:HE2	1.94	0.48
2:3C:309:ARG:H	2:3C:372:THR:HG22	1.79	0.48
2:3E:200:GLN:HB3	2:3E:268:ILE:HD11	1.94	0.48
2:3E:293:MET:HG3	2:3E:367:PHE:HB2	1.94	0.48
2:3F:58:ARG:HD3	2:3G:281:TYR:CE1	2.48	0.48
2:3H:5:VAL:HB	2:3H:133:PHE:CD1	2.48	0.48
1:4E:274:PRO:HG3	1:4E:286:LEU:CD2	2.43	0.48
1:4F:377:MET:HE2	1:4F:379:SER:HB3	1.96	0.48
1:4G:177:VAL:HG13	2:5G:327:ASP:HB3	1.96	0.48
1:4I:215:ARG:NH2	1:4I:299:ALA:O	2.46	0.48
2:5D:54:ALA:CB	2:5E:281:TYR:O	2.61	0.48
2:5H:289:LEU:HD12	2:5H:365:VAL:HG12	1.96	0.48
1:2I:5:ILE:HG12	1:2I:132:LEU:HD11	1.96	0.48
2:3A:267:LEU:CD2	2:3A:374:ILE:HD11	2.34	0.48
2:3C:122:LYS:CE	2:3D:281:TYR:OH	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3C:311:LEU:HD12	2:3C:342:VAL:HG11	1.95	0.48
1:4E:151:CYS:SG	1:4E:193:SER:OG	2.40	0.48
1:4G:136:LEU:HD22	1:4G:167:LEU:HD23	1.96	0.48
1:4G:309:HIS:HE2	1:4G:386:GLU:CD	2.22	0.48
1:4H:178:SER:HB2	2:5H:347:ASN:ND2	2.29	0.48
1:4I:53:PHE:HB3	1:4I:61:HIS:HB3	1.95	0.48
2:5D:54:ALA:HB1	2:5E:282:ARG:C	2.39	0.48
2:5D:178:THR:OG1	2:5D:181:GLU:OE2	2.31	0.48
2:5D:284:LEU:HD23	2:5D:362:LYS:HG2	1.95	0.48
2:5E:213:ARG:HH12	2:5E:297:LYS:HB2	1.79	0.48
2:5I:193:VAL:HG21	2:5I:418:LEU:HD12	1.94	0.48
1:2D:75:VAL:O	1:2D:78:VAL:HG12	2.14	0.48
1:2E:174:SER:HB3	1:2E:207:GLU:HG2	1.96	0.48
1:2H:4:VAL:HG21	1:2H:136:LEU:HD13	1.95	0.48
1:2H:210:TYR:CG	2:3H:324:LYS:HE3	2.42	0.48
2:3A:258:ILE:HG13	2:3A:258:ILE:O	2.13	0.48
1:4D:99:ALA:O	1:4D:105:ARG:HD3	2.13	0.48
1:4E:11:GLN:HG3	1:4E:74:VAL:HG21	1.95	0.48
2:5A:109:GLY:O	2:5A:113:ILE:HG12	2.14	0.48
2:5G:55:THR:HG23	2:5H:283:ALA:CB	2.44	0.48
1:2H:71:GLU:HB3	1:2H:98:ASP:HB3	1.96	0.48
2:3C:181:GLU:CG	2:3C:182:PRO:HD3	2.44	0.48
2:3E:274:THR:HG21	2:3E:282:ARG:HD2	1.95	0.48
2:3F:202:ILE:HD11	2:3F:268:ILE:HG21	1.96	0.48
2:3G:101:TRP:CD1	2:3G:145:SER:HG	2.32	0.48
2:3G:107:THR:OG1	2:3G:401:GLU:OE2	2.31	0.48
2:3G:196:ALA:O	2:3G:264:HIS:NE2	2.47	0.48
1:4E:178:SER:OG	2:5E:347:ASN:ND2	2.47	0.48
1:4F:306:ASP:HB3	1:4F:309:HIS:HE1	1.79	0.48
2:5A:133:PHE:HZ	2:5A:159:TYR:HD2	1.62	0.48
2:5B:311:LEU:HD12	2:5B:342:VAL:HG11	1.96	0.48
2:5F:173:PRO:HD2	2:5F:205:GLU:OE2	2.14	0.48
1:2E:76:ASP:OD2	2:3E:46:ARG:NH1	2.40	0.48
1:2G:212:ILE:HG23	1:2G:275:ILE:CD1	2.41	0.48
1:2G:269:LEU:HD11	1:2G:384:ILE:HD11	1.95	0.48
1:2H:406:HIS:HA	1:2H:409:VAL:HG22	1.96	0.48
2:3E:55:THR:HG22	2:3F:283:ALA:HA	1.90	0.48
2:3H:64:ILE:HD12	2:3H:119:VAL:HG12	1.96	0.48
2:5F:98:GLY:H	2:5F:103:LYS:HD3	1.78	0.48
1:2A:397:LEU:HD23	2:3A:346:PRO:HD3	1.96	0.47
1:2D:269:LEU:CD2	1:2D:301:MET:HG2	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2H:223:THR:OG1	2:3H:245:GLN:OE1	2.32	0.47
2:3E:155:VAL:HG13	2:3E:164:MET:HE2	1.94	0.47
2:3F:323:THR:HA	2:3F:326:VAL:HG12	1.95	0.47
1:4C:105:ARG:HH12	2:5C:251:ARG:HD3	1.79	0.47
1:4F:335:ILE:HG23	1:4F:341:ILE:HD13	1.96	0.47
2:5D:375:GLN:HG3	2:5D:419:VAL:HG13	1.96	0.47
1:2H:51:THR:HG23	1:2H:52:PHE:HD1	1.79	0.47
1:2I:52:PHE:HD2	1:2I:243:ARG:HD3	1.78	0.47
2:3C:86:ARG:HG3	2:3D:280:GLN:OE1	2.13	0.47
1:4E:5:ILE:HD13	1:4E:64:ARG:HB3	1.95	0.47
1:4E:217:LEU:HD11	1:4E:275:ILE:CG2	2.43	0.47
1:4H:33:ASP:O	1:4H:60:LYS:NZ	2.25	0.47
1:4H:399:TYR:OH	1:4H:415:GLU:OE2	2.32	0.47
2:5A:272:PRO:HD2	2:5A:361:LEU:HD21	1.95	0.47
2:5C:88:ASP:OD2	2:5D:281:TYR:CE2	2.67	0.47
1:2G:100:ALA:O	2:3G:255:VAL:HG11	2.14	0.47
2:3A:220:PRO:HD2	1:4A:326:LYS:HE3	1.78	0.47
2:3E:258:ILE:HG13	2:3E:258:ILE:O	2.14	0.47
2:3F:334:GLN:HE22	2:3F:348:ASN:H	1.61	0.47
2:3G:220:PRO:CD	1:4G:326:LYS:HD3	2.45	0.47
1:4B:72:PRO:HD2	2:5B:2:ARG:HH22	1.79	0.47
1:4B:103:PHE:CD2	1:4B:413:MET:HE1	2.48	0.47
1:4D:178:SER:CB	2:5D:347:ASN:HD22	2.19	0.47
1:4I:70:LEU:HD12	1:4I:99:ALA:HB2	1.96	0.47
2:5E:114:ASP:N	2:5E:114:ASP:OD1	2.47	0.47
2:5G:311:LEU:HD12	2:5G:342:VAL:HG11	1.96	0.47
2:5H:10:GLY:O	2:5H:14:ASN:ND2	2.48	0.47
2:5H:249:ASP:H	2:5H:252:LYS:HB2	1.79	0.47
1:2E:403:ALA:HB2	2:3E:344:TRP:CZ3	2.48	0.47
1:2F:168:ASN:ND2	1:2F:170:CYS:SG	2.88	0.47
1:2G:189:LEU:HD11	1:2G:418:PHE:CD1	2.49	0.47
1:2H:178:SER:HB3	2:3H:347:ASN:ND2	2.29	0.47
2:3A:179:VAL:HG11	1:4A:258:ASN:O	2.15	0.47
2:3B:309:ARG:NH1	2:3B:341:PHE:O	2.48	0.47
2:3C:163:ILE:HD12	2:3C:250:LEU:HB2	1.95	0.47
2:3E:98:GLY:O	1:4E:257:THR:HG21	2.14	0.47
2:3F:58:ARG:HD3	2:3G:281:TYR:CD1	2.49	0.47
1:4A:50:ASN:O	1:4A:64:ARG:NH2	2.46	0.47
1:4A:70:LEU:HD12	1:4A:99:ALA:HB2	1.96	0.47
1:4F:60:LYS:HZ3	1:4F:62:VAL:HB	1.79	0.47
2:5E:215:LEU:HB3	2:5E:217:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5G:169:VAL:HG12	2:5G:202:ILE:HB	1.96	0.47
1:2B:221:ARG:HD2	1:2B:221:ARG:HA	1.43	0.47
1:2C:223:THR:OG1	2:3C:245:GLN:NE2	2.47	0.47
2:3B:94:GLN:C	1:4B:2:ARG:HH22	2.22	0.47
1:4D:16:ILE:HD11	1:4D:138:PHE:HB3	1.96	0.47
2:5A:200:GLN:HG3	2:5A:268:ILE:HD11	1.96	0.47
2:5D:135:ILE:HG22	2:5D:137:HIS:CD2	2.49	0.47
1:2H:11:GLN:NE2	1:2H:15:GLN:OE1	2.48	0.47
1:2H:168:ASN:HD22	1:2H:198:THR:HG21	1.80	0.47
1:2I:71:GLU:OE2	1:2I:73:THR:HG23	2.14	0.47
2:3A:121:ARG:NH2	2:3A:158:GLU:OE2	2.47	0.47
2:3C:99:ASN:HD21	1:4C:258:ASN:HD21	1.61	0.47
2:3D:309:ARG:NH1	2:3D:341:PHE:O	2.48	0.47
2:3G:52:ASN:ND2	2:3G:123:GLU:OE2	2.34	0.47
2:3G:69:GLU:HG2	1:4G:2:ARG:NH2	2.29	0.47
1:4A:269:LEU:HD11	1:4A:384:ILE:HD11	1.97	0.47
1:4C:8:HIS:CD2	1:4C:65:CYS:SG	3.07	0.47
1:4G:154:LEU:HD21	1:4G:198:THR:OG1	2.14	0.47
1:2A:406:HIS:HA	1:2A:409:VAL:HG22	1.96	0.47
1:2B:221:ARG:NH2	2:3B:325:GLU:N	2.61	0.47
1:2C:50:ASN:O	1:2C:64:ARG:NH2	2.48	0.47
1:2E:269:LEU:HD11	1:2E:384:ILE:HD11	1.97	0.47
1:2G:60:LYS:CE	1:2H:283:HIS:CD2	2.98	0.47
1:2G:137:MET:HB3	1:2G:168:ASN:HA	1.95	0.47
1:2H:100:ALA:O	2:3H:255:VAL:HG11	2.15	0.47
2:3A:169:VAL:HG12	2:3A:202:ILE:HB	1.96	0.47
2:3D:64:ILE:HD12	2:3D:119:VAL:HG12	1.96	0.47
2:3E:55:THR:HG21	2:3F:284:LEU:H	1.80	0.47
2:3H:391:ARG:HD2	1:4H:346:TRP:CD1	2.49	0.47
1:4A:407:TRP:CZ2	2:5A:258:ILE:HD11	2.50	0.47
1:4C:259:LEU:HB3	1:4C:268:MET:HE1	1.97	0.47
1:4D:57:GLY:N	1:4E:285:GLN:CB	2.67	0.47
1:4E:181:VAL:HG22	2:5E:256:ASN:ND2	2.30	0.47
1:4E:260:VAL:HG23	1:4E:260:VAL:O	2.15	0.47
2:5A:207:LEU:HD21	2:5A:225:LEU:CB	2.38	0.47
2:5A:313:ALA:HB1	2:5A:367:PHE:HE1	1.79	0.47
2:5D:239:CYS:SG	2:5D:248:SER:N	2.83	0.47
2:5F:290:THR:HA	2:5F:293:MET:HE2	1.96	0.47
2:5H:106:TYR:CE1	2:5H:403:MET:HE1	2.50	0.47
2:5H:293:MET:HE1	2:5H:365:VAL:HG21	1.97	0.47
1:2A:90:GLU:O	1:2A:93:ILE:HD11	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2E:259:LEU:HD13	1:2E:268:MET:HE2	1.95	0.47
1:2H:411:GLU:N	1:2H:411:GLU:OE1	2.48	0.47
1:2I:396:ASP:OD2	1:2I:422:ARG:NH2	2.47	0.47
2:3B:213:ARG:HH12	2:3B:297:LYS:HB3	1.80	0.47
2:3C:181:GLU:HG2	2:3C:182:PRO:HD3	1.97	0.47
2:3D:290:THR:HG21	2:3D:329:GLN:HB3	1.97	0.47
2:3F:347:ASN:OD1	2:3F:349:MET:HB3	2.15	0.47
1:4C:212:ILE:HD11	1:4C:300:SER:HA	1.97	0.47
1:4G:340:THR:HG23	1:4G:341:ILE:HG13	1.97	0.47
2:5D:309:ARG:H	2:5D:372:THR:HG22	1.80	0.47
2:5I:211:CYS:SG	2:5I:220:PRO:HB3	2.55	0.47
1:2B:12:ALA:HB3	1:2B:140:ALA:HB2	1.96	0.47
1:2E:60:LYS:NZ	1:2F:283:HIS:CD2	2.83	0.47
1:2F:30:ILE:HG22	1:2F:36:MET:HG2	1.97	0.47
1:2F:105:ARG:HH12	2:3F:251:ARG:HG2	1.80	0.47
1:2G:108:TYR:O	1:2G:112:LYS:NZ	2.47	0.47
2:3G:175:VAL:HG21	1:4G:332:VAL:HG23	1.96	0.47
2:3H:12:CYS:HB3	2:3H:138:SER:OG	2.14	0.47
1:4A:57:GLY:CA	1:4B:285:GLN:HG2	2.45	0.47
1:4A:68:LEU:HD23	1:4A:149:LEU:HD21	1.97	0.47
1:4A:254:GLU:OE1	1:4A:352:LYS:NZ	2.40	0.47
1:4H:142:GLY:CA	1:4H:183:GLU:HG2	2.45	0.47
1:4H:404:PHE:HE2	2:5H:345:ILE:HD12	1.80	0.47
2:5D:58:ARG:HD2	2:5E:280:GLN:C	2.36	0.47
2:5E:155:VAL:HG13	2:5E:164:MET:CE	2.45	0.47
2:5E:192:LEU:HD21	2:5E:199:VAL:HG11	1.97	0.47
2:5I:293:MET:HE2	2:5I:365:VAL:HG11	1.96	0.47
1:2D:57:GLY:N	1:2E:285:GLN:CB	2.76	0.47
2:3F:417:ASP:O	2:3F:421:GLU:OE1	2.33	0.47
2:3I:137:HIS:HE1	2:3I:166:THR:CG2	2.27	0.47
1:4F:60:LYS:NZ	1:4G:283:HIS:ND1	2.57	0.47
1:4G:135:PHE:HB2	1:4G:166:LYS:HG2	1.97	0.47
1:4G:181:VAL:HB	2:5G:256:ASN:OD1	2.14	0.47
1:4G:298:PRO:O	1:4G:301:MET:HE1	2.15	0.47
2:5D:58:ARG:NH2	2:5E:281:TYR:CD1	2.78	0.47
2:5G:135:ILE:HD13	2:5G:152:ILE:HG12	1.96	0.47
1:2A:60:LYS:NZ	1:2B:283:HIS:HD2	2.13	0.46
1:2A:306:ASP:N	1:2A:386:GLU:OE2	2.45	0.46
1:2H:35:GLN:OE1	1:2H:35:GLN:N	2.47	0.46
2:3D:309:ARG:H	2:3D:372:THR:HG22	1.80	0.46
2:3G:135:ILE:CG1	2:3G:166:THR:HG22	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3I:178:THR:HA	1:4I:258:ASN:HD21	1.79	0.46
1:4D:11:GLN:NE2	2:5D:247:ASN:OD1	2.48	0.46
1:4D:60:LYS:CE	1:4E:283:HIS:HA	2.40	0.46
1:4G:398:MET:SD	2:5G:346:PRO:HD2	2.55	0.46
1:4I:246:GLY:HA2	1:4I:357:TYR:HD1	1.79	0.46
2:5B:284:LEU:HB3	2:5B:362:LYS:HE3	1.96	0.46
2:5E:141:GLY:O	2:5E:145:SER:OG	2.29	0.46
1:2A:402:ARG:NH1	1:2A:405:VAL:HG11	2.30	0.46
1:2G:401:LYS:NZ	2:3G:425:TYR:CD1	2.83	0.46
1:2I:241:SER:HB2	1:2I:249:ASN:HB2	1.97	0.46
2:3D:10:GLY:HA2	2:3D:143:THR:HG23	1.96	0.46
2:3F:309:ARG:H	2:3F:372:THR:HG22	1.80	0.46
2:3G:97:ALA:HB3	2:3G:143:THR:HB	1.98	0.46
2:3H:169:VAL:HG12	2:3H:202:ILE:HB	1.96	0.46
1:4B:306:ASP:HB3	1:4B:309:HIS:CE1	2.49	0.46
1:4C:70:LEU:HD12	1:4C:99:ALA:HB2	1.97	0.46
1:4D:238:LEU:HD11	1:4D:255:PHE:CE2	2.50	0.46
1:4I:213:CYS:SG	1:4I:222:PRO:HG3	2.56	0.46
2:5H:181:GLU:CG	2:5H:182:PRO:HD3	2.45	0.46
2:5I:272:PRO:HG3	2:5I:284:LEU:HD11	1.96	0.46
1:2B:98:ASP:O	1:2B:105:ARG:NH1	2.48	0.46
1:2G:287:SER:N	1:2G:290:GLU:OE2	2.45	0.46
2:3A:311:LEU:HD12	2:3A:342:VAL:HG11	1.96	0.46
2:3E:99:ASN:CG	1:4E:254:GLU:OE1	2.59	0.46
2:3F:238:CYS:SG	2:3F:318:ARG:NE	2.88	0.46
2:3H:397:TRP:CH2	1:4H:260:VAL:HG23	2.50	0.46
2:3I:192:LEU:HD21	2:3I:199:VAL:HG21	1.97	0.46
1:4A:340:THR:HG23	1:4A:341:ILE:HG13	1.96	0.46
1:4D:33:ASP:O	1:4D:60:LYS:NZ	2.48	0.46
1:4E:241:SER:OG	1:4E:250:VAL:O	2.21	0.46
1:4G:358:GLN:OE1	1:4G:359:PRO:HD2	2.15	0.46
2:5B:105:HIS:CD2	2:5B:150:LEU:HB2	2.51	0.46
2:5H:20:PHE:CD2	2:5H:233:MET:HE3	2.47	0.46
2:5I:252:LYS:HG3	2:5I:350:LYS:HE3	1.98	0.46
1:2D:391:MET:HE3	1:2D:391:MET:HB2	1.83	0.46
1:2H:183:GLU:HG3	1:2H:184:PRO:HD3	1.97	0.46
2:3A:55:THR:HG21	2:3B:283:ALA:HB1	1.90	0.46
2:3C:249:ASP:OD1	2:3C:252:LYS:HG2	2.15	0.46
2:3G:55:THR:HG23	2:3H:283:ALA:CB	2.46	0.46
2:3H:179:VAL:HG11	1:4H:258:ASN:O	2.15	0.46
1:4B:419:SER:O	1:4B:423:GLU:OE1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4H:406:HIS:HA	1:4H:409:VAL:HG22	1.98	0.46
2:5B:19:LYS:HE3	2:5B:227:HIS:HB2	1.97	0.46
2:5B:156:ARG:NH1	2:5B:162:ARG:O	2.49	0.46
2:5B:284:LEU:HD23	2:5B:362:LYS:HG3	1.97	0.46
1:2B:221:ARG:NH2	2:3B:322:SER:C	2.74	0.46
1:2C:124:LYS:CD	1:2D:283:HIS:NE2	2.69	0.46
1:2G:403:ALA:HB2	2:3G:344:TRP:CH2	2.51	0.46
2:3B:16:ILE:HD11	2:3B:136:THR:HB	1.97	0.46
2:3G:189:VAL:HG11	2:3G:415:MET:SD	2.55	0.46
2:3G:407:GLU:OE1	2:3G:407:GLU:N	2.47	0.46
1:4B:316:CYS:SG	1:4B:378:ILE:HB	2.55	0.46
1:4D:1:MET:N	1:4D:3:GLU:OE2	2.35	0.46
1:4G:244:PHE:HB2	1:4G:356:ASN:HD21	1.81	0.46
2:5B:341:PHE:CZ	2:5B:349:MET:HE1	2.50	0.46
2:5E:404:ASP:OD1	2:5E:405:GLU:N	2.47	0.46
1:2A:10:GLY:HA2	1:2A:145:THR:HG23	1.96	0.46
1:2C:192:HIS:NE2	1:2C:420:GLU:OE2	2.49	0.46
1:2D:306:ASP:HB3	1:2D:309:HIS:CE1	2.50	0.46
1:2E:184:PRO:HG2	1:2E:398:MET:HE3	1.97	0.46
2:3D:324:LYS:O	2:3D:328:GLU:HG2	2.15	0.46
2:3E:169:VAL:HG12	2:3E:202:ILE:HB	1.96	0.46
2:3G:265:PHE:CE2	2:3G:418:LEU:HD21	2.51	0.46
2:3H:372:THR:HA	2:3H:422:TYR:HD2	1.79	0.46
1:4A:80:THR:HA	1:4A:84:ARG:HE	1.80	0.46
1:4C:298:PRO:HB3	1:4C:307:PRO:HD2	1.98	0.46
1:4D:50:ASN:O	1:4D:64:ARG:NH2	2.49	0.46
1:4E:179:THR:HG21	2:5E:327:ASP:OD1	2.16	0.46
1:4G:121:ARG:NH1	1:4G:124:LYS:HE3	2.28	0.46
1:4I:265:ILE:HG21	1:4I:313:MET:HE1	1.98	0.46
2:5A:7:VAL:HG22	2:5A:64:ILE:HG21	1.98	0.46
2:5D:16:ILE:HG22	2:5D:136:THR:HG21	1.98	0.46
2:5E:1:MET:N	2:5E:128:ASP:OD2	2.45	0.46
2:5H:202:ILE:HD12	2:5H:300:MET:HE2	1.97	0.46
1:2A:323:VAL:HG13	1:2A:355:ILE:HG23	1.97	0.46
1:2A:397:LEU:HG	2:3A:344:TRP:O	2.15	0.46
1:2B:256:GLN:HE21	1:2B:256:GLN:H	1.63	0.46
1:2I:223:THR:HG22	2:3I:322:SER:HA	1.96	0.46
2:3A:171:PRO:HG3	2:3A:181:GLU:OE1	2.16	0.46
2:3B:94:GLN:O	1:4B:2:ARG:CZ	2.63	0.46
2:3D:282:ARG:NH1	2:3D:288:GLU:OE2	2.49	0.46
1:4C:238:LEU:HD13	1:4C:255:PHE:HE2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4F:370:LYS:HZ1	1:4F:372:MET:HE1	1.80	0.46
1:4G:135:PHE:HD2	1:4G:166:LYS:HG2	1.81	0.46
1:4G:259:LEU:HD11	1:4G:316:CYS:HB2	1.98	0.46
2:5C:178:THR:HG23	2:5C:181:GLU:HG3	1.98	0.46
1:2F:215:ARG:NH2	1:2F:300:SER:HB2	2.31	0.46
1:2H:133:GLN:NE2	1:2H:253:THR:HG23	2.31	0.46
2:3C:397:TRP:HZ2	1:4C:260:VAL:HB	1.81	0.46
2:3D:94:GLN:O	1:4D:2:ARG:NH2	2.49	0.46
2:3E:397:TRP:NE1	1:4E:256:GLN:OE1	2.49	0.46
2:3F:10:GLY:HA2	2:3F:143:THR:HG23	1.98	0.46
2:3F:54:ALA:HB1	2:3G:281:TYR:O	2.16	0.46
2:3G:397:TRP:CZ3	1:4G:256:GLN:O	2.69	0.46
1:4D:203:MET:HE1	1:4D:384:ILE:HD12	1.98	0.46
1:4G:167:LEU:HA	1:4G:200:VAL:HG13	1.98	0.46
2:5E:169:VAL:HG12	2:5E:202:ILE:HB	1.98	0.46
2:5F:135:ILE:HB	2:5F:166:THR:HG22	1.97	0.46
2:5G:7:VAL:HG11	2:5G:151:LEU:HD22	1.98	0.46
1:2A:60:LYS:HE2	1:2B:283:HIS:CD2	2.50	0.46
1:2G:213:CYS:SG	1:2G:222:PRO:HG3	2.56	0.46
2:3A:7:VAL:HB	2:3A:135:ILE:CD1	2.46	0.46
2:3C:332:ASN:CG	2:3C:336:LYS:HZ1	2.23	0.46
2:3D:326:VAL:HG22	2:3D:351:SER:HB2	1.98	0.46
2:3E:10:GLY:HA2	2:3E:143:THR:HG23	1.98	0.46
2:3F:2:ARG:HB3	2:3F:131:GLN:HB2	1.98	0.46
2:3G:99:ASN:OD1	2:3G:99:ASN:N	2.49	0.46
2:3H:113:ILE:HA	2:3H:116:VAL:HG12	1.98	0.46
1:4I:274:PRO:HB2	1:4I:276:ILE:HG12	1.98	0.46
2:5B:407:GLU:OE2	2:5B:407:GLU:N	2.47	0.46
2:5D:54:ALA:HA	2:5E:283:ALA:CA	2.45	0.46
2:5D:139:LEU:HD11	2:5D:192:LEU:HD13	1.97	0.46
2:5E:54:ALA:CB	2:5F:281:TYR:O	2.45	0.46
1:2A:65:CYS:O	1:2A:91:GLN:HG3	2.16	0.46
1:2D:265:ILE:HG21	1:2D:313:MET:HE1	1.98	0.46
1:2F:27:GLU:OE1	1:2F:320:ARG:NH2	2.40	0.46
2:3A:5:VAL:HB	2:3A:133:PHE:HD1	1.81	0.46
2:3B:68:LEU:HD11	2:3B:147:MET:CE	2.46	0.46
2:3G:174:LYS:HE2	1:4G:333:ALA:HB1	1.97	0.46
2:3H:149:THR:HG22	2:3H:191:GLN:NE2	2.31	0.46
1:4A:97:GLU:HG3	1:4A:105:ARG:HH21	1.81	0.46
1:4E:172:TRP:HZ2	1:4E:391:MET:HE1	1.80	0.46
1:4H:269:LEU:CD2	1:4H:384:ILE:HD11	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:172:SER:HB2	2:5A:205:GLU:OE1	2.16	0.46
2:5C:103:LYS:HA	2:5C:107:THR:HB	1.98	0.46
2:5D:107:THR:HG1	2:5D:108:GLU:CD	2.23	0.46
1:2B:173:PRO:HG2	1:2B:391:MET:HE1	1.98	0.45
1:2C:76:ASP:HA	1:2C:79:ARG:HD2	1.98	0.45
2:3G:175:VAL:HG11	1:4G:332:VAL:CG2	2.47	0.45
1:4C:238:LEU:HD21	1:4C:378:ILE:HD11	1.98	0.45
2:5C:274:THR:HG21	2:5C:282:ARG:HD3	1.98	0.45
2:5E:68:LEU:HB3	2:5E:96:GLY:HA2	1.98	0.45
2:5G:403:MET:HB3	2:5G:408:PHE:HE1	1.81	0.45
1:2D:138:PHE:CZ	1:2D:235:ILE:HD12	2.47	0.45
1:2I:234:VAL:HG21	1:2I:302:MET:HE1	1.97	0.45
2:3B:173:PRO:HB3	2:3B:380:ARG:CZ	2.46	0.45
2:3G:309:ARG:H	2:3G:372:THR:HG22	1.82	0.45
1:4A:256:GLN:O	1:4A:260:VAL:HG22	2.16	0.45
1:4F:99:ALA:HA	1:4F:105:ARG:HG2	1.97	0.45
1:4G:88:HIS:HB3	1:4G:91:GLN:HE22	1.82	0.45
1:4H:72:PRO:HD2	2:5H:2:ARG:NH2	2.31	0.45
1:4H:251:ASP:OD1	1:4H:254:GLU:N	2.49	0.45
1:4I:167:LEU:HD22	1:4I:200:VAL:HB	1.98	0.45
1:4I:215:ARG:HH22	1:4I:299:ALA:C	2.25	0.45
1:4I:397:LEU:CD2	2:5I:344:TRP:HA	2.43	0.45
2:5G:86:ARG:NE	2:5G:86:ARG:HA	2.31	0.45
2:5H:169:VAL:HG12	2:5H:202:ILE:HB	1.97	0.45
1:2C:306:ASP:OD1	1:2C:308:ARG:NH1	2.50	0.45
1:2I:181:VAL:HG22	2:3I:347:ASN:O	2.16	0.45
2:3E:113:ILE:HD12	2:3E:113:ILE:HA	1.86	0.45
2:3F:14:ASN:ND2	2:3F:67:ASP:OD2	2.50	0.45
2:3G:7:VAL:HG11	2:3G:151:LEU:HD23	1.98	0.45
1:4A:51:THR:HG23	1:4A:52:PHE:CD2	2.51	0.45
1:4H:269:LEU:HD21	1:4H:384:ILE:HD11	1.99	0.45
1:4I:269:LEU:HD12	1:4I:303:ALA:HB3	1.99	0.45
2:5A:363:MET:HE2	2:5A:363:MET:HB2	1.89	0.45
2:5E:58:ARG:NH1	2:5F:281:TYR:CE1	2.84	0.45
1:2D:57:GLY:N	1:2E:285:GLN:CA	2.79	0.45
2:3C:66:MET:HG2	2:3C:147:MET:HE1	1.98	0.45
2:3F:54:ALA:HB1	2:3G:281:TYR:C	2.42	0.45
2:3F:208:TYR:HA	1:4F:326:LYS:HE2	1.98	0.45
1:4C:75:VAL:HG21	1:4C:94:SER:HB2	1.98	0.45
1:4F:230:LEU:HD21	1:4F:368:LEU:HD21	1.98	0.45
1:4G:241:SER:HB2	1:4G:249:ASN:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5G:5:VAL:HB	2:5G:133:PHE:CD1	2.51	0.45
1:2A:17:GLY:HA2	1:2A:20:CYS:SG	2.56	0.45
1:2B:221:ARG:HH12	2:3B:324:LYS:CB	2.29	0.45
1:2D:5:ILE:HG12	1:2D:132:LEU:HD11	1.99	0.45
1:2F:217:LEU:CD2	1:2F:275:ILE:HG22	2.46	0.45
1:2F:377:MET:SD	1:2F:379:SER:HB3	2.56	0.45
1:2G:48:ALA:O	1:2G:51:THR:HG22	2.16	0.45
1:2H:270:SER:O	1:2H:301:MET:HE3	2.17	0.45
2:3C:60:VAL:CG1	2:3D:280:GLN:NE2	2.69	0.45
2:3C:284:LEU:HD23	2:3C:362:LYS:HG2	1.97	0.45
2:3E:177:ASP:OD1	1:4E:353:CYS:SG	2.74	0.45
2:3H:94:GLN:O	1:4H:2:ARG:NH2	2.50	0.45
2:3I:274:THR:HG21	2:3I:282:ARG:HD2	1.98	0.45
1:4A:238:LEU:HD13	1:4A:378:ILE:HD13	1.99	0.45
1:4A:301:MET:HE2	1:4A:301:MET:HB3	1.86	0.45
1:4C:101:ASN:ND2	2:5C:256:ASN:OD1	2.50	0.45
1:4F:50:ASN:O	1:4F:64:ARG:NH2	2.48	0.45
1:4G:287:SER:OG	1:4G:290:GLU:OE2	2.35	0.45
2:5H:7:VAL:HB	2:5H:135:ILE:HD13	1.98	0.45
1:2B:210:TYR:CE1	2:3B:324:LYS:HB2	2.51	0.45
1:2C:89:PRO:HD3	1:2D:282:TYR:CD2	2.52	0.45
1:2F:11:GLN:OE1	2:3F:247:ASN:ND2	2.49	0.45
1:2I:70:LEU:HD12	1:2I:99:ALA:HB2	1.98	0.45
2:3C:10:GLY:HA2	2:3C:143:THR:HG23	1.96	0.45
2:3F:98:GLY:CA	1:4F:254:GLU:HB3	2.47	0.45
2:3F:220:PRO:CG	1:4F:326:LYS:HE3	2.39	0.45
2:3G:5:VAL:HB	2:3G:133:PHE:CD1	2.52	0.45
2:3G:329:GLN:OE1	2:3G:332:ASN:ND2	2.42	0.45
2:3H:35:THR:OG1	2:3H:36:TYR:N	2.50	0.45
1:4A:100:ALA:O	2:5A:255:VAL:HG11	2.17	0.45
1:4F:401:LYS:HE2	2:5F:344:TRP:CD2	2.52	0.45
2:5D:150:LEU:CD2	2:5D:154:LYS:HD2	2.46	0.45
2:5F:202:ILE:HD11	2:5F:268:ILE:HG21	1.99	0.45
2:5I:354:CYS:SG	2:5I:355:ASP:N	2.90	0.45
1:2B:301:MET:SD	1:2B:307:PRO:HG3	2.56	0.45
1:2C:244:PHE:HB2	1:2C:356:ASN:HD21	1.82	0.45
2:3B:211:CYS:SG	2:3B:220:PRO:HB3	2.57	0.45
2:3C:66:MET:HE2	2:3C:116:VAL:HG21	1.99	0.45
2:3E:1:MET:N	2:3E:128:ASP:OD2	2.40	0.45
2:3E:294:PHE:HE1	2:3E:367:PHE:CE1	2.35	0.45
1:4A:105:ARG:NH2	2:5A:251:ARG:HH12	2.13	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4C:107:HIS:NE2	1:4C:151:CYS:SG	2.89	0.45
1:4D:132:LEU:HG	1:4D:164:LYS:HD3	1.99	0.45
2:5C:284:LEU:CD2	2:5C:363:MET:HB2	2.46	0.45
2:5H:35:THR:OG1	2:5H:36:TYR:N	2.50	0.45
1:2G:186:ASN:OD1	1:2G:408:TYR:OH	2.34	0.45
2:3C:332:ASN:HD21	2:3C:336:LYS:NZ	2.15	0.45
2:3G:100:ASN:HB3	2:3G:103:LYS:HG2	1.98	0.45
2:3G:239:CYS:SG	2:3G:248:SER:N	2.89	0.45
1:4C:216:ASN:O	1:4C:280:LYS:HE2	2.17	0.45
1:4E:306:ASP:HB3	1:4E:309:HIS:CE1	2.51	0.45
1:4F:306:ASP:HB3	1:4F:309:HIS:CE1	2.51	0.45
2:5A:156:ARG:NH2	2:5A:197:ASP:OD1	2.50	0.45
2:5B:176:SER:OG	2:5B:181:GLU:OE1	2.34	0.45
2:5C:172:SER:OG	2:5C:205:GLU:OE1	2.34	0.45
2:5D:54:ALA:HA	2:5E:283:ALA:N	2.31	0.45
2:5F:173:PRO:HD3	2:5F:380:ARG:CZ	2.46	0.45
2:5G:309:ARG:H	2:5G:372:THR:HG22	1.81	0.45
1:2D:154:LEU:HB3	1:2D:197:HIS:HB3	1.98	0.45
1:2D:301:MET:HG3	1:2D:302:MET:H	1.81	0.45
1:2G:121:ARG:NH1	1:2G:121:ARG:HA	2.32	0.45
2:3A:133:PHE:HB2	2:3A:164:MET:HB3	1.99	0.45
2:3B:248:SER:HA	2:3B:252:LYS:HG2	1.98	0.45
2:3D:113:ILE:HA	2:3D:116:VAL:HG12	1.99	0.45
2:5A:358:PRO:HG2	2:5A:361:LEU:HB3	1.98	0.45
2:5E:239:CYS:SG	2:5E:248:SER:N	2.85	0.45
2:5G:267:LEU:HD21	2:5G:374:ILE:CG2	2.47	0.45
1:2A:265:ILE:HG23	1:2A:432:TYR:HE1	1.82	0.45
1:2D:102:ASN:ND2	1:2D:411:GLU:OE1	2.50	0.45
1:2E:195:LEU:HD22	1:2E:264:ARG:HG3	1.99	0.45
1:2I:88:HIS:HB3	1:2I:91:GLN:HG3	1.99	0.45
2:3B:20:PHE:HA	2:3B:230:SER:OG	2.17	0.45
2:3D:323:THR:O	2:3D:326:VAL:HG12	2.16	0.45
2:3E:67:ASP:OD1	2:3E:68:LEU:N	2.50	0.45
2:3I:10:GLY:HA2	2:3I:143:THR:HG23	1.98	0.45
1:4A:306:ASP:HB3	1:4A:309:HIS:CE1	2.51	0.45
1:4D:35:GLN:OE1	1:4E:282:TYR:CZ	2.70	0.45
1:4G:172:TRP:HB3	1:4G:205:ASP:OD1	2.17	0.45
1:4H:142:GLY:HA2	1:4H:183:GLU:HG2	1.98	0.45
2:5B:7:VAL:HG11	2:5B:151:LEU:HD22	1.99	0.45
2:5B:211:CYS:SG	2:5B:220:PRO:HG3	2.56	0.45
2:5C:368:VAL:HG23	2:5C:368:VAL:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5E:238:CYS:SG	2:5E:318:ARG:NE	2.90	0.45
2:5I:318:ARG:HD3	2:5I:356:ILE:O	2.16	0.45
1:2F:298:PRO:HB3	1:2F:307:PRO:HD2	1.98	0.44
1:2H:269:LEU:HD21	1:2H:384:ILE:HD11	1.97	0.44
1:2H:309:HIS:HE1	1:2H:386:GLU:CD	2.25	0.44
1:2I:195:LEU:HD21	1:2I:264:ARG:HE	1.81	0.44
2:3A:183:TYR:OH	2:3A:388:MET:O	2.30	0.44
2:3B:290:THR:HG22	2:3B:330:MET:HE1	1.98	0.44
2:3C:391:ARG:HD2	1:4C:346:TRP:CD1	2.53	0.44
2:3E:397:TRP:CZ2	1:4E:260:VAL:CG2	2.99	0.44
2:3H:117:LEU:HD13	2:3H:154:LYS:HG2	1.99	0.44
1:4B:183:GLU:HG3	1:4B:184:PRO:HD3	1.99	0.44
1:4C:215:ARG:NH2	1:4C:300:SER:HB2	2.32	0.44
1:4F:269:LEU:HD12	1:4F:384:ILE:HD11	1.98	0.44
1:4H:200:VAL:HG13	1:4H:268:MET:HE3	1.98	0.44
1:4I:88:HIS:HB3	1:4I:91:GLN:HG3	1.99	0.44
2:5D:54:ALA:HB1	2:5E:281:TYR:O	2.16	0.44
1:2A:225:THR:O	1:2A:229:ARG:HG2	2.17	0.44
1:2E:33:ASP:OD1	1:2E:34:GLY:N	2.51	0.44
1:2H:122:ILE:HG21	1:2H:157:LEU:HD11	2.00	0.44
2:3B:68:LEU:HD13	2:3B:143:THR:OG1	2.16	0.44
2:3D:27:GLU:OE1	2:3D:318:ARG:NH2	2.46	0.44
2:3F:113:ILE:HA	2:3F:116:VAL:HG12	2.00	0.44
2:3H:228:LEU:HG	2:3H:300:MET:HE2	1.99	0.44
2:3H:318:ARG:HD3	2:3H:358:PRO:HD3	1.99	0.44
1:4B:210:TYR:CE1	2:5B:324:LYS:HB2	2.53	0.44
1:4D:204:LEU:HD13	1:4D:231:ILE:HD12	1.98	0.44
1:4I:246:GLY:HA2	1:4I:357:TYR:CD1	2.52	0.44
1:4I:250:VAL:HG23	1:4I:254:GLU:HG2	1.99	0.44
2:5B:315:ALA:HB3	2:5B:330:MET:HE1	2.00	0.44
2:5C:290:THR:HA	2:5C:293:MET:HE2	1.98	0.44
2:5D:58:ARG:HH11	2:5E:280:GLN:HB2	1.82	0.44
1:2A:271:SER:HB3	1:2A:377:MET:HB3	2.00	0.44
1:2C:311:LYS:NZ	1:2C:342:GLN:OE1	2.47	0.44
1:2F:259:LEU:HD21	1:2F:316:CYS:HB2	1.99	0.44
1:2I:220:GLU:O	2:3I:324:LYS:HD3	2.17	0.44
2:3B:169:VAL:HG12	2:3B:202:ILE:HB	1.99	0.44
2:3G:334:GLN:HG3	2:3G:341:PHE:CD2	2.53	0.44
2:3H:211:CYS:HA	2:3H:215:LEU:HB2	2.00	0.44
2:3I:165:GLU:HG2	2:3I:198:GLU:HG3	2.00	0.44
1:4B:250:VAL:HA	1:4B:254:GLU:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4D:262:TYR:HB2	1:4D:265:ILE:HD12	2.00	0.44
1:4F:107:HIS:NE2	1:4F:151:CYS:SG	2.90	0.44
2:5A:30:ILE:HD12	2:5A:51:TYR:HE2	1.82	0.44
2:5A:77:ARG:HH22	2:5A:92:PHE:HZ	1.66	0.44
2:5C:87:PRO:CA	2:5D:281:TYR:OH	2.65	0.44
2:5C:169:VAL:HG12	2:5C:202:ILE:HB	1.98	0.44
1:2A:306:ASP:HB3	1:2A:309:HIS:CE1	2.52	0.44
1:2B:338:LYS:HE3	1:2B:338:LYS:HB3	1.91	0.44
1:2C:271:SER:OG	1:2C:377:MET:HB3	2.18	0.44
2:3A:106:TYR:CE1	2:3A:403:MET:HE1	2.52	0.44
2:3D:73:MET:HE1	2:3D:92:PHE:HA	1.99	0.44
2:3E:388:MET:HE3	1:4E:348:PRO:HD2	2.00	0.44
2:3H:257:LEU:HD21	2:3H:314:SER:HB2	2.00	0.44
2:3I:137:HIS:HE1	2:3I:166:THR:HG23	1.82	0.44
1:4A:265:ILE:HG23	1:4A:432:TYR:HE1	1.81	0.44
1:4C:392:ASP:OD1	1:4C:422:ARG:NH1	2.50	0.44
2:5B:139:LEU:HA	2:5B:145:SER:HB2	2.00	0.44
2:5D:267:LEU:HD11	2:5D:374:ILE:CG2	2.47	0.44
2:5F:55:THR:CG2	2:5G:283:ALA:CA	2.90	0.44
2:5H:187:LEU:HD13	2:5H:190:HIS:HE1	1.82	0.44
2:5I:67:ASP:OD1	2:5I:68:LEU:N	2.50	0.44
1:2B:164:LYS:HB3	1:2B:164:LYS:HE3	1.74	0.44
1:2C:221:ARG:HG3	2:3C:325:GLU:OE1	2.18	0.44
1:2F:217:LEU:HD21	1:2F:275:ILE:HG22	1.99	0.44
1:2F:401:LYS:NZ	2:3F:344:TRP:CG	2.83	0.44
1:2I:10:GLY:HA2	1:2I:145:THR:HG23	1.99	0.44
1:2I:339:ARG:NH1	1:2I:342:GLN:OE1	2.51	0.44
2:3A:398:TYR:HB3	2:3A:403:MET:HG3	1.99	0.44
2:3D:257:LEU:HD23	2:3D:312:THR:HG22	1.99	0.44
2:3D:383:ASP:HA	2:3D:386:THR:HG22	2.00	0.44
2:3G:178:THR:HA	1:4G:352:LYS:HD3	2.00	0.44
1:4C:50:ASN:O	1:4C:64:ARG:NH2	2.50	0.44
1:4C:258:ASN:C	1:4C:259:LEU:HD22	2.43	0.44
1:4I:188:VAL:HG23	1:4I:189:LEU:HD12	1.99	0.44
1:4I:408:TYR:HB3	1:4I:413:MET:HE2	1.99	0.44
2:5C:16:ILE:HD11	2:5C:229:VAL:HG11	1.99	0.44
2:5G:53:GLU:OE2	2:5G:54:ALA:N	2.48	0.44
2:5G:325:GLU:HA	2:5G:328:GLU:HG2	1.99	0.44
2:5H:200:GLN:HG3	2:5H:268:ILE:HD11	1.98	0.44
2:5H:267:LEU:HD11	2:5H:374:ILE:HD13	1.98	0.44
2:5I:241:ARG:HH11	2:5I:241:ARG:HD2	1.67	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2D:390:ARG:NH2	1:2D:390:ARG:HB3	2.32	0.44
1:2F:28:HIS:CE1	1:2F:243:ARG:HH11	2.36	0.44
1:2G:154:LEU:HD21	1:2G:198:THR:HB	1.99	0.44
1:2I:241:SER:OG	1:2I:250:VAL:O	2.23	0.44
2:3A:109:GLY:O	2:3A:113:ILE:HG12	2.17	0.44
2:3A:391:ARG:NH2	1:4A:346:TRP:NE1	2.66	0.44
2:3B:95:THR:C	1:4B:2:ARG:HH12	2.24	0.44
2:3F:7:VAL:HB	2:3F:135:ILE:HG12	1.99	0.44
2:3F:137:HIS:HE1	2:3F:166:THR:HB	1.82	0.44
1:4A:175:PRO:HA	1:4A:390:ARG:NE	2.33	0.44
1:4E:269:LEU:HD23	1:4E:303:ALA:HB3	1.98	0.44
1:4G:427:ALA:O	1:4G:430:LYS:HG3	2.17	0.44
1:4H:155:GLU:HG2	1:4H:197:HIS:CD2	2.53	0.44
2:5D:55:THR:OG1	2:5E:283:ALA:CA	2.66	0.44
1:2D:57:GLY:N	1:2E:285:GLN:HB3	2.31	0.44
1:2D:223:THR:OG1	2:3D:245:GLN:OE1	2.34	0.44
1:2E:225:THR:O	1:2E:229:ARG:HG2	2.18	0.44
1:2H:12:ALA:HB3	1:2H:140:ALA:HB2	1.99	0.44
1:2I:100:ALA:O	2:3I:255:VAL:HG11	2.17	0.44
2:3A:208:TYR:CD1	1:4A:326:LYS:HB3	2.52	0.44
2:3G:101:TRP:HZ3	2:3G:403:MET:HE2	1.83	0.44
1:4B:88:HIS:ND1	1:4C:283:HIS:CB	2.80	0.44
1:4D:56:THR:HA	1:4E:285:GLN:CB	2.47	0.44
1:4H:398:MET:HE1	2:5H:345:ILE:HD12	1.98	0.44
2:5D:113:ILE:HA	2:5D:116:VAL:HG12	1.99	0.44
2:5H:211:CYS:HA	2:5H:215:LEU:HB2	2.00	0.44
1:2A:212:ILE:HD11	1:2A:300:SER:HA	1.99	0.44
1:2B:269:LEU:HD23	1:2B:303:ALA:HB3	1.99	0.44
1:2H:222:PRO:HD2	2:3H:324:LYS:HG2	2.00	0.44
2:3H:309:ARG:H	2:3H:372:THR:HG22	1.83	0.44
1:4G:121:ARG:NH1	1:4G:121:ARG:HA	2.33	0.44
2:5D:58:ARG:HD3	2:5E:280:GLN:C	2.41	0.44
2:5D:229:VAL:HG12	2:5D:233:MET:HE3	2.00	0.44
2:5E:383:ASP:HA	2:5E:386:THR:HG22	1.98	0.44
2:5G:1:MET:N	2:5G:128:ASP:OD2	2.41	0.44
2:5I:6:HIS:CD2	2:5I:8:GLN:HG3	2.53	0.44
1:2B:338:LYS:NZ	1:2B:341:ILE:HG12	2.25	0.44
1:2D:204:LEU:HD13	1:2D:231:ILE:HD12	1.99	0.44
1:2F:323:VAL:HG13	1:2F:323:VAL:O	2.18	0.44
1:2I:252:VAL:HG22	1:2I:252:VAL:O	2.18	0.44
1:2I:255:PHE:CE1	1:2I:318:MET:HE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3B:105:HIS:HD2	2:3B:150:LEU:HD22	1.83	0.44
2:3B:139:LEU:HA	2:3B:145:SER:HB2	1.99	0.44
2:3B:156:ARG:HD2	2:3B:156:ARG:HA	1.86	0.44
2:3C:16:ILE:HG22	2:3C:136:THR:HG21	2.00	0.44
2:3E:317:PHE:CD2	2:3E:365:VAL:HG22	2.53	0.44
2:3G:382:SER:HB2	2:3G:415:MET:HE3	1.99	0.44
2:3H:200:GLN:HG3	2:3H:268:ILE:HD11	2.00	0.44
1:4A:9:VAL:HG13	1:4A:149:LEU:HD23	2.00	0.44
1:4E:225:THR:O	1:4E:229:ARG:HG2	2.18	0.44
2:5A:268:ILE:HB	2:5A:300:MET:HE2	1.99	0.44
2:5A:382:SER:HB2	2:5A:415:MET:HE1	2.00	0.44
2:5D:12:CYS:SG	2:5D:138:SER:N	2.91	0.44
2:5G:83:GLN:N	2:5G:83:GLN:OE1	2.51	0.44
1:2F:7:ILE:HG21	1:2F:153:LEU:HD21	2.00	0.43
1:2G:195:LEU:HD21	1:2G:264:ARG:HE	1.83	0.43
1:2G:217:LEU:HD23	1:2G:217:LEU:O	2.18	0.43
2:3B:309:ARG:H	2:3B:372:THR:HG22	1.83	0.43
2:3B:326:VAL:O	2:3B:330:MET:HG2	2.18	0.43
2:3D:178:THR:HA	1:4D:352:LYS:HD3	2.00	0.43
2:3E:325:GLU:HA	2:3E:328:GLU:HG2	1.99	0.43
2:3F:101:TRP:HB3	2:3F:398:TYR:HE1	1.82	0.43
1:4A:60:LYS:HE3	1:4A:60:LYS:HB3	1.90	0.43
1:4G:198:THR:O	1:4G:266:HIS:NE2	2.51	0.43
1:4G:276:ILE:HD12	1:4G:281:ALA:HA	1.99	0.43
1:4H:259:LEU:HD21	1:4H:316:CYS:HB2	2.00	0.43
1:4H:425:LEU:HD23	1:4H:425:LEU:HA	1.87	0.43
1:4I:108:TYR:O	1:4I:112:LYS:NZ	2.50	0.43
1:4I:223:THR:HG22	2:5I:322:SER:HA	2.00	0.43
2:5D:200:GLN:HG2	2:5D:268:ILE:HD11	2.00	0.43
2:5G:5:VAL:HB	2:5G:133:PHE:HD1	1.83	0.43
2:5G:66:MET:HE2	2:5G:116:VAL:HG11	1.99	0.43
1:2G:309:HIS:HE2	1:2G:386:GLU:CD	2.25	0.43
2:3A:105:HIS:CD2	2:3A:150:LEU:HD12	2.51	0.43
2:3D:267:LEU:HD21	2:3D:374:ILE:CG2	2.48	0.43
2:3E:141:GLY:O	2:3E:145:SER:OG	2.29	0.43
2:3E:309:ARG:H	2:3E:372:THR:HG22	1.82	0.43
2:3F:220:PRO:CG	1:4F:326:LYS:HG3	2.44	0.43
2:3F:244:GLY:HA2	2:3F:355:ASP:HB2	2.00	0.43
2:3G:203:ASP:O	2:3G:207:LEU:HD13	2.18	0.43
1:4B:70:LEU:HD23	1:4B:145:THR:OG1	2.18	0.43
1:4B:107:HIS:NE2	1:4B:151:CYS:SG	2.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4F:104:ALA:HB2	1:4F:413:MET:HE3	1.99	0.43
1:2A:292:THR:HG21	1:2A:331:ALA:HB1	2.00	0.43
1:2B:272:TYR:HB3	1:2B:275:ILE:HD11	2.00	0.43
1:2B:309:HIS:NE2	1:2B:386:GLU:OE1	2.40	0.43
1:2C:88:HIS:HD1	1:2C:90:GLU:H	1.65	0.43
1:2E:265:ILE:HD11	1:2E:435:VAL:HG21	1.99	0.43
1:2G:230:LEU:HD23	1:2G:302:MET:HE2	2.00	0.43
2:3A:28:HIS:HB2	2:3A:30:ILE:HD12	2.00	0.43
2:3C:394:PHE:HD1	2:3C:397:TRP:HZ3	1.66	0.43
2:3F:170:PHE:HD1	2:3F:171:PRO:HD2	1.83	0.43
1:4A:338:LYS:HG2	1:4A:340:THR:HG22	2.00	0.43
1:4F:175:PRO:HB3	1:4F:390:ARG:HD3	2.00	0.43
2:5A:293:MET:HE3	2:5A:367:PHE:HB2	2.00	0.43
2:5G:68:LEU:HD13	2:5G:93:GLY:HA3	1.99	0.43
1:2A:214:ARG:HH22	1:2A:220:GLU:HG2	1.83	0.43
1:2B:352:LYS:HD3	1:2B:352:LYS:HA	1.87	0.43
1:2D:402:ARG:HG3	1:2D:405:VAL:CG2	2.48	0.43
1:2F:15:GLN:HE21	1:2F:74:VAL:CG2	2.32	0.43
1:2G:205:ASP:HB2	1:2G:303:ALA:HA	2.01	0.43
2:3F:203:ASP:O	2:3F:207:LEU:HD23	2.18	0.43
2:3F:353:VAL:HG13	2:3F:353:VAL:O	2.19	0.43
2:3G:164:MET:SD	2:3G:196:ALA:HA	2.58	0.43
2:3H:392:LYS:HA	2:3H:395:LEU:HD23	1.99	0.43
1:4D:225:THR:O	1:4D:229:ARG:HG2	2.19	0.43
1:4D:276:ILE:HD12	1:4D:281:ALA:HA	2.01	0.43
1:4H:205:ASP:HB2	1:4H:303:ALA:HA	2.00	0.43
2:5B:420:SER:O	2:5B:424:GLN:HG3	2.19	0.43
2:5D:124:ALA:HB1	2:5D:130:LEU:HD22	2.01	0.43
2:5G:107:THR:OG1	2:5G:401:GLU:OE2	2.29	0.43
1:2C:166:LYS:N	1:2C:199:ASP:OD2	2.48	0.43
1:2C:282:TYR:HB2	1:2C:283:HIS:CD2	2.53	0.43
1:2D:85:HIS:HB3	1:2E:283:HIS:NE2	2.33	0.43
1:2D:133:GLN:NE2	1:2D:251:ASP:OD1	2.52	0.43
2:3B:394:PHE:CE1	1:4B:261:PRO:HB3	2.53	0.43
2:3C:156:ARG:NH1	2:3C:162:ARG:O	2.51	0.43
2:3E:94:GLN:OE1	1:4E:2:ARG:HG3	2.18	0.43
1:4B:223:THR:CG2	1:4B:225:THR:HG22	2.47	0.43
1:4E:391:MET:HE3	1:4E:391:MET:HB2	1.85	0.43
1:4I:183:GLU:HG3	1:4I:184:PRO:HD3	1.99	0.43
2:5D:54:ALA:CA	2:5E:283:ALA:N	2.81	0.43
1:2A:210:TYR:HE2	2:3A:327:ASP:OD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2B:306:ASP:HB3	1:2B:309:HIS:HE1	1.83	0.43
1:2E:203:MET:HE1	1:2E:384:ILE:HG23	2.01	0.43
1:2G:153:LEU:O	1:2G:157:LEU:HD23	2.18	0.43
1:2H:210:TYR:HE1	1:2H:227:LEU:HD11	1.84	0.43
1:2I:269:LEU:CD2	1:2I:384:ILE:HD11	2.47	0.43
2:3D:16:ILE:HG22	2:3D:136:THR:HG21	2.01	0.43
2:3D:176:SER:HB2	1:4D:349:THR:OG1	2.18	0.43
2:3E:68:LEU:HB3	2:3E:96:GLY:HA2	2.01	0.43
2:3G:169:VAL:HG12	2:3G:202:ILE:HB	1.99	0.43
2:3G:207:LEU:HB3	2:3G:225:LEU:CD1	2.48	0.43
2:3G:209:ASP:HA	2:3G:212:PHE:CD2	2.54	0.43
2:3G:293:MET:HE2	2:3G:293:MET:HB2	1.66	0.43
1:4F:7:ILE:HG21	1:4F:153:LEU:HD21	2.00	0.43
1:4G:28:HIS:HE1	1:4G:243:ARG:HD2	1.84	0.43
1:4H:358:GLN:OE1	1:4H:359:PRO:HD2	2.18	0.43
2:5A:117:LEU:HB3	2:5A:121:ARG:HH22	1.83	0.43
2:5B:341:PHE:HZ	2:5B:349:MET:HE1	1.82	0.43
2:5C:293:MET:HG3	2:5C:367:PHE:HB2	2.01	0.43
2:5D:58:ARG:HD3	2:5E:280:GLN:O	2.01	0.43
2:5G:165:GLU:HG3	2:5G:198:GLU:HG3	1.99	0.43
1:2D:181:VAL:H	2:3D:256:ASN:HD22	1.67	0.43
1:2F:98:ASP:OD1	1:2F:99:ALA:N	2.52	0.43
1:2F:164:LYS:O	1:2F:166:LYS:NZ	2.51	0.43
2:3A:229:VAL:HG12	2:3A:233:MET:HE2	2.00	0.43
2:3E:165:GLU:HG3	2:3E:198:GLU:HG3	2.00	0.43
2:3E:238:CYS:SG	2:3E:318:ARG:NE	2.92	0.43
1:4C:224:TYR:HD1	1:4C:227:LEU:HD12	1.84	0.43
1:4E:181:VAL:HG21	2:5E:256:ASN:O	2.18	0.43
1:4E:258:ASN:CG	1:4E:352:LYS:HD3	2.44	0.43
2:5A:237:THR:O	2:5A:241:ARG:NH1	2.51	0.43
2:5C:141:GLY:O	2:5C:145:SER:OG	2.32	0.43
2:5C:257:LEU:HD11	2:5C:368:VAL:CG2	2.48	0.43
2:5G:100:ASN:HB3	2:5G:103:LYS:HG2	1.99	0.43
2:5H:69:GLU:HG2	2:5H:71:GLY:H	1.83	0.43
2:5H:274:THR:OG1	2:5H:279:GLN:OE1	2.32	0.43
1:2E:203:MET:HE2	1:2E:267:PHE:HB3	2.00	0.43
1:2I:77:GLU:OE1	2:3I:243:PRO:HB3	2.18	0.43
1:4A:223:THR:O	1:4A:227:LEU:HD23	2.18	0.43
1:4F:210:TYR:CG	2:5F:324:LYS:HD2	2.54	0.43
1:4G:168:ASN:ND2	1:4G:194:LEU:HD11	2.20	0.43
1:4H:105:ARG:HH21	1:4H:110:ILE:HG21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4H:141:VAL:HG21	1:4H:172:TRP:CZ3	2.53	0.43
2:5F:10:GLY:O	2:5F:14:ASN:ND2	2.51	0.43
2:5G:295:ASP:HB3	2:5G:298:ASN:HB2	2.01	0.43
2:5H:318:ARG:HD3	2:5H:358:PRO:HD3	1.99	0.43
1:2A:88:HIS:HB3	1:2A:91:GLN:NE2	2.33	0.43
1:2C:183:GLU:HG3	1:2C:184:PRO:HD3	2.01	0.43
1:2F:241:SER:OG	1:2F:250:VAL:O	2.22	0.43
1:2H:225:THR:O	1:2H:229:ARG:HG2	2.18	0.43
1:2H:259:LEU:HD21	1:2H:316:CYS:HB2	2.01	0.43
2:3F:330:MET:CB	2:3F:349:MET:SD	3.04	0.43
2:3I:169:VAL:HG12	2:3I:202:ILE:HB	2.01	0.43
1:4F:370:LYS:O	1:4F:370:LYS:HG3	2.18	0.43
1:4I:301:MET:HE1	1:4I:377:MET:CE	2.49	0.43
2:5A:65:LEU:HB3	2:5A:73:MET:HE3	2.00	0.43
2:5A:67:ASP:OD1	2:5A:68:LEU:N	2.48	0.43
2:5C:284:LEU:HD23	2:5C:363:MET:HE2	2.00	0.43
2:5D:176:SER:OG	2:5D:181:GLU:HG3	2.19	0.43
2:5G:66:MET:HE3	2:5G:151:LEU:CD1	2.49	0.43
1:2C:98:ASP:OD1	1:2C:99:ALA:N	2.52	0.43
1:2D:119:LEU:HA	1:2D:122:ILE:HG22	2.01	0.43
1:2I:269:LEU:HD21	1:2I:384:ILE:CD1	2.49	0.43
2:3A:139:LEU:HD23	2:3A:139:LEU:HA	1.87	0.43
2:3C:20:PHE:HA	2:3C:230:SER:OG	2.19	0.43
2:3E:101:TRP:CE3	2:3E:403:MET:HE1	2.54	0.43
2:3G:151:LEU:HD12	2:3G:151:LEU:HA	1.90	0.43
1:4B:181:VAL:N	2:5B:350:LYS:HZ2	2.17	0.43
1:4G:177:VAL:HB	1:4G:207:GLU:HB3	2.01	0.43
1:4G:178:SER:HG	2:5G:347:ASN:ND2	2.04	0.43
1:4G:251:ASP:N	1:4G:254:GLU:OE2	2.40	0.43
1:4G:298:PRO:O	1:4G:301:MET:SD	2.77	0.43
2:5E:139:LEU:HD12	2:5E:170:PHE:HE1	1.83	0.43
2:5F:268:ILE:HG23	2:5F:300:MET:HB2	2.01	0.43
1:2D:11:GLN:NE2	1:2D:15:GLN:OE1	2.44	0.42
1:2D:398:MET:HE1	2:3D:345:ILE:HG23	2.00	0.42
1:2G:222:PRO:HD2	2:3G:324:LYS:HB3	2.01	0.42
1:2I:239:THR:OG1	1:2I:243:ARG:NH1	2.52	0.42
2:3C:103:LYS:HG2	2:3C:108:GLU:HG2	2.01	0.42
2:3D:377:MET:HB2	2:3D:377:MET:HE3	1.82	0.42
2:3E:58:ARG:HD2	2:3F:281:TYR:CD1	2.52	0.42
2:3E:350:LYS:NZ	2:3E:352:SER:OG	2.52	0.42
2:3G:68:LEU:HD12	2:3G:97:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3G:320:ARG:NH1	2:3G:320:ARG:HB2	2.34	0.42
2:5C:295:ASP:OD2	2:5C:297:LYS:HG2	2.19	0.42
2:5D:150:LEU:HD23	2:5D:154:LYS:HD2	2.01	0.42
2:5E:318:ARG:HB3	2:5E:357:PRO:HA	2.00	0.42
2:5F:192:LEU:HD21	2:5F:199:VAL:HG11	2.01	0.42
2:5G:10:GLY:HA2	2:5G:143:THR:OG1	2.19	0.42
1:2A:76:ASP:OD2	2:3A:46:ARG:NH1	2.52	0.42
1:2D:222:PRO:HD2	2:3D:324:LYS:HE3	2.01	0.42
1:2F:306:ASP:HB3	1:2F:309:HIS:CE1	2.54	0.42
1:2H:109:THR:OG1	1:2H:110:ILE:N	2.52	0.42
1:2I:250:VAL:CG1	1:2I:318:MET:HE1	2.49	0.42
2:3B:179:VAL:N	1:4B:352:LYS:HZ3	2.16	0.42
2:3D:117:LEU:HA	2:3D:120:VAL:HG12	1.99	0.42
2:3F:19:LYS:HA	2:3F:22:GLU:OE1	2.19	0.42
2:3H:149:THR:O	2:3H:191:GLN:NE2	2.52	0.42
1:4G:26:LEU:HD21	1:4G:363:VAL:HG12	2.00	0.42
2:5B:68:LEU:HD23	2:5B:112:LEU:HD13	2.01	0.42
2:5F:55:THR:HG23	2:5G:283:ALA:CA	2.48	0.42
1:2A:96:LYS:CG	2:3A:129:CYS:SG	3.07	0.42
1:2B:224:TYR:HA	1:2B:227:LEU:HD23	2.02	0.42
1:2D:298:PRO:HG2	1:2D:308:ARG:HH11	1.84	0.42
1:2E:97:GLU:OE2	2:3E:162:ARG:NH1	2.51	0.42
1:2H:31:GLN:HG2	1:2H:35:GLN:O	2.19	0.42
2:3B:105:HIS:CD2	2:3B:150:LEU:HB2	2.53	0.42
2:3D:69:GLU:OE2	2:3D:96:GLY:HA3	2.19	0.42
2:3F:320:ARG:HD2	2:3F:320:ARG:HA	1.79	0.42
1:4A:26:LEU:HD21	1:4A:363:VAL:HG12	2.00	0.42
1:4B:181:VAL:N	2:5B:350:LYS:HE3	2.29	0.42
1:4F:98:ASP:OD1	1:4F:99:ALA:N	2.52	0.42
1:4G:121:ARG:HH11	1:4G:121:ARG:HD2	1.69	0.42
2:5B:87:PRO:CD	2:5C:281:TYR:HE2	2.25	0.42
2:5F:140:GLY:O	2:5F:184:ASN:ND2	2.49	0.42
2:5F:309:ARG:H	2:5F:372:THR:HG22	1.84	0.42
2:5H:113:ILE:HA	2:5H:116:VAL:HG12	2.01	0.42
2:5I:13:GLY:HA2	2:5I:136:THR:HG22	2.01	0.42
2:5I:246:LEU:HA	2:5I:246:LEU:HD12	1.81	0.42
1:2A:296:PHE:CZ	1:2A:317:LEU:HD21	2.55	0.42
1:2B:10:GLY:HA2	1:2B:145:THR:HG23	2.01	0.42
1:2B:221:ARG:CZ	2:3B:322:SER:OG	2.67	0.42
1:2B:404:PHE:HZ	2:3B:312:THR:HG21	1.85	0.42
1:2C:65:CYS:SG	1:2C:66:VAL:N	2.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2D:60:LYS:HE2	1:2E:283:HIS:CD2	2.45	0.42
1:2D:178:SER:CB	2:3D:347:ASN:ND2	2.82	0.42
1:2D:259:LEU:HD21	1:2D:316:CYS:HB2	2.01	0.42
1:2F:154:LEU:HB3	1:2F:197:HIS:HB3	2.01	0.42
1:2G:401:LYS:HE3	2:3G:344:TRP:CE2	2.54	0.42
1:2I:52:PHE:CD2	1:2I:243:ARG:HD3	2.54	0.42
2:3B:206:ALA:HB2	2:3B:302:ALA:HB2	2.00	0.42
2:3C:131:GLN:OE1	2:3C:163:ILE:HD11	2.20	0.42
2:3D:8:GLN:NE2	2:3D:65:LEU:HD22	2.34	0.42
2:3D:55:THR:HG1	2:3E:283:ALA:HA	1.80	0.42
2:3E:155:VAL:HG13	2:3E:164:MET:CE	2.50	0.42
2:3H:372:THR:HA	2:3H:422:TYR:CD2	2.54	0.42
1:4C:302:MET:HE2	1:4C:302:MET:HB2	1.92	0.42
1:4D:2:ARG:HG3	1:4D:51:THR:HG22	2.00	0.42
1:4D:33:ASP:CG	1:4E:282:TYR:CE2	2.95	0.42
1:4E:294:SER:O	1:4E:297:GLU:HG2	2.19	0.42
1:4F:145:THR:O	1:4F:149:LEU:HB2	2.20	0.42
1:4G:14:ILE:HD12	1:4G:67:PHE:CD1	2.55	0.42
1:4H:100:ALA:O	2:5H:255:VAL:HG11	2.20	0.42
2:5A:404:ASP:HB3	2:5A:406:MET:HG3	2.01	0.42
2:5F:7:VAL:HB	2:5F:135:ILE:HG12	2.02	0.42
2:5I:8:GLN:O	2:5I:66:MET:HB2	2.19	0.42
1:2B:71:GLU:HB3	1:2B:98:ASP:HB2	2.02	0.42
1:2B:256:GLN:HE21	1:2B:256:GLN:N	2.17	0.42
1:2G:60:LYS:HD2	1:2H:283:HIS:CD2	2.52	0.42
1:2G:313:MET:HE3	1:2G:380:ASN:HB3	2.02	0.42
2:3I:179:VAL:HG22	1:4I:258:ASN:OD1	2.19	0.42
1:4G:79:ARG:NH1	1:4G:92:LEU:O	2.53	0.42
1:4G:100:ALA:HA	2:5G:252:LYS:HB3	2.00	0.42
1:4H:35:GLN:OE1	1:4H:35:GLN:N	2.53	0.42
2:5G:200:GLN:HB3	2:5G:266:PHE:HB2	2.02	0.42
1:2B:109:THR:HG23	1:2B:411:GLU:OE1	2.20	0.42
1:2D:81:GLY:O	1:2D:84:ARG:HG3	2.19	0.42
1:2H:269:LEU:HD21	1:2H:384:ILE:CD1	2.49	0.42
2:3A:55:THR:OG1	2:3B:282:ARG:C	2.63	0.42
2:3G:135:ILE:CD1	2:3G:152:ILE:HD11	2.45	0.42
2:3H:25:SER:HB2	2:3H:30:ILE:HG22	2.01	0.42
2:3H:391:ARG:NH2	1:4H:437:ILE:O	2.52	0.42
1:4B:213:CYS:SG	1:4B:222:PRO:HG3	2.60	0.42
1:4C:406:HIS:HA	1:4C:409:VAL:HG12	2.01	0.42
1:4D:393:HIS:O	1:4D:397:LEU:HD13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4E:60:LYS:HD3	1:4F:283:HIS:HA	2.01	0.42
1:4H:377:MET:SD	1:4H:379:SER:OG	2.69	0.42
1:4I:107:HIS:CE1	1:4I:151:CYS:HB3	2.55	0.42
2:5D:267:LEU:HB3	2:5D:299:MET:CE	2.46	0.42
2:5E:64:ILE:HD11	2:5E:123:GLU:HG3	2.01	0.42
2:5G:19:LYS:HD2	2:5G:227:HIS:ND1	2.35	0.42
2:5G:135:ILE:CD1	2:5G:152:ILE:HG12	2.49	0.42
2:5I:16:ILE:CG2	2:5I:136:THR:HG21	2.49	0.42
1:2C:386:GLU:OE1	1:2C:390:ARG:NH1	2.53	0.42
1:2E:338:LYS:HG2	1:2E:340:THR:HG22	2.02	0.42
1:2I:152:LEU:O	1:2I:155:GLU:HG3	2.18	0.42
2:3E:180:VAL:O	2:3E:184:ASN:ND2	2.52	0.42
2:3E:383:ASP:HA	2:3E:386:THR:HG22	2.00	0.42
1:4C:185:TYR:CZ	1:4C:398:MET:HE3	2.55	0.42
1:4C:209:ILE:CD1	1:4C:302:MET:HG3	2.47	0.42
1:4E:326:LYS:NZ	1:4E:327:ASP:OD1	2.40	0.42
1:4G:114:ILE:HD12	1:4G:114:ILE:HA	1.92	0.42
2:5H:309:ARG:H	2:5H:372:THR:HG22	1.85	0.42
1:2A:100:ALA:O	2:3A:255:VAL:HG11	2.20	0.42
1:2A:301:MET:HE2	1:2A:301:MET:HB3	1.87	0.42
1:2E:172:TRP:NE1	1:2E:391:MET:SD	2.90	0.42
1:2E:189:LEU:HD21	1:2E:413:MET:HE1	2.00	0.42
1:2F:153:LEU:O	1:2F:157:LEU:HD23	2.20	0.42
2:3D:326:VAL:O	2:3D:330:MET:HG2	2.20	0.42
2:3E:282:ARG:NH2	2:3E:292:GLN:OE1	2.48	0.42
2:3F:311:LEU:HD12	2:3F:342:VAL:HG11	2.01	0.42
1:4F:298:PRO:HB3	1:4F:307:PRO:HD2	2.02	0.42
1:4G:177:VAL:HG13	2:5G:327:ASP:CB	2.49	0.42
1:4H:414:GLU:HG2	1:4H:417:GLU:OE2	2.20	0.42
2:5A:7:VAL:HG11	2:5A:151:LEU:HD23	2.01	0.42
2:5A:249:ASP:H	2:5A:252:LYS:HB3	1.85	0.42
2:5B:309:ARG:NH2	2:5B:343:GLU:OE2	2.53	0.42
2:5E:385:PHE:HE2	2:5E:412:GLU:HB2	1.84	0.42
2:5F:407:GLU:HA	2:5F:410:GLU:HG3	2.02	0.42
2:5G:6:HIS:CD2	2:5G:134:GLN:HG3	2.55	0.42
1:2D:98:ASP:OD1	1:2D:99:ALA:N	2.52	0.42
1:2H:121:ARG:HD2	1:2H:121:ARG:HA	1.75	0.42
1:2H:176:GLN:O	2:3H:347:ASN:ND2	2.53	0.42
1:2I:408:TYR:HB3	1:2I:413:MET:HE2	2.01	0.42
2:3A:66:MET:HE3	2:3A:66:MET:HB3	1.98	0.42
2:3A:135:ILE:HB	2:3A:166:THR:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3C:211:CYS:HB3	2:3C:220:PRO:HG3	2.02	0.42
2:3D:267:LEU:HD21	2:3D:374:ILE:HG22	2.02	0.42
2:3F:54:ALA:O	2:3G:280:GLN:O	2.38	0.42
2:3F:236:VAL:HG13	2:3F:237:THR:HG23	2.02	0.42
2:3H:16:ILE:HG22	2:3H:136:THR:HG21	2.01	0.42
2:3H:130:LEU:HD11	2:3H:133:PHE:HE1	1.85	0.42
2:3H:295:ASP:HB3	2:3H:297:LYS:HG2	2.01	0.42
2:3H:330:MET:HB3	2:3H:349:MET:HG2	2.02	0.42
1:4B:64:ARG:HB3	1:4B:125:LEU:HD21	2.02	0.42
1:4D:388:PHE:HD1	1:4D:391:MET:HE2	1.84	0.42
1:4I:81:GLY:O	1:4I:84:ARG:HG3	2.19	0.42
2:5B:67:ASP:OD1	2:5B:68:LEU:N	2.50	0.42
2:5C:10:GLY:HA2	2:5C:143:THR:HG23	2.02	0.42
2:5D:2:ARG:HD3	2:5D:240:LEU:HD22	2.02	0.42
2:5E:237:THR:HG22	2:5E:250:LEU:HD21	2.02	0.42
2:5F:27:GLU:OE1	2:5F:318:ARG:NH2	2.47	0.42
2:5G:167:PHE:HZ	2:5G:236:VAL:HG11	1.85	0.42
2:5I:5:VAL:HB	2:5I:133:PHE:HD1	1.85	0.42
1:2A:269:LEU:CD2	1:2A:384:ILE:HD11	2.50	0.42
1:2A:323:VAL:CG1	1:2A:355:ILE:HG23	2.50	0.42
1:2F:189:LEU:HD11	1:2F:418:PHE:CD1	2.55	0.42
2:3C:77:ARG:HH22	2:3C:92:PHE:HZ	1.67	0.42
2:3D:112:LEU:HD12	2:3D:112:LEU:HA	1.92	0.42
2:3E:73:MET:HG2	2:3E:90:PHE:HD2	1.85	0.42
2:3G:186:THR:O	2:3G:189:VAL:HG12	2.20	0.42
1:4E:276:ILE:HD12	1:4E:281:ALA:HA	2.02	0.42
2:5D:139:LEU:HD12	2:5D:170:PHE:CE1	2.55	0.42
2:5E:68:LEU:HD12	2:5E:143:THR:HG22	2.02	0.42
2:5E:73:MET:HE3	2:5E:92:PHE:CD1	2.55	0.42
2:5E:172:SER:HB3	2:5E:205:GLU:HG2	2.02	0.42
2:5G:55:THR:CG2	2:5H:283:ALA:CB	2.98	0.42
2:5G:138:SER:HA	2:5G:169:VAL:HG22	2.01	0.42
1:2E:6:SER:OG	1:2E:8:HIS:NE2	2.52	0.41
1:2E:81:GLY:O	1:2E:84:ARG:HG3	2.20	0.41
1:2E:145:THR:O	1:2E:149:LEU:HB2	2.20	0.41
1:2F:403:ALA:HB2	2:3F:344:TRP:HZ3	1.84	0.41
2:3B:303:SER:HB3	2:3B:377:MET:HE3	2.02	0.41
2:3C:388:MET:HG2	1:4C:346:TRP:O	2.19	0.41
2:3C:397:TRP:CZ2	1:4C:260:VAL:HB	2.54	0.41
2:3F:189:VAL:HG11	2:3F:415:MET:SD	2.60	0.41
2:3G:113:ILE:HA	2:3G:116:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3H:25:SER:HA	2:3H:30:ILE:HG22	2.00	0.41
1:4A:231:ILE:O	1:4A:235:ILE:HG12	2.20	0.41
1:4C:124:LYS:HD2	1:4D:283:HIS:NE2	2.35	0.41
1:4E:75:VAL:HG11	1:4E:94:SER:HB3	2.01	0.41
1:4F:181:VAL:HG22	2:5F:347:ASN:O	2.20	0.41
1:4G:231:ILE:O	1:4G:235:ILE:HG12	2.20	0.41
1:4H:210:TYR:CZ	2:5H:324:LYS:HG2	2.55	0.41
1:4H:260:VAL:O	1:4H:260:VAL:HG23	2.19	0.41
2:5A:215:LEU:HB3	2:5A:217:LEU:HD23	2.02	0.41
2:5A:292:GLN:O	2:5A:298:ASN:ND2	2.41	0.41
2:5G:228:LEU:CD1	2:5G:300:MET:HE2	2.49	0.41
2:5I:113:ILE:HD12	2:5I:113:ILE:HA	1.91	0.41
2:5I:192:LEU:HD21	2:5I:199:VAL:HG21	2.02	0.41
1:2A:274:PRO:HG3	1:2A:286:LEU:HD13	2.01	0.41
1:2G:399:TYR:OH	1:2G:415:GLU:OE2	2.37	0.41
2:3A:208:TYR:HE2	1:4A:329:ASN:ND2	2.17	0.41
2:3B:290:THR:HA	2:3B:293:MET:HE3	2.02	0.41
2:3C:259:PRO:HD2	2:3C:263:LEU:HD11	2.03	0.41
2:3G:293:MET:HE1	2:3G:365:VAL:HG21	2.02	0.41
2:3H:268:ILE:CD1	2:3H:368:VAL:HG12	2.50	0.41
2:3I:139:LEU:HD23	2:3I:139:LEU:HA	1.86	0.41
1:4A:224:TYR:CD2	2:5A:323:THR:HG21	2.55	0.41
1:4A:427:ALA:O	1:4A:430:LYS:HG3	2.19	0.41
1:4B:328:VAL:HG12	1:4B:353:CYS:SG	2.60	0.41
1:4G:103:PHE:HB3	1:4G:189:LEU:HD23	2.02	0.41
1:4G:212:ILE:HD13	1:4G:215:ARG:HH22	1.85	0.41
2:5B:130:LEU:HD23	2:5B:130:LEU:H	1.85	0.41
2:5D:272:PRO:HB2	2:5D:282:ARG:HH22	1.85	0.41
2:5E:330:MET:HG2	2:5E:349:MET:HE2	2.01	0.41
2:5F:375:GLN:HG3	2:5F:419:VAL:HG13	2.02	0.41
2:5G:67:ASP:HB3	2:5G:73:MET:HE1	2.02	0.41
2:5I:19:LYS:HA	2:5I:22:GLU:HG2	2.02	0.41
2:3D:238:CYS:SG	2:3D:318:ARG:NE	2.94	0.41
2:3E:239:CYS:SG	2:3E:248:SER:N	2.85	0.41
2:3I:156:ARG:HG3	2:3I:195:ASN:O	2.20	0.41
2:3I:293:MET:HE3	2:3I:367:PHE:HB2	2.01	0.41
1:4A:10:GLY:O	1:4A:14:ILE:HG12	2.20	0.41
1:4C:183:GLU:HG3	1:4C:184:PRO:HD3	2.02	0.41
1:4E:269:LEU:HD11	1:4E:384:ILE:HD11	2.02	0.41
1:4H:36:MET:HE3	1:4H:61:HIS:NE2	2.36	0.41
1:4H:70:LEU:HD12	1:4H:99:ALA:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4I:98:ASP:OD1	1:4I:99:ALA:N	2.52	0.41
1:4I:265:ILE:HG21	1:4I:313:MET:CE	2.50	0.41
1:4I:265:ILE:HG22	1:4I:380:ASN:HD21	1.85	0.41
2:5D:238:CYS:SG	2:5D:318:ARG:NE	2.94	0.41
1:2A:65:CYS:SG	1:2A:66:VAL:N	2.93	0.41
1:2A:91:GLN:OE1	1:2A:91:GLN:N	2.53	0.41
1:2D:56:THR:CA	1:2E:285:GLN:H	2.28	0.41
1:2D:183:GLU:HG3	1:2D:184:PRO:HD3	2.03	0.41
1:2H:54:SER:OG	1:2H:55:GLU:N	2.53	0.41
2:3C:113:ILE:HA	2:3C:116:VAL:HG12	2.03	0.41
2:3E:16:ILE:HD11	2:3E:229:VAL:HG11	2.02	0.41
2:3E:101:TRP:HE3	2:3E:403:MET:HE1	1.85	0.41
2:3G:388:MET:HE2	1:4G:348:PRO:HD2	2.03	0.41
2:3H:99:ASN:ND2	1:4H:254:GLU:CD	2.52	0.41
2:3I:8:GLN:HG2	2:3I:14:ASN:HA	2.03	0.41
1:4A:230:LEU:HD21	1:4A:368:LEU:HD21	2.02	0.41
1:4A:259:LEU:HD21	1:4A:316:CYS:HB2	2.02	0.41
1:4D:56:THR:HA	1:4E:285:GLN:HB3	2.02	0.41
1:4H:173:PRO:O	1:4H:390:ARG:NH1	2.50	0.41
1:4I:133:GLN:HG3	1:4I:252:VAL:HB	2.01	0.41
2:5B:323:THR:HA	2:5B:326:VAL:HG12	2.02	0.41
2:5E:4:ILE:HD11	2:5E:240:LEU:HD13	2.03	0.41
1:2E:11:GLN:HE21	1:2E:15:GLN:NE2	2.19	0.41
1:2E:259:LEU:HD21	1:2E:316:CYS:HB2	2.02	0.41
1:2G:60:LYS:NZ	1:2H:283:HIS:HD2	2.05	0.41
1:2G:132:LEU:HB3	1:2G:164:LYS:NZ	2.35	0.41
1:2I:34:GLY:HA3	1:2I:60:LYS:NZ	2.35	0.41
2:3B:117:LEU:HA	2:3B:120:VAL:HG12	2.02	0.41
2:3B:163:ILE:HD13	2:3B:250:LEU:HB3	2.03	0.41
2:3F:53:GLU:OE2	2:3F:54:ALA:N	2.46	0.41
2:3F:245:GLN:HB2	2:3F:353:VAL:CG1	2.51	0.41
2:3I:141:GLY:O	2:3I:145:SER:OG	2.32	0.41
2:3I:294:PHE:HZ	2:3I:349:MET:HE1	1.85	0.41
1:4A:218:ASP:OD2	1:4A:280:LYS:NZ	2.42	0.41
1:4I:306:ASP:OD2	1:4I:308:ARG:NH2	2.52	0.41
2:5B:107:THR:HG21	2:5B:401:GLU:OE2	2.20	0.41
2:5C:7:VAL:HG11	2:5C:151:LEU:HD23	2.02	0.41
2:5E:363:MET:HE3	2:5E:363:MET:HB2	1.97	0.41
2:5F:68:LEU:HD13	2:5F:108:GLU:OE2	2.21	0.41
2:5H:73:MET:HB3	2:5H:77:ARG:NH2	2.35	0.41
2:5H:119:VAL:O	2:5H:122:LYS:HG3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5I:200:GLN:HB2	2:5I:268:ILE:HD11	2.02	0.41
1:2D:96:LYS:CE	2:3D:129:CYS:HB2	2.49	0.41
1:2G:301:MET:HE2	1:2G:301:MET:HB2	1.87	0.41
2:3B:178:THR:HA	1:4B:352:LYS:HZ3	1.68	0.41
2:3H:391:ARG:HD2	1:4H:346:TRP:CG	2.56	0.41
1:4F:370:LYS:NZ	1:4F:372:MET:HE1	2.36	0.41
1:4G:154:LEU:HG	1:4G:197:HIS:HB3	2.01	0.41
1:4H:432:TYR:O	1:4H:436:GLY:N	2.52	0.41
1:4I:224:TYR:HB2	2:5I:245:GLN:NE2	2.36	0.41
2:5I:5:VAL:HB	2:5I:133:PHE:CD1	2.55	0.41
1:2B:401:LYS:HE2	2:3B:344:TRP:CE2	2.55	0.41
1:2D:276:ILE:HD12	1:2D:281:ALA:HA	2.03	0.41
1:2F:15:GLN:HE21	1:2F:74:VAL:HG23	1.86	0.41
1:2G:135:PHE:HB2	1:2G:166:LYS:HA	2.02	0.41
2:3B:67:ASP:OD1	2:3B:68:LEU:N	2.54	0.41
2:3B:228:LEU:HG	2:3B:300:MET:HE2	2.02	0.41
2:3C:13:GLY:HA2	2:3C:136:THR:HG22	2.03	0.41
2:3I:16:ILE:CG2	2:3I:136:THR:HG21	2.50	0.41
2:3I:137:HIS:CE1	2:3I:166:THR:HG23	2.55	0.41
2:3I:267:LEU:HB3	2:3I:299:MET:HE2	2.03	0.41
1:4E:66:VAL:HG21	1:4E:122:ILE:HD11	2.03	0.41
1:4F:180:ALA:HB3	1:4F:183:GLU:CD	2.45	0.41
1:4G:71:GLU:HB3	1:4G:98:ASP:HB3	2.03	0.41
1:4G:168:ASN:HB2	1:4G:201:ALA:HA	2.03	0.41
1:4H:270:SER:O	1:4H:301:MET:HE3	2.19	0.41
2:5A:386:THR:HG23	2:5A:412:GLU:OE2	2.21	0.41
2:5G:65:LEU:CD1	2:5G:76:VAL:HG11	2.51	0.41
2:5G:133:PHE:HB2	2:5G:164:MET:HB3	2.02	0.41
1:2G:114:ILE:HD12	1:2G:114:ILE:HA	1.88	0.41
1:2G:191:THR:HB	1:2G:425:LEU:HD21	2.03	0.41
1:2H:60:LYS:HE2	1:2H:60:LYS:HB2	1.90	0.41
2:3D:139:LEU:HA	2:3D:145:SER:HB2	2.02	0.41
2:3E:6:HIS:HE2	2:3E:136:THR:HG23	1.86	0.41
2:3E:191:GLN:HA	2:3E:194:GLU:HG2	2.02	0.41
2:3E:385:PHE:HE2	2:3E:412:GLU:HB2	1.85	0.41
2:3F:388:MET:HG2	1:4F:346:TRP:O	2.20	0.41
2:3G:391:ARG:NE	2:3G:391:ARG:HA	2.35	0.41
2:3H:113:ILE:HA	2:3H:113:ILE:HD13	1.96	0.41
1:4A:152:LEU:HD11	1:4A:156:ARG:HH11	1.84	0.41
1:4D:269:LEU:HD21	1:4D:384:ILE:CD1	2.50	0.41
1:4F:36:MET:SD	1:4F:61:HIS:NE2	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4F:168:ASN:C	1:4F:169:PHE:HD1	2.29	0.41
1:4G:230:LEU:HD11	1:4G:275:ILE:HD13	2.02	0.41
2:5A:209:ASP:OD1	2:5A:213:ARG:NH1	2.54	0.41
2:5D:272:PRO:HB2	2:5D:282:ARG:NH2	2.35	0.41
2:5E:92:PHE:O	2:5E:112:LEU:HD11	2.21	0.41
2:5G:54:ALA:O	2:5H:281:TYR:C	2.64	0.41
2:5I:156:ARG:HG3	2:5I:195:ASN:O	2.20	0.41
1:2A:193:SER:O	1:2A:197:HIS:ND1	2.52	0.41
1:2B:177:VAL:HG13	2:3B:327:ASP:CG	2.46	0.41
1:2B:221:ARG:HH12	2:3B:324:LYS:N	2.19	0.41
1:2B:241:SER:OG	1:2B:250:VAL:O	2.23	0.41
1:2D:12:ALA:HB3	1:2D:140:ALA:HB2	2.01	0.41
1:2D:76:ASP:HA	1:2D:79:ARG:HG2	2.03	0.41
1:2F:7:ILE:HD13	1:2F:153:LEU:HD21	2.02	0.41
1:2F:50:ASN:O	1:2F:64:ARG:NH2	2.46	0.41
1:2G:231:ILE:O	1:2G:235:ILE:HG12	2.21	0.41
1:2G:306:ASP:HB3	1:2G:309:HIS:CE1	2.56	0.41
1:2H:176:GLN:O	2:3H:331:LEU:HD21	2.21	0.41
1:2I:77:GLU:OE1	2:3I:243:PRO:CB	2.69	0.41
2:3A:309:ARG:H	2:3A:372:THR:HG22	1.85	0.41
2:3B:178:THR:N	1:4B:352:LYS:HZ3	2.19	0.41
2:3E:7:VAL:HG11	2:3E:151:LEU:HD23	2.03	0.41
2:3F:18:ALA:O	2:3F:22:GLU:OE1	2.39	0.41
2:3G:265:PHE:HE2	2:3G:418:LEU:HD21	1.86	0.41
2:3H:121:ARG:NH2	2:3H:158:GLU:OE1	2.54	0.41
1:4B:259:LEU:HD11	1:4B:316:CYS:SG	2.61	0.41
1:4E:28:HIS:CE1	1:4E:243:ARG:HD2	2.56	0.41
1:4F:238:LEU:HD12	1:4F:318:MET:HE3	2.03	0.41
1:4H:107:HIS:NE2	1:4H:151:CYS:SG	2.83	0.41
1:4H:258:ASN:OD1	1:4H:258:ASN:C	2.64	0.41
2:5A:47:ILE:HD12	2:5A:47:ILE:HA	1.97	0.41
2:5A:263:LEU:H	2:5A:263:LEU:HD23	1.86	0.41
2:5A:374:ILE:O	2:5A:374:ILE:CG2	2.67	0.41
2:5B:349:MET:HE2	2:5B:349:MET:HB2	1.83	0.41
1:2A:296:PHE:CE2	1:2A:335:ILE:HG21	2.56	0.41
1:2B:60:LYS:CE	1:2C:282:TYR:HD2	2.30	0.41
1:2F:189:LEU:HD21	1:2F:413:MET:HE1	2.03	0.41
1:2G:211:ASP:HA	1:2G:214:ARG:HG2	2.03	0.41
1:2H:231:ILE:HD13	1:2H:231:ILE:HA	1.89	0.41
2:3D:19:LYS:HD2	2:3D:19:LYS:HA	1.89	0.41
2:3F:65:LEU:HB3	2:3F:73:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3F:397:TRP:HZ2	1:4F:260:VAL:HB	1.86	0.41
2:3G:334:GLN:HG3	2:3G:341:PHE:HD2	1.86	0.41
1:4A:90:GLU:O	1:4A:93:ILE:HD11	2.20	0.41
1:4A:274:PRO:HG3	1:4A:286:LEU:HD13	2.02	0.41
1:4B:102:ASN:HB3	1:4B:105:ARG:HB2	2.02	0.41
1:4D:251:ASP:H	1:4D:254:GLU:HG3	1.85	0.41
1:4D:301:MET:HE3	1:4D:307:PRO:HG3	2.03	0.41
1:4F:76:ASP:O	1:4F:79:ARG:HG2	2.20	0.41
1:4H:180:ALA:HB3	1:4H:183:GLU:HB2	2.02	0.41
2:5B:66:MET:CG	2:5B:116:VAL:HG21	2.51	0.41
2:5B:289:LEU:HD12	2:5B:365:VAL:HG12	2.02	0.41
2:5F:169:VAL:HG12	2:5F:202:ILE:HB	2.03	0.41
2:5F:270:PHE:O	2:5F:298:ASN:ND2	2.54	0.41
1:2A:96:LYS:HZ1	2:3A:1:MET:C	2.15	0.40
1:2B:98:ASP:OD1	1:2B:99:ALA:N	2.54	0.40
1:2C:422:ARG:HH12	1:2C:426:ALA:HB2	1.86	0.40
1:2G:96:LYS:HA	1:2G:96:LYS:HE2	2.03	0.40
1:2I:339:ARG:O	1:2I:339:ARG:HG3	2.21	0.40
2:3A:5:VAL:HG22	2:3A:123:GLU:OE1	2.21	0.40
2:3A:7:VAL:HB	2:3A:135:ILE:HD13	2.02	0.40
2:3A:133:PHE:HB2	2:3A:164:MET:CB	2.51	0.40
2:3B:403:MET:HE3	2:3B:403:MET:HB2	1.86	0.40
2:3F:64:ILE:HD11	2:3F:123:GLU:HG3	2.04	0.40
2:3F:173:PRO:HB3	2:3F:380:ARG:HD3	2.02	0.40
2:3G:173:PRO:HD2	2:3G:205:GLU:HG2	2.03	0.40
2:3I:107:THR:HG21	2:3I:401:GLU:OE2	2.20	0.40
2:3I:403:MET:HE2	2:3I:403:MET:HB3	1.98	0.40
1:4C:151:CYS:SG	1:4C:193:SER:OG	2.40	0.40
1:4I:338:LYS:NZ	1:4I:340:THR:OG1	2.44	0.40
2:5B:113:ILE:HA	2:5B:116:VAL:HG12	2.03	0.40
2:5C:113:ILE:HA	2:5C:116:VAL:HG12	2.03	0.40
2:5D:54:ALA:CA	2:5E:283:ALA:CA	2.98	0.40
2:5D:103:LYS:HB2	2:5D:108:GLU:OE1	2.21	0.40
2:5F:42:LEU:HD12	2:5F:42:LEU:HA	1.94	0.40
2:5G:20:PHE:O	2:5G:24:ILE:HG12	2.22	0.40
2:5G:86:ARG:HB2	2:5G:89:ASN:OD1	2.21	0.40
2:5G:97:ALA:HB3	2:5G:143:THR:HG22	2.02	0.40
1:2D:10:GLY:HA2	1:2D:145:THR:HG23	2.04	0.40
1:2E:332:VAL:O	1:2E:336:LYS:HG3	2.21	0.40
1:2G:296:PHE:CE2	1:2G:335:ILE:HG21	2.57	0.40
1:2H:275:ILE:HD12	1:2H:368:LEU:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3A:177:ASP:OD1	1:4A:353:CYS:SG	2.77	0.40
2:3D:99:ASN:ND2	1:4D:254:GLU:OE1	2.54	0.40
2:3D:284:LEU:HD23	2:3D:362:LYS:HG2	2.01	0.40
1:4A:103:PHE:CD2	1:4A:189:LEU:HB3	2.56	0.40
1:4A:313:MET:HE3	1:4A:346:TRP:CZ2	2.56	0.40
1:4E:185:TYR:HE1	1:4E:398:MET:HB3	1.85	0.40
1:4G:15:GLN:HA	1:4G:18:ASN:ND2	2.36	0.40
2:5D:83:GLN:HB3	2:5E:281:TYR:OH	2.21	0.40
2:5G:324:LYS:HG3	2:5G:325:GLU:N	2.36	0.40
1:2A:219:ILE:HD13	1:2A:219:ILE:HA	1.83	0.40
1:2A:231:ILE:O	1:2A:235:ILE:HG12	2.21	0.40
1:2D:292:THR:CG2	1:2D:331:ALA:HB1	2.50	0.40
1:2H:269:LEU:CD2	1:2H:384:ILE:HD11	2.51	0.40
2:3B:228:LEU:O	2:3B:300:MET:HE1	2.21	0.40
2:3C:207:LEU:HB3	2:3C:225:LEU:HD22	2.02	0.40
2:3E:391:ARG:CD	1:4E:346:TRP:CD1	3.04	0.40
1:4B:65:CYS:SG	1:4B:66:VAL:N	2.93	0.40
1:4F:231:ILE:O	1:4F:235:ILE:HG12	2.21	0.40
1:4G:15:GLN:HA	1:4G:18:ASN:HD21	1.86	0.40
1:4G:176:GLN:HB3	2:5G:331:LEU:HD22	2.03	0.40
1:4G:399:TYR:OH	1:4G:415:GLU:OE2	2.35	0.40
1:4H:225:THR:O	1:4H:229:ARG:HG2	2.22	0.40
1:4H:346:TRP:HZ2	1:4H:435:VAL:HG13	1.86	0.40
2:5A:66:MET:HE2	2:5A:147:MET:HG3	2.03	0.40
2:5G:171:PRO:HG3	2:5G:181:GLU:OE1	2.21	0.40
2:5H:211:CYS:SG	2:5H:217:LEU:HB2	2.61	0.40
1:2A:2:ARG:NE	1:2A:133:GLN:HE21	2.16	0.40
1:2C:302:MET:HE2	1:2C:302:MET:HB2	1.71	0.40
1:2E:98:ASP:OD1	1:2E:99:ALA:N	2.54	0.40
1:2F:101:ASN:ND2	2:3F:256:ASN:HD21	2.19	0.40
1:2H:155:GLU:HG2	1:2H:197:HIS:CE1	2.57	0.40
2:3B:246:LEU:HD12	2:3B:246:LEU:HA	1.84	0.40
2:3C:141:GLY:O	2:3C:145:SER:OG	2.33	0.40
2:3C:284:LEU:HD12	2:3C:284:LEU:HA	1.95	0.40
2:3E:117:LEU:HA	2:3E:120:VAL:HG12	2.03	0.40
2:3F:25:SER:OG	2:3F:81:PHE:HE2	2.04	0.40
2:3I:290:THR:HA	2:3I:293:MET:HG2	2.03	0.40
1:4A:88:HIS:HB3	1:4A:91:GLN:HE22	1.85	0.40
1:4C:274:PRO:HB2	1:4C:276:ILE:HG12	2.04	0.40
2:5B:117:LEU:HA	2:5B:120:VAL:HG12	2.04	0.40
2:5F:355:ASP:O	2:5F:355:ASP:OD1	2.40	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2D:50:ASN:O	1:2D:64:ARG:NH2	2.52	0.40
1:2E:243:ARG:HH11	1:2E:243:ARG:HD2	1.72	0.40
1:2G:189:LEU:HD11	1:2G:418:PHE:HD1	1.87	0.40
1:2G:310:GLY:HA3	1:2G:383:ALA:HB2	2.03	0.40
1:2H:108:TYR:CE2	1:2H:413:MET:HB3	2.56	0.40
2:3B:258:ILE:HD11	2:3B:266:PHE:CZ	2.56	0.40
2:3B:280:GLN:HG2	2:3B:281:TYR:CD1	2.56	0.40
2:3E:100:ASN:ND2	2:3E:397:TRP:O	2.54	0.40
2:3E:396:HIS:HE1	1:4E:262:TYR:HA	1.86	0.40
2:3G:294:PHE:O	2:3G:306:ARG:NH2	2.41	0.40
2:3I:11:GLN:HE22	1:4I:248:LEU:HD12	1.86	0.40
2:3I:16:ILE:HG22	2:3I:136:THR:HG21	2.02	0.40
2:3I:354:CYS:SG	2:3I:355:ASP:N	2.95	0.40
1:4C:88:HIS:HD1	1:4C:90:GLU:H	1.68	0.40
1:4C:185:TYR:HE2	1:4C:404:PHE:HB2	1.86	0.40
1:4H:306:ASP:N	1:4H:386:GLU:OE2	2.54	0.40
1:4H:395:PHE:O	1:4H:398:MET:HB2	2.22	0.40
1:4I:65:CYS:SG	1:4I:66:VAL:N	2.94	0.40
1:4I:230:LEU:HD21	1:4I:368:LEU:HD11	2.03	0.40
2:5A:256:ASN:ND2	2:5A:350:LYS:HG3	2.37	0.40
2:5F:151:LEU:HD12	2:5F:151:LEU:HA	1.90	0.40
2:5H:192:LEU:HD21	2:5H:199:VAL:HG11	2.04	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	2A	424/437 (97%)	416 (98%)	7 (2%)	1 (0%)	43	78
1	2B	424/437 (97%)	416 (98%)	8 (2%)	0	100	100
1	2C	424/437 (97%)	419 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2D	424/437 (97%)	418 (99%)	6 (1%)	0	100	100
1	2E	424/437 (97%)	417 (98%)	7 (2%)	0	100	100
1	2F	424/437 (97%)	415 (98%)	9 (2%)	0	100	100
1	2G	424/437 (97%)	411 (97%)	13 (3%)	0	100	100
1	2H	424/437 (97%)	414 (98%)	10 (2%)	0	100	100
1	2I	424/437 (97%)	418 (99%)	6 (1%)	0	100	100
1	4A	424/437 (97%)	414 (98%)	10 (2%)	0	100	100
1	4B	424/437 (97%)	413 (97%)	11 (3%)	0	100	100
1	4C	424/437 (97%)	416 (98%)	8 (2%)	0	100	100
1	4D	424/437 (97%)	417 (98%)	7 (2%)	0	100	100
1	4E	424/437 (97%)	414 (98%)	10 (2%)	0	100	100
1	4F	424/437 (97%)	417 (98%)	7 (2%)	0	100	100
1	4G	424/437 (97%)	415 (98%)	9 (2%)	0	100	100
1	4H	424/437 (97%)	411 (97%)	13 (3%)	0	100	100
1	4I	424/437 (97%)	419 (99%)	5 (1%)	0	100	100
2	3A	424/426 (100%)	411 (97%)	13 (3%)	0	100	100
2	3B	424/426 (100%)	408 (96%)	16 (4%)	0	100	100
2	3C	424/426 (100%)	409 (96%)	15 (4%)	0	100	100
2	3D	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	3E	424/426 (100%)	406 (96%)	18 (4%)	0	100	100
2	3F	424/426 (100%)	406 (96%)	18 (4%)	0	100	100
2	3G	424/426 (100%)	413 (97%)	11 (3%)	0	100	100
2	3H	424/426 (100%)	411 (97%)	13 (3%)	0	100	100
2	3I	424/426 (100%)	411 (97%)	13 (3%)	0	100	100
2	5A	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	5B	424/426 (100%)	406 (96%)	18 (4%)	0	100	100
2	5C	424/426 (100%)	410 (97%)	14 (3%)	0	100	100
2	5D	424/426 (100%)	409 (96%)	15 (4%)	0	100	100
2	5E	424/426 (100%)	405 (96%)	19 (4%)	0	100	100
2	5F	424/426 (100%)	407 (96%)	17 (4%)	0	100	100
2	5G	424/426 (100%)	410 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	5H	424/426 (100%)	411 (97%)	12 (3%)	1 (0%)	43	78
2	5I	424/426 (100%)	412 (97%)	12 (3%)	0	100	100
All	All	15264/15534 (98%)	14845 (97%)	417 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2A	304	LYS
2	5H	180	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2A	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2B	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	2C	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2D	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2E	359/368 (98%)	359 (100%)	0	100	100
1	2F	359/368 (98%)	358 (100%)	1 (0%)	86	86
1	2G	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	2H	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	2I	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	4A	359/368 (98%)	353 (98%)	6 (2%)	53	69
1	4B	359/368 (98%)	356 (99%)	3 (1%)	73	80
1	4C	359/368 (98%)	356 (99%)	3 (1%)	73	80
1	4D	359/368 (98%)	355 (99%)	4 (1%)	65	76
1	4E	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	4F	359/368 (98%)	357 (99%)	2 (1%)	78	83
1	4G	359/368 (98%)	352 (98%)	7 (2%)	50	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4H	359/368 (98%)	356 (99%)	3 (1%)	73	80
1	4I	359/368 (98%)	354 (99%)	5 (1%)	59	72
2	3A	364/366 (100%)	362 (100%)	2 (0%)	81	83
2	3B	364/366 (100%)	363 (100%)	1 (0%)	86	86
2	3C	364/366 (100%)	363 (100%)	1 (0%)	86	86
2	3D	364/366 (100%)	362 (100%)	2 (0%)	81	83
2	3E	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	3F	364/366 (100%)	357 (98%)	7 (2%)	50	67
2	3G	364/366 (100%)	361 (99%)	3 (1%)	73	80
2	3H	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	3I	364/366 (100%)	361 (99%)	3 (1%)	73	80
2	5A	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5B	364/366 (100%)	362 (100%)	2 (0%)	81	83
2	5C	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5D	364/366 (100%)	363 (100%)	1 (0%)	86	86
2	5E	364/366 (100%)	357 (98%)	7 (2%)	50	67
2	5F	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5G	364/366 (100%)	360 (99%)	4 (1%)	65	76
2	5H	364/366 (100%)	361 (99%)	3 (1%)	73	80
2	5I	364/366 (100%)	361 (99%)	3 (1%)	73	80
All	All	13014/13212 (98%)	12899 (99%)	115 (1%)	68	79

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2A	154	LEU
1	2A	227	LEU
1	2B	86	LEU
1	2B	153	LEU
1	2B	238	LEU
1	2B	256	GLN
1	2C	302	MET
1	2C	386	GLU
1	2D	35	GLN
1	2D	342	GLN

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Mol	Chain	Res	Type
1	2F	390	ARG
1	2G	200	VAL
1	2G	401	LYS
1	2H	154	LEU
1	2H	196	GLU
1	2H	326	LYS
1	2H	372	MET
1	2I	114	ILE
1	2I	125	LEU
1	2I	159	VAL
1	2I	334	THR
2	3A	69	GLU
2	3A	375	GLN
2	3B	179	VAL
2	3C	328	GLU
2	3D	53	GLU
2	3D	117	LEU
2	3E	44	LEU
2	3E	84	LEU
2	3E	191	GLN
2	3E	255	VAL
2	3F	112	LEU
2	3F	147	MET
2	3F	155	VAL
2	3F	175	VAL
2	3F	215	LEU
2	3F	255	VAL
2	3F	333	VAL
2	3G	155	VAL
2	3G	255	VAL
2	3G	300	MET
2	3H	45	GLU
2	3H	117	LEU
2	3H	359	LYS
2	3H	395	LEU
2	3I	42	LEU
2	3I	256	ASN
2	3I	349	MET
1	4A	132	LEU
1	4A	159	VAL
1	4A	167	LEU
1	4A	336	LYS

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Mol	Chain	Res	Type
1	4A	401	LYS
1	4A	435	VAL
1	4B	217	LEU
1	4B	238	LEU
1	4B	280	LYS
1	4C	107	HIS
1	4C	124	LYS
1	4C	153	LEU
1	4D	96	LYS
1	4D	125	LEU
1	4D	153	LEU
1	4D	326	LYS
1	4E	31	GLN
1	4E	315	CYS
1	4F	66	VAL
1	4F	112	LYS
1	4G	31	GLN
1	4G	183	GLU
1	4G	200	VAL
1	4G	238	LEU
1	4G	280	LYS
1	4G	334	THR
1	4G	425	LEU
1	4H	196	GLU
1	4H	227	LEU
1	4H	325	PRO
1	4I	114	ILE
1	4I	125	LEU
1	4I	297	GLU
1	4I	334	THR
1	4I	425	LEU
2	5A	2	ARG
2	5A	23	VAL
2	5A	123	GLU
2	5A	169	VAL
2	5B	262	ARG
2	5B	323	THR
2	5C	39	ASP
2	5C	147	MET
2	5C	247	ASN
2	5C	342	VAL
2	5D	423	GLN

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Mol	Chain	Res	Type
2	5E	48	ASN
2	5E	112	LEU
2	5E	190	HIS
2	5E	255	VAL
2	5E	280	GLN
2	5E	297	LYS
2	5E	423	GLN
2	5F	46	ARG
2	5F	99	ASN
2	5F	117	LEU
2	5F	155	VAL
2	5G	2	ARG
2	5G	339	SER
2	5G	364	SER
2	5G	365	VAL
2	5H	112	LEU
2	5H	117	LEU
2	5H	395	LEU
2	5I	66	MET
2	5I	280	GLN
2	5I	377	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (207) such sidechains are listed below:

Mol	Chain	Res	Type
1	2A	28	HIS
1	2A	128	ASN
1	2A	133	GLN
1	2A	342	GLN
1	2B	18	ASN
1	2B	31	GLN
1	2B	85	HIS
1	2B	283	HIS
1	2B	342	GLN
1	2C	31	GLN
1	2C	102	ASN
1	2C	216	ASN
1	2C	258	ASN
1	2D	85	HIS
1	2D	91	GLN
1	2D	226	ASN
1	2D	356	ASN

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Mol	Chain	Res	Type
1	2D	380	ASN
1	2D	393	HIS
1	2E	11	GLN
1	2E	101	ASN
1	2E	216	ASN
1	2F	11	GLN
1	2F	15	GLN
1	2F	28	HIS
1	2F	50	ASN
1	2F	85	HIS
1	2F	102	ASN
1	2F	283	HIS
1	2F	406	HIS
1	2G	133	GLN
1	2G	380	ASN
1	2H	11	GLN
1	2H	168	ASN
1	2H	176	GLN
1	2H	216	ASN
1	2H	233	GLN
1	2H	283	HIS
1	2H	342	GLN
1	2I	50	ASN
1	2I	102	ASN
1	2I	206	ASN
1	2I	329	ASN
1	2I	393	HIS
2	3A	11	GLN
2	3A	94	GLN
2	3A	99	ASN
2	3A	105	HIS
2	3A	195	ASN
2	3A	264	HIS
2	3A	335	ASN
2	3A	348	ASN
2	3A	375	GLN
2	3A	423	GLN
2	3B	247	ASN
2	3B	348	ASN
2	3B	423	GLN
2	3C	11	GLN
2	3C	14	ASN

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Mol	Chain	Res	Type
2	3C	329	GLN
2	3C	347	ASN
2	3C	348	ASN
2	3C	414	ASN
2	3D	14	ASN
2	3D	43	GLN
2	3D	52	ASN
2	3D	99	ASN
2	3D	190	HIS
2	3D	191	GLN
2	3D	204	ASN
2	3D	247	ASN
2	3D	334	GLN
2	3D	347	ASN
2	3D	348	ASN
2	3D	375	GLN
2	3D	426	GLN
2	3E	43	GLN
2	3E	134	GLN
2	3E	195	ASN
2	3E	247	ASN
2	3E	256	ASN
2	3E	264	HIS
2	3E	347	ASN
2	3E	396	HIS
2	3E	426	GLN
2	3F	6	HIS
2	3F	11	GLN
2	3F	14	ASN
2	3F	94	GLN
2	3F	99	ASN
2	3F	245	GLN
2	3F	247	ASN
2	3F	334	GLN
2	3G	11	GLN
2	3G	14	ASN
2	3G	43	GLN
2	3G	190	HIS
2	3G	245	GLN
2	3G	335	ASN
2	3G	337	ASN
2	3G	348	ASN

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Mol	Chain	Res	Type
2	3H	8	GLN
2	3H	14	ASN
2	3H	99	ASN
2	3H	195	ASN
2	3H	264	HIS
2	3I	105	HIS
2	3I	137	HIS
2	3I	190	HIS
2	3I	264	HIS
2	3I	307	HIS
2	3I	423	GLN
1	4A	329	ASN
1	4B	31	GLN
1	4B	206	ASN
1	4B	216	ASN
1	4B	283	HIS
1	4C	176	GLN
1	4C	216	ASN
1	4C	258	ASN
1	4C	309	HIS
1	4D	91	GLN
1	4D	283	HIS
1	4D	356	ASN
1	4D	380	ASN
1	4E	11	GLN
1	4E	35	GLN
1	4E	380	ASN
1	4F	91	GLN
1	4F	102	ASN
1	4F	139	ASN
1	4F	168	ASN
1	4F	258	ASN
1	4F	283	HIS
1	4G	28	HIS
1	4G	168	ASN
1	4G	406	HIS
1	4H	226	ASN
1	4H	233	GLN
1	4H	329	ASN
1	4H	380	ASN
1	4I	8	HIS
1	4I	11	GLN

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Mol	Chain	Res	Type
1	4I	176	GLN
1	4I	206	ASN
1	4I	216	ASN
2	5A	14	ASN
2	5A	105	HIS
2	5A	134	GLN
2	5A	137	HIS
2	5A	247	ASN
2	5A	264	HIS
2	5A	279	GLN
2	5A	335	ASN
2	5A	337	ASN
2	5B	11	GLN
2	5B	52	ASN
2	5B	195	ASN
2	5B	348	ASN
2	5B	375	GLN
2	5B	414	ASN
2	5C	6	HIS
2	5C	329	GLN
2	5C	347	ASN
2	5D	6	HIS
2	5D	8	GLN
2	5D	52	ASN
2	5D	204	ASN
2	5D	280	GLN
2	5D	348	ASN
2	5D	414	ASN
2	5E	137	HIS
2	5E	195	ASN
2	5E	245	GLN
2	5E	337	ASN
2	5E	347	ASN
2	5E	348	ASN
2	5F	11	GLN
2	5F	15	GLN
2	5F	43	GLN
2	5F	94	GLN
2	5F	99	ASN
2	5F	247	ASN
2	5F	335	ASN
2	5F	337	ASN

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Mol	Chain	Res	Type
2	5F	414	ASN
2	5F	426	GLN
2	5G	14	ASN
2	5G	52	ASN
2	5G	131	GLN
2	5G	245	GLN
2	5G	247	ASN
2	5G	280	GLN
2	5G	335	ASN
2	5G	347	ASN
2	5H	14	ASN
2	5H	105	HIS
2	5H	137	HIS
2	5H	190	HIS
2	5H	195	ASN
2	5H	204	ASN
2	5H	347	ASN
2	5I	134	GLN
2	5I	204	ASN
2	5I	245	GLN
2	5I	347	ASN
2	5I	423	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

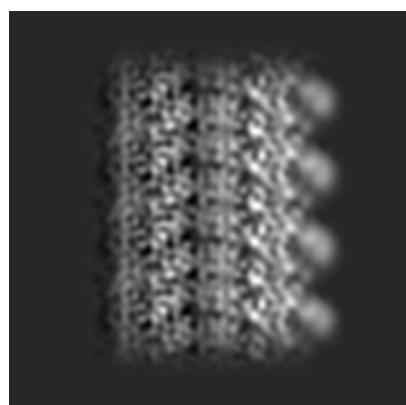
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26020. These allow visual inspection of the internal detail of the map and identification of artifacts.

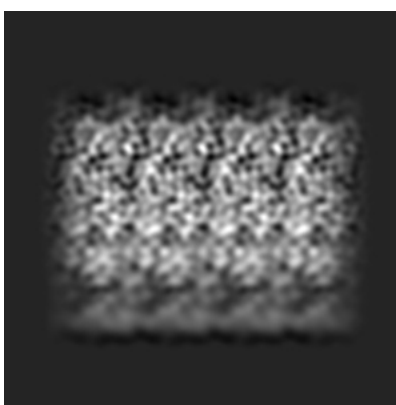
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

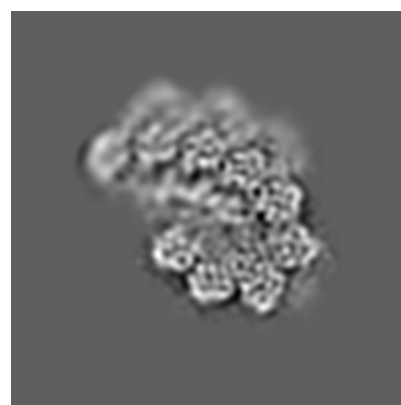
6.1.1 Primary map



X



Y

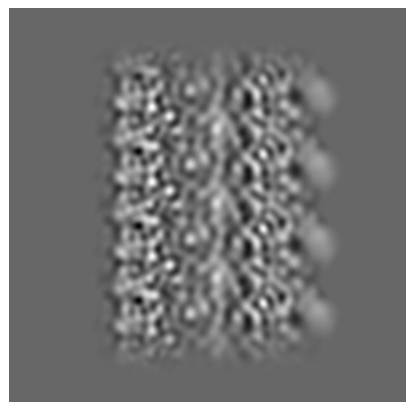


Z

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

6.2 Central slices [i](#)

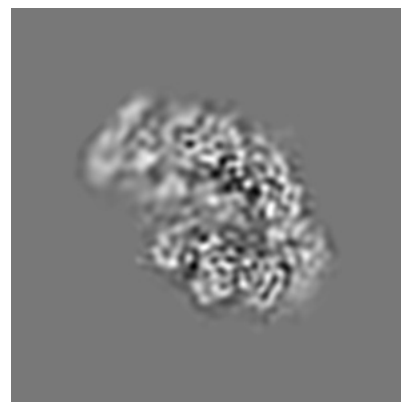
6.2.1 Primary map



X Index: 64



Y Index: 64

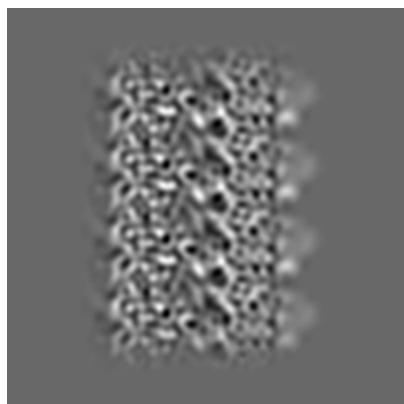


Z Index: 64

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

6.3 Largest variance slices [i](#)

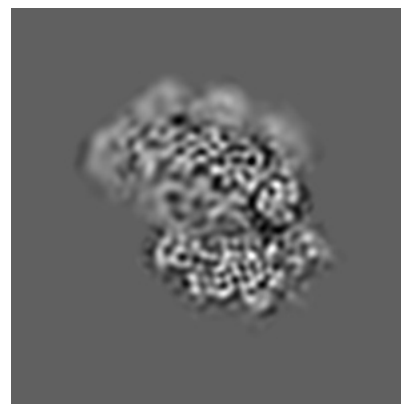
6.3.1 Primary map



X Index: 76



Y Index: 79

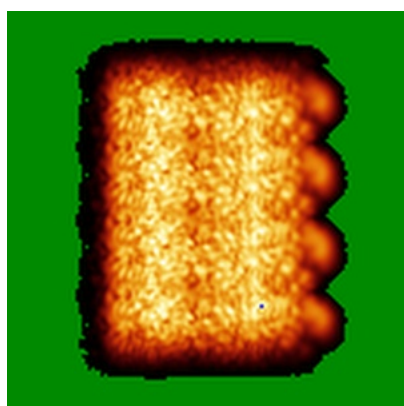


Z Index: 32

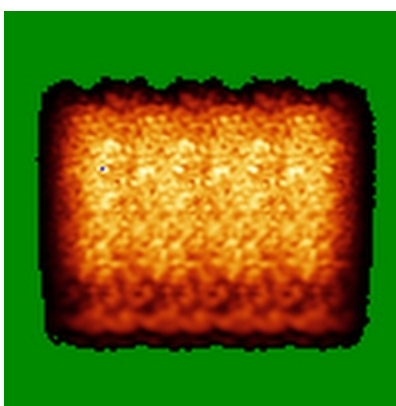
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

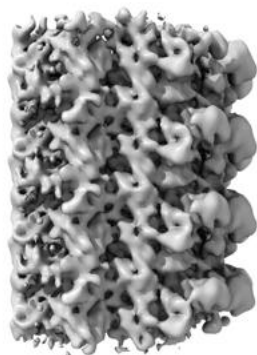


Z

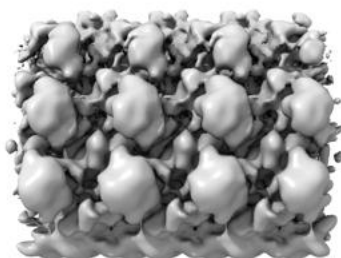
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

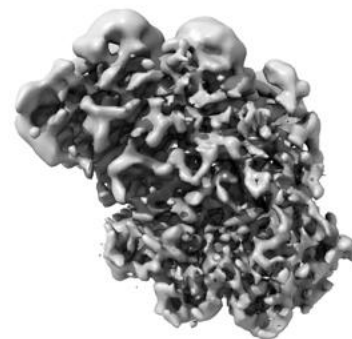
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

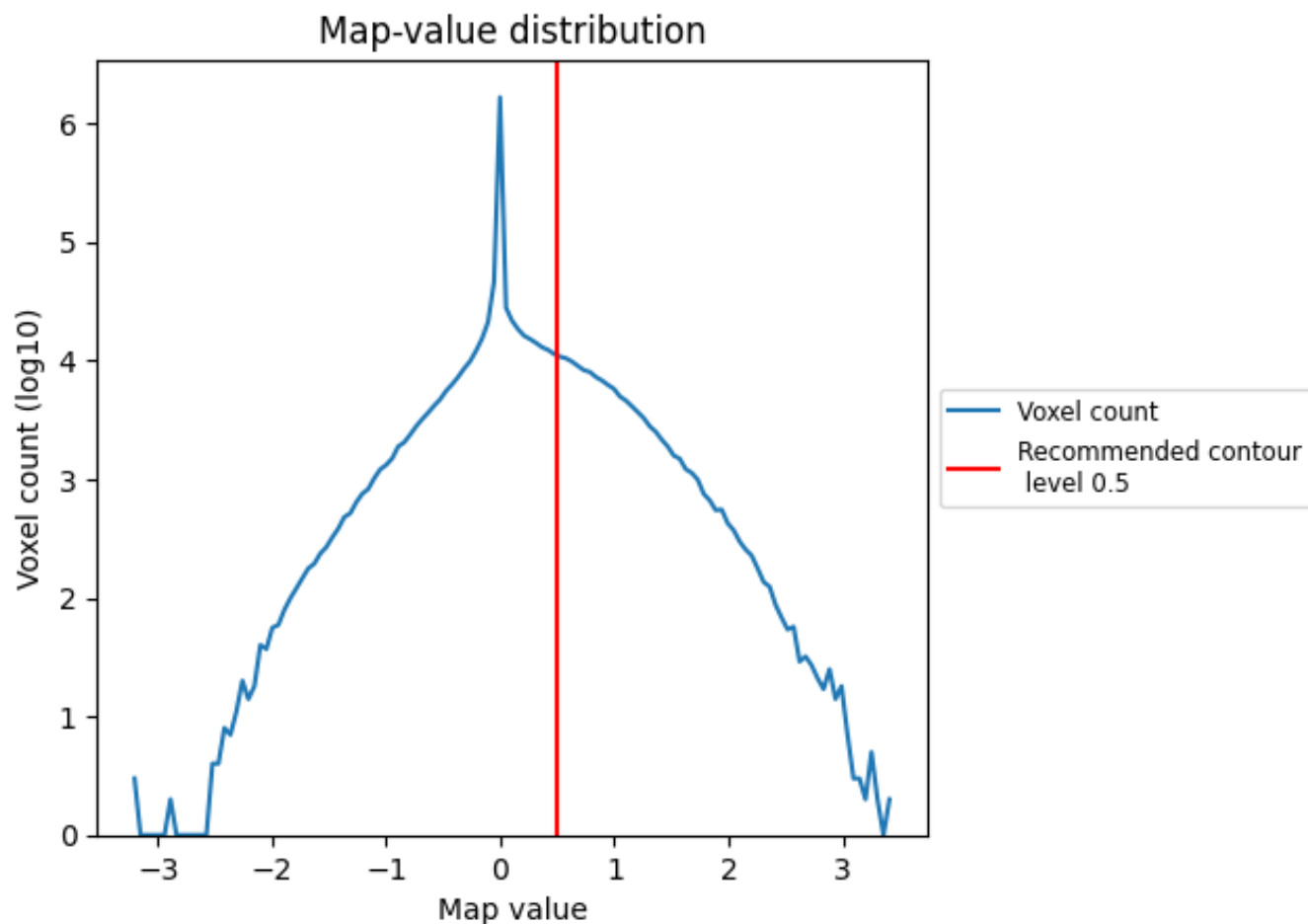
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

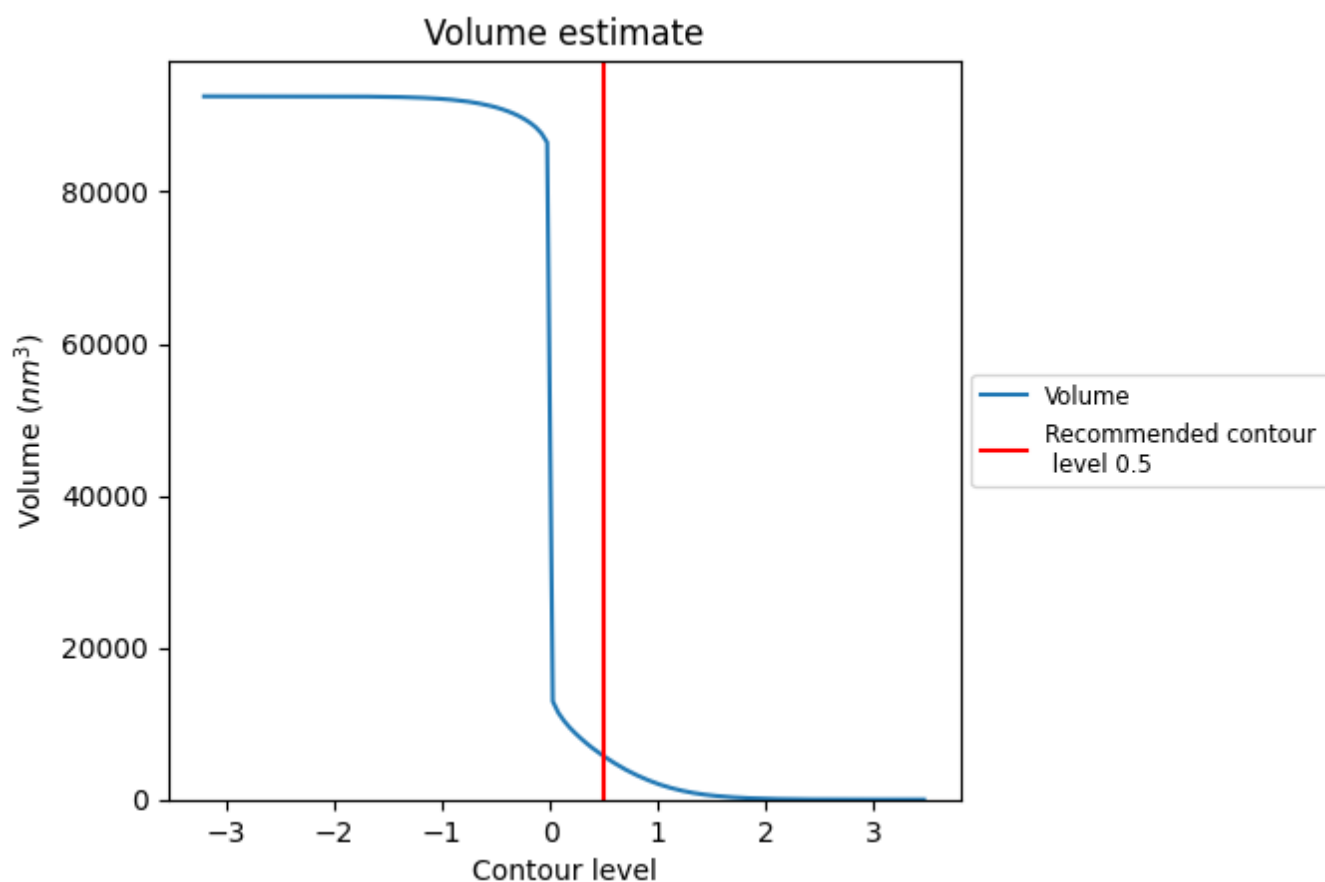
This section contains the results of statistical analysis of the map.

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.

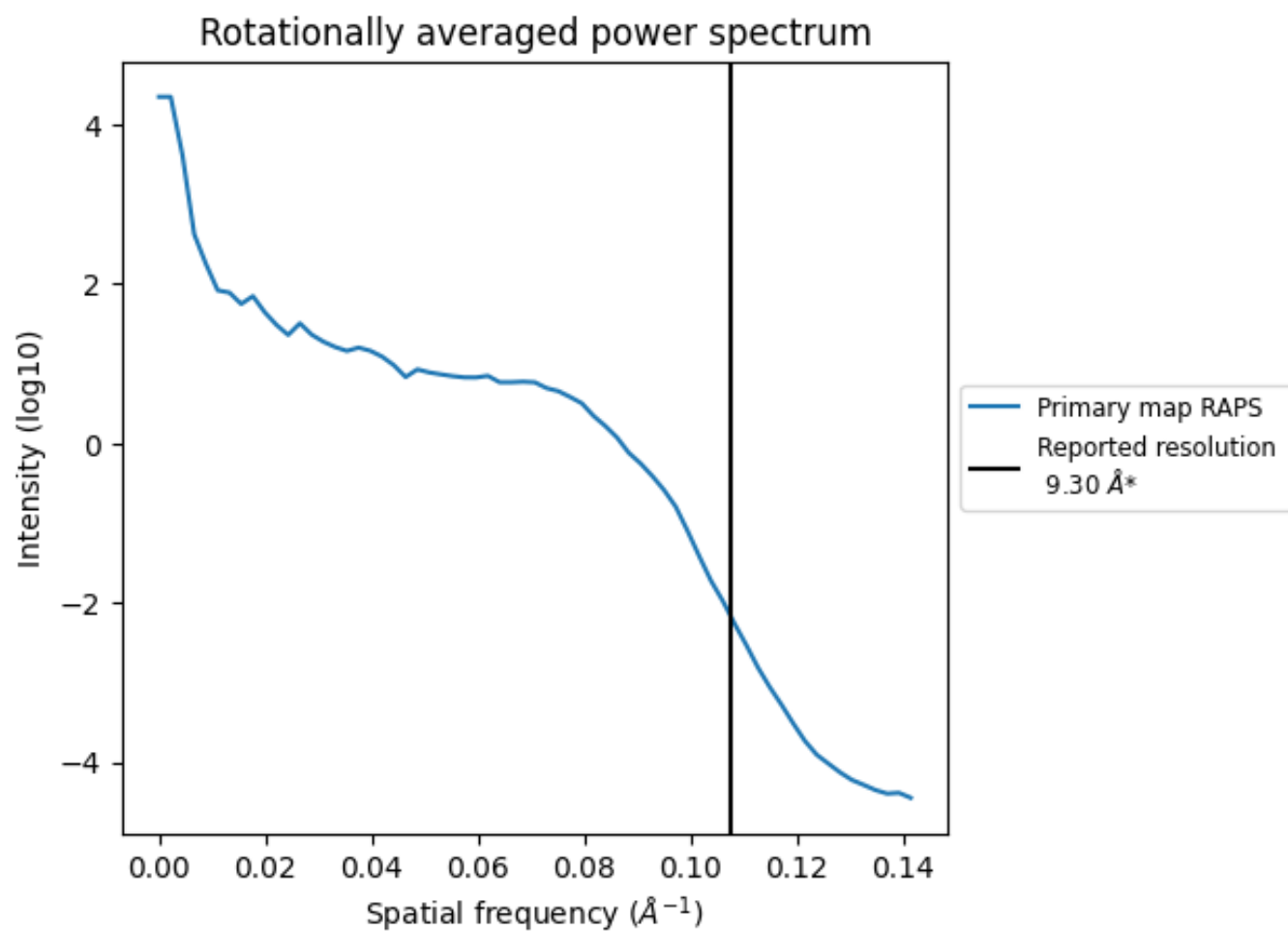
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5688 nm³; this corresponds to an approximate mass of 5138 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 0.108 Å⁻¹

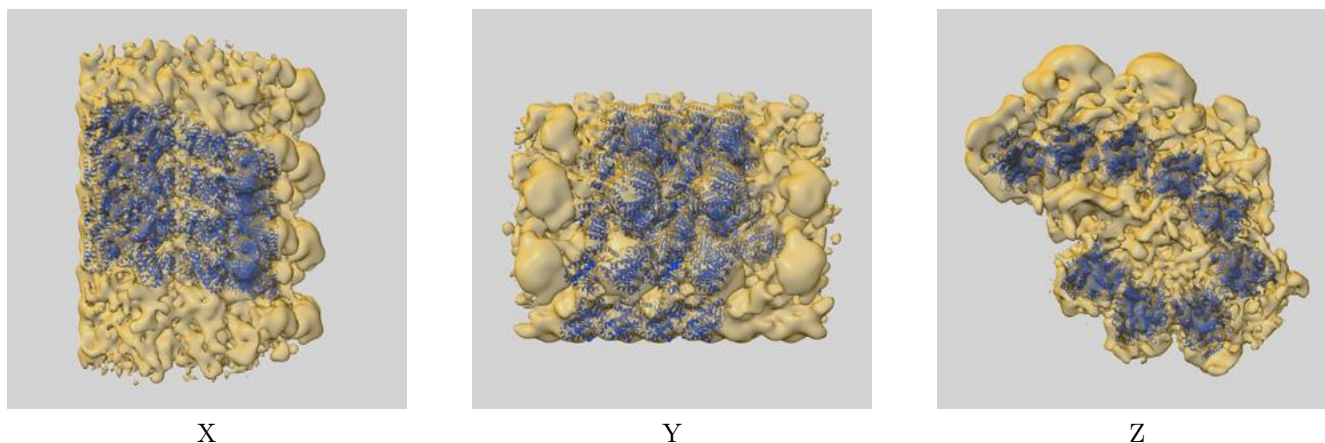
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

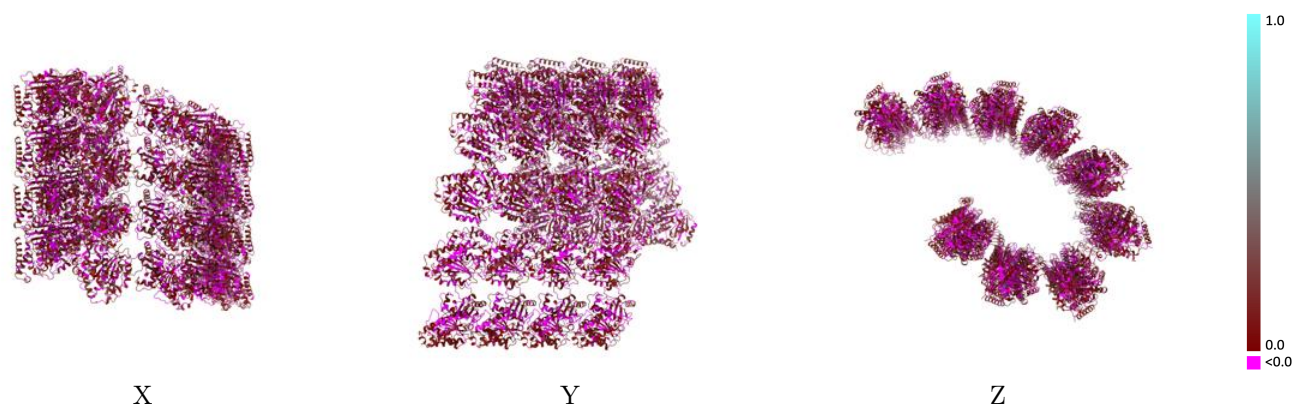
This section contains information regarding the fit between EMDB map EMD-26020 and PDB model 7TNT. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



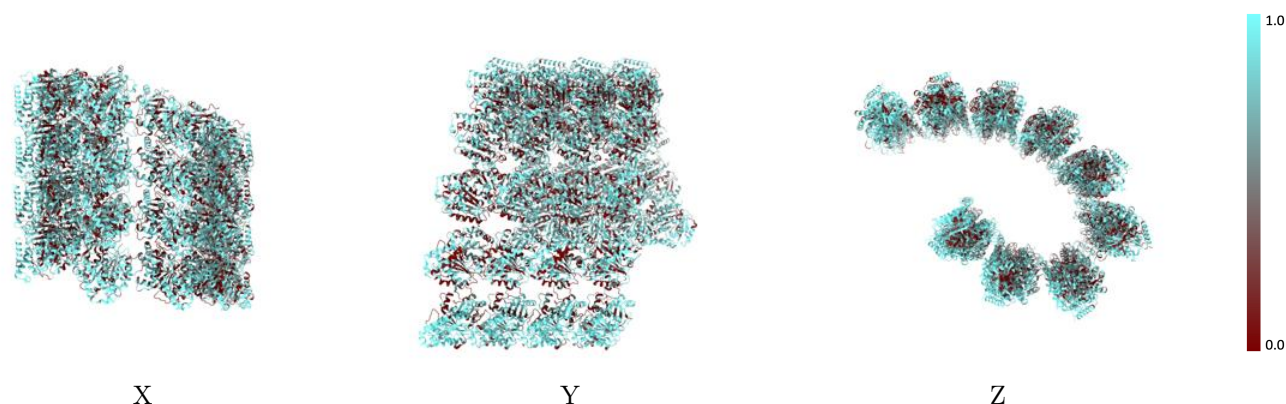
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



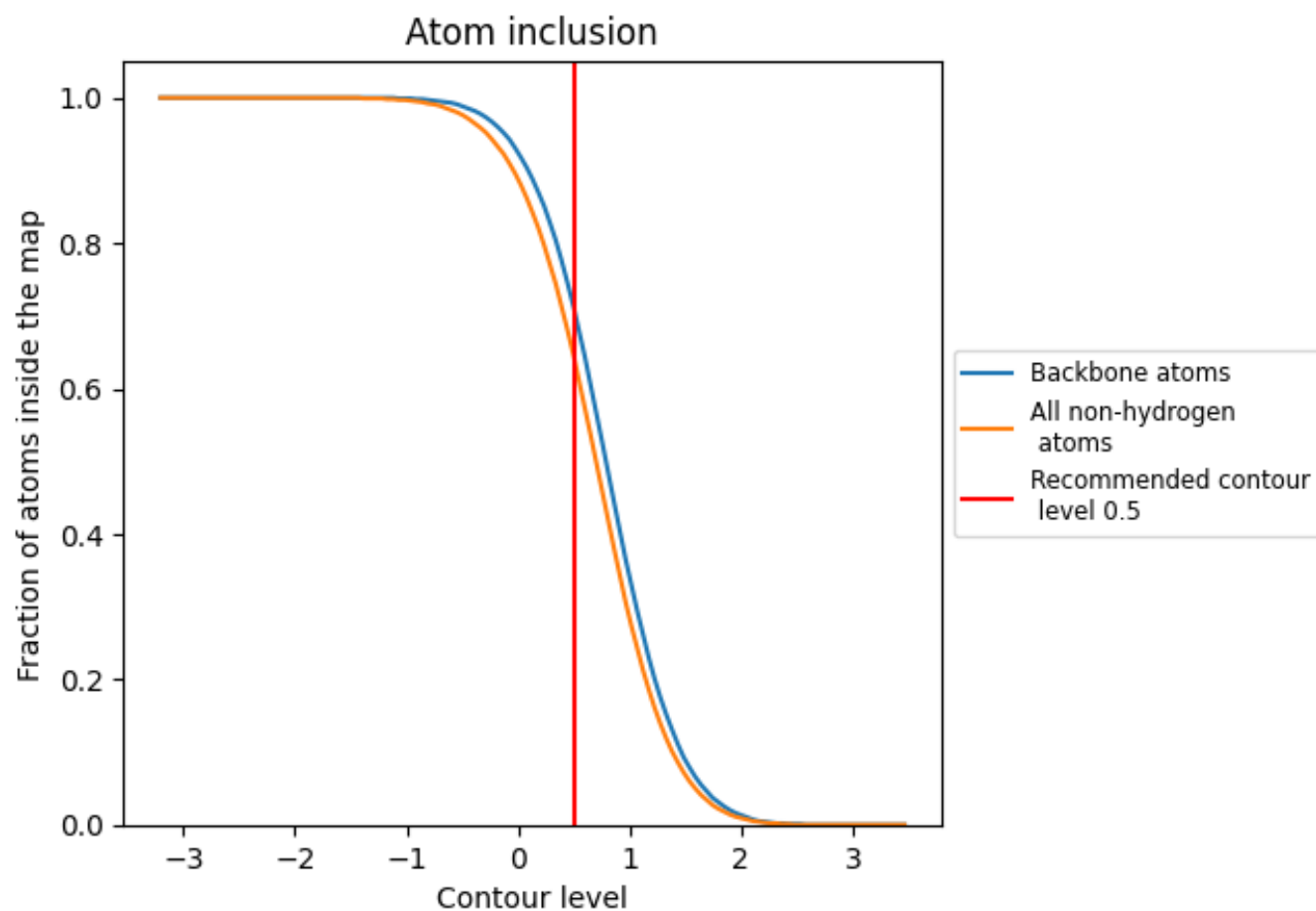
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6440	 0.0530
2A	 0.7180	 0.0590
2B	 0.6580	 0.0530
2C	 0.6420	 0.0620
2D	 0.5940	 0.0530
2E	 0.5920	 0.0500
2F	 0.5900	 0.0480
2G	 0.6300	 0.0580
2H	 0.6000	 0.0350
2I	 0.7640	 0.0390
3A	 0.7140	 0.0620
3B	 0.6630	 0.0700
3C	 0.6540	 0.0620
3D	 0.6530	 0.0650
3E	 0.6030	 0.0510
3F	 0.5930	 0.0610
3G	 0.5680	 0.0410
3H	 0.5900	 0.0380
3I	 0.7520	 0.0330
4A	 0.7220	 0.0590
4B	 0.6720	 0.0680
4C	 0.6470	 0.0650
4D	 0.6030	 0.0540
4E	 0.6060	 0.0530
4F	 0.6110	 0.0610
4G	 0.6360	 0.0590
4H	 0.6160	 0.0390
4I	 0.7810	 0.0400
5A	 0.7070	 0.0650
5B	 0.6580	 0.0640
5C	 0.6430	 0.0630
5D	 0.6500	 0.0700
5E	 0.5900	 0.0470
5F	 0.5820	 0.0490
5G	 0.5630	 0.0350



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Chain	Atom inclusion	Q-score
5H	 0.5740	 0.0330
5I	 0.7390	 0.0260