



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 08:33 AM UTC

PDB ID : 7TAU / pdb_00007tau
EMDB ID : EMD-25786
Title : Refined capsid structure of human adenovirus D26 at 3.4 Å resolution
Authors : Reddy, V.S.; Yu, X.; Barry, M.A.
Deposited on : 2021-12-21
Resolution : 3.38 Å (reported)
Based on initial model : 5TX1

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

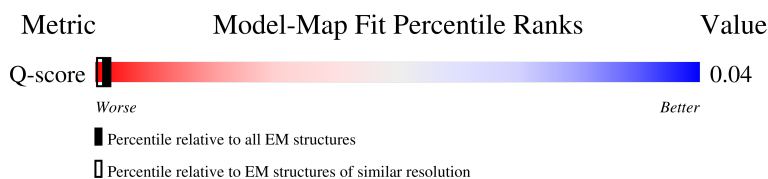
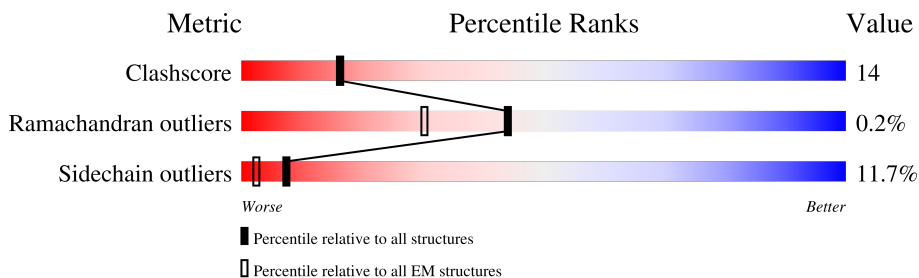
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.38 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	14261 (2.88 - 3.88)

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

Mol	Chain	Length	Quality of chain
1	A	952	
1	B	952	
1	C	952	
1	D	952	

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Mol	Chain	Length	Quality of chain
1	E	952	
1	F	952	
1	G	952	
1	H	952	
1	I	952	
1	J	952	
1	K	952	
1	L	952	
2	N	519	
3	O	374	
4	M	560	
5	P	134	
5	Q	134	
5	R	134	
5	S	134	
6	U	227	
6	V	227	
7	1	234	
7	2	234	
7	3	234	
7	4	234	
7	5	234	
7	6	234	
7	7	234	
7	8	234	

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Mol	Chain	Length	Quality of chain
7	9	234	
8	X	15	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 105672 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 Hexon protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	951	Total	C	N	O	S	0	0
			7551	4796	1276	1444	35		
1	B	949	Total	C	N	O	S	0	0
			7536	4787	1274	1441	34		
1	C	946	Total	C	N	O	S	0	0
			7519	4777	1271	1437	34		
1	D	947	Total	C	N	O	S	0	0
			7526	4780	1272	1440	34		
1	E	947	Total	C	N	O	S	0	0
			7526	4780	1272	1440	34		
1	F	949	Total	C	N	O	S	0	0
			7539	4789	1274	1441	35		
1	G	947	Total	C	N	O	S	0	0
			7526	4780	1272	1440	34		
1	H	947	Total	C	N	O	S	0	0
			7526	4780	1272	1440	34		
1	I	949	Total	C	N	O	S	0	0
			7536	4787	1274	1441	34		
1	J	951	Total	C	N	O	S	0	0
			7551	4795	1276	1446	34		
1	K	950	Total	C	N	O	S	0	0
			7546	4792	1275	1445	34		
1	L	947	Total	C	N	O	S	0	0
			7524	4780	1272	1438	34		

- Molecule 2 is a protein called Penton protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	471	Total	C	N	O	S	0	0
			3786	2404	640	728	14		

- Molecule 3 is a protein called Fiber.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	O	17	Total	C	N	O	0	0
			147	96	24	27		

- Molecule 4 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	362	Total	C	N	O	S	0	0
			2829	1771	508	541	9		

- Molecule 5 is a protein called PIX.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	122	Total	C	N	O	S	0	0
			889	547	157	181	4		
5	Q	114	Total	C	N	O	S	0	0
			821	508	143	166	4		
5	R	133	Total	C	N	O	S	0	0
			957	587	168	198	4		
5	S	122	Total	C	N	O	S	0	0
			887	545	157	182	3		

- Molecule 6 is a protein called PVIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	U	190	Total	C	N	O	S	0	0
			1462	919	252	285	6		
6	V	188	Total	C	N	O	S	0	0
			1449	911	250	282	6		

- Molecule 7 is a protein called Pre-protein VI.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1	30	Total	C	N	O	S	0	0
			236	147	43	45	1		
7	2	26	Total	C	N	O	S	0	0
			203	128	38	36	1		
7	3	27	Total	C	N	O	S	0	0
			211	132	40	38	1		
7	4	29	Total	C	N	O	S	0	0
			227	142	42	42	1		
7	5	28	Total	C	N	O	S	0	0
			219	138	41	39	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	27	Total	C	N	O	S	0	0
			211	132	40	38	1		
7	7	27	Total	C	N	O	S	0	0
			211	132	40	38	1		
7	8	29	Total	C	N	O	S	0	0
			227	142	42	42	1		
7	9	28	Total	C	N	O	S	0	0
			219	138	41	39	1		

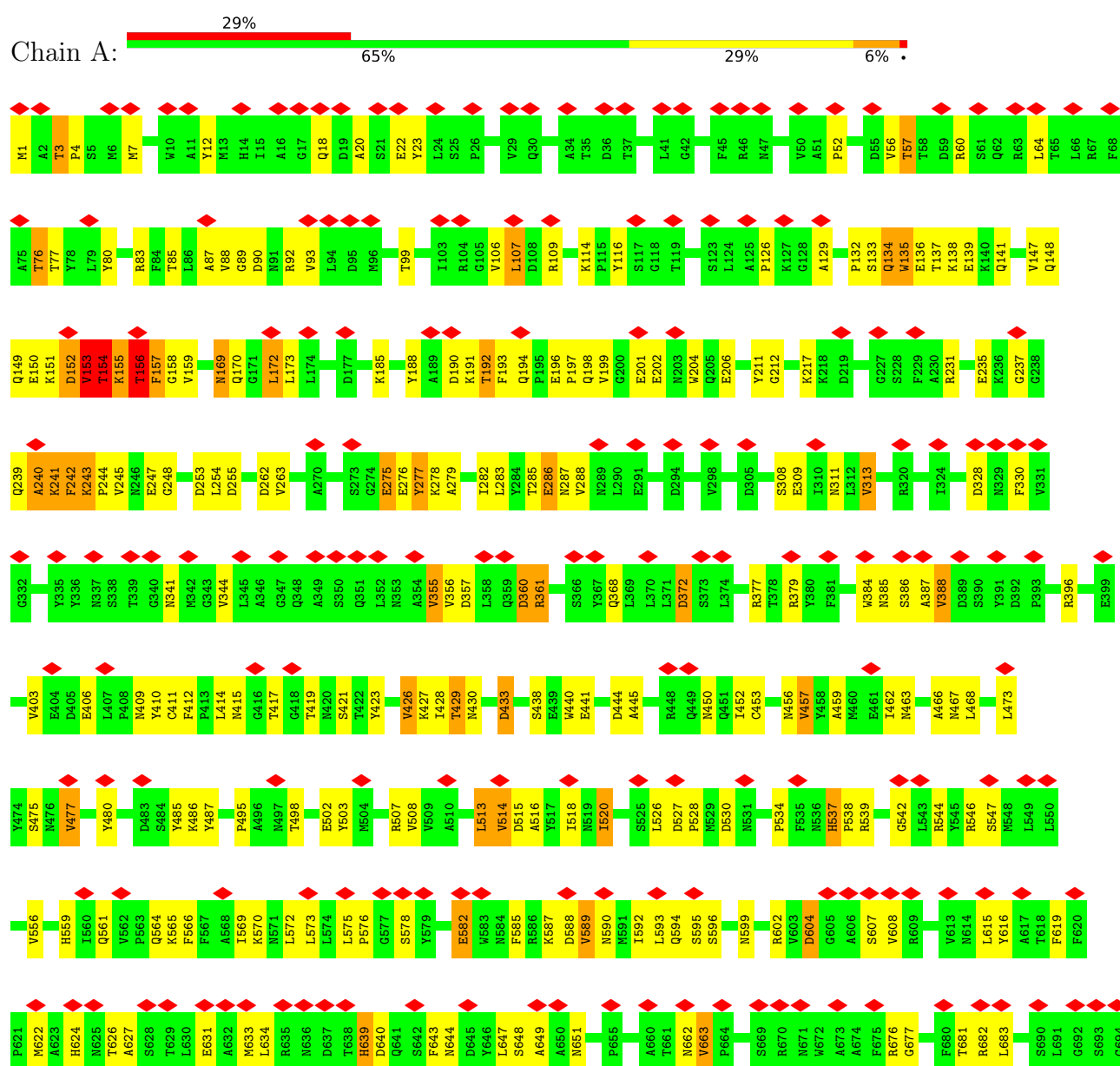
- Molecule 8 is a protein called Unknown fragment.

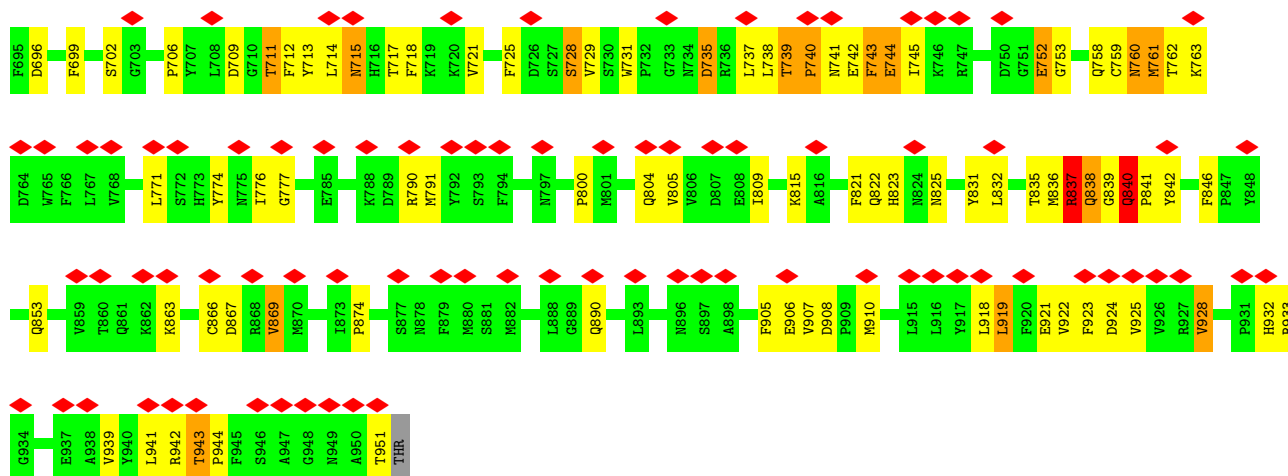
Mol	Chain	Residues	Atoms				AltConf	Trace
8	X	15	Total	C	N	O	0	0
			75	45	15	15		

3 Residue-property plots

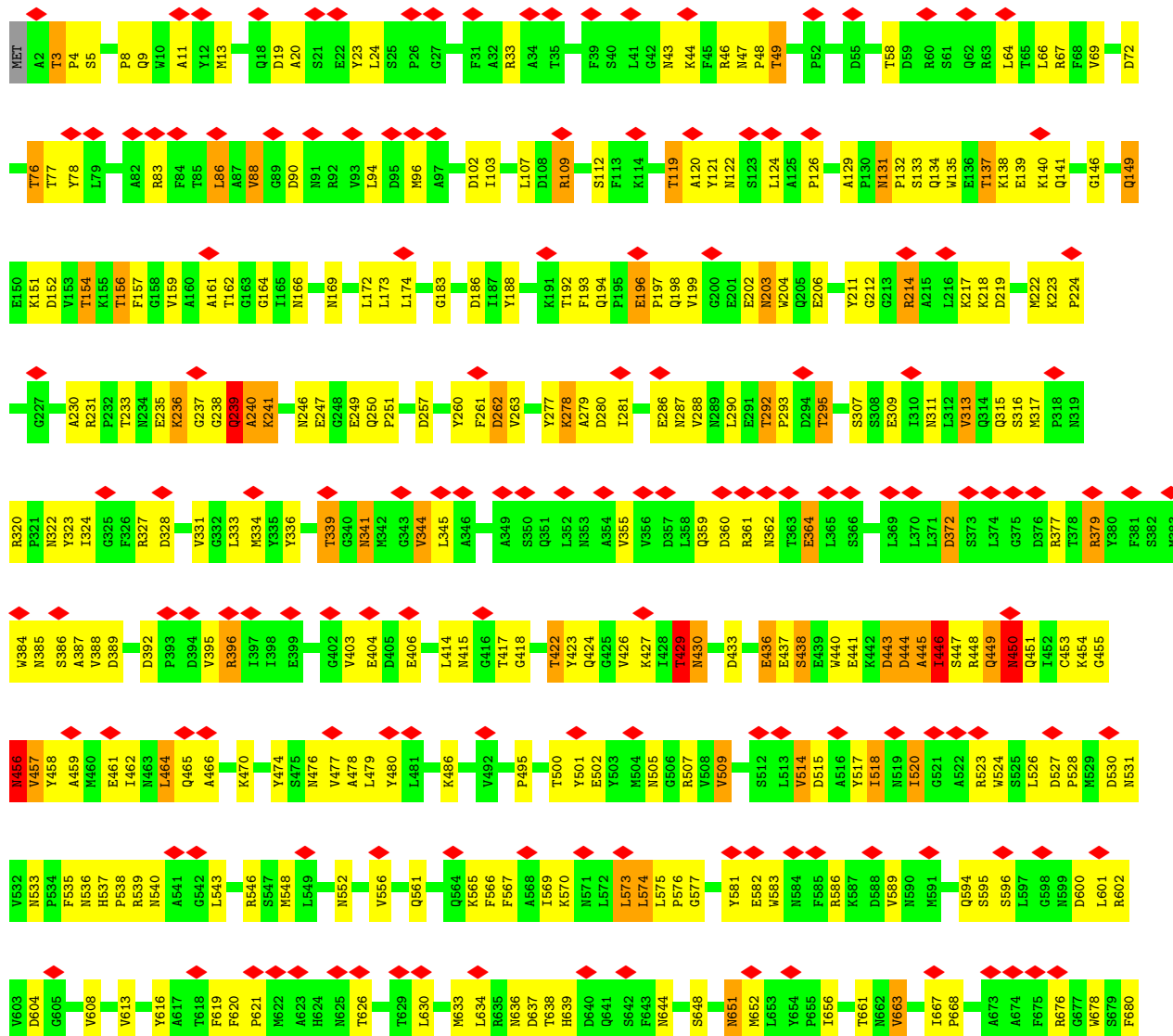
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

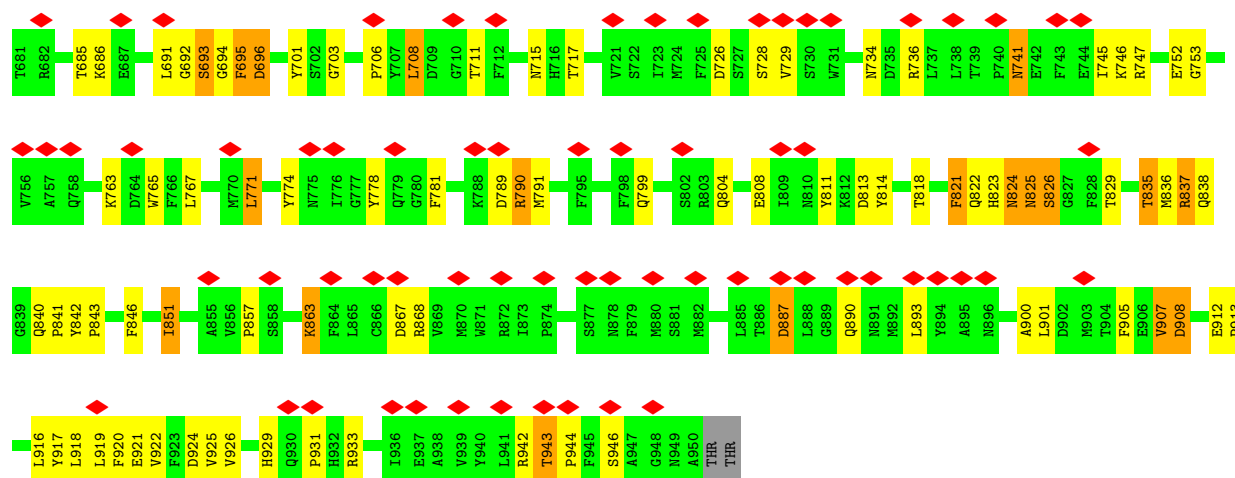
• Molecule 1: Hexon protein



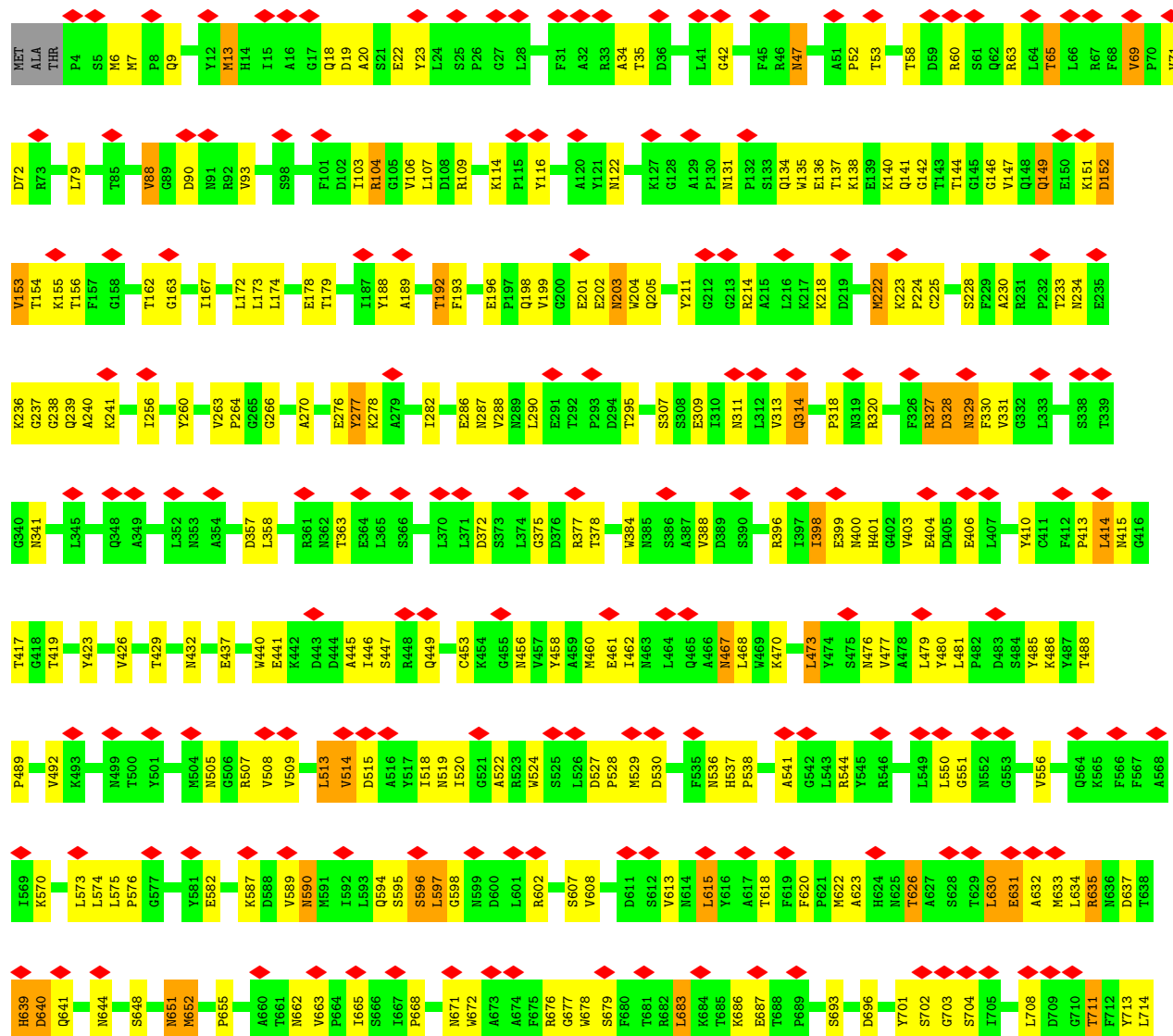


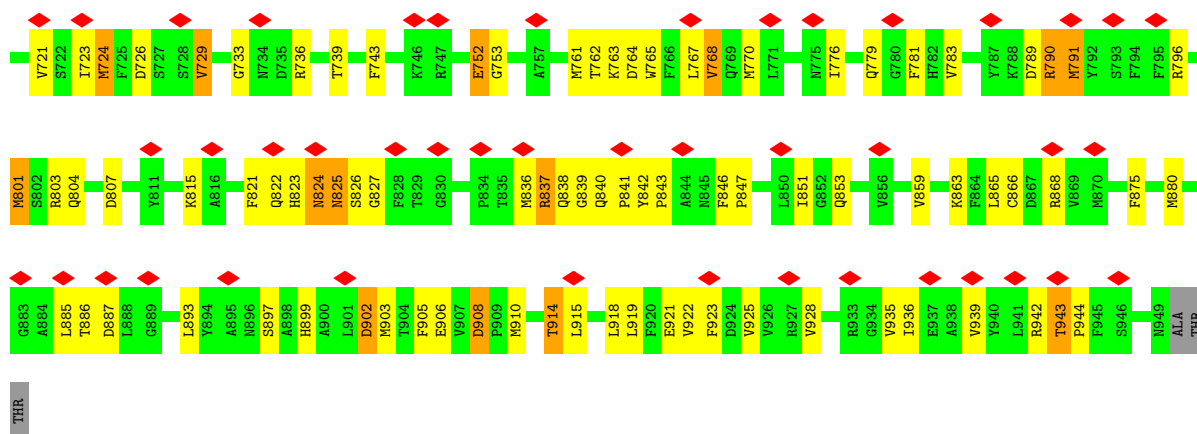
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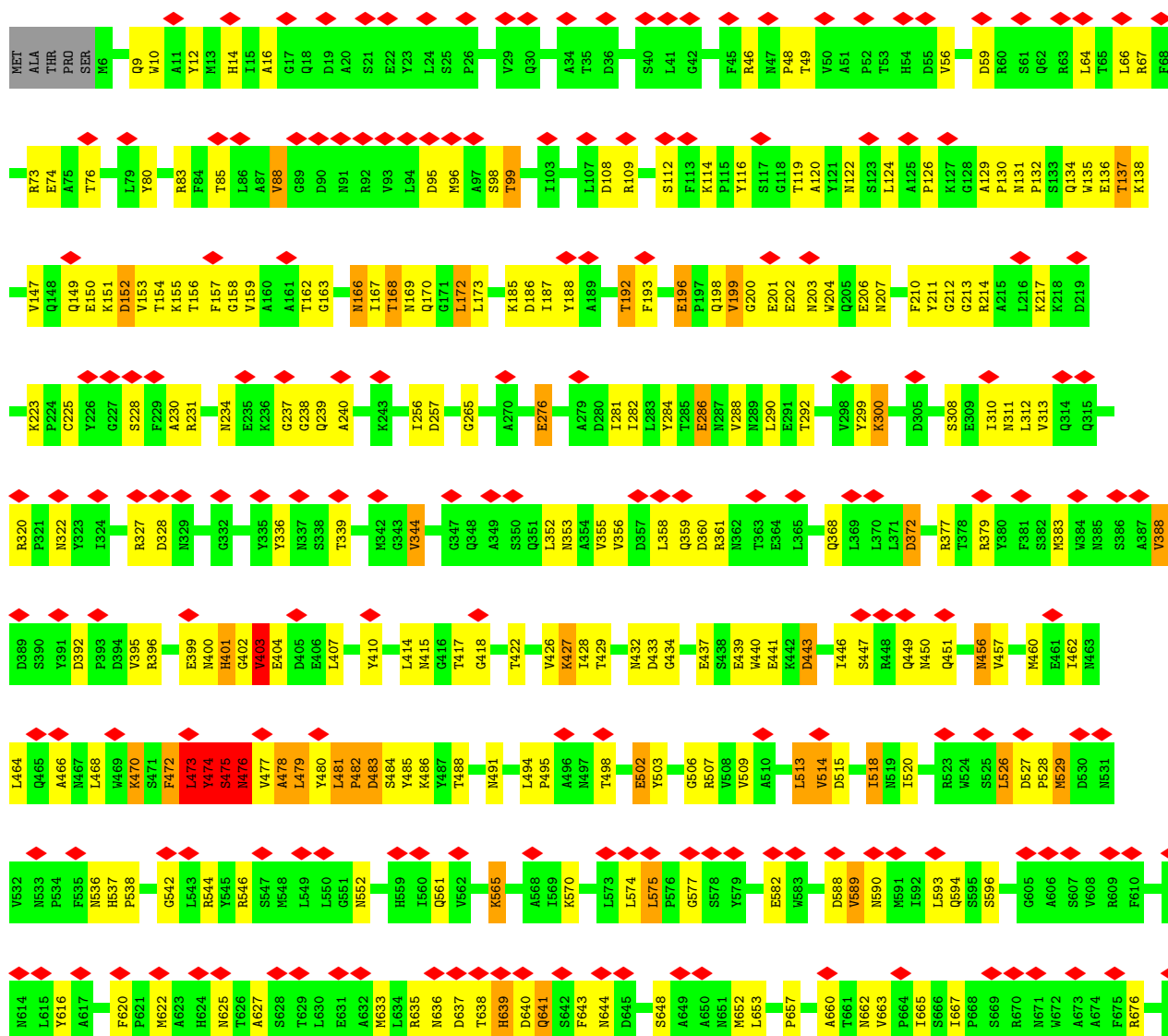


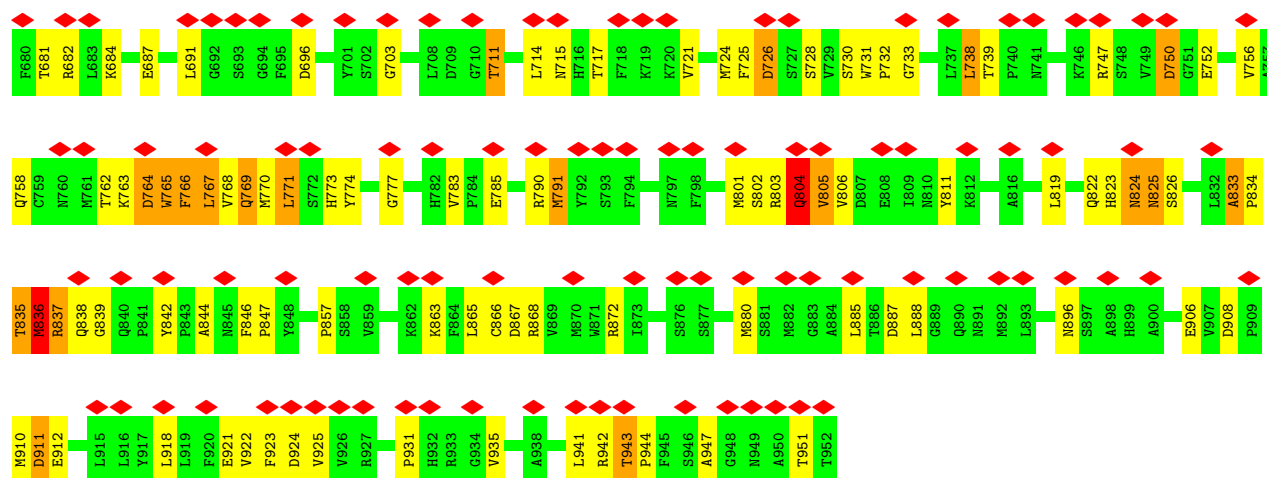
• Molecule 1: Hexon protein



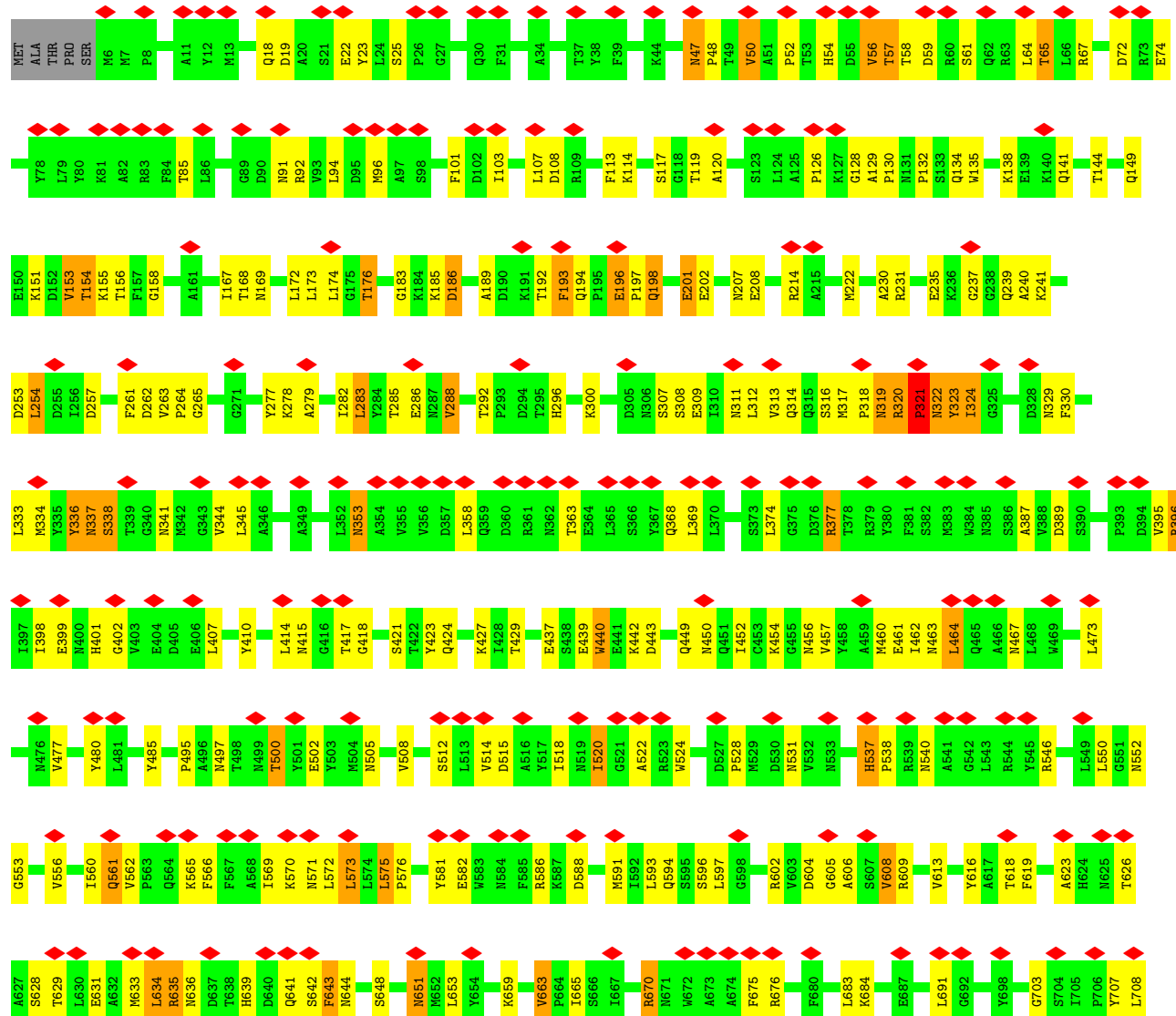


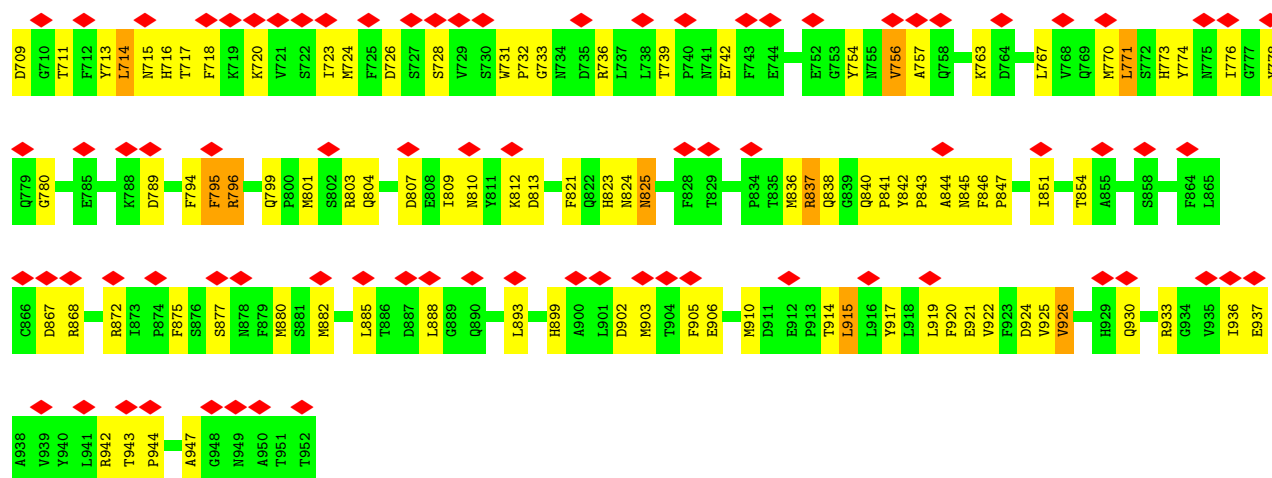
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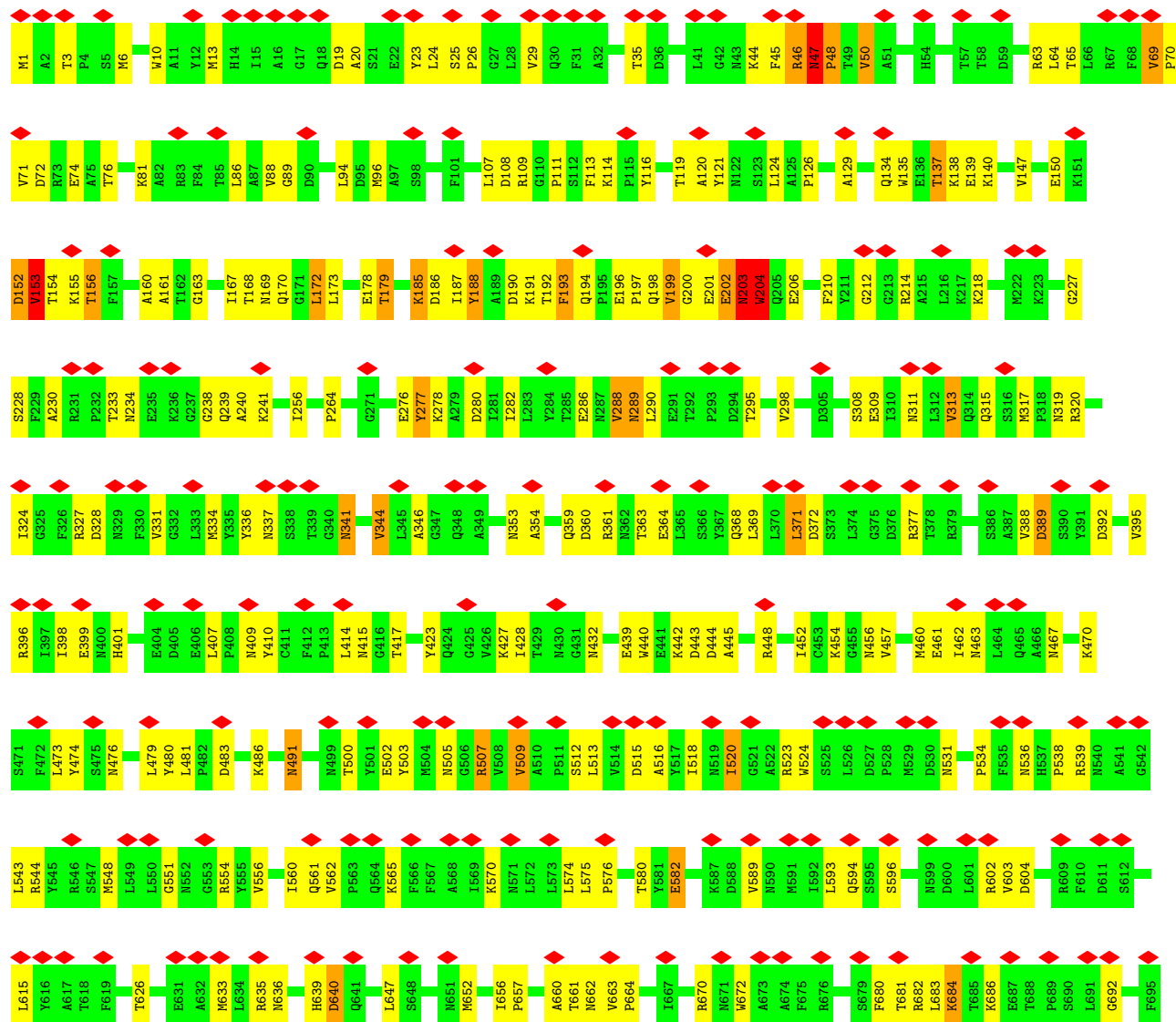


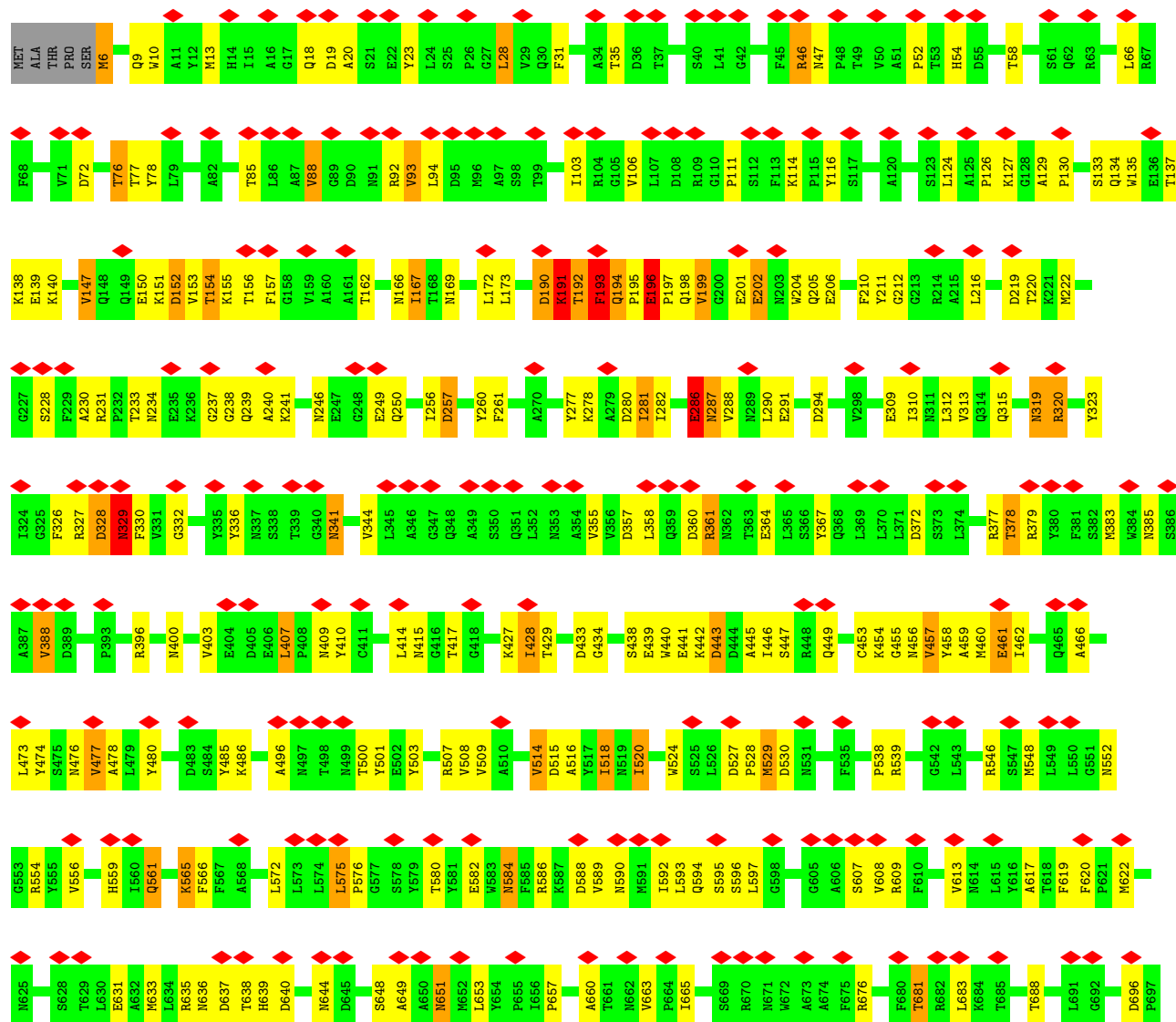
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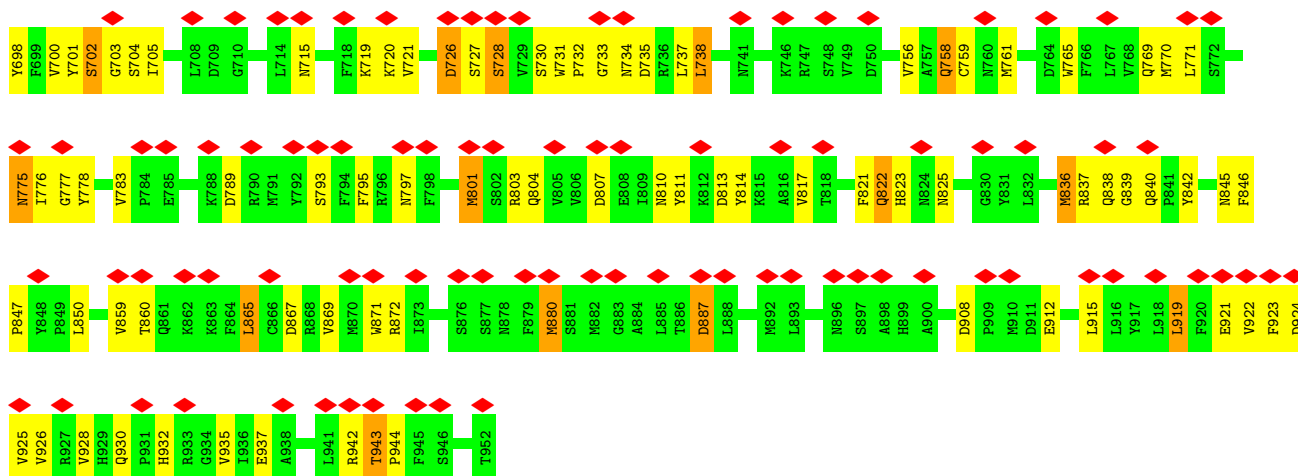




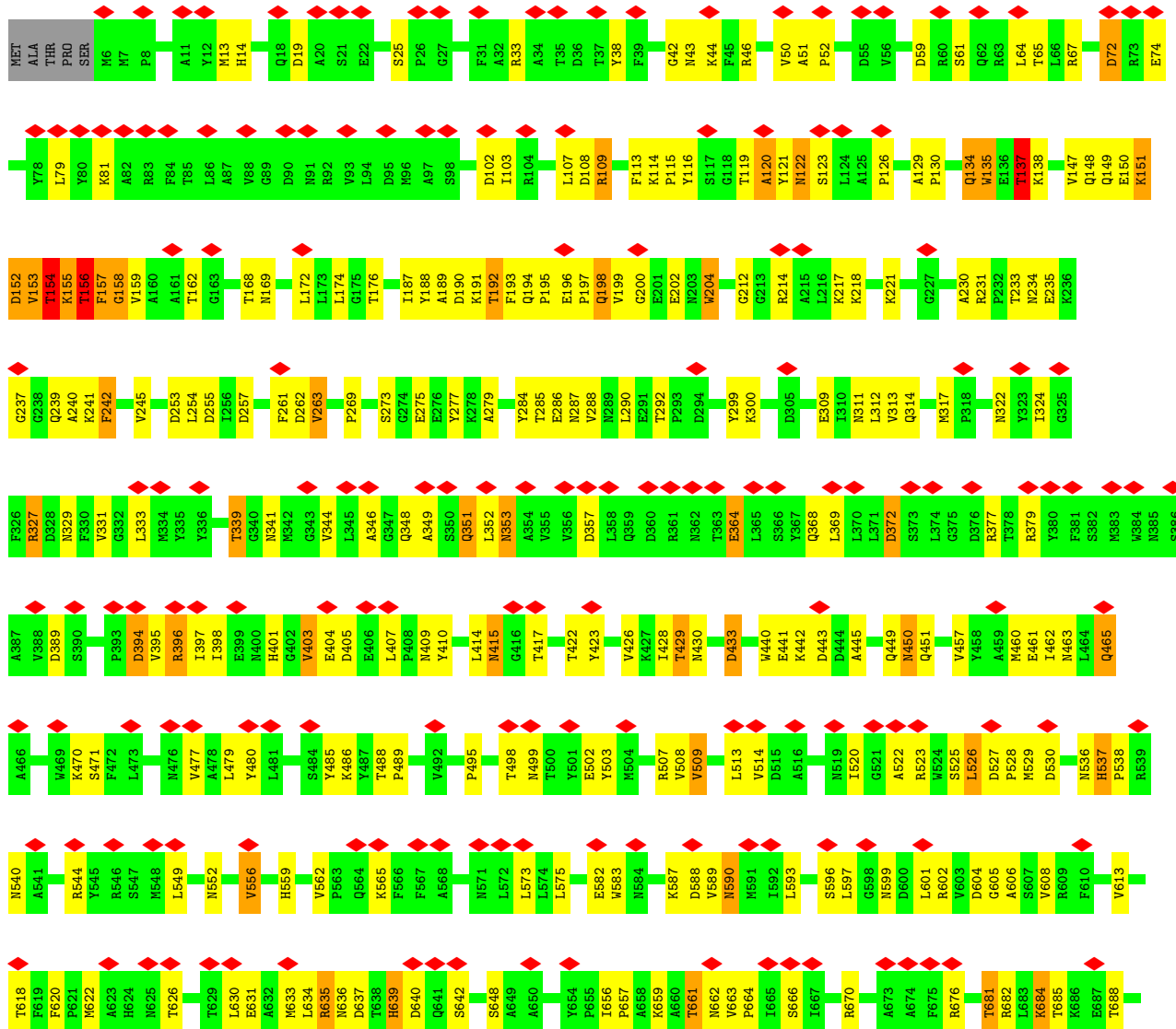
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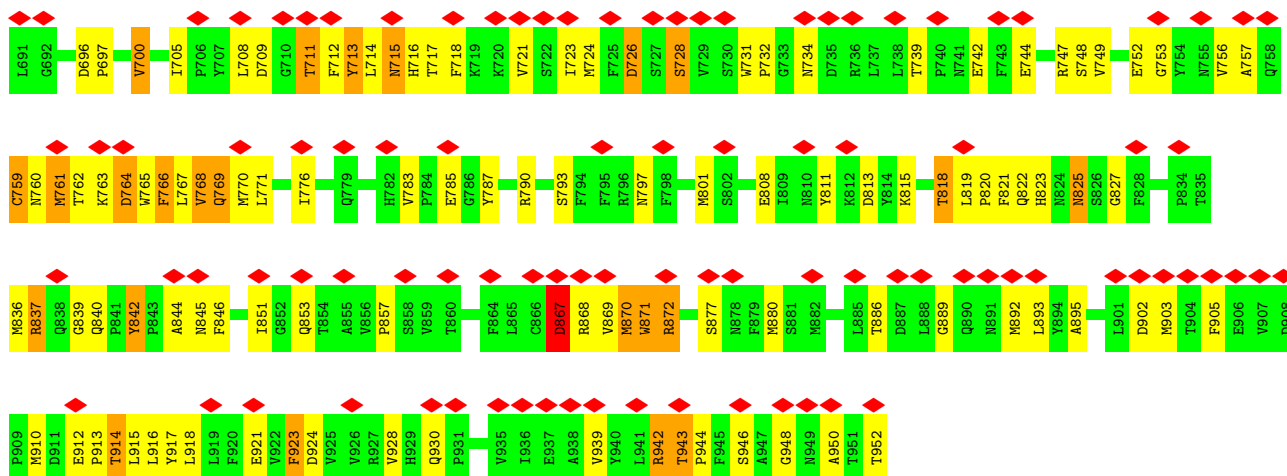




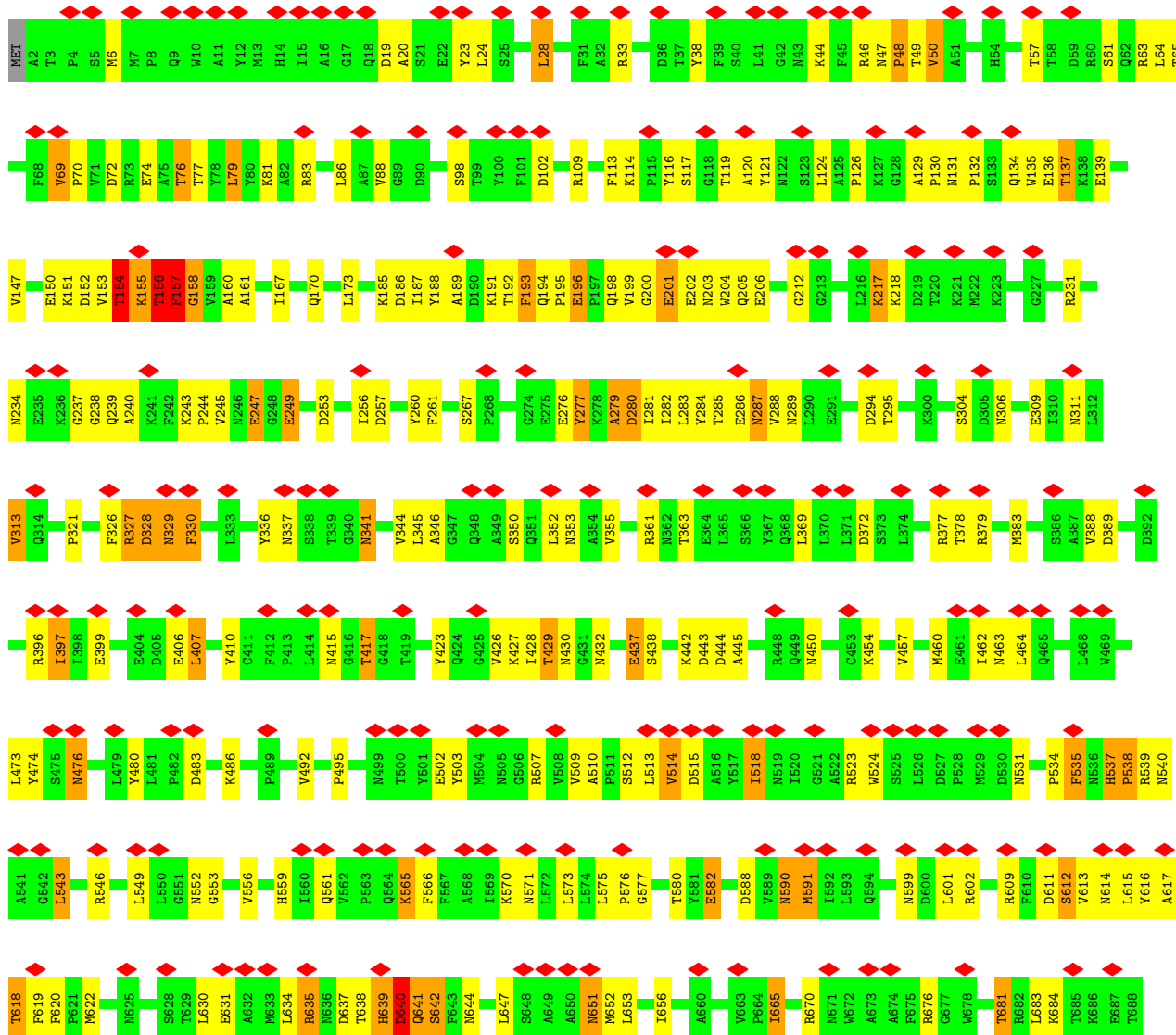


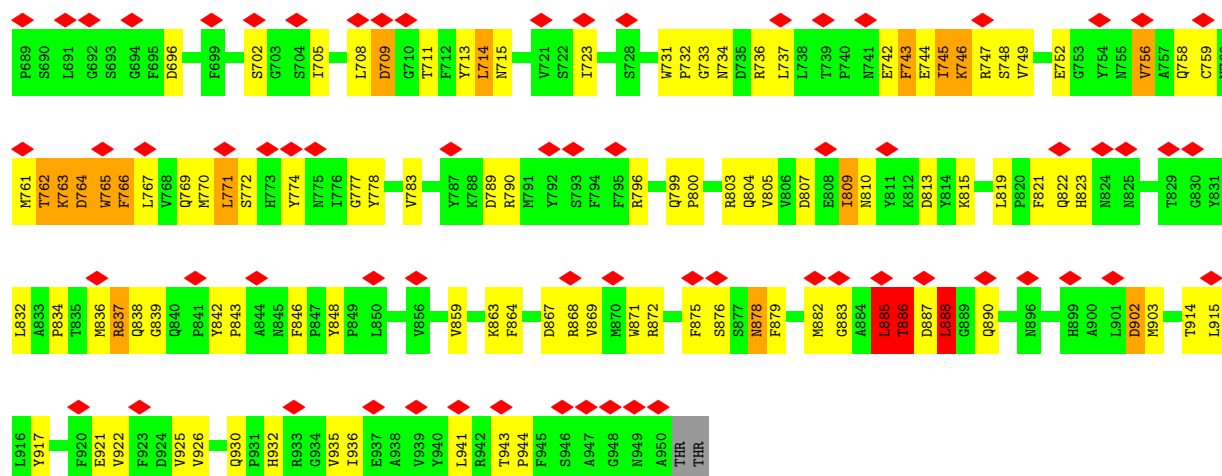
• Molecule 1: Hexon protein



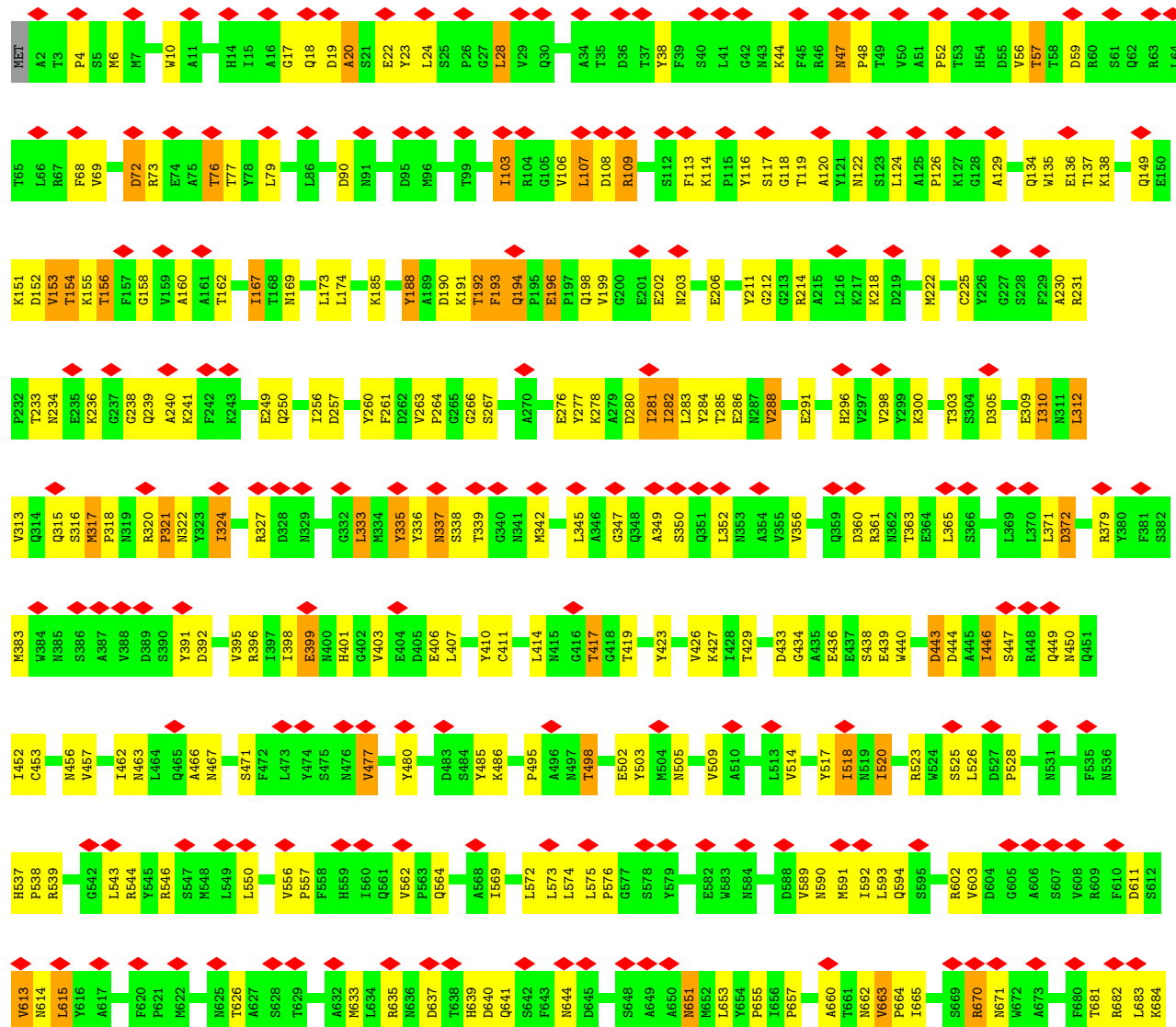


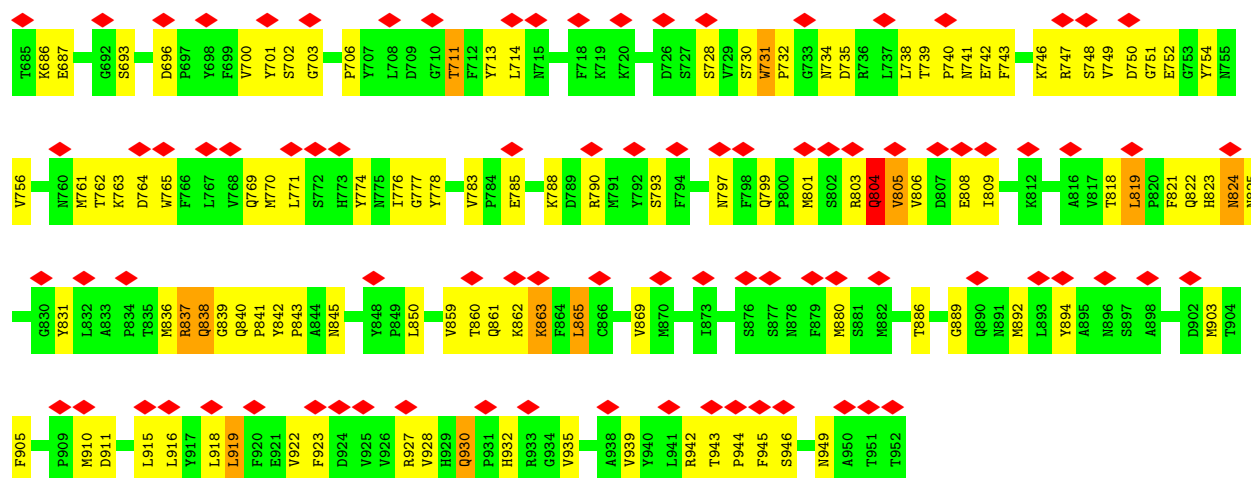
• Molecule 1: Hexon protein



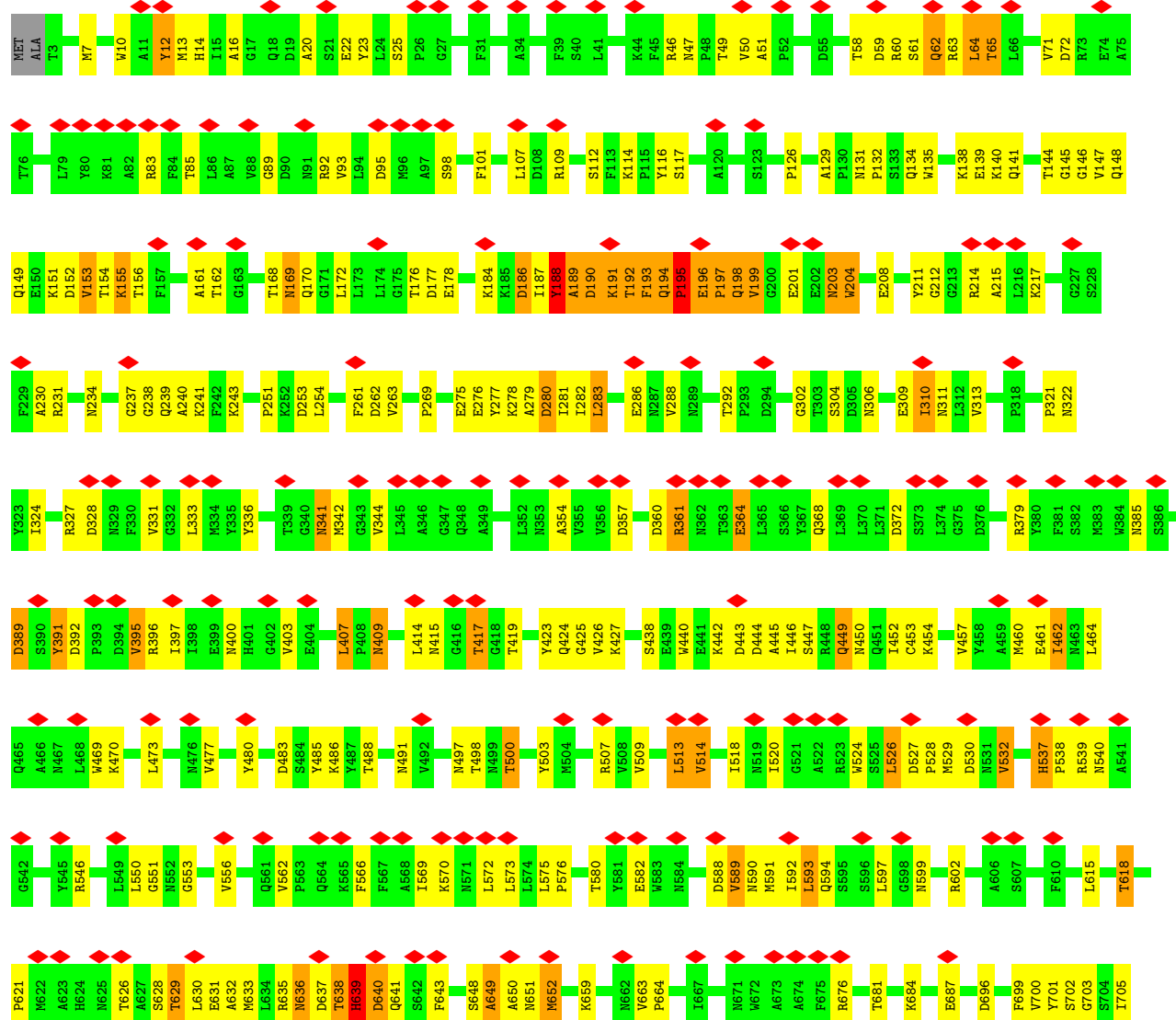


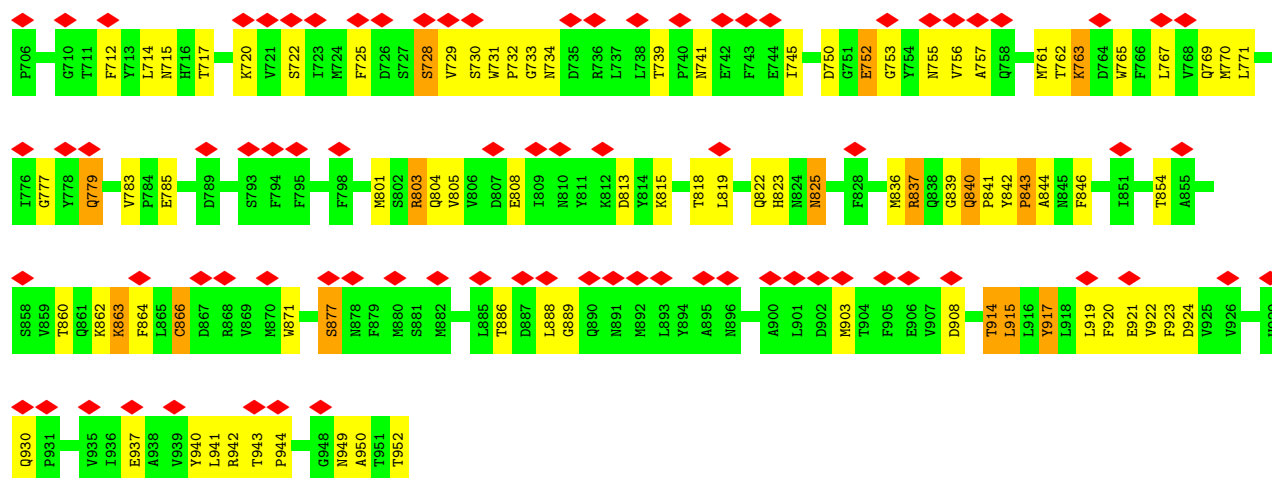
• Molecule 1: Hexon protein



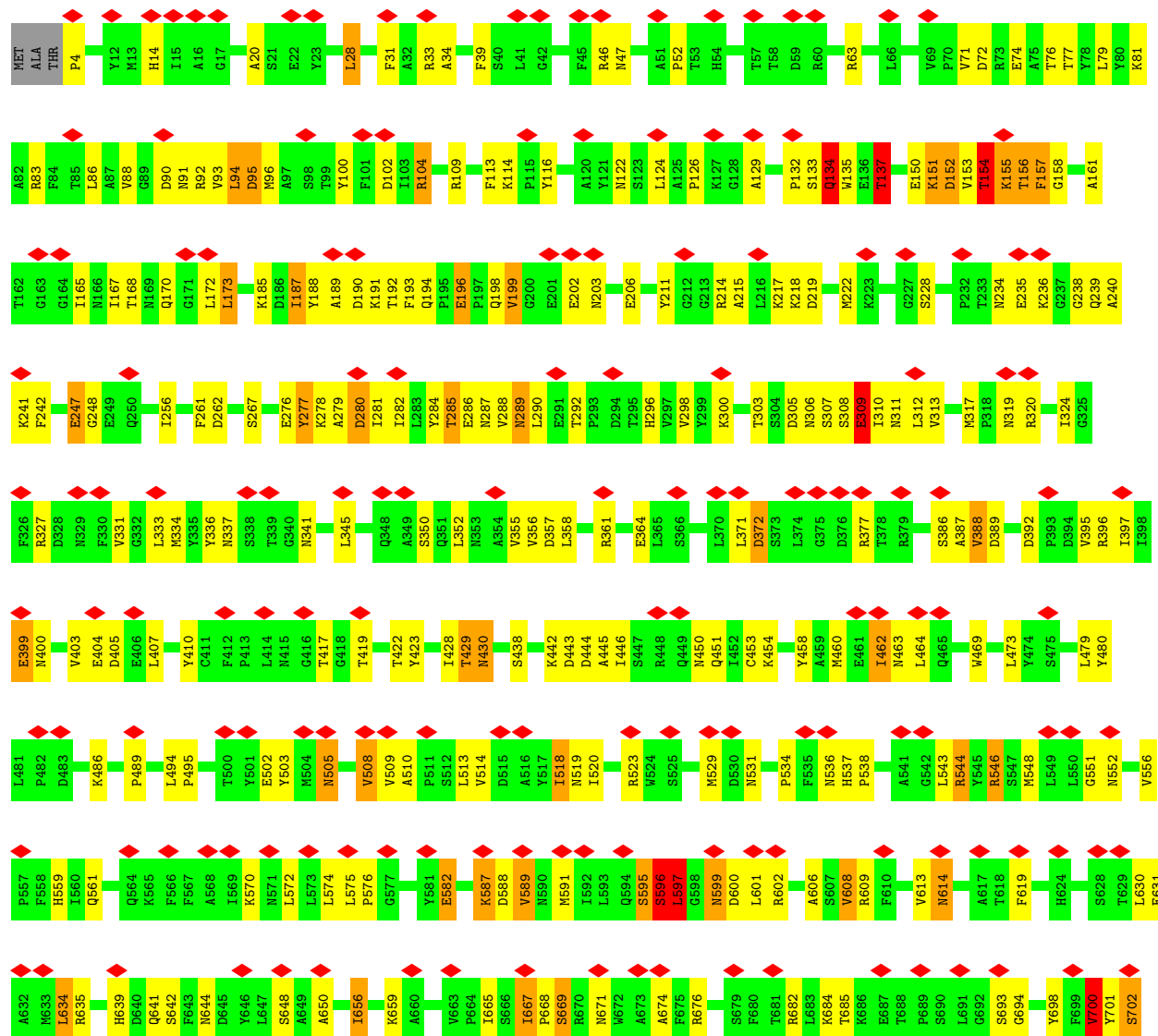


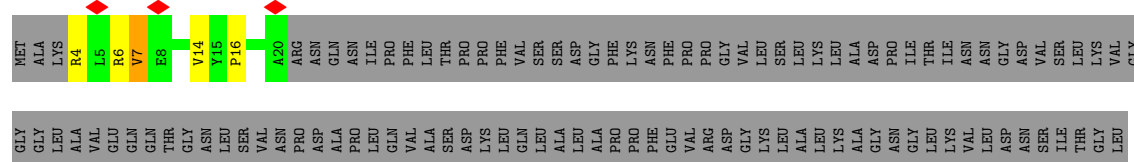
• Molecule 1: Hexon protein

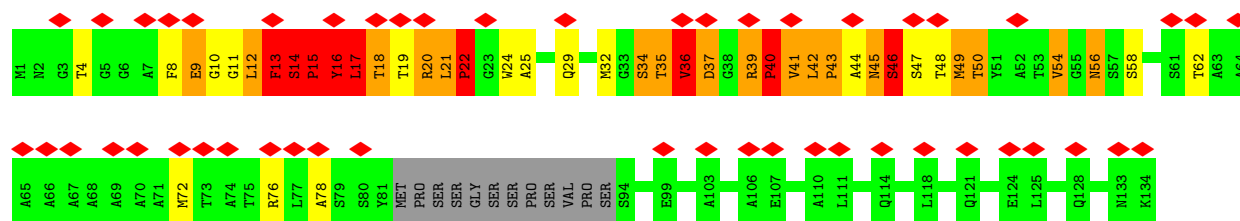




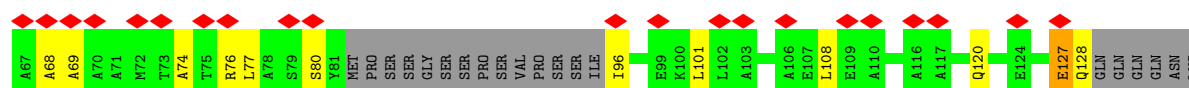
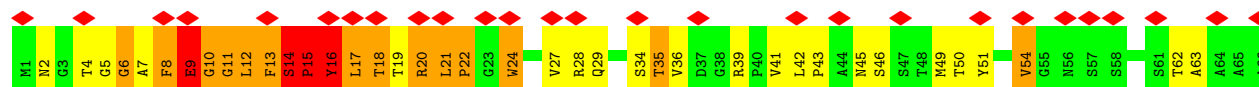
• Molecule 1: Hexon protein



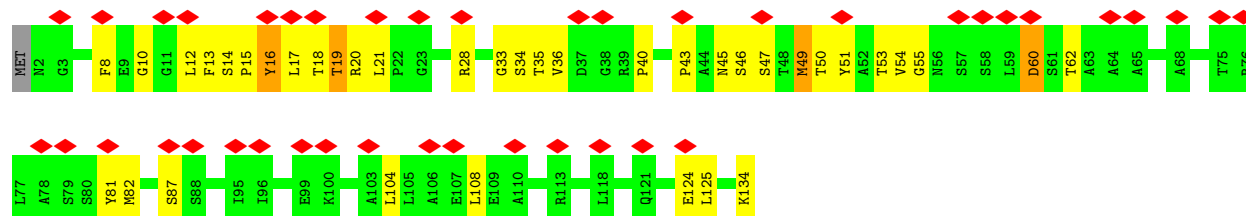




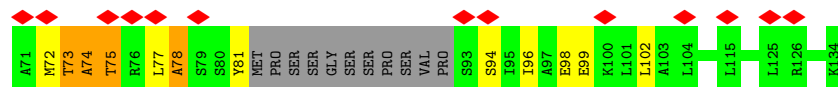
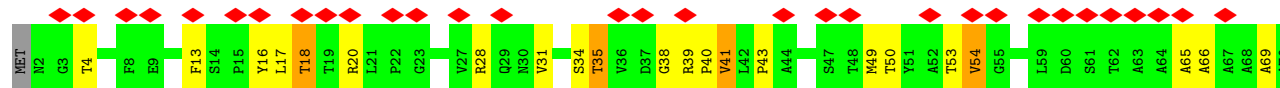
• Molecule 5: PIX



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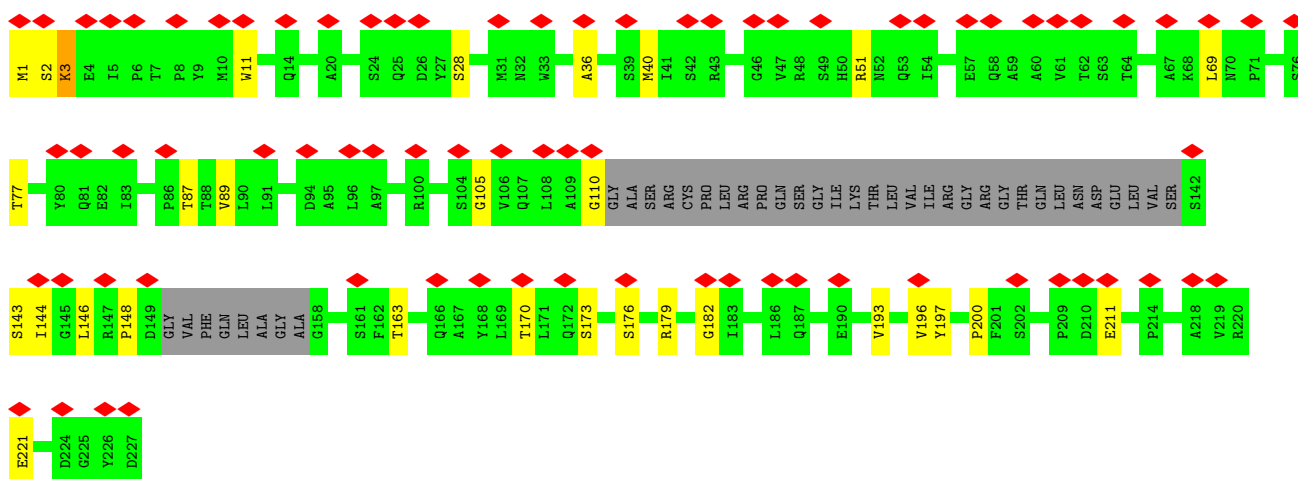
• Molecule 5: PIX



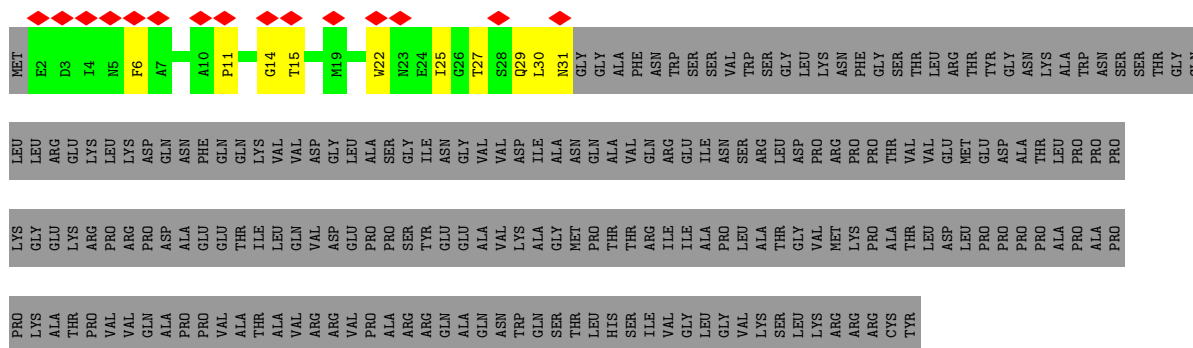
• Molecule 6: PVIII



- Molecule 6: PVIII

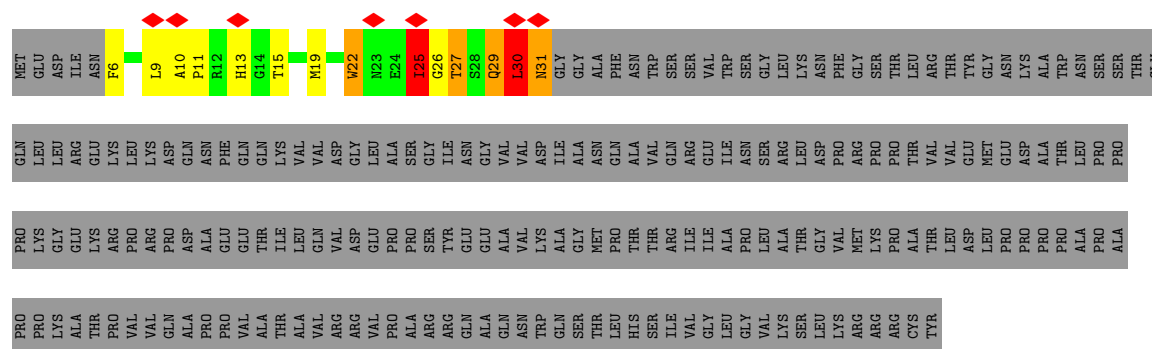


- Molecule 7: Pre-protein VI

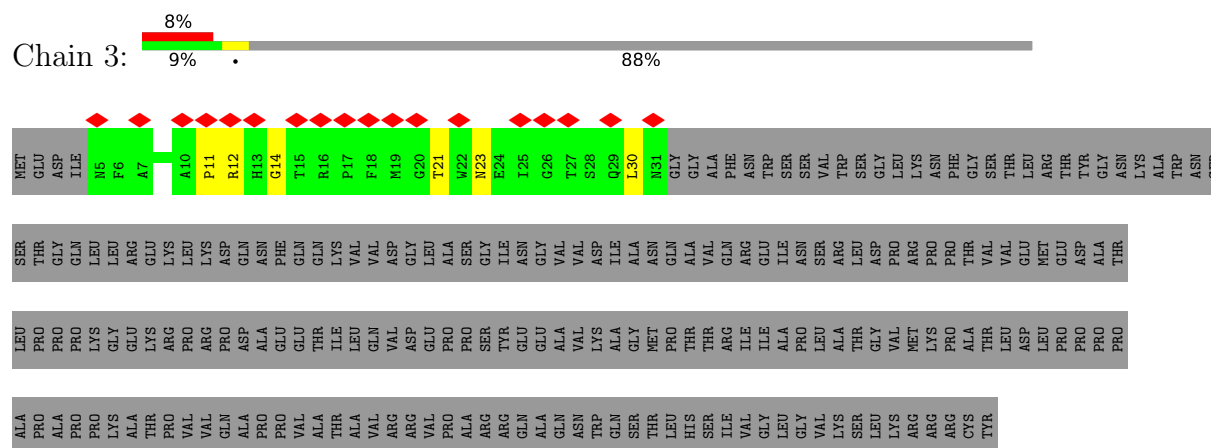


- Molecule 7: Pre-protein VI

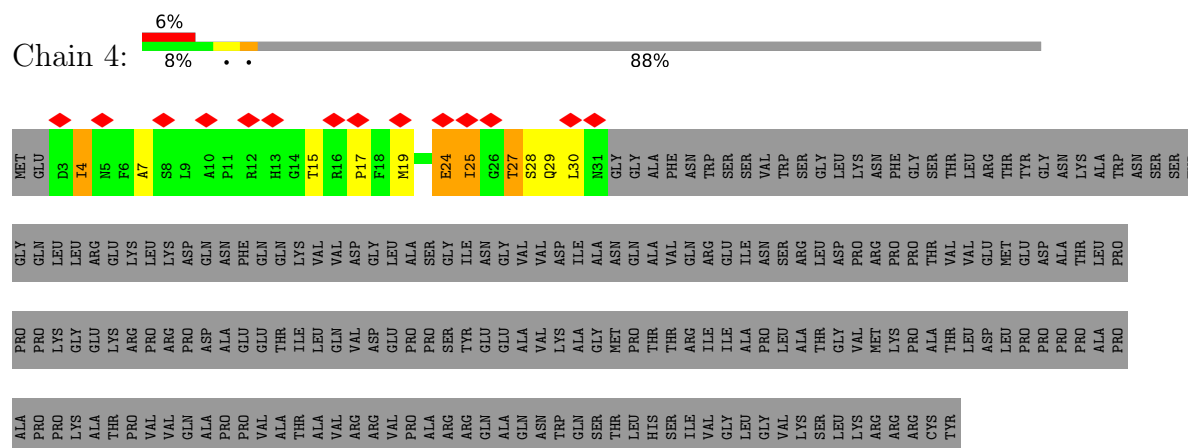




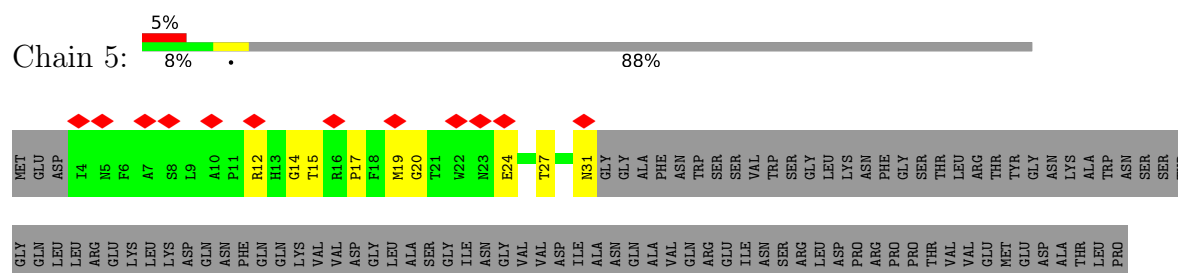
• Molecule 7: Pre-protein VI

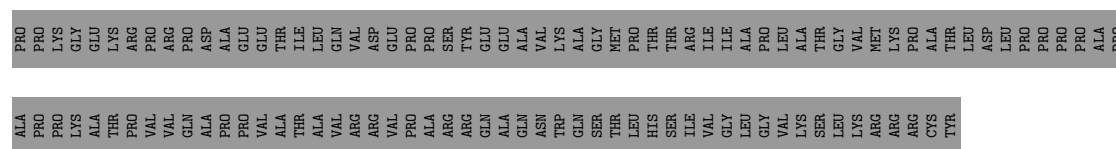


• Molecule 7: Pre-protein VI

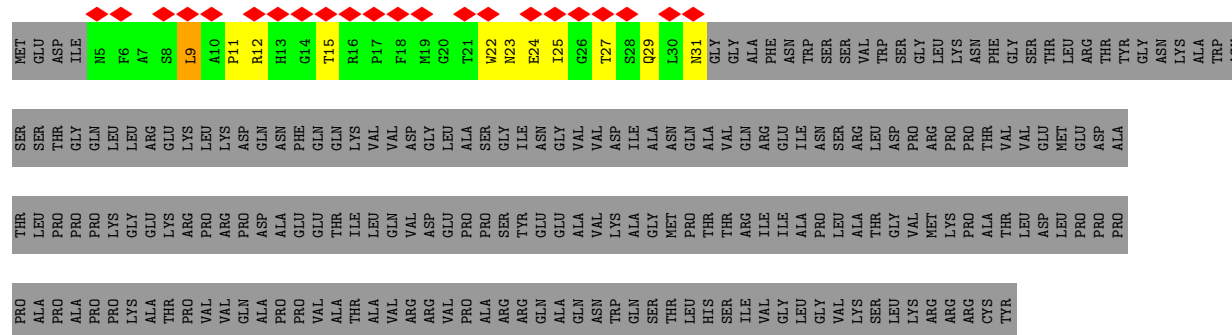


• Molecule 7: Pre-protein VI

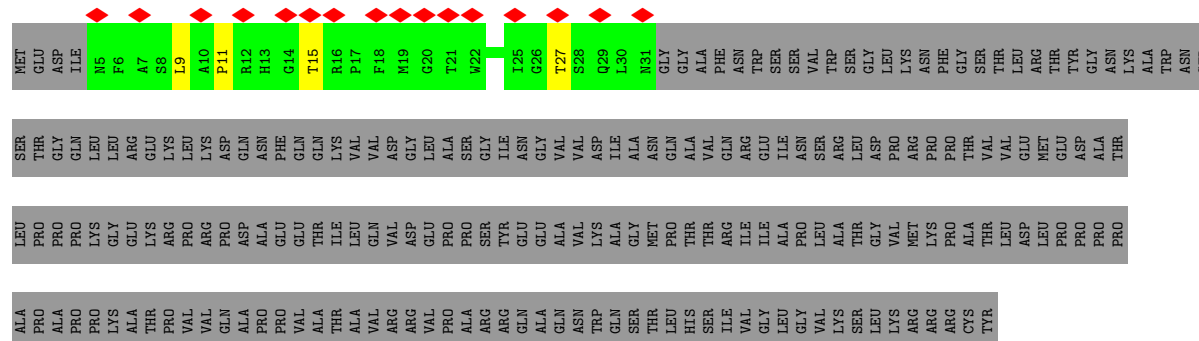




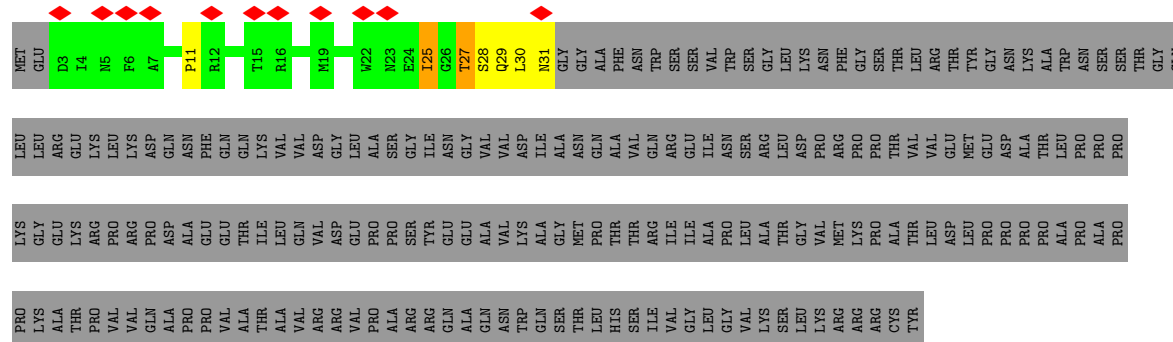
• Molecule 7: Pre-protein VI



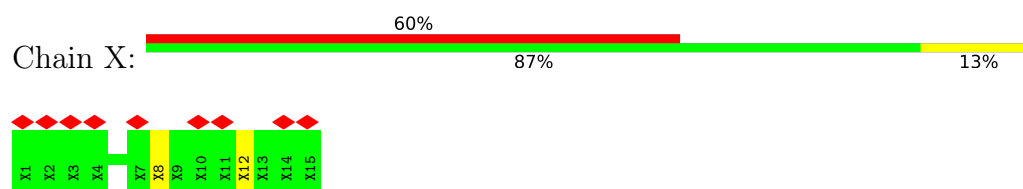
• Molecule 7: Pre-protein VI



• Molecule 7: Pre-protein VI



• Molecule 7: Pre-protein VI



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	30834	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	54.450	Depositor
Minimum map value	-32.776	Depositor
Average map value	-0.056	Depositor
Map value standard deviation	3.692	Depositor
Recommended contour level	1.8	Depositor
Map size ($\text{\AA}$)	1089.9199, 1089.9199, 1089.9199	wwPDB
Map dimensions	832, 832, 832	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.31, 1.31, 1.31	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.55	24/7758 (0.3%)	0.54	15/10554 (0.1%)
1	B	0.66	28/7743 (0.4%)	0.63	20/10534 (0.2%)
1	C	0.53	20/7726 (0.3%)	0.49	5/10509 (0.0%)
1	D	0.80	49/7732 (0.6%)	0.66	30/10517 (0.3%)
1	E	0.63	25/7732 (0.3%)	0.56	14/10517 (0.1%)
1	F	0.72	33/7746 (0.4%)	0.60	21/10537 (0.2%)
1	G	0.62	29/7732 (0.4%)	0.58	8/10517 (0.1%)
1	H	0.74	39/7732 (0.5%)	0.64	20/10517 (0.2%)
1	I	0.94	71/7743 (0.9%)	0.73	31/10534 (0.3%)
1	J	0.65	27/7758 (0.3%)	0.59	16/10554 (0.2%)
1	K	0.87	76/7753 (1.0%)	0.62	21/10547 (0.2%)
1	L	0.75	40/7731 (0.5%)	0.64	27/10516 (0.3%)
2	N	0.88	20/3879 (0.5%)	0.77	21/5280 (0.4%)
3	O	0.91	1/152 (0.7%)	1.10	1/207 (0.5%)
4	M	0.94	17/2884 (0.6%)	0.83	20/3926 (0.5%)
5	P	2.05	33/898 (3.7%)	1.96	42/1216 (3.5%)
5	Q	1.63	18/830 (2.2%)	1.52	25/1127 (2.2%)
5	R	0.20	0/970	0.41	0/1318
5	S	0.57	1/896 (0.1%)	0.81	3/1214 (0.2%)
6	U	1.45	40/1499 (2.7%)	0.93	10/2041 (0.5%)
6	V	0.25	0/1486	0.37	0/2023
7	1	0.16	0/242	0.50	0/328
7	2	1.44	5/209 (2.4%)	2.12	4/283 (1.4%)
7	3	0.16	0/217	0.33	0/294
7	4	1.13	2/233 (0.9%)	1.19	5/316 (1.6%)
7	5	0.14	0/225	0.32	0/305
7	6	0.84	0/217	1.00	2/294 (0.7%)
7	7	0.15	0/217	0.33	0/294
7	8	0.84	1/233 (0.4%)	1.43	4/316 (1.3%)
7	9	0.18	0/225	0.31	0/305
All	All	0.77	599/108398 (0.6%)	0.67	365/147440 (0.2%)

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	D	0	3
1	K	0	1
1	L	0	1
2	N	0	3
4	M	0	1
All	All	0	9

All (599) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	P	17	LEU	CA-C	-17.95	1.33	1.53
5	Q	17	LEU	CA-C	-14.38	1.33	1.52
5	P	15	PRO	CA-C	-12.61	1.34	1.52
2	N	185	TYR	CA-C	-12.32	1.37	1.52
5	Q	13	PHE	CA-C	-12.04	1.35	1.52
5	P	34	SER	CA-C	-11.86	1.36	1.52
1	I	155	LYS	CA-C	-11.34	1.40	1.53
1	I	746	LYS	CA-C	-11.28	1.40	1.53
1	K	16	ALA	CA-C	-11.15	1.43	1.53
5	P	16	TYR	N-CA	-11.13	1.32	1.46
5	P	14	SER	CA-C	-11.00	1.38	1.52
1	I	875	PHE	CA-C	-11.00	1.42	1.53
1	I	157	PHE	CA-C	-10.88	1.39	1.53
1	H	155	LYS	CA-C	-10.84	1.40	1.53
1	G	192	THR	CA-C	-10.84	1.38	1.52
1	K	631	GLU	CA-C	-10.74	1.38	1.52
1	G	194	GLN	C-N	-10.72	1.24	1.33
5	Q	9	GLU	CA-C	-10.62	1.38	1.52
5	P	42	LEU	CA-C	-10.56	1.39	1.52
1	F	202	GLU	CA-C	-10.36	1.40	1.53
1	D	474	TYR	CA-C	-10.34	1.40	1.52
1	C	595	SER	CA-C	-10.18	1.40	1.52
1	K	648	SER	CA-C	-10.14	1.42	1.53
5	P	37	ASP	CA-C	-10.01	1.40	1.52
5	P	13	PHE	CA-C	-9.95	1.40	1.52
1	H	154	THR	N-CA	-9.94	1.34	1.46
1	D	473	LEU	CA-C	-9.93	1.40	1.52
5	P	35	THR	CA-C	-9.79	1.40	1.52
1	L	945	PHE	CA-C	-9.69	1.41	1.52
5	Q	15	PRO	CA-C	-9.66	1.38	1.52
1	L	133	SER	CA-CB	-9.65	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	630	LEU	CA-C	-9.64	1.40	1.52
1	G	194	GLN	CA-C	-9.63	1.40	1.52
2	N	185	TYR	C-O	-9.61	1.13	1.24
5	P	14	SER	C-O	-9.50	1.15	1.24
1	H	151	LYS	CA-C	-9.49	1.43	1.53
5	P	36	VAL	N-CA	-9.49	1.33	1.46
1	F	763	LYS	CA-C	-9.47	1.39	1.52
5	P	22	PRO	CA-C	-9.44	1.42	1.52
1	I	615	LEU	CA-C	-9.41	1.41	1.52
1	K	194	GLN	CA-C	-9.36	1.43	1.53
1	K	12	TYR	CA-C	-9.35	1.40	1.52
1	J	824	ASN	CA-C	-9.32	1.41	1.52
1	J	335	TYR	CA-C	-9.23	1.41	1.52
1	J	803	ARG	CA-C	-9.23	1.41	1.52
1	D	473	LEU	C-O	-9.20	1.13	1.24
1	B	239	GLN	CA-C	-9.14	1.41	1.53
1	D	826	SER	CA-C	-9.10	1.41	1.52
1	D	803	ARG	CA-C	-9.09	1.41	1.52
1	I	154	THR	N-CA	-9.05	1.35	1.46
1	F	826	SER	CA-C	-9.02	1.41	1.52
6	U	20	ALA	CA-C	-9.01	1.40	1.53
1	D	478	ALA	CA-C	-9.01	1.40	1.52
5	Q	15	PRO	CA-CB	-9.01	1.41	1.53
1	F	759	CYS	CA-C	-8.79	1.42	1.53
1	I	156	THR	CA-C	-8.79	1.41	1.52
1	D	475	SER	CA-C	-8.77	1.42	1.52
5	P	22	PRO	CA-CB	-8.73	1.42	1.53
5	Q	13	PHE	CA-CB	-8.68	1.42	1.54
1	G	459	ALA	CA-C	-8.67	1.41	1.52
7	4	24	GLU	CA-C	-8.58	1.43	1.53
2	N	187	GLN	C-O	8.54	1.33	1.24
1	K	192	THR	CA-C	-8.40	1.41	1.52
1	L	151	LYS	CA-C	-8.40	1.41	1.52
1	G	194	GLN	N-CA	-8.39	1.37	1.46
1	H	153	VAL	CA-C	-8.37	1.42	1.52
1	E	337	ASN	CA-C	-8.36	1.42	1.53
5	Q	22	PRO	CA-C	-8.30	1.43	1.52
1	E	338	SER	CA-C	-8.28	1.42	1.52
5	Q	21	LEU	CA-C	-8.28	1.43	1.53
1	K	630	LEU	C-O	-8.27	1.14	1.24
1	K	650	ALA	CA-C	-8.24	1.42	1.52
1	J	320	ARG	CA-C	-8.23	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	U	58	GLN	CA-C	-8.21	1.42	1.52
1	G	454	LYS	CA-C	-8.20	1.45	1.53
5	P	21	LEU	CA-C	-8.20	1.44	1.53
1	C	594	GLN	CA-C	-8.16	1.43	1.52
1	D	766	PHE	CA-C	-8.15	1.42	1.52
1	B	240	ALA	N-CA	-8.11	1.35	1.45
1	I	328	ASP	CA-C	-8.11	1.42	1.52
1	I	878	ASN	CA-C	-8.11	1.42	1.52
1	F	716	HIS	CA-C	-8.10	1.41	1.52
1	I	329	ASN	CA-C	-8.06	1.42	1.53
1	D	472	PHE	CA-C	-8.04	1.42	1.52
1	G	459	ALA	CA-CB	-8.04	1.41	1.53
1	C	702	SER	CA-C	-8.03	1.43	1.52
1	L	155	LYS	CA-C	-8.01	1.41	1.53
1	I	745	ILE	C-O	-7.99	1.16	1.24
6	U	17	MET	CA-C	-7.98	1.41	1.52
5	Q	12	LEU	CA-C	-7.98	1.44	1.52
1	F	203	ASN	CA-C	-7.98	1.42	1.52
5	P	18	THR	CA-C	-7.94	1.42	1.52
7	2	30	LEU	CA-C	-7.94	1.42	1.52
2	N	387	TRP	CA-C	-7.94	1.43	1.52
1	B	454	LYS	CA-C	-7.91	1.43	1.52
1	L	944	PRO	CA-CB	-7.86	1.42	1.53
1	L	154	THR	N-CA	-7.86	1.35	1.45
1	K	197	PRO	CA-C	-7.83	1.41	1.52
1	K	840	GLN	CA-C	-7.79	1.44	1.52
5	P	19	THR	N-CA	-7.78	1.36	1.46
1	K	631	GLU	C-O	-7.76	1.15	1.24
1	C	328	ASP	CA-C	-7.76	1.42	1.52
1	A	240	ALA	CA-C	-7.75	1.43	1.52
1	K	193	PHE	CA-CB	-7.73	1.42	1.52
1	K	639	HIS	CA-CB	-7.70	1.43	1.53
1	G	193	PHE	N-CA	-7.66	1.36	1.46
1	E	324	ILE	C-O	-7.65	1.16	1.24
4	M	116	LEU	C-O	-7.64	1.15	1.24
1	L	133	SER	CA-C	-7.60	1.46	1.53
5	P	35	THR	N-CA	-7.55	1.37	1.46
1	A	132	PRO	CA-C	-7.54	1.44	1.52
1	L	600	ASP	CA-C	-7.50	1.42	1.52
1	H	870	MET	CA-C	-7.49	1.43	1.52
1	I	763	LYS	CA-C	-7.47	1.43	1.52
1	H	716	HIS	CA-C	-7.45	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	920	PHE	CA-C	-7.42	1.43	1.52
1	J	840	GLN	CA-C	-7.41	1.44	1.52
6	U	51	ARG	CA-C	-7.40	1.43	1.52
5	Q	13	PHE	N-CA	-7.39	1.36	1.45
1	D	824	ASN	CA-C	-7.38	1.43	1.53
1	E	320	ARG	CA-C	-7.38	1.44	1.53
1	I	156	THR	N-CA	-7.37	1.37	1.46
1	L	867	ASP	CA-C	-7.37	1.43	1.52
1	I	641	GLN	CA-C	-7.36	1.43	1.53
1	H	718	PHE	C-O	-7.35	1.15	1.23
1	I	640	ASP	CA-C	-7.35	1.43	1.52
1	J	321	PRO	CA-CB	-7.31	1.43	1.53
1	G	191	LYS	CA-C	-7.31	1.43	1.52
1	C	826	SER	CA-C	-7.30	1.43	1.52
1	A	156	THR	CA-C	-7.29	1.43	1.53
1	A	739	THR	CA-C	-7.29	1.43	1.52
1	D	476	ASN	C-O	7.28	1.32	1.24
6	U	24	SER	CA-C	-7.28	1.43	1.52
6	U	49	SER	CA-C	-7.28	1.42	1.52
1	E	794	PHE	CA-C	-7.27	1.43	1.52
1	K	650	ALA	CA-CB	-7.26	1.43	1.53
1	D	482	PRO	CA-C	-7.24	1.44	1.52
1	I	642	SER	C-O	-7.24	1.15	1.23
1	F	825	ASN	CA-C	-7.24	1.43	1.53
1	H	844	ALA	CA-CB	-7.23	1.43	1.53
1	D	477	VAL	CA-C	-7.22	1.44	1.52
1	J	336	TYR	CA-C	-7.19	1.44	1.52
1	K	629	THR	CA-C	-7.19	1.43	1.52
5	P	32	MET	CA-C	-7.18	1.42	1.52
1	E	321	PRO	CA-CB	-7.18	1.44	1.53
1	F	199	VAL	CA-C	-7.15	1.43	1.52
1	L	837	ARG	CA-C	-7.15	1.43	1.52
1	F	717	THR	CA-C	-7.12	1.43	1.53
5	P	15	PRO	N-CA	-7.11	1.38	1.47
1	E	799	GLN	N-CA	-7.11	1.40	1.46
2	N	186	LEU	N-CA	-7.08	1.38	1.46
1	B	824	ASN	CA-C	-7.04	1.44	1.52
1	K	60	ARG	CA-C	-7.04	1.45	1.53
1	F	759	CYS	CA-CB	-7.02	1.44	1.54
6	U	20	ALA	CA-CB	-7.01	1.41	1.53
1	B	826	SER	CA-C	-7.00	1.44	1.52
1	F	204	TRP	N-CA	-7.00	1.37	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	132	PRO	CA-C	-6.99	1.44	1.52
1	L	156	THR	N-CA	-6.98	1.38	1.46
6	U	48	ARG	CA-C	-6.98	1.43	1.52
7	2	26	GLY	N-CA	6.96	1.51	1.44
1	H	872	ARG	CA-C	-6.95	1.44	1.52
1	K	651	ASN	N-CA	-6.95	1.37	1.46
1	L	946	SER	CA-C	-6.95	1.44	1.52
1	C	596	SER	CA-C	-6.92	1.44	1.52
1	B	458	TYR	CA-C	-6.92	1.43	1.52
1	J	336	TYR	N-CA	-6.90	1.37	1.45
1	E	321	PRO	C-O	-6.89	1.16	1.23
1	J	324	ILE	C-O	-6.87	1.16	1.24
1	I	617	ALA	CA-CB	-6.86	1.42	1.54
4	M	18	PRO	CA-C	-6.85	1.43	1.52
6	U	54	ILE	CA-CB	-6.85	1.45	1.54
1	D	769	GLN	CA-CB	-6.83	1.42	1.53
1	C	825	ASN	CA-C	-6.83	1.44	1.53
6	U	23	ALA	CA-CB	-6.83	1.42	1.53
1	K	919	LEU	C-O	-6.81	1.16	1.24
5	P	13	PHE	N-CA	-6.81	1.38	1.46
2	N	258	GLN	CA-C	-6.81	1.43	1.52
5	Q	22	PRO	CA-CB	-6.81	1.46	1.54
5	Q	19	THR	N-CA	-6.80	1.37	1.46
1	F	46	ARG	CA-C	-6.78	1.44	1.52
1	D	470	LYS	CA-C	-6.78	1.44	1.52
1	D	478	ALA	N-CA	-6.76	1.37	1.45
1	I	876	SER	CA-C	-6.76	1.44	1.52
1	E	322	ASN	C-O	-6.75	1.16	1.23
5	P	43	PRO	CA-C	-6.74	1.44	1.52
1	H	717	THR	CA-C	-6.74	1.44	1.53
1	K	651	ASN	CA-C	-6.74	1.44	1.52
1	K	920	PHE	N-CA	-6.73	1.37	1.46
1	K	640	ASP	CA-C	-6.71	1.44	1.52
1	C	596	SER	C-O	-6.71	1.16	1.24
1	H	714	LEU	CA-C	-6.71	1.42	1.52
1	G	702	SER	CA-CB	-6.70	1.43	1.54
2	N	45	SER	CA-C	-6.70	1.44	1.52
1	F	871	TRP	N-CA	-6.69	1.37	1.46
1	D	768	VAL	CA-CB	-6.69	1.45	1.54
1	G	458	TYR	CA-C	-6.69	1.44	1.52
1	I	612	SER	C-O	-6.69	1.16	1.23
4	M	105	ASN	CA-C	-6.69	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	241	LYS	N-CA	-6.68	1.37	1.46
6	U	25	GLN	CA-C	-6.68	1.44	1.52
1	B	825	ASN	CA-C	-6.68	1.44	1.53
1	G	328	ASP	C-O	-6.67	1.15	1.23
5	Q	16	TYR	N-CA	-6.66	1.36	1.45
1	D	834	PRO	CA-CB	-6.66	1.48	1.53
1	L	599	ASN	CA-C	-6.65	1.44	1.53
2	N	184	ASN	CA-C	-6.64	1.44	1.52
4	M	108	ASN	CA-C	-6.64	1.44	1.52
1	G	287	ASN	CA-C	-6.62	1.44	1.53
1	I	641	GLN	N-CA	-6.62	1.36	1.45
1	K	921	GLU	C-O	-6.60	1.15	1.23
1	A	155	LYS	CA-C	-6.58	1.44	1.53
1	I	639	HIS	CA-CB	-6.57	1.44	1.52
1	K	628	SER	CA-CB	-6.57	1.42	1.53
1	F	759	CYS	C-O	-6.55	1.18	1.24
5	P	15	PRO	C-O	-6.55	1.15	1.24
1	I	886	THR	CA-C	-6.54	1.44	1.52
1	E	799	GLN	C-O	-6.54	1.17	1.24
6	U	14	GLN	CA-C	-6.53	1.44	1.52
1	K	63	ARG	CA-C	-6.52	1.44	1.52
1	H	122	ASN	CA-C	-6.52	1.44	1.53
1	I	637	ASP	CA-C	-6.51	1.44	1.52
6	U	42	SER	CA-C	-6.51	1.44	1.52
1	D	400	ASN	CA-C	-6.50	1.45	1.53
1	I	44	LYS	C-O	-6.50	1.17	1.23
4	M	395	TYR	C-O	-6.50	1.16	1.24
1	E	321	PRO	CA-C	-6.50	1.43	1.52
1	G	190	ASP	CA-C	-6.50	1.46	1.52
1	K	16	ALA	CA-CB	-6.50	1.41	1.52
1	A	743	PHE	CA-C	-6.50	1.44	1.52
1	H	867	ASP	CA-C	-6.47	1.44	1.52
6	U	12	SER	CA-CB	-6.47	1.42	1.53
1	H	156	THR	N-CA	-6.46	1.38	1.46
1	H	156	THR	CA-C	-6.45	1.44	1.52
1	A	837	ARG	CA-C	-6.45	1.44	1.52
5	P	44	ALA	N-CA	-6.44	1.38	1.46
1	K	193	PHE	N-CA	-6.43	1.38	1.46
1	K	651	ASN	CA-CB	-6.43	1.44	1.53
1	I	641	GLN	C-O	-6.43	1.15	1.23
1	B	240	ALA	CA-C	-6.43	1.44	1.52
4	M	126	GLN	CA-C	-6.42	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	871	TRP	N-CA	-6.40	1.38	1.46
5	Q	16	TYR	CA-CB	-6.39	1.44	1.54
1	E	336	TYR	CA-C	-6.38	1.45	1.52
1	F	762	THR	CA-C	-6.38	1.44	1.53
1	F	714	LEU	CA-C	-6.36	1.44	1.53
1	I	761	MET	CA-C	-6.35	1.44	1.52
6	U	47	VAL	CA-CB	-6.35	1.46	1.54
1	B	717	THR	CA-C	-6.34	1.45	1.53
1	K	649	ALA	CA-C	-6.33	1.44	1.52
5	Q	20	ARG	CA-C	-6.33	1.44	1.52
1	D	478	ALA	CA-CB	-6.33	1.45	1.54
1	H	158	GLY	C-N	-6.33	1.25	1.33
1	J	338	SER	CA-C	-6.32	1.44	1.52
1	I	328	ASP	C-O	-6.31	1.16	1.23
1	K	915	LEU	C-O	-6.31	1.16	1.23
3	O	16	PRO	CA-C	-6.31	1.45	1.52
5	Q	14	SER	CA-C	-6.31	1.44	1.52
2	N	186	LEU	CA-C	-6.30	1.44	1.52
1	L	596	SER	C-O	-6.30	1.16	1.23
2	N	389	LEU	CA-C	-6.30	1.46	1.52
1	F	718	PHE	C-N	-6.29	1.27	1.33
1	F	870	MET	CA-C	-6.27	1.45	1.52
1	I	157	PHE	N-CA	-6.27	1.38	1.46
1	I	743	PHE	CA-C	-6.27	1.45	1.52
1	I	762	THR	CA-C	-6.25	1.44	1.53
1	I	642	SER	CA-CB	-6.25	1.43	1.53
1	K	632	ALA	CA-CB	-6.25	1.43	1.53
6	U	25	GLN	N-CA	-6.25	1.37	1.46
1	I	330	PHE	N-CA	-6.24	1.37	1.46
1	D	474	TYR	C-O	-6.23	1.17	1.24
1	I	744	GLU	C-O	-6.22	1.16	1.24
2	N	98	ILE	CA-C	-6.22	1.45	1.52
1	H	157	PHE	N-CA	-6.22	1.38	1.45
1	I	616	TYR	N-CA	-6.21	1.38	1.46
1	F	867	ASP	CA-C	-6.21	1.45	1.52
1	H	157	PHE	CA-C	-6.19	1.45	1.52
6	U	45	ASN	C-O	-6.19	1.16	1.24
1	F	48	PRO	CA-CB	-6.19	1.45	1.53
1	K	919	LEU	CA-C	-6.19	1.45	1.52
1	D	805	VAL	CA-CB	-6.18	1.46	1.54
1	G	703	GLY	C-O	-6.17	1.17	1.23
1	B	448	ARG	CA-C	-6.17	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	156	THR	CA-C	-6.16	1.44	1.52
1	F	762	THR	C-O	-6.16	1.15	1.23
1	L	836	MET	CA-C	-6.15	1.44	1.53
1	J	803	ARG	C-O	-6.14	1.16	1.23
1	I	535	PHE	CA-C	-6.14	1.43	1.52
1	B	826	SER	CA-CB	-6.13	1.44	1.53
1	B	453	CYS	CA-C	-6.13	1.44	1.52
1	J	316	SER	C-O	-6.10	1.16	1.24
2	N	385	VAL	CA-C	-6.09	1.45	1.52
1	C	701	TYR	CA-C	-6.09	1.45	1.52
1	K	638	THR	CA-C	-6.08	1.44	1.52
1	D	838	GLN	CA-C	-6.07	1.45	1.52
1	F	844	ALA	CA-C	-6.07	1.45	1.53
1	L	596	SER	CA-CB	-6.06	1.43	1.53
1	L	596	SER	CA-C	-6.05	1.45	1.53
1	F	843	PRO	CA-CB	-6.05	1.45	1.53
1	I	327	ARG	CA-C	-6.05	1.45	1.53
1	L	137	THR	CA-C	-6.04	1.47	1.53
6	U	11	TRP	C-O	-6.03	1.16	1.24
1	I	879	PHE	CA-C	-6.02	1.43	1.52
1	L	715	ASN	CA-C	-6.02	1.44	1.52
1	L	714	LEU	CA-C	-6.01	1.45	1.52
1	D	401	HIS	CA-C	-6.01	1.44	1.52
1	F	869	VAL	C-O	-6.01	1.18	1.24
6	U	11	TRP	CA-C	-6.00	1.45	1.52
1	C	702	SER	CA-CB	-6.00	1.44	1.53
1	K	844	ALA	CA-C	-6.00	1.45	1.53
1	G	701	TYR	C-O	-5.99	1.17	1.23
6	U	41	ILE	CA-C	-5.98	1.45	1.52
1	E	316	SER	C-O	-5.97	1.17	1.24
1	K	639	HIS	C-O	-5.97	1.16	1.23
1	C	329	ASN	CA-C	-5.97	1.44	1.53
1	K	650	ALA	N-CA	-5.97	1.39	1.46
1	L	838	GLN	CA-C	-5.97	1.45	1.52
6	U	52	ASN	N-CA	-5.97	1.39	1.46
1	C	824	ASN	CA-C	-5.97	1.45	1.52
1	K	14	HIS	CA-CB	-5.96	1.44	1.53
1	E	717	THR	CA-CB	-5.96	1.45	1.52
1	D	479	LEU	CA-C	-5.96	1.44	1.52
1	J	316	SER	CA-C	-5.96	1.45	1.52
1	I	46	ARG	CA-C	-5.96	1.45	1.52
7	4	25	ILE	CA-C	-5.95	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Q	18	THR	CA-C	-5.94	1.44	1.52
2	N	182	LEU	C-O	-5.93	1.16	1.24
1	D	403	VAL	CA-CB	-5.92	1.47	1.54
1	L	943	THR	CA-C	-5.92	1.45	1.52
1	B	446	ILE	CA-C	-5.92	1.45	1.52
1	K	64	LEU	CA-C	-5.91	1.45	1.52
1	H	770	MET	CA-CB	-5.90	1.44	1.53
1	K	639	HIS	CA-C	-5.89	1.45	1.53
1	I	765	TRP	CA-C	-5.88	1.45	1.52
1	J	803	ARG	CA-CB	-5.88	1.43	1.53
2	N	44	TYR	CA-C	-5.88	1.45	1.52
2	N	190	ARG	CA-C	-5.88	1.45	1.52
1	I	614	ASN	C-O	-5.87	1.17	1.23
1	B	132	PRO	CA-C	-5.86	1.45	1.52
2	N	488	ARG	CA-C	-5.85	1.45	1.52
1	D	402	GLY	CA-C	-5.85	1.45	1.52
1	I	639	HIS	CA-C	-5.84	1.47	1.53
1	K	632	ALA	N-CA	-5.84	1.39	1.46
1	E	341	ASN	CA-C	-5.84	1.45	1.53
1	K	631	GLU	N-CA	-5.83	1.39	1.46
1	J	805	VAL	CA-CB	-5.83	1.45	1.54
1	K	844	ALA	CA-CB	-5.83	1.44	1.53
1	F	761	MET	CA-C	-5.82	1.45	1.53
4	M	395	TYR	CA-C	-5.82	1.45	1.52
1	C	704	SER	CA-C	-5.82	1.45	1.52
1	I	157	PHE	C-N	-5.81	1.28	1.33
1	D	834	PRO	N-CA	-5.81	1.43	1.47
1	K	195	PRO	CA-CB	-5.81	1.45	1.53
7	2	22	TRP	CA-C	-5.81	1.44	1.52
1	B	238	GLY	CA-C	-5.81	1.46	1.52
6	U	23	ALA	CA-C	-5.81	1.45	1.52
1	F	844	ALA	CA-CB	-5.80	1.44	1.53
1	A	838	GLN	CA-C	-5.80	1.45	1.52
1	I	744	GLU	CA-C	-5.79	1.45	1.52
1	K	193	PHE	CA-C	-5.78	1.45	1.52
1	D	825	ASN	CA-C	-5.77	1.45	1.53
1	I	47	ASN	C-O	-5.77	1.18	1.24
1	F	824	ASN	CA-C	-5.76	1.45	1.52
1	G	701	TYR	CA-C	-5.76	1.45	1.52
1	H	715	ASN	N-CA	-5.76	1.38	1.46
1	G	328	ASP	CA-C	-5.76	1.45	1.52
2	N	264	PHE	CA-C	-5.75	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	317	MET	CA-C	-5.75	1.46	1.52
1	D	766	PHE	C-O	-5.74	1.17	1.24
1	B	826	SER	N-CA	-5.73	1.38	1.46
1	I	330	PHE	CA-C	-5.73	1.45	1.53
1	L	671	ASN	CA-C	-5.73	1.45	1.52
1	K	637	ASP	CA-C	-5.72	1.45	1.52
1	D	834	PRO	CA-C	-5.72	1.46	1.53
5	P	42	LEU	C-N	-5.72	1.27	1.33
6	U	18	GLY	CA-C	-5.71	1.45	1.51
1	I	763	LYS	N-CA	-5.70	1.39	1.46
1	D	835	THR	CA-C	-5.70	1.47	1.53
1	K	631	GLU	CA-CB	-5.70	1.44	1.53
1	I	765	TRP	N-CA	-5.70	1.39	1.46
1	I	887	ASP	CA-C	-5.70	1.45	1.52
1	B	444	ASP	CA-C	-5.69	1.45	1.52
6	U	40	MET	N-CA	-5.69	1.39	1.46
1	C	596	SER	N-CA	-5.69	1.39	1.46
6	U	23	ALA	N-CA	-5.68	1.39	1.46
1	G	195	PRO	N-CA	-5.68	1.40	1.47
1	A	739	THR	C-O	-5.67	1.19	1.24
6	U	54	ILE	C-O	-5.67	1.17	1.24
1	K	188	TYR	CA-C	-5.67	1.45	1.52
1	K	917	TYR	C-O	-5.66	1.15	1.23
1	J	805	VAL	CA-C	-5.66	1.46	1.52
1	G	329	ASN	C-O	-5.66	1.16	1.24
1	F	870	MET	C-O	-5.65	1.17	1.24
6	U	41	ILE	CA-CB	-5.65	1.47	1.54
1	A	240	ALA	N-CA	-5.64	1.39	1.46
1	K	921	GLU	CA-CB	-5.63	1.44	1.53
1	C	701	TYR	C-O	-5.63	1.17	1.24
1	D	826	SER	CA-CB	-5.62	1.44	1.53
5	Q	15	PRO	N-CA	-5.62	1.40	1.47
1	J	838	GLN	CA-C	-5.62	1.45	1.52
1	I	153	VAL	CA-C	-5.61	1.45	1.52
7	2	25	ILE	CA-C	5.61	1.59	1.52
5	S	74	ALA	CA-CB	5.60	1.62	1.53
1	D	479	LEU	N-CA	-5.60	1.38	1.46
1	I	48	PRO	CA-C	-5.59	1.45	1.52
6	U	13	TYR	CA-C	-5.59	1.45	1.52
1	H	155	LYS	CA-CB	-5.59	1.45	1.52
1	D	770	MET	CA-C	-5.58	1.44	1.52
1	L	870	MET	CA-C	-5.58	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	617	ALA	CA-C	-5.58	1.45	1.52
1	F	762	THR	CA-CB	-5.56	1.44	1.53
1	K	842	TYR	CA-CB	-5.56	1.46	1.54
1	E	322	ASN	CA-C	-5.56	1.45	1.52
1	J	823	HIS	CA-C	-5.56	1.45	1.53
1	K	649	ALA	CA-CB	-5.54	1.44	1.53
1	B	715	ASN	CA-C	-5.54	1.44	1.52
1	H	154	THR	CA-C	-5.54	1.45	1.52
1	D	804	GLN	CA-C	-5.54	1.46	1.52
1	K	16	ALA	C-O	-5.53	1.18	1.23
1	F	712	PHE	CA-C	-5.52	1.46	1.52
5	P	35	THR	C-N	-5.52	1.27	1.33
1	L	153	VAL	CA-C	-5.51	1.45	1.52
6	U	22	GLY	C-O	-5.51	1.18	1.24
1	A	157	PHE	N-CA	-5.51	1.38	1.46
1	L	155	LYS	C-N	-5.50	1.27	1.33
1	E	715	ASN	CA-C	-5.50	1.45	1.52
1	H	842	TYR	CA-C	-5.50	1.45	1.52
1	C	327	ARG	CA-C	-5.50	1.45	1.53
5	P	40	PRO	CA-C	-5.49	1.44	1.52
1	H	122	ASN	C-O	-5.49	1.16	1.23
1	J	321	PRO	C-O	-5.49	1.17	1.23
4	M	116	LEU	CA-C	-5.48	1.45	1.52
1	H	766	PHE	CA-C	-5.48	1.45	1.52
1	H	844	ALA	CA-C	-5.47	1.45	1.53
1	I	743	PHE	C-O	-5.47	1.17	1.24
1	D	803	ARG	C-O	-5.47	1.17	1.23
1	H	123	SER	CA-C	-5.46	1.45	1.52
1	D	136	GLU	CA-C	-5.46	1.45	1.53
6	U	59	ALA	CA-C	-5.46	1.45	1.52
1	L	871	TRP	C-O	-5.45	1.17	1.23
1	L	669	SER	C-O	-5.45	1.17	1.23
1	I	613	VAL	C-O	-5.44	1.17	1.23
5	P	36	VAL	C-O	-5.44	1.17	1.24
1	A	838	GLN	N-CA	-5.44	1.39	1.46
1	I	879	PHE	N-CA	-5.44	1.38	1.46
1	H	120	ALA	CA-CB	-5.44	1.46	1.54
1	K	187	ILE	CA-C	-5.44	1.45	1.52
1	I	326	PHE	N-CA	-5.43	1.38	1.45
1	J	342	MET	CA-C	-5.43	1.46	1.52
6	U	24	SER	C-O	-5.43	1.17	1.24
1	K	921	GLU	CA-C	-5.43	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	13	MET	CA-CB	-5.42	1.44	1.53
1	D	826	SER	N-CA	-5.42	1.39	1.45
1	G	702	SER	C-O	-5.42	1.16	1.24
1	K	920	PHE	C-O	-5.42	1.17	1.24
1	E	336	TYR	N-CA	-5.42	1.39	1.45
1	B	131	ASN	CA-C	-5.42	1.47	1.53
1	A	136	GLU	CA-C	-5.41	1.45	1.52
1	J	316	SER	CA-CB	-5.41	1.45	1.53
1	D	768	VAL	N-CA	-5.41	1.39	1.46
1	I	762	THR	N-CA	-5.41	1.38	1.45
6	U	54	ILE	CA-C	-5.40	1.45	1.52
1	I	44	LYS	CA-CB	-5.40	1.46	1.53
1	I	746	LYS	CA-CB	-5.40	1.48	1.53
1	L	869	VAL	CA-CB	-5.40	1.45	1.55
1	A	837	ARG	CA-CB	-5.39	1.45	1.53
1	L	702	SER	CA-CB	-5.39	1.45	1.53
1	B	436	GLU	CA-C	-5.39	1.45	1.52
1	K	14	HIS	CA-C	-5.38	1.45	1.53
6	U	24	SER	CA-CB	-5.38	1.44	1.53
1	A	713	TYR	CA-C	-5.38	1.45	1.52
1	H	872	ARG	C-O	-5.38	1.17	1.23
6	U	50	HIS	C-O	-5.38	1.17	1.24
1	I	762	THR	CA-CB	-5.37	1.44	1.53
1	K	843	PRO	CA-C	-5.36	1.46	1.52
1	K	631	GLU	C-N	-5.36	1.26	1.33
1	B	693	SER	CA-C	-5.36	1.45	1.52
1	E	316	SER	CA-CB	-5.36	1.45	1.53
4	M	97	LEU	N-CA	-5.36	1.39	1.46
1	E	796	ARG	CA-C	-5.36	1.45	1.52
1	J	337	ASN	CA-C	-5.35	1.46	1.53
1	I	878	ASN	CA-CB	-5.35	1.45	1.53
1	G	286	GLU	CA-CB	-5.35	1.43	1.54
1	H	713	TYR	CA-C	-5.35	1.46	1.52
1	K	649	ALA	N-CA	-5.35	1.39	1.46
1	K	190	ASP	CA-C	-5.34	1.45	1.52
1	L	716	HIS	CA-C	-5.34	1.44	1.52
5	P	18	THR	C-N	-5.34	1.26	1.33
4	M	109	VAL	CA-C	-5.34	1.46	1.52
1	E	337	ASN	CA-CB	-5.34	1.45	1.53
1	K	61	SER	CA-CB	-5.34	1.44	1.53
1	A	241	LYS	CA-C	-5.33	1.46	1.52
1	C	327	ARG	CA-CB	-5.32	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	616	TYR	C-O	-5.32	1.17	1.23
1	D	137	THR	CA-C	-5.32	1.46	1.52
1	H	135	TRP	CA-C	-5.32	1.46	1.52
1	G	326	PHE	N-CA	-5.32	1.38	1.45
1	E	323	TYR	C-O	-5.31	1.18	1.24
1	I	885	LEU	CA-C	-5.31	1.45	1.52
5	P	15	PRO	CA-CB	-5.31	1.46	1.53
1	I	879	PHE	CA-CB	-5.30	1.45	1.53
1	D	767	LEU	C-O	-5.30	1.17	1.24
6	U	51	ARG	C-O	-5.30	1.18	1.24
1	D	477	VAL	CA-CB	-5.30	1.48	1.54
4	M	19	SER	CA-C	-5.30	1.45	1.52
1	C	596	SER	CA-CB	-5.29	1.45	1.53
1	I	535	PHE	C-O	-5.29	1.17	1.24
1	D	479	LEU	C-O	-5.29	1.17	1.24
1	D	837	ARG	CA-C	-5.29	1.45	1.52
1	A	135	TRP	CA-C	-5.28	1.46	1.52
1	A	717	THR	C-O	-5.28	1.17	1.23
1	D	483	ASP	CA-C	-5.27	1.46	1.52
1	K	843	PRO	CA-CB	-5.27	1.46	1.53
1	G	457	VAL	C-O	-5.27	1.18	1.24
1	I	765	TRP	C-O	-5.26	1.17	1.24
5	P	42	LEU	C-O	-5.26	1.19	1.24
6	U	10	MET	CA-C	-5.25	1.46	1.52
1	H	152	ASP	CA-C	5.24	1.59	1.52
1	J	318	PRO	CA-CB	-5.24	1.46	1.53
1	K	12	TYR	CA-CB	-5.24	1.46	1.53
5	P	41	VAL	CA-C	-5.23	1.46	1.52
5	P	24	TRP	CA-C	-5.23	1.46	1.52
4	M	115	ARG	CA-C	-5.23	1.46	1.52
1	J	804	GLN	C-O	-5.22	1.18	1.24
1	L	702	SER	CA-C	-5.21	1.46	1.53
1	H	868	ARG	CA-CB	-5.21	1.47	1.54
4	M	15	GLN	CA-C	-5.21	1.46	1.52
1	B	459	ALA	CA-C	-5.21	1.46	1.52
1	K	919	LEU	N-CA	-5.20	1.40	1.46
1	E	716	HIS	CA-C	-5.20	1.45	1.52
1	E	795	PHE	CA-C	-5.20	1.46	1.52
1	I	616	TYR	CA-C	-5.19	1.46	1.52
1	H	764	ASP	C-O	-5.19	1.17	1.24
4	M	109	VAL	CA-CB	-5.19	1.48	1.54
1	A	740	PRO	CA-CB	-5.18	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	U	17	MET	C-O	-5.18	1.17	1.24
7	2	29	GLN	CA-CB	-5.18	1.47	1.53
1	H	870	MET	N-CA	-5.17	1.40	1.46
1	J	322	ASN	CA-C	-5.17	1.46	1.52
1	K	632	ALA	CA-C	-5.17	1.46	1.52
1	L	597	LEU	CA-C	-5.17	1.45	1.52
1	D	765	TRP	CA-C	-5.16	1.46	1.52
1	K	13	MET	CA-C	-5.16	1.45	1.52
1	H	154	THR	CA-CB	-5.15	1.45	1.53
1	I	761	MET	C-O	-5.15	1.17	1.23
1	L	947	ALA	CA-C	-5.15	1.46	1.53
1	A	715	ASN	CA-C	-5.15	1.45	1.52
1	G	459	ALA	N-CA	-5.15	1.40	1.46
1	G	704	SER	CA-C	-5.14	1.46	1.52
1	K	62	GLN	CA-C	-5.14	1.46	1.52
1	A	154	THR	N-CA	-5.13	1.39	1.45
1	F	50	VAL	C-O	-5.13	1.19	1.24
1	L	157	PHE	N-CA	-5.13	1.39	1.46
1	I	539	ARG	CA-CB	-5.13	1.46	1.53
1	B	454	LYS	N-CA	-5.12	1.40	1.46
1	H	764	ASP	CA-CB	-5.12	1.45	1.53
1	I	537	HIS	C-O	-5.12	1.18	1.24
4	M	119	ASP	N-CA	-5.12	1.40	1.46
1	B	445	ALA	CA-C	-5.11	1.46	1.53
1	C	329	ASN	C-O	-5.11	1.16	1.23
1	I	617	ALA	C-O	-5.11	1.17	1.23
1	B	450	ASN	CA-C	-5.11	1.46	1.52
1	G	705	ILE	C-O	-5.10	1.18	1.24
2	N	388	SER	CA-C	-5.10	1.46	1.52
2	N	219	VAL	CA-C	-5.09	1.47	1.52
6	U	53	GLN	N-CA	-5.09	1.40	1.46
1	E	318	PRO	C-O	-5.09	1.18	1.23
1	F	46	ARG	C-O	-5.09	1.17	1.23
1	K	628	SER	CA-C	-5.08	1.45	1.52
1	G	329	ASN	N-CA	-5.08	1.39	1.46
1	B	695	PHE	CA-C	-5.08	1.46	1.52
1	L	701	TYR	CA-C	-5.08	1.47	1.52
1	A	742	GLU	CA-C	-5.07	1.46	1.52
1	J	824	ASN	C-N	-5.07	1.26	1.33
1	L	599	ASN	C-O	-5.07	1.17	1.23
1	K	194	GLN	N-CA	-5.07	1.39	1.45
1	D	481	LEU	CA-C	-5.06	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	8	30	LEU	CA-C	-5.06	1.46	1.52
2	N	43	ARG	CA-C	-5.06	1.46	1.52
1	K	188	TYR	N-CA	-5.06	1.40	1.46
1	C	597	LEU	CA-C	-5.06	1.45	1.52
1	K	640	ASP	C-O	-5.06	1.18	1.24
1	K	921	GLU	N-CA	-5.05	1.39	1.46
1	L	597	LEU	N-CA	-5.04	1.39	1.46
1	L	870	MET	C-O	-5.04	1.18	1.24
1	K	62	GLN	C-O	-5.04	1.17	1.23
4	M	96	ALA	CA-CB	-5.04	1.45	1.53
1	F	872	ARG	CA-C	-5.04	1.46	1.52
6	U	44	VAL	CA-CB	-5.03	1.48	1.54
1	B	695	PHE	N-CA	-5.03	1.39	1.46
1	A	156	THR	N-CA	-5.03	1.39	1.45
1	J	286	GLU	CA-CB	-5.03	1.45	1.53
4	M	17	GLN	CA-C	-5.03	1.47	1.52
1	G	455	GLY	CA-C	-5.02	1.46	1.51
6	U	10	MET	CA-CB	-5.02	1.45	1.53
1	H	870	MET	CA-CB	-5.02	1.46	1.53
1	K	12	TYR	C-O	-5.02	1.16	1.23
5	P	39	ARG	N-CA	-5.01	1.37	1.45
1	I	763	LYS	C-O	-5.00	1.18	1.24

All (365) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	2	26	GLY	N-CA-C	27.47	151.25	111.14
5	P	44	ALA	N-CA-C	-24.70	64.52	107.49
5	Q	11	GLY	N-CA-C	-20.59	85.77	113.37
1	G	194	GLN	N-CA-C	-19.00	91.12	108.22
5	P	14	SER	CA-C-N	-16.42	99.32	119.84
5	P	14	SER	C-N-CA	-16.42	99.32	119.84
1	I	156	THR	N-CA-C	16.06	128.48	111.14
5	P	16	TYR	N-CA-C	-16.04	84.71	109.25
1	I	280	ASP	N-CA-C	15.99	131.94	108.60
5	P	42	LEU	CA-C-N	-15.64	103.48	119.90
5	P	42	LEU	C-N-CA	-15.64	103.48	119.90
1	H	152	ASP	N-CA-C	15.49	128.23	111.03
1	G	193	PHE	N-CA-C	-14.90	79.06	110.80
4	M	395	TYR	CA-C-O	14.73	136.04	120.42
1	H	157	PHE	N-CA-C	-14.44	86.69	109.50
1	G	192	THR	N-CA-C	-14.43	95.75	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	8	28	SER	N-CA-C	14.16	130.76	110.23
1	G	194	GLN	CA-C-N	-13.92	106.63	120.83
1	G	194	GLN	C-N-CA	-13.92	106.63	120.83
5	Q	16	TYR	N-CA-C	-13.05	96.76	113.72
7	8	27	THR	N-CA-C	13.02	125.47	111.28
1	D	823	HIS	N-CA-C	12.84	129.68	108.49
1	I	888	LEU	N-CA-C	-11.70	99.39	112.72
1	J	321	PRO	CB-CA-C	-11.38	96.77	111.46
1	B	436	GLU	N-CA-C	-11.32	92.28	109.14
1	D	479	LEU	N-CA-C	-11.00	99.87	113.18
5	P	48	THR	N-CA-C	-10.96	87.45	110.80
4	M	395	TYR	O-C-N	-10.90	109.73	122.15
5	Q	19	THR	N-CA-C	-10.80	93.77	109.96
5	P	11	GLY	N-CA-C	-10.33	88.70	113.18
5	Q	15	PRO	N-CA-C	10.25	133.59	112.47
7	2	27	THR	N-CA-C	10.23	126.08	109.40
1	E	321	PRO	CB-CA-C	-10.23	97.61	111.21
1	A	241	LYS	N-CA-C	-10.22	91.50	108.76
1	K	189	ALA	N-CA-C	10.18	122.13	111.14
1	L	839	GLY	N-CA-C	10.03	124.31	111.37
5	P	20	ARG	N-CA-C	-9.96	97.10	110.55
1	C	703	GLY	N-CA-C	-9.94	95.62	110.42
1	D	771	LEU	N-CA-C	-9.87	101.36	113.50
1	B	455	GLY	N-CA-C	9.59	130.81	115.08
5	Q	20	ARG	N-CA-C	-9.58	93.86	109.96
5	P	17	LEU	N-CA-C	-9.52	95.34	109.62
1	L	943	THR	CA-C-N	-9.44	108.56	118.85
1	L	943	THR	C-N-CA	-9.44	108.56	118.85
4	M	391	PRO	CA-C-N	-9.42	110.71	120.03
4	M	391	PRO	C-N-CA	-9.42	110.71	120.03
5	P	17	LEU	CB-CA-C	-9.39	98.04	112.12
2	N	44	TYR	N-CA-C	-9.32	95.12	109.95
1	E	320	ARG	N-CA-C	9.26	122.86	110.08
1	I	281	ILE	N-CA-C	-9.26	95.59	108.27
1	H	123	SER	N-CA-C	9.16	121.35	111.36
1	I	279	ALA	N-CA-C	-9.12	98.77	110.53
1	D	766	PHE	N-CA-C	-9.11	101.32	111.07
2	N	262	GLU	N-CA-C	9.09	123.92	110.48
5	Q	63	ALA	N-CA-C	9.08	121.18	111.28
1	C	823	HIS	N-CA-C	8.96	127.07	108.53
5	S	66	ALA	N-CA-C	8.92	122.89	112.72
5	S	65	ALA	N-CA-C	8.86	122.82	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	4	27	THR	N-CA-C	8.83	123.62	107.99
1	B	696	ASP	N-CA-C	-8.80	92.30	109.10
1	C	597	LEU	N-CA-C	-8.76	102.50	113.01
1	L	156	THR	N-CA-C	8.69	121.54	111.11
2	N	389	LEU	N-CA-C	-8.69	95.50	109.40
1	C	596	SER	N-CA-C	8.64	120.48	111.14
1	E	316	SER	N-CA-C	8.63	122.49	108.34
1	B	448	ARG	N-CA-C	-8.52	99.85	111.87
5	P	18	THR	CA-C-N	-8.52	108.77	120.87
5	P	18	THR	C-N-CA	-8.52	108.77	120.87
4	M	394	PHE	N-CA-C	-8.51	102.08	111.36
3	O	16	PRO	N-CA-C	-8.51	97.92	111.03
1	J	823	HIS	N-CA-C	8.49	122.50	108.49
5	P	35	THR	N-CA-C	8.48	120.99	108.60
1	B	133	SER	N-CA-C	8.47	120.97	108.60
5	Q	15	PRO	CB-CA-C	-8.46	97.60	111.56
2	N	185	TYR	N-CA-C	-8.45	102.03	111.07
1	I	137	THR	N-CA-C	8.43	119.07	108.45
1	H	137	THR	N-CA-C	8.41	123.13	108.75
1	H	844	ALA	N-CA-C	8.40	122.46	109.60
1	B	694	GLY	N-CA-C	8.40	123.53	112.77
1	I	158	GLY	N-CA-C	8.37	121.15	111.36
1	L	595	SER	O-C-N	-8.32	113.62	123.03
6	U	50	HIS	N-CA-C	-8.30	101.77	112.23
1	K	920	PHE	N-CA-C	-8.26	95.77	109.24
5	P	39	ARG	N-CA-C	-8.24	98.34	110.20
5	P	12	LEU	N-CA-C	8.17	125.44	108.53
1	F	823	HIS	N-CA-C	8.14	121.77	108.26
1	H	717	THR	CB-CA-C	-8.11	98.47	111.28
4	M	393	GLY	N-CA-C	-8.10	104.17	114.37
5	P	21	LEU	N-CA-C	-8.03	99.44	109.64
1	J	840	GLN	CA-C-N	-7.97	112.50	120.31
1	J	840	GLN	C-N-CA	-7.97	112.50	120.31
5	S	69	ALA	N-CA-C	-7.95	102.61	111.28
5	Q	6	GLY	N-CA-C	-7.89	103.89	113.99
2	N	190	ARG	N-CA-C	-7.88	102.69	111.28
1	J	324	ILE	N-CA-C	7.88	119.80	107.28
1	A	839	GLY	N-CA-C	7.87	121.71	110.46
7	6	27	THR	N-CA-C	7.87	121.34	108.52
1	L	945	PHE	N-CA-C	-7.82	96.48	109.07
1	K	14	HIS	N-CA-C	7.81	122.23	112.24
1	I	156	THR	CA-C-N	-7.80	111.55	123.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	156	THR	C-N-CA	-7.80	111.55	123.17
1	I	243	LYS	N-CA-C	-7.77	99.01	110.20
1	B	137	THR	N-CA-C	7.76	118.83	107.88
1	D	477	VAL	CA-C-N	-7.74	110.08	122.24
1	D	477	VAL	C-N-CA	-7.74	110.08	122.24
1	D	483	ASP	N-CA-C	7.73	119.71	111.28
1	L	133	SER	CB-CA-C	-7.73	103.20	114.87
1	I	156	THR	CB-CA-C	-7.71	98.71	110.90
5	P	19	THR	N-CA-C	-7.66	98.94	110.28
1	A	741	ASN	N-CA-C	7.61	119.65	111.36
1	E	321	PRO	CA-C-O	-7.61	112.18	121.31
1	F	203	ASN	CB-CA-C	-7.52	95.45	110.42
7	4	25	ILE	CB-CA-C	-7.50	98.98	111.29
5	P	46	SER	N-CA-C	7.43	126.62	110.80
1	D	478	ALA	CA-C-N	-7.42	107.10	121.58
1	D	478	ALA	C-N-CA	-7.42	107.10	121.58
1	I	46	ARG	CB-CA-C	-7.40	96.99	109.50
1	J	839	GLY	N-CA-C	7.40	121.04	110.46
1	D	475	SER	CA-C-N	-7.37	110.92	120.65
1	D	475	SER	C-N-CA	-7.37	110.92	120.65
1	J	819	LEU	CA-C-N	-7.37	112.60	119.82
1	J	819	LEU	C-N-CA	-7.37	112.60	119.82
1	A	154	THR	N-CA-C	-7.37	100.60	110.55
1	L	702	SER	N-CA-C	7.27	121.70	111.52
1	J	324	ILE	CB-CA-C	-7.20	101.64	110.99
5	Q	18	THR	CA-C-N	-7.18	110.89	120.95
5	Q	18	THR	C-N-CA	-7.18	110.89	120.95
1	I	639	HIS	CB-CA-C	-7.16	101.38	112.12
1	K	840	GLN	CA-C-N	-7.16	111.49	120.51
1	K	840	GLN	C-N-CA	-7.16	111.49	120.51
2	N	493	ASP	N-CA-C	7.16	120.29	109.63
7	2	27	THR	CB-CA-C	-7.16	95.70	109.37
1	B	692	GLY	N-CA-C	-7.14	96.27	113.18
2	N	186	LEU	CA-C-N	-7.12	111.25	120.65
2	N	186	LEU	C-N-CA	-7.12	111.25	120.65
1	H	156	THR	N-CA-C	7.12	118.69	111.07
1	B	429	THR	N-CA-C	7.10	125.93	110.80
1	J	321	PRO	CA-C-O	-7.07	113.28	121.34
1	D	802	SER	N-CA-C	7.07	119.92	108.76
1	E	717	THR	CB-CA-C	-7.03	101.58	112.12
2	N	389	LEU	CA-C-N	-7.01	111.08	119.84
2	N	389	LEU	C-N-CA	-7.01	111.08	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	48	PRO	CB-CA-C	-6.97	101.85	110.98
4	M	395	TYR	N-CA-C	6.97	118.95	111.36
1	I	886	THR	N-CA-C	-6.96	95.97	110.80
5	P	43	PRO	N-CA-C	6.92	121.24	110.80
1	H	842	TYR	CA-C-N	-6.91	112.87	119.85
1	H	842	TYR	C-N-CA	-6.91	112.87	119.85
1	I	538	PRO	N-CA-C	-6.91	103.93	113.53
7	2	25	ILE	CB-CA-C	6.88	121.72	111.26
1	I	612	SER	N-CA-C	6.86	118.98	108.42
5	P	15	PRO	CB-CA-C	-6.86	100.25	111.56
1	K	192	THR	N-CA-C	-6.85	96.22	110.80
1	A	713	TYR	N-CA-C	6.82	120.70	112.38
1	H	154	THR	CB-CA-C	-6.82	99.48	110.79
1	D	833	ALA	CA-C-N	-6.77	112.77	121.91
1	D	833	ALA	C-N-CA	-6.77	112.77	121.91
1	E	336	TYR	N-CA-C	-6.74	99.20	109.85
5	Q	9	GLU	N-CA-C	6.73	125.14	110.80
6	U	22	GLY	N-CA-C	6.73	121.59	112.17
1	L	837	ARG	CB-CA-C	-6.72	99.13	109.89
1	K	60	ARG	N-CA-C	-6.72	99.77	109.31
1	K	637	ASP	N-CA-C	6.71	118.59	111.28
5	P	34	SER	CB-CA-C	-6.70	97.08	110.42
5	P	15	PRO	N-CA-C	6.69	126.24	112.47
1	J	336	TYR	N-CA-C	-6.68	99.04	109.72
1	D	399	GLU	N-CA-C	6.67	121.54	113.41
1	D	474	TYR	CA-C-O	-6.66	114.00	121.00
1	D	403	VAL	CB-CA-C	-6.65	100.78	110.63
1	K	636	ASN	N-CA-C	-6.63	99.11	109.72
1	L	943	THR	N-CA-C	6.63	124.46	109.81
6	U	54	ILE	N-CA-C	-6.61	104.04	110.72
2	N	96	GLN	N-CA-C	6.54	119.24	110.35
1	H	840	GLN	N-CA-C	-6.51	102.64	110.13
1	K	915	LEU	CB-CA-C	-6.50	98.75	109.80
1	K	639	HIS	CB-CA-C	-6.46	100.45	111.31
5	Q	12	LEU	CB-CA-C	-6.45	101.82	110.79
5	P	14	SER	CA-C-O	6.45	124.26	118.33
2	N	190	ARG	CA-C-N	-6.44	109.96	120.72
2	N	190	ARG	C-N-CA	-6.44	109.96	120.72
1	K	919	LEU	N-CA-C	-6.43	97.79	108.34
1	K	842	TYR	CA-C-N	-6.42	113.05	119.92
1	K	842	TYR	C-N-CA	-6.42	113.05	119.92
5	P	21	LEU	CA-C-N	-6.42	112.87	120.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	P	21	LEU	C-N-CA	-6.42	112.87	120.13
1	L	154	THR	N-CA-C	-6.41	100.42	110.36
1	F	202	GLU	N-CA-C	-6.39	97.44	108.56
5	Q	8	PHE	N-CA-C	6.39	116.43	108.19
1	L	840	GLN	N-CA-C	-6.38	102.04	110.40
2	N	43	ARG	N-CA-C	6.35	119.30	109.07
1	B	438	SER	N-CA-C	-6.35	98.17	108.52
1	I	243	LYS	CA-C-N	-6.35	113.75	120.03
1	I	243	LYS	C-N-CA	-6.35	113.75	120.03
5	Q	21	LEU	N-CA-C	-6.34	100.34	109.48
1	D	474	TYR	CB-CA-C	-6.34	101.19	110.96
1	D	476	ASN	N-CA-C	6.34	117.88	110.97
1	L	869	VAL	CB-CA-C	-6.33	100.56	110.69
1	I	743	PHE	N-CA-C	-6.32	98.60	108.90
7	4	15	THR	CA-C-N	6.29	129.41	120.49
7	4	15	THR	C-N-CA	6.29	129.41	120.49
1	F	717	THR	CB-CA-C	-6.28	102.40	111.70
1	L	134	GLN	N-CA-C	-6.25	99.22	108.79
1	E	794	PHE	N-CA-C	6.24	117.96	111.03
1	I	746	LYS	CB-CA-C	-6.24	101.44	111.86
5	P	49	MET	N-CA-C	6.22	124.04	110.80
1	F	757	ALA	CA-C-N	-6.22	113.01	122.21
1	F	757	ALA	C-N-CA	-6.22	113.01	122.21
2	N	46	GLU	N-CA-C	6.20	118.12	111.36
1	B	458	TYR	N-CA-C	-6.19	101.77	110.50
1	L	714	LEU	N-CA-C	-6.15	104.41	112.41
4	M	389	LEU	CA-C-N	-6.15	114.05	120.38
4	M	389	LEU	C-N-CA	-6.15	114.05	120.38
1	D	833	ALA	O-C-N	6.15	125.64	121.71
1	D	823	HIS	CB-CA-C	-6.14	102.82	111.85
1	L	667	ILE	CA-C-N	-6.14	112.17	119.84
1	L	667	ILE	C-N-CA	-6.14	112.17	119.84
6	U	18	GLY	N-CA-C	6.13	124.80	113.76
1	F	48	PRO	CB-CA-C	-6.08	103.01	110.98
1	B	823	HIS	N-CA-C	6.08	118.59	108.20
1	L	137	THR	CB-CA-C	-6.08	99.28	114.11
1	F	840	GLN	N-CA-C	-6.07	99.62	109.82
5	Q	62	THR	N-CA-C	6.05	120.08	110.70
5	P	13	PHE	CB-CA-C	-6.04	100.58	110.85
1	D	472	PHE	N-CA-C	-6.00	104.65	111.07
5	Q	9	GLU	CB-CA-C	-5.97	98.54	110.42
1	L	842	TYR	N-CA-C	-5.97	102.85	108.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	185	TYR	CB-CA-C	-5.95	101.53	110.88
1	F	201	GLU	N-CA-C	5.94	117.43	111.07
1	L	717	THR	CB-CA-C	-5.94	101.31	111.41
5	P	22	PRO	CB-CA-C	-5.94	104.16	111.11
4	M	108	ASN	N-CA-C	-5.93	104.90	111.36
1	L	700	VAL	CB-CA-C	-5.92	101.58	111.29
4	M	126	GLN	N-CA-C	-5.92	104.83	111.28
1	A	242	PHE	N-CA-C	-5.91	102.17	110.50
1	I	612	SER	CB-CA-C	-5.90	100.51	110.43
1	H	156	THR	CA-C-N	-5.89	113.44	122.62
1	H	156	THR	C-N-CA	-5.89	113.44	122.62
1	D	836	MET	N-CA-C	5.86	118.27	110.53
1	G	286	GLU	N-CA-C	5.86	118.09	109.24
5	P	47	SER	N-CA-C	5.86	119.63	111.90
1	B	430	ASN	N-CA-C	5.85	117.65	111.28
1	B	447	SER	N-CA-C	5.84	117.32	111.07
1	C	823	HIS	CB-CA-C	-5.83	102.47	111.74
1	K	12	TYR	N-CA-C	-5.82	106.72	113.88
1	K	197	PRO	CB-CA-C	-5.81	101.97	111.56
1	I	47	ASN	CB-CA-C	-5.80	102.35	110.13
1	L	669	SER	N-CA-C	5.80	118.64	110.23
6	U	62	THR	CB-CA-C	-5.79	100.37	109.34
1	K	637	ASP	CB-CA-C	-5.79	101.19	110.79
1	F	206	GLU	CB-CA-C	-5.78	103.82	112.09
1	A	840	GLN	CA-C-N	-5.78	114.00	119.89
1	A	840	GLN	C-N-CA	-5.78	114.00	119.89
2	N	261	GLN	N-CA-C	-5.78	101.86	110.23
7	8	25	ILE	N-CA-C	5.77	118.48	108.95
1	F	47	ASN	CB-CA-C	5.77	117.53	108.88
1	I	639	HIS	N-CA-C	5.77	118.28	109.62
1	I	641	GLN	N-CA-CB	-5.77	102.11	110.36
1	J	321	PRO	N-CA-C	5.77	120.14	111.14
2	N	260	PHE	N-CA-C	5.77	117.57	111.28
7	4	24	GLU	CB-CA-C	-5.77	103.28	112.05
1	H	153	VAL	N-CA-C	-5.76	97.35	109.34
6	U	17	MET	N-CA-C	-5.76	105.83	112.92
1	D	766	PHE	CB-CA-C	-5.74	101.87	110.88
5	Q	21	LEU	CA-C-N	-5.71	112.54	120.25
5	Q	21	LEU	C-N-CA	-5.71	112.54	120.25
1	H	844	ALA	CB-CA-C	-5.69	101.04	112.99
1	E	337	ASN	CB-CA-C	-5.66	103.69	111.73
4	M	141	LEU	N-CA-C	-5.66	105.21	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	843	PRO	CA-C-O	-5.65	115.01	121.56
4	M	97	LEU	N-CA-C	-5.64	105.13	111.28
1	B	236	LYS	N-CA-C	-5.59	106.66	112.93
1	F	844	ALA	N-CA-C	5.59	119.02	110.36
1	E	316	SER	N-CA-CB	-5.57	102.02	110.77
7	6	24	GLU	N-CA-C	-5.57	98.93	110.80
1	A	743	PHE	N-CA-C	-5.56	100.62	109.96
1	H	153	VAL	CA-C-N	-5.55	112.84	120.28
1	H	153	VAL	C-N-CA	-5.55	112.84	120.28
1	I	612	SER	N-CA-CB	-5.55	103.13	111.56
5	Q	68	ALA	N-CA-C	-5.53	105.25	111.28
5	Q	22	PRO	N-CA-C	-5.52	100.81	111.69
1	I	247	GLU	CB-CA-C	-5.51	109.13	117.07
5	P	36	VAL	N-CA-C	-5.51	101.07	109.78
1	A	243	LYS	N-CA-C	-5.51	102.47	110.08
1	I	249	GLU	N-CA-C	5.51	117.80	110.53
1	L	156	THR	CA-C-N	-5.50	114.31	123.33
1	L	156	THR	C-N-CA	-5.50	114.31	123.33
5	Q	12	LEU	CA-C-N	-5.50	113.61	122.24
5	Q	12	LEU	C-N-CA	-5.50	113.61	122.24
1	H	123	SER	CB-CA-C	-5.49	101.51	110.85
1	J	337	ASN	N-CA-C	5.49	119.15	111.74
1	F	718	PHE	CA-C-N	5.47	129.39	122.16
1	F	718	PHE	C-N-CA	5.47	129.39	122.16
1	I	766	PHE	N-CA-C	-5.47	105.22	111.07
4	M	145	LEU	N-CA-C	-5.47	105.31	111.28
1	K	841	PRO	CA-C-O	-5.44	115.33	122.19
1	A	739	THR	N-CA-C	-5.44	96.78	108.64
6	U	40	MET	N-CA-C	-5.43	105.52	111.82
1	G	190	ASP	CB-CA-C	-5.42	102.27	111.26
1	A	156	THR	CB-CA-C	-5.41	99.21	110.40
4	M	134	GLY	O-C-N	-5.40	117.65	122.57
5	P	42	LEU	CA-C-O	5.40	123.58	118.34
1	F	714	LEU	N-CA-C	-5.39	104.27	111.87
5	Q	24	TRP	CA-CB-CG	5.39	123.84	113.60
5	P	41	VAL	CB-CA-C	5.38	120.11	111.29
1	K	194	GLN	CA-C-N	-5.37	113.08	119.05
1	K	194	GLN	C-N-CA	-5.37	113.08	119.05
1	D	836	MET	CB-CG-SD	-5.34	96.66	112.70
1	A	133	SER	N-CA-C	5.34	116.26	108.14
5	Q	17	LEU	CB-CA-C	-5.33	99.81	110.42
7	8	25	ILE	CB-CA-C	-5.33	102.45	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	194	GLN	N-CA-CB	-5.32	105.51	111.10
1	H	153	VAL	CB-CA-C	-5.32	102.57	111.29
1	F	713	TYR	N-CA-C	5.31	120.94	113.02
4	M	135	LEU	N-CA-C	5.31	118.86	112.38
5	P	34	SER	CA-C-N	-5.30	112.73	121.80
5	P	34	SER	C-N-CA	-5.30	112.73	121.80
1	J	338	SER	N-CA-C	-5.30	99.80	108.76
1	I	154	THR	N-CA-C	5.29	116.86	111.14
5	P	14	SER	N-CA-C	5.28	120.79	113.45
1	B	696	ASP	CA-C-N	-5.27	114.60	120.45
1	B	696	ASP	C-N-CA	-5.27	114.60	120.45
1	F	204	TRP	CA-C-N	-5.27	113.91	122.34
1	F	204	TRP	C-N-CA	-5.27	113.91	122.34
1	A	158	GLY	CA-C-N	-5.27	112.49	121.97
1	A	158	GLY	C-N-CA	-5.27	112.49	121.97
1	B	238	GLY	N-CA-C	-5.25	105.36	112.14
2	N	184	ASN	N-CA-C	-5.25	105.64	111.36
1	J	841	PRO	CA-C-O	-5.24	115.62	122.12
1	E	713	TYR	N-CA-C	5.24	121.40	114.12
1	E	341	ASN	CA-C-N	-5.23	113.72	122.92
1	E	341	ASN	C-N-CA	-5.23	113.72	122.92
5	P	22	PRO	N-CA-C	-5.22	102.05	110.55
4	M	139	VAL	CB-CA-C	-5.21	105.11	112.14
1	D	837	ARG	CB-CA-C	-5.21	102.66	110.16
4	M	123	ALA	N-CA-C	5.20	116.95	111.28
1	J	316	SER	CB-CA-C	-5.19	103.05	110.62
5	P	45	ASN	N-CA-C	5.19	119.59	113.16
1	D	476	ASN	O-C-N	-5.16	116.66	122.03
1	H	120	ALA	N-CA-C	-5.16	108.01	114.56
6	U	44	VAL	CB-CA-C	-5.15	105.19	112.14
1	B	313	VAL	N-CA-CB	-5.14	104.60	112.15
1	F	716	HIS	CB-CA-C	-5.13	102.47	110.94
2	N	197	SER	N-CA-C	-5.13	106.61	112.92
1	B	239	GLN	N-CA-C	-5.12	101.80	109.79
5	Q	16	TYR	CA-CB-CG	5.11	123.10	113.90
1	L	151	LYS	CB-CA-C	-5.10	100.26	110.42
1	L	703	GLY	N-CA-C	-5.10	100.98	110.66
1	I	614	ASN	CA-C-O	-5.09	115.99	121.38
5	P	17	LEU	CA-C-N	-5.08	114.59	122.67
5	P	17	LEU	C-N-CA	-5.08	114.59	122.67
4	M	138	LEU	CA-C-N	-5.07	113.51	120.46
4	M	138	LEU	C-N-CA	-5.07	113.51	120.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	715	ASN	CB-CA-C	-5.06	101.26	110.63
6	U	12	SER	N-CA-C	5.06	117.99	109.95
1	D	473	LEU	CA-C-O	-5.05	115.52	120.82
1	F	45	PHE	N-CA-CB	-5.05	102.62	110.29
1	E	718	PHE	N-CA-C	-5.04	101.62	109.24
1	D	475	SER	CB-CA-C	-5.04	103.19	110.96
1	D	132	PRO	CB-CA-C	-5.04	105.16	111.56
6	U	41	ILE	N-CA-C	-5.03	105.49	110.62
5	P	40	PRO	N-CA-C	-5.02	102.14	112.47
1	F	48	PRO	N-CA-C	5.01	119.35	111.38
2	N	259	PRO	N-CA-C	5.01	120.11	113.40
1	K	12	TYR	CA-CB-CG	5.01	122.92	113.90
5	P	43	PRO	CB-CA-C	-5.00	105.41	111.46

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	474	TYR	Mainchain
1	D	475	SER	Mainchain
1	D	476	ASN	Mainchain
1	K	186	ASP	Mainchain
1	L	595	SER	Mainchain
4	M	395	TYR	Mainchain
2	N	185	TYR	Mainchain
2	N	186	LEU	Mainchain
2	N	187	GLN	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	A	7551	0	7226	245	0
1	B	7536	0	7207	275	0
1	C	7519	0	7191	246	0
1	D	7526	0	7197	261	0
1	E	7526	0	7197	237	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	7539	0	7214	283	0
1	G	7526	0	7197	243	0
1	H	7526	0	7197	282	0
1	I	7536	0	7207	261	0
1	J	7551	0	7221	251	0
1	K	7546	0	7216	256	0
1	L	7524	0	7196	260	0
2	N	3786	0	3699	60	0
3	O	147	0	132	2	0
4	M	2829	0	2795	28	0
5	P	889	0	889	48	0
5	Q	821	0	822	62	0
5	R	957	0	950	46	0
5	S	887	0	882	21	0
6	U	1462	0	1416	35	0
6	V	1449	0	1402	14	0
7	1	236	0	219	8	0
7	2	203	0	192	5	0
7	3	211	0	198	7	0
7	4	227	0	213	9	0
7	5	219	0	209	9	0
7	6	211	0	198	9	0
7	7	211	0	198	1	0
7	8	227	0	213	4	0
7	9	219	0	209	9	0
8	X	75	0	17	1	0
All	All	105672	0	101319	2940	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 14.

All (2940) 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)
5:Q:15:PRO:HB2	5:Q:17:LEU:H	1.22	1.01
1:A:154:THR:HG23	1:A:155:LYS:HG2	1.47	0.96
1:K:196:GLU:HG2	1:L:823:HIS:HB3	1.47	0.94
1:K:194:GLN:HB2	1:K:197:PRO:HD2	1.52	0.91
1:I:762:THR:HG22	1:I:763:LYS:N	1.84	0.90
1:E:337:ASN:HD21	1:E:363:THR:H	1.18	0.89
1:A:135:TRP:CZ2	1:A:153:VAL:HB	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:449:GLN:HB3	1:H:153:VAL:HG13	1.54	0.86
1:G:194:GLN:HB3	1:G:197:PRO:HD2	1.55	0.85
1:J:134:GLN:HB2	1:J:154:THR:HG23	1.56	0.85
1:D:837:ARG:HD2	1:E:457:VAL:HG23	1.59	0.85
1:A:152:ASP:O	1:C:445:ALA:HB2	1.77	0.84
1:A:721:VAL:HG12	1:A:743:PHE:HB2	1.58	0.84
1:L:822:GLN:HB2	1:L:846:PHE:HB2	1.59	0.84
5:P:35:THR:HG21	5:P:40:PRO:HA	1.59	0.84
1:E:824:ASN:HA	1:E:844:ALA:HB1	1.58	0.84
1:A:262:ASP:HA	1:A:279:ALA:HB3	1.59	0.83
1:C:897:SER:HG	1:C:899:HIS:HE2	1.24	0.83
1:F:170:GLN:HB2	1:F:185:LYS:HD2	1.61	0.83
1:H:822:GLN:HB2	1:H:846:PHE:HB2	1.62	0.82
1:A:151:LYS:HB3	1:A:154:THR:HG21	1.60	0.82
1:I:267:SER:HB2	1:I:276:GLU:HA	1.60	0.82
1:C:138:LYS:HG2	1:C:149:GLN:HB3	1.61	0.81
1:L:155:LYS:HG3	1:L:261:PHE:HZ	1.43	0.81
1:A:403:VAL:HG11	1:A:466:ALA:HA	1.63	0.81
1:K:138:LYS:HG2	1:K:149:GLN:HB2	1.63	0.81
1:A:822:GLN:HB2	1:A:846:PHE:HB2	1.62	0.80
1:J:126:PRO:HG2	1:J:129:ALA:HB2	1.61	0.80
1:F:822:GLN:HB2	1:F:846:PHE:HB2	1.63	0.80
1:E:19:ASP:HA	1:E:48:PRO:HD2	1.62	0.80
1:I:244:PRO:HG3	1:I:253:ASP:HB3	1.62	0.79
1:D:126:PRO:HG2	1:D:129:ALA:HB2	1.65	0.79
1:F:203:ASN:HB2	1:F:204:TRP:HD1	1.47	0.79
5:Q:16:TYR:HB3	5:Q:18:THR:HG22	1.65	0.79
1:K:193:PHE:CZ	1:K:212:GLY:HA3	2.18	0.78
1:B:239:GLN:HE21	1:B:240:ALA:H	1.32	0.78
1:E:240:ALA:HB3	1:E:288:VAL:HB	1.64	0.78
1:I:762:THR:CG2	1:I:763:LYS:N	2.45	0.78
1:B:445:ALA:HB3	1:B:449:GLN:NE2	1.99	0.78
1:F:20:ALA:HB3	7:4:25:ILE:HG22	1.65	0.77
1:D:822:GLN:HB2	1:D:846:PHE:HB2	1.65	0.77
1:A:126:PRO:HG2	1:A:129:ALA:HB2	1.66	0.77
1:K:822:GLN:HB2	1:K:846:PHE:HB2	1.65	0.77
1:D:377:ARG:HB3	1:D:388:VAL:HG11	1.66	0.77
1:K:189:ALA:HA	1:K:241:LYS:HE3	1.65	0.77
1:L:267:SER:HB3	1:L:276:GLU:HA	1.65	0.77
1:C:822:GLN:HB2	1:C:846:PHE:HB2	1.67	0.76
1:H:67:ARG:HH12	1:I:752:GLU:HB2	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:908:ASP:OD1	1:L:908:ASP:N	2.19	0.76
1:I:126:PRO:HG2	1:I:129:ALA:HB2	1.68	0.75
1:L:399:GLU:HB3	1:L:523:ARG:HA	1.69	0.75
1:B:887:ASP:OD1	1:B:887:ASP:N	2.20	0.75
1:J:249:GLU:HG3	1:J:250:GLN:HG2	1.67	0.75
1:I:377:ARG:HB3	1:I:388:VAL:HG21	1.68	0.75
1:K:140:LYS:HB3	1:K:147:VAL:HG13	1.68	0.75
1:B:444:ASP:HA	1:C:151:LYS:O	1.87	0.75
1:F:698:TYR:HD1	5:R:33:GLY:HA3	1.50	0.75
1:H:344:VAL:HG22	1:H:582:GLU:HG2	1.68	0.75
1:K:438:SER:HB2	1:L:278:LYS:HD2	1.68	0.74
1:J:135:TRP:HE1	1:J:156:THR:HG1	1.36	0.74
1:K:922:VAL:HB	1:K:944:PRO:HD2	1.70	0.74
1:H:525:SER:OG	1:H:801:MET:SD	2.46	0.74
5:Q:15:PRO:HB2	5:Q:17:LEU:N	1.99	0.74
1:F:377:ARG:HB3	1:F:388:VAL:HG21	1.70	0.74
1:A:244:PRO:HD2	1:A:253:ASP:O	1.87	0.74
5:S:41:VAL:H	5:S:43:PRO:HG3	1.53	0.73
1:F:204:TRP:H	1:F:204:TRP:CD1	2.03	0.73
1:H:162:THR:HB	1:H:212:GLY:H	1.53	0.73
1:I:167:ILE:HD12	1:I:280:ASP:HB3	1.68	0.73
1:B:72:ASP:OD2	1:B:83:ARG:NH1	2.21	0.73
1:L:126:PRO:HG2	1:L:129:ALA:HB2	1.71	0.73
1:A:188:TYR:HA	1:A:192:THR:HB	1.69	0.73
1:I:114:LYS:HE2	1:I:294:ASP:HB2	1.70	0.73
1:K:361:ARG:NH1	1:K:924:ASP:OD2	2.22	0.73
1:D:552:ASN:O	1:E:804:GLN:NE2	2.21	0.73
1:G:681:THR:HG22	1:G:715:ASN:HB3	1.71	0.72
1:G:715:ASN:ND2	1:G:869:VAL:O	2.22	0.72
1:G:822:GLN:HB2	1:G:846:PHE:HB2	1.70	0.72
1:F:198:GLN:C	1:F:200:GLY:H	1.97	0.72
1:L:135:TRP:CZ3	1:L:309:GLU:HB3	2.24	0.72
1:E:427:LYS:HB3	1:E:439:GLU:HB2	1.71	0.72
1:F:74:GLU:HB3	1:F:81:LYS:HB3	1.70	0.72
1:D:410:TYR:HE1	1:E:414:LEU:HD21	1.54	0.72
1:J:160:ALA:HB3	1:J:281:ILE:HD11	1.72	0.72
1:C:188:TYR:O	1:C:241:LYS:NZ	2.22	0.72
1:B:633:MET:O	1:B:639:HIS:NE2	2.23	0.72
1:D:726:ASP:OD1	1:D:726:ASP:N	2.20	0.72
1:C:122:ASN:ND2	1:C:225:CYS:SG	2.61	0.71
1:F:602:ARG:HB2	5:R:35:THR:HB	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:7:MET:O	1:C:9:GLN:N	2.23	0.71
1:H:152:ASP:C	1:H:154:THR:H	1.96	0.71
1:C:633:MET:O	1:C:639:HIS:NE2	2.23	0.71
1:L:389:ASP:OD1	1:L:546:ARG:NH2	2.21	0.71
1:A:153:VAL:HG13	1:C:449:GLN:HB3	1.73	0.71
1:B:822:GLN:HB2	1:B:846:PHE:HB2	1.72	0.71
1:C:135:TRP:N	1:C:154:THR:OG1	2.23	0.71
1:D:589:VAL:HG23	1:D:593:LEU:HD12	1.73	0.71
1:H:726:ASP:N	1:H:726:ASP:OD1	2.20	0.71
1:F:114:LYS:NZ	1:F:116:TYR:O	2.24	0.71
1:H:114:LYS:NZ	1:H:116:TYR:O	2.21	0.71
1:F:203:ASN:HB2	1:F:204:TRP:CD1	2.25	0.71
1:D:457:VAL:O	1:F:837:ARG:NH1	2.23	0.71
1:I:715:ASN:ND2	1:I:869:VAL:O	2.23	0.71
1:A:172:LEU:HD11	1:A:212:GLY:HA3	1.71	0.70
1:F:657:PRO:HB3	5:Q:13:PHE:HZ	1.55	0.70
1:G:486:LYS:HG2	1:G:509:VAL:HG22	1.72	0.70
1:G:648:SER:OG	1:G:676:ARG:NH1	2.24	0.70
1:K:551:GLY:HA3	1:L:804:GLN:HE21	1.55	0.70
1:E:553:GLY:H	1:F:804:GLN:HG3	1.54	0.70
5:R:34:SER:HA	5:R:43:PRO:HD2	1.74	0.70
1:E:922:VAL:HB	1:E:944:PRO:HD2	1.74	0.70
1:G:924:ASP:HB3	1:G:942:ARG:HG3	1.73	0.70
1:L:943:THR:HB	1:L:944:PRO:HD3	1.72	0.70
1:B:88:VAL:HG22	1:B:576:PRO:HA	1.73	0.70
1:J:135:TRP:NE1	1:J:156:THR:HG1	1.87	0.70
1:L:168:THR:HG23	1:L:170:GLN:H	1.57	0.70
1:H:329:ASN:OD1	1:H:377:ARG:NH2	2.23	0.70
1:B:20:ALA:H	1:B:47:ASN:HB3	1.57	0.70
1:E:155:LYS:HD3	1:E:283:LEU:HD13	1.72	0.70
1:C:188:TYR:HA	1:C:192:THR:HB	1.73	0.70
1:D:154:THR:HG23	1:D:155:LYS:HD2	1.74	0.70
1:J:315:GLN:NE2	1:L:203:ASN:OD1	2.24	0.70
1:A:134:GLN:HB2	1:A:155:LYS:HD3	1.73	0.70
1:H:151:LYS:HB3	1:H:154:THR:HG21	1.74	0.70
1:J:450:ASN:ND2	1:K:154:THR:O	2.24	0.70
1:B:246:ASN:ND2	1:B:249:GLU:O	2.25	0.69
1:I:709:ASP:HB3	1:I:711:THR:HG22	1.73	0.69
1:L:151:LYS:O	1:L:154:THR:HB	1.92	0.69
5:Q:12:LEU:HG	5:Q:15:PRO:HD3	1.75	0.69
1:D:198:GLN:OE1	1:F:456:ASN:ND2	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:463:ASN:O	1:J:467:ASN:ND2	2.25	0.69
1:B:126:PRO:HG2	1:B:129:ALA:HB2	1.74	0.69
1:B:693:SER:HB2	2:N:69:LEU:O	1.91	0.69
1:D:401:HIS:CD2	1:F:548:MET:HE1	2.28	0.69
1:H:633:MET:O	1:H:639:HIS:NE2	2.25	0.69
1:K:172:LEU:HD13	1:K:193:PHE:HZ	1.57	0.69
1:H:192:THR:HB	1:H:214:ARG:HD2	1.74	0.69
1:J:401:HIS:NE2	1:L:548:MET:SD	2.63	0.69
1:D:124:LEU:HB2	1:E:825:ASN:HD21	1.58	0.69
1:F:230:ALA:O	1:F:239:GLN:NE2	2.26	0.69
1:J:653:LEU:HD22	1:J:915:LEU:HD23	1.74	0.69
1:J:603:VAL:HA	5:P:40:PRO:HB3	1.73	0.69
1:D:620:PHE:HE1	1:E:880:MET:HE1	1.57	0.69
1:I:389:ASP:OD1	1:I:540:ASN:ND2	2.24	0.69
1:I:822:GLN:HB2	1:I:846:PHE:HB2	1.75	0.69
1:J:135:TRP:NE1	1:J:156:THR:OG1	2.25	0.69
1:K:172:LEU:CD1	1:K:193:PHE:HZ	2.05	0.69
1:D:169:ASN:OD1	1:F:432:ASN:ND2	2.25	0.68
1:D:486:LYS:O	1:D:507:ARG:NH2	2.26	0.68
1:G:726:ASP:O	1:G:728:SER:N	2.26	0.68
1:J:456:ASN:HB3	1:L:837:ARG:HH12	1.57	0.68
1:L:14:HIS:O	1:L:46:ARG:NH1	2.27	0.68
1:B:449:GLN:HG3	1:B:450:ASN:OD1	1.94	0.68
1:C:239:GLN:HE21	1:C:240:ALA:H	1.40	0.68
1:J:17:GLY:H	1:J:48:PRO:HG3	1.58	0.68
1:G:196:GLU:HG3	1:G:197:PRO:HD3	1.75	0.68
1:J:19:ASP:HB2	7:9:14:GLY:HA3	1.75	0.68
1:B:415:ASN:HD21	1:B:418:GLY:HA2	1.59	0.68
1:K:109:ARG:HD3	1:K:324:ILE:HB	1.75	0.68
1:B:686:LYS:HE2	1:B:701:TYR:HB2	1.75	0.68
1:D:681:THR:HG23	1:D:715:ASN:HB3	1.73	0.68
1:J:230:ALA:O	1:J:239:GLN:NE2	2.26	0.68
1:H:214:ARG:HH22	1:H:241:LYS:HE2	1.58	0.68
1:I:543:LEU:HD23	1:I:546:ARG:HH21	1.57	0.68
1:L:240:ALA:HB3	1:L:288:VAL:HB	1.74	0.68
1:C:536:ASN:HB3	1:C:596:SER:O	1.93	0.68
1:F:135:TRP:N	1:F:154:THR:OG1	2.20	0.68
1:C:20:ALA:H	1:C:47:ASN:HB3	1.58	0.68
1:D:747:ARG:HE	1:D:750:ASP:HB2	1.59	0.68
1:I:415:ASN:ND2	1:I:417:THR:O	2.27	0.68
2:N:170:GLU:HB3	2:N:378:VAL:HG12	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:173:LEU:HB2	1:J:185:LYS:HZ2	1.59	0.67
1:A:589:VAL:HG23	1:A:593:LEU:HD12	1.76	0.67
1:K:194:GLN:CB	1:K:197:PRO:HD2	2.23	0.67
1:B:196:GLU:HG3	1:B:197:PRO:HD3	1.75	0.67
1:A:415:ASN:ND2	1:A:417:THR:O	2.21	0.67
1:C:676:ARG:NH1	1:C:921:GLU:OE1	2.27	0.67
1:D:198:GLN:NE2	1:D:199:VAL:O	2.26	0.67
5:Q:45:ASN:HB2	5:Q:49:MET:HG2	1.76	0.67
1:A:409:ASN:ND2	1:C:467:ASN:OD1	2.27	0.67
1:H:769:GLN:NE2	1:H:872:ARG:H	1.92	0.67
2:N:334:ASP:OD1	2:N:334:ASP:N	2.25	0.67
1:E:837:ARG:NH1	1:F:457:VAL:O	2.28	0.67
1:F:196:GLU:OE1	1:F:196:GLU:N	2.24	0.67
1:J:633:MET:O	1:J:639:HIS:NE2	2.27	0.67
1:K:327:ARG:NH1	1:K:591:MET:O	2.28	0.67
1:L:155:LYS:HZ3	1:L:285:THR:HG23	1.59	0.67
1:G:414:LEU:HD21	1:I:410:TYR:HE1	1.58	0.67
1:J:414:LEU:HD21	1:L:410:TYR:HE1	1.60	0.67
1:B:46:ARG:NH1	1:C:644:ASN:OD1	2.28	0.67
1:B:202:GLU:HA	1:C:313:VAL:HG11	1.75	0.67
1:H:723:ILE:HG12	1:H:903:MET:HE3	1.77	0.67
5:S:35:THR:HG1	5:S:39:ARG:H	1.43	0.67
1:A:56:VAL:HG13	1:A:57:THR:HG22	1.77	0.67
1:K:937:GLU:HB2	6:U:36:ALA:HA	1.76	0.67
2:N:282:VAL:HG13	2:N:283:PRO:HD3	1.76	0.67
1:H:697:PRO:O	5:Q:34:SER:N	2.27	0.67
1:H:771:LEU:HD22	1:H:880:MET:HG2	1.76	0.67
1:K:47:ASN:HD21	7:8:25:ILE:HG22	1.59	0.67
1:L:47:ASN:ND2	7:9:24:GLU:O	2.28	0.67
1:H:135:TRP:CZ3	1:H:137:THR:HB	2.30	0.66
1:K:25:SER:H	1:L:639:HIS:CE1	2.12	0.66
1:K:440:TRP:CZ2	1:L:276:GLU:HB3	2.31	0.66
1:G:199:VAL:HG11	1:G:206:GLU:HG3	1.76	0.66
1:I:399:GLU:HB3	1:I:523:ARG:HA	1.77	0.66
1:C:908:ASP:OD1	1:C:908:ASP:N	2.15	0.66
1:F:922:VAL:HB	1:F:944:PRO:HD2	1.78	0.66
1:I:287:ASN:OD1	1:I:287:ASN:N	2.27	0.66
1:K:240:ALA:HB3	1:K:288:VAL:HB	1.77	0.66
1:A:444:ASP:HA	1:B:152:ASP:HA	1.78	0.66
1:B:134:GLN:HA	1:B:154:THR:O	1.95	0.66
1:H:135:TRP:CH2	1:H:309:GLU:HB2	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:117:SER:HA	1:I:321:PRO:HG3	1.78	0.66
1:B:836:MET:O	1:B:837:ARG:NE	2.28	0.66
1:J:837:ARG:NE	1:J:837:ARG:O	2.28	0.66
2:N:280:LEU:HD13	2:N:328:VAL:HG13	1.76	0.66
6:V:179:ARG:NH2	6:V:182:GLY:O	2.28	0.66
1:H:233:THR:O	1:I:815:LYS:NZ	2.24	0.66
1:I:681:THR:HG22	1:I:715:ASN:HB3	1.78	0.66
1:J:124:LEU:HB2	1:K:825:ASN:HD21	1.60	0.66
2:N:164:PRO:HD2	2:N:176:LEU:HD21	1.78	0.66
1:B:211:TYR:H	1:B:281:ILE:HG22	1.61	0.66
1:D:159:VAL:HG21	1:E:841:PRO:HD2	1.76	0.66
1:E:107:LEU:HD13	1:E:608:VAL:HG12	1.76	0.66
1:K:126:PRO:HG2	1:K:129:ALA:HB2	1.78	0.66
1:G:474:TYR:HA	1:G:478:ALA:HB3	1.78	0.66
1:K:280:ASP:OD1	1:K:280:ASP:N	2.29	0.66
1:L:134:GLN:HA	1:L:155:LYS:H	1.61	0.66
6:U:179:ARG:NH2	6:U:182:GLY:O	2.29	0.66
1:B:194:GLN:O	1:B:198:GLN:NE2	2.29	0.65
1:E:684:LYS:HA	1:E:914:THR:HG22	1.77	0.65
1:J:333:LEU:HD22	1:J:562:VAL:HG21	1.76	0.65
1:K:46:ARG:HG2	1:L:642:SER:HB2	1.78	0.65
1:A:426:VAL:HA	1:A:440:TRP:HA	1.78	0.65
1:A:542:GLY:O	1:A:546:ARG:NH1	2.29	0.65
1:A:815:LYS:NZ	1:C:233:THR:O	2.27	0.65
1:C:440:TRP:HD1	1:C:441:GLU:HG2	1.60	0.65
1:D:676:ARG:NH2	1:D:921:GLU:OE1	2.27	0.65
1:K:409:ASN:ND2	1:K:462:ILE:O	2.28	0.65
1:K:681:THR:HG23	1:K:715:ASN:HB3	1.77	0.65
1:F:241:LYS:HD3	1:F:256:ILE:HD11	1.77	0.65
1:G:154:THR:HG23	1:G:155:LYS:HG2	1.77	0.65
1:K:114:LYS:NZ	1:K:116:TYR:O	2.28	0.65
1:K:681:THR:HG21	1:K:712:PHE:HB3	1.78	0.65
1:D:198:GLN:NE2	1:D:200:GLY:O	2.30	0.65
1:E:189:ALA:O	1:E:241:LYS:NZ	2.28	0.65
1:G:427:LYS:HB2	1:G:441:GLU:HG2	1.77	0.65
1:K:168:THR:HG23	1:K:170:GLN:H	1.61	0.65
5:Q:35:THR:HA	5:Q:43:PRO:HD2	1.77	0.65
1:J:240:ALA:HB3	1:J:288:VAL:HB	1.78	0.65
1:L:289:ASN:OD1	1:L:289:ASN:N	2.29	0.65
4:M:246:VAL:HB	4:M:249:ASN:HB2	1.76	0.65
1:B:344:VAL:HG13	1:B:582:GLU:HB3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:ASN:ND2	1:D:225:CYS:SG	2.70	0.65
1:D:503:TYR:OH	1:D:507:ARG:NH1	2.30	0.65
1:H:255:ASP:OD2	1:H:287:ASN:ND2	2.30	0.65
1:K:162:THR:HB	1:K:193:PHE:HE1	1.61	0.65
1:L:33:ARG:HE	7:9:22:TRP:HB3	1.61	0.65
1:H:711:THR:OG1	1:H:711:THR:O	2.14	0.65
1:L:188:TYR:O	1:L:241:LYS:NZ	2.29	0.65
5:R:49:MET:SD	5:R:50:THR:N	2.69	0.65
1:I:217:LYS:NZ	1:I:287:ASN:OD1	2.29	0.65
1:I:762:THR:HG22	1:I:764:ASP:H	1.61	0.65
1:K:135:TRP:NE1	1:K:156:THR:OG1	2.29	0.65
1:G:443:ASP:N	1:G:443:ASP:OD1	2.30	0.65
1:J:114:LYS:NZ	1:J:116:TYR:O	2.29	0.65
1:K:837:ARG:NE	1:K:837:ARG:O	2.30	0.65
1:L:150:GLU:C	1:L:152:ASP:H	2.05	0.65
2:N:247:ARG:NH2	2:N:380:CYS:O	2.29	0.65
1:F:657:PRO:HD3	5:Q:13:PHE:HE2	1.61	0.65
1:G:323:TYR:H	1:G:596:SER:HB3	1.62	0.65
1:J:135:TRP:O	1:J:154:THR:OG1	2.14	0.65
1:J:526:LEU:HG	1:J:528:PRO:HD2	1.79	0.65
1:L:744:GLU:O	1:L:762:THR:OG1	2.14	0.64
5:Q:34:SER:OG	5:Q:35:THR:N	2.30	0.64
1:A:633:MET:O	1:A:639:HIS:NE2	2.30	0.64
1:D:14:HIS:O	1:D:46:ARG:NH1	2.30	0.64
1:F:837:ARG:NE	1:F:837:ARG:O	2.28	0.64
1:G:201:GLU:OE1	1:G:201:GLU:N	2.29	0.64
1:G:845:ASN:HB3	1:I:239:GLN:HE22	1.62	0.64
1:K:161:ALA:HB2	1:L:840:GLN:HE21	1.63	0.64
1:A:648:SER:OG	1:A:676:ARG:NH2	2.30	0.64
1:H:552:ASN:O	1:I:804:GLN:NE2	2.29	0.64
1:I:922:VAL:HB	1:I:944:PRO:HD2	1.80	0.64
1:J:403:VAL:HG11	1:J:466:ALA:HA	1.78	0.64
1:A:907:VAL:HG23	1:A:908:ASP:H	1.62	0.64
1:C:140:LYS:HA	1:C:147:VAL:HG22	1.78	0.64
1:F:320:ARG:NH1	1:F:479:LEU:O	2.31	0.64
1:F:681:THR:CG2	1:F:715:ASN:ND2	2.60	0.64
1:I:762:THR:CG2	1:I:763:LYS:H	2.11	0.64
5:P:42:LEU:HB2	5:P:43:PRO:HD3	1.79	0.64
1:E:155:LYS:HZ3	1:E:283:LEU:HD22	1.62	0.64
1:G:230:ALA:O	1:G:239:GLN:NE2	2.29	0.64
1:G:403:VAL:HG11	1:G:466:ALA:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:415:ASN:OD1	1:H:415:ASN:N	2.31	0.64
5:S:35:THR:OG1	5:S:39:ARG:N	2.28	0.64
1:B:443:ASP:OD1	1:B:443:ASP:N	2.31	0.64
1:C:375:GLY:O	1:C:790:ARG:NH1	2.30	0.64
1:D:152:ASP:O	1:D:154:THR:N	2.31	0.64
1:E:103:ILE:HG13	1:E:613:VAL:HG22	1.79	0.64
1:E:512:SER:HA	1:E:515:ASP:HB2	1.79	0.64
1:I:114:LYS:NZ	1:I:116:TYR:O	2.30	0.64
1:J:154:THR:HG22	1:J:155:LYS:HG2	1.80	0.64
1:K:198:GLN:HG2	1:L:839:GLY:N	2.11	0.64
5:R:54:VAL:HG12	5:R:55:GLY:H	1.63	0.64
1:I:731:TRP:O	1:I:733:GLY:N	2.31	0.64
1:C:426:VAL:HG12	1:C:440:TRP:HB3	1.79	0.64
1:F:196:GLU:HG2	1:F:197:PRO:HD3	1.79	0.64
1:G:19:ASP:OD1	1:G:47:ASN:ND2	2.31	0.64
1:G:126:PRO:HG2	1:G:129:ALA:HB2	1.79	0.64
1:H:759:CYS:SG	1:H:760:ASN:N	2.70	0.64
1:A:468:LEU:HD21	1:B:464:LEU:HD22	1.79	0.64
1:D:747:ARG:NH2	1:D:752:GLU:OE2	2.29	0.64
1:E:138:LYS:HD3	1:E:149:GLN:HB2	1.80	0.64
1:L:211:TYR:H	1:L:281:ILE:HG22	1.63	0.64
1:A:328:ASP:OD2	1:A:368:GLN:NE2	2.26	0.64
1:F:328:ASP:OD2	1:F:368:GLN:NE2	2.31	0.64
1:C:224:PRO:HD3	1:C:314:GLN:HG2	1.79	0.63
1:D:328:ASP:OD2	1:D:377:ARG:NH2	2.31	0.63
1:F:789:ASP:OD1	1:F:796:ARG:NH1	2.31	0.63
1:H:14:HIS:O	1:H:46:ARG:NH1	2.31	0.63
1:I:756:VAL:HG13	1:I:763:LYS:HG2	1.80	0.63
1:K:98:SER:HB2	1:K:618:THR:HG23	1.81	0.63
6:U:69:LEU:HB2	6:U:211:GLU:HG3	1.79	0.63
1:B:139:GLU:HG3	1:B:152:ASP:HB2	1.79	0.63
1:B:379:ARG:NH2	1:C:789:ASP:OD2	2.31	0.63
1:C:295:THR:HG22	1:C:318:PRO:HA	1.80	0.63
1:E:186:ASP:OD1	1:E:186:ASP:N	2.31	0.63
1:E:389:ASP:O	1:E:868:ARG:NH2	2.30	0.63
1:F:682:ARG:NH2	1:F:914:THR:OG1	2.30	0.63
1:L:422:THR:HB	1:L:450:ASN:H	1.63	0.63
1:L:538:PRO:O	1:L:544:ARG:NE	2.32	0.63
1:I:24:LEU:HD13	1:I:28:LEU:HD12	1.81	0.63
1:J:651:ASN:HB3	1:J:919:LEU:HB3	1.81	0.63
1:L:167:ILE:HD13	1:L:282:ILE:HG23	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:526:LEU:HG	1:A:528:PRO:HD2	1.80	0.63
1:D:750:ASP:OD1	1:D:750:ASP:N	2.32	0.63
1:J:337:ASN:HD21	1:J:363:THR:H	1.45	0.63
1:B:449:GLN:HE21	1:B:450:ASN:H	1.47	0.63
1:L:79:LEU:O	1:L:587:LYS:NZ	2.30	0.63
1:B:533:ASN:ND2	1:B:536:ASN:OD1	2.32	0.63
1:E:633:MET:O	1:E:639:HIS:NE2	2.31	0.63
1:F:137:THR:OG1	1:F:138:LYS:N	2.32	0.63
1:D:228:SER:HB2	1:D:290:LEU:HD11	1.80	0.62
1:H:344:VAL:HB	1:H:353:ASN:HB2	1.81	0.62
1:I:943:THR:HB	1:I:944:PRO:HD3	1.81	0.62
1:A:546:ARG:NH2	1:A:594:GLN:OE1	2.30	0.62
1:B:135:TRP:CH2	1:B:309:GLU:HB2	2.34	0.62
1:B:162:THR:HG21	1:B:172:LEU:HD13	1.81	0.62
1:B:747:ARG:NH2	1:B:752:GLU:OE1	2.32	0.62
1:E:345:LEU:HD13	1:E:581:TYR:HD1	1.63	0.62
1:G:6:MET:SD	1:G:6:MET:N	2.72	0.62
1:A:89:GLY:HA3	1:A:92:ARG:HE	1.64	0.62
1:F:657:PRO:HB3	5:Q:13:PHE:CZ	2.34	0.62
1:H:52:PRO:HD3	7:7:11:PRO:HA	1.79	0.62
1:H:914:THR:OG1	1:H:915:LEU:N	2.30	0.62
1:K:89:GLY:HA3	1:K:92:ARG:HD3	1.80	0.62
1:A:590:ASN:ND2	1:A:699:PHE:O	2.32	0.62
1:B:13:MET:HB3	1:C:925:VAL:HG21	1.80	0.62
1:E:594:GLN:HB2	1:E:703:GLY:HA2	1.80	0.62
1:F:152:ASP:O	1:F:154:THR:N	2.33	0.62
1:L:486:LYS:HG2	1:L:509:VAL:HG22	1.82	0.62
1:A:202:GLU:HA	1:B:313:VAL:HG11	1.81	0.62
1:I:537:HIS:CG	1:I:538:PRO:HD2	2.34	0.62
1:J:233:THR:O	1:K:815:LYS:NZ	2.29	0.62
6:U:143:SER:OG	7:1:6:PHE:N	2.32	0.62
1:A:198:GLN:HG2	1:B:838:GLN:HB2	1.82	0.62
1:B:539:ARG:NH1	1:C:404:GLU:OE2	2.32	0.62
1:E:25:SER:H	1:F:639:HIS:CE1	2.18	0.62
1:G:364:GLU:OE1	1:G:565:LYS:NZ	2.32	0.62
1:I:135:TRP:CZ2	1:I:309:GLU:HB3	2.34	0.62
1:L:262:ASP:OD1	1:L:279:ALA:N	2.27	0.62
1:D:308:SER:OG	1:D:311:ASN:ND2	2.32	0.62
1:F:701:TYR:CZ	1:F:703:GLY:HA3	2.35	0.62
1:I:244:PRO:HD3	1:I:253:ASP:C	2.25	0.62
1:I:902:ASP:OD1	1:I:902:ASP:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:300:LYS:HB3	1:D:491:ASN:HD21	1.64	0.62
1:G:360:ASP:OD1	1:G:361:ARG:N	2.33	0.62
1:J:202:GLU:HA	1:K:313:VAL:HG11	1.81	0.62
1:B:474:TYR:HA	1:B:478:ALA:HB3	1.82	0.62
1:E:594:GLN:NE2	1:E:703:GLY:O	2.33	0.62
1:F:813:ASP:OD1	1:F:813:ASP:N	2.29	0.62
1:B:741:ASN:OD1	1:B:741:ASN:N	2.23	0.62
1:D:415:ASN:ND2	1:D:417:THR:O	2.33	0.62
1:F:240:ALA:HB3	1:F:288:VAL:HB	1.82	0.62
1:J:886:THR:HG23	1:J:889:GLY:H	1.65	0.62
1:C:902:ASP:OD1	1:C:902:ASP:N	2.33	0.61
1:D:636:ASN:OD1	1:D:637:ASP:N	2.29	0.61
1:H:682:ARG:HH21	1:H:910:MET:HE3	1.65	0.61
1:K:231:ARG:NH1	1:L:813:ASP:OD2	2.33	0.61
1:G:503:TYR:OH	1:G:507:ARG:NH1	2.33	0.61
1:I:88:VAL:HG12	1:I:619:PHE:HE2	1.65	0.61
1:K:360:ASP:OD1	1:K:942:ARG:NH1	2.33	0.61
1:K:450:ASN:HB2	1:L:156:THR:HA	1.82	0.61
1:D:653:LEU:HD13	1:D:691:LEU:HD11	1.83	0.61
1:J:327:ARG:NH2	1:J:703:GLY:O	2.34	0.61
1:F:192:THR:HB	1:F:214:ARG:HD2	1.80	0.61
1:H:837:ARG:NH1	1:I:457:VAL:O	2.34	0.61
5:Q:35:THR:OG1	5:Q:36:VAL:O	2.19	0.61
1:D:327:ARG:NH1	1:D:703:GLY:O	2.30	0.61
1:E:173:LEU:HB2	1:E:185:LYS:HZ3	1.66	0.61
1:F:756:VAL:HB	1:F:763:LYS:HA	1.82	0.61
1:G:635:ARG:NH1	1:G:932:HIS:O	2.34	0.61
1:H:379:ARG:NH2	1:I:789:ASP:OD2	2.33	0.61
1:K:417:THR:HB	1:K:457:VAL:HG12	1.83	0.61
1:B:648:SER:OG	1:B:676:ARG:NH2	2.33	0.61
1:D:482:PRO:HD3	1:D:529:MET:HB3	1.82	0.61
1:H:25:SER:H	1:I:639:HIS:CE1	2.18	0.61
1:H:445:ALA:HB3	1:H:449:GLN:HG3	1.81	0.61
1:L:280:ASP:OD1	1:L:280:ASP:N	2.16	0.61
1:A:463:ASN:O	1:A:467:ASN:ND2	2.33	0.61
1:B:470:LYS:NZ	1:B:515:ASP:OD1	2.32	0.61
1:D:135:TRP:N	1:D:154:THR:OG1	2.34	0.61
1:E:47:ASN:OD1	1:E:47:ASN:N	2.33	0.61
1:F:234:ASN:HD21	1:F:238:GLY:HA3	1.65	0.61
1:F:575:LEU:HB3	1:F:576:PRO:HD2	1.83	0.61
1:F:640:ASP:N	1:F:640:ASP:OD1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:461:GLU:HG2	1:I:126:PRO:HB3	1.83	0.61
1:H:346:ALA:HB2	1:H:353:ASN:HA	1.82	0.61
1:H:648:SER:OG	1:H:676:ARG:NH2	2.33	0.61
5:R:12:LEU:HD21	5:R:17:LEU:HD11	1.82	0.61
1:A:90:ASP:OD2	1:A:933:ARG:NH1	2.34	0.61
1:H:311:ASN:OD1	1:H:314:GLN:NE2	2.33	0.61
1:H:656:ILE:HD11	1:H:916:LEU:HB2	1.82	0.61
1:H:749:VAL:HG22	5:R:51:TYR:HE2	1.66	0.61
1:B:449:GLN:NE2	1:B:450:ASN:H	1.98	0.61
1:E:723:ILE:HG12	1:E:903:MET:HE3	1.82	0.61
1:D:239:GLN:OE1	1:E:823:HIS:NE2	2.31	0.61
1:D:514:VAL:HA	1:D:518:ILE:HG21	1.82	0.61
1:F:698:TYR:CD1	5:R:33:GLY:HA3	2.33	0.61
1:A:922:VAL:HB	1:A:944:PRO:HD2	1.83	0.60
1:C:135:TRP:CH2	1:C:309:GLU:HB3	2.36	0.60
1:F:173:LEU:HA	1:F:185:LYS:HA	1.83	0.60
1:H:262:ASP:OD1	1:H:263:VAL:N	2.34	0.60
1:I:566:PHE:O	1:I:570:LYS:HB2	2.01	0.60
2:N:408:TYR:O	2:N:496:ARG:NH2	2.34	0.60
1:B:222:MET:HE3	1:B:307:SER:HB2	1.82	0.60
1:G:162:THR:H	1:G:211:TYR:HD1	1.48	0.60
1:H:952:THR:OXT	1:J:734:ASN:ND2	2.34	0.60
1:A:774:TYR:HB2	1:A:776:ILE:HG12	1.83	0.60
1:B:540:ASN:O	1:B:543:LEU:N	2.31	0.60
1:E:117:SER:HA	1:E:321:PRO:HG3	1.82	0.60
1:F:760:ASN:HD22	5:P:54:VAL:HB	1.66	0.60
1:G:813:ASP:OD2	1:I:231:ARG:NH1	2.34	0.60
1:H:449:GLN:HG2	1:H:450:ASN:H	1.65	0.60
1:K:589:VAL:HG23	1:K:593:LEU:HD12	1.83	0.60
7:6:23:ASN:C	7:6:25:ILE:H	2.10	0.60
1:C:240:ALA:HB3	1:C:288:VAL:HB	1.82	0.60
1:H:135:TRP:CD1	1:H:156:THR:HG1	2.19	0.60
1:H:916:LEU:HD13	1:H:918:LEU:H	1.66	0.60
1:L:135:TRP:CH2	1:L:309:GLU:HB3	2.36	0.60
1:E:644:ASN:HB3	1:E:925:VAL:HG12	1.84	0.60
1:F:445:ALA:HB1	1:F:448:ARG:HB2	1.83	0.60
1:G:887:ASP:OD1	1:G:887:ASP:N	2.33	0.60
1:I:234:ASN:HD21	1:I:238:GLY:HA3	1.65	0.60
1:L:669:SER:HA	1:L:899:HIS:O	2.02	0.60
1:C:47:ASN:N	1:C:47:ASN:OD1	2.34	0.60
1:H:351:GLN:O	1:L:92:ARG:NH2	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:486:LYS:HB3	1:J:509:VAL:HG22	1.84	0.60
1:A:80:TYR:HB2	1:A:587:LYS:HE3	1.83	0.60
1:B:917:TYR:CZ	1:B:919:LEU:HD21	2.37	0.60
1:C:131:ASN:ND2	1:C:223:LYS:O	2.30	0.60
1:D:403:VAL:HG11	1:D:466:ALA:HA	1.84	0.60
1:E:415:ASN:HD21	1:E:418:GLY:HA2	1.67	0.60
1:G:441:GLU:OE1	1:G:442:LYS:N	2.32	0.60
1:H:331:VAL:HG13	1:H:364:GLU:HG2	1.82	0.60
1:H:886:THR:HG23	1:H:889:GLY:H	1.66	0.60
5:Q:96:ILE:N	5:S:94:SER:HG	1.99	0.60
1:C:587:LYS:NZ	1:C:608:VAL:O	2.35	0.60
1:F:399:GLU:HB3	1:F:523:ARG:HG3	1.84	0.60
1:F:515:ASP:OD1	1:F:516:ALA:N	2.30	0.60
1:F:640:ASP:OD2	1:F:927:ARG:NH1	2.35	0.60
1:K:715:ASN:ND2	1:K:866:CYS:O	2.31	0.60
1:L:20:ALA:HB3	7:9:24:GLU:HB3	1.84	0.60
1:G:837:ARG:NH2	1:H:457:VAL:O	2.31	0.60
1:K:327:ARG:NH2	1:K:703:GLY:O	2.35	0.60
1:L:72:ASP:OD2	1:L:83:ARG:NH1	2.35	0.60
1:D:633:MET:O	1:D:639:HIS:ND1	2.34	0.60
1:E:588:ASP:OD2	1:E:602:ARG:NH2	2.35	0.60
1:J:122:ASN:ND2	1:J:225:CYS:SG	2.75	0.60
1:J:664:PRO:HG2	5:P:15:PRO:O	2.02	0.60
5:P:10:GLY:O	5:P:12:LEU:N	2.35	0.60
1:A:313:VAL:HG22	1:C:204:TRP:HE3	1.66	0.59
1:E:231:ARG:NH1	1:F:813:ASP:OD2	2.35	0.59
1:F:427:LYS:HB3	1:F:439:GLU:HB3	1.83	0.59
1:F:486:LYS:HG2	1:F:509:VAL:HG12	1.84	0.59
1:I:575:LEU:HD21	1:I:634:LEU:HD23	1.84	0.59
1:K:162:THR:HB	1:K:193:PHE:CE1	2.36	0.59
1:B:575:LEU:HB3	1:B:576:PRO:HD2	1.85	0.59
1:C:22:GLU:OE1	7:1:15:THR:OG1	2.21	0.59
1:E:277:TYR:CZ	1:E:279:ALA:HB2	2.37	0.59
1:F:341:ASN:OD1	1:F:341:ASN:N	2.35	0.59
1:G:496:ALA:HB3	5:R:87:SER:HA	1.82	0.59
1:H:589:VAL:HG23	1:H:593:LEU:HD12	1.83	0.59
1:C:519:ASN:OD1	1:C:803:ARG:NH1	2.35	0.59
1:F:214:ARG:NH2	1:F:286:GLU:OE2	2.34	0.59
1:J:731:TRP:CD1	1:J:732:PRO:HD3	2.37	0.59
2:N:94:SER:O	2:N:485:GLY:HA3	2.02	0.59
1:A:544:ARG:HA	1:A:547:SER:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:648:SER:OG	1:C:676:ARG:NH2	2.35	0.59
1:D:401:HIS:HD2	1:F:548:MET:HE1	1.63	0.59
1:E:196:GLU:HB2	1:F:831:TYR:HD1	1.67	0.59
1:G:433:ASP:OD1	1:G:434:GLY:N	2.35	0.59
1:H:202:GLU:HA	1:I:313:VAL:HG11	1.85	0.59
1:L:95:ASP:OD1	1:L:96:MET:N	2.36	0.59
1:A:196:GLU:N	1:A:196:GLU:OE2	2.35	0.59
1:B:90:ASP:OD1	1:B:933:ARG:NH2	2.36	0.59
1:D:135:TRP:NE1	1:D:156:THR:OG1	2.36	0.59
1:F:137:THR:HG23	1:F:152:ASP:HB2	1.85	0.59
1:F:523:ARG:NH2	1:F:799:GLN:OE1	2.34	0.59
1:G:88:VAL:HG23	1:G:92:ARG:HB2	1.83	0.59
1:G:731:TRP:CD1	1:G:732:PRO:HD3	2.37	0.59
1:G:758:GLN:HG3	1:I:549:LEU:HD21	1.85	0.59
1:A:387:ALA:O	1:A:546:ARG:NH1	2.35	0.59
1:D:839:GLY:HA2	1:F:198:GLN:HG2	1.83	0.59
1:E:396:ARG:NH1	1:E:867:ASP:OD2	2.35	0.59
1:F:539:ARG:HA	1:F:544:ARG:HH21	1.67	0.59
1:K:239:GLN:OE1	1:L:823:HIS:NE2	2.32	0.59
1:L:247:GLU:OE1	1:L:248:GLY:N	2.35	0.59
1:C:18:GLN:HA	7:1:15:THR:HG23	1.84	0.59
1:C:19:ASP:OD1	1:C:20:ALA:N	2.35	0.59
1:E:132:PRO:HB3	1:E:158:GLY:HA2	1.84	0.59
1:H:286:GLU:OE2	1:I:842:TYR:OH	2.21	0.59
1:J:590:ASN:ND2	1:J:701:TYR:O	2.36	0.59
1:L:113:PHE:HD1	1:L:324:ILE:HG13	1.67	0.59
1:L:306:ASN:O	1:L:311:ASN:ND2	2.32	0.59
2:N:247:ARG:NH2	2:N:383:GLU:OE2	2.36	0.59
1:C:486:LYS:HG2	1:C:509:VAL:HG12	1.85	0.59
1:D:426:VAL:HG12	1:D:440:TRP:HA	1.84	0.59
1:E:214:ARG:NH2	1:E:241:LYS:HE2	2.17	0.59
1:E:337:ASN:HD21	1:E:363:THR:N	1.97	0.59
1:G:261:PHE:HB2	1:G:281:ILE:HG23	1.84	0.59
1:G:880:MET:HE3	1:H:38:TYR:HB2	1.85	0.59
1:H:333:LEU:HD23	1:H:562:VAL:HG11	1.85	0.59
1:H:676:ARG:NH2	1:H:921:GLU:OE1	2.35	0.59
1:J:222:MET:HE1	1:J:312:LEU:HD22	1.84	0.59
1:J:337:ASN:ND2	1:J:363:THR:H	2.00	0.59
1:A:309:GLU:O	1:C:205:GLN:NE2	2.34	0.59
1:E:214:ARG:HH22	1:E:241:LYS:HE2	1.67	0.59
1:E:424:GLN:HA	1:E:449:GLN:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:573:LEU:HB3	1:E:641:GLN:HE21	1.67	0.59
1:C:230:ALA:O	1:C:239:GLN:NE2	2.35	0.59
1:E:495:PRO:HG3	1:E:502:GLU:HG3	1.83	0.59
1:H:134:GLN:HG3	1:H:155:LYS:NZ	2.18	0.59
1:J:738:LEU:HB3	1:J:754:TYR:HE2	1.67	0.59
1:F:47:ASN:HB3	7:4:25:ILE:HB	1.84	0.58
1:K:590:ASN:ND2	1:K:699:PHE:O	2.36	0.58
1:L:214:ARG:NH2	1:L:286:GLU:OE2	2.36	0.58
5:P:29:GLN:N	5:R:8:PHE:O	2.29	0.58
1:C:541:ALA:HA	1:C:544:ARG:HD3	1.84	0.58
1:D:449:GLN:HB3	1:E:153:VAL:HG13	1.84	0.58
1:E:670:ARG:NH1	1:E:944:PRO:O	2.36	0.58
1:G:589:VAL:HG23	1:G:593:LEU:HD22	1.86	0.58
2:N:325:LYS:O	3:O:6:ARG:NH2	2.35	0.58
1:D:804:GLN:HE21	1:F:551:GLY:HA3	1.68	0.58
1:G:922:VAL:HB	1:G:944:PRO:HD2	1.85	0.58
1:L:731:TRP:O	1:L:733:GLY:N	2.35	0.58
1:A:410:TYR:HE1	1:B:414:LEU:HD21	1.69	0.58
1:A:760:ASN:O	1:A:760:ASN:ND2	2.35	0.58
1:C:93:VAL:HG21	1:C:630:LEU:HD12	1.85	0.58
1:D:202:GLU:HB3	1:E:313:VAL:HG11	1.84	0.58
1:D:842:TYR:OH	1:F:286:GLU:OE2	2.22	0.58
1:E:344:VAL:HG22	1:E:582:GLU:HG2	1.84	0.58
1:E:893:LEU:O	1:E:899:HIS:NE2	2.34	0.58
1:G:124:LEU:HB2	1:H:825:ASN:HD21	1.69	0.58
1:G:726:ASP:N	1:G:726:ASP:OD1	2.33	0.58
1:G:737:LEU:O	1:I:63:ARG:NH1	2.35	0.58
1:K:239:GLN:HE21	1:K:240:ALA:H	1.49	0.58
1:K:483:ASP:OD1	1:K:507:ARG:NH1	2.37	0.58
1:L:300:LYS:NZ	1:L:305:ASP:OD1	2.34	0.58
5:P:17:LEU:HA	5:R:14:SER:O	2.04	0.58
1:B:451:GLN:OE1	1:B:451:GLN:N	2.37	0.58
1:G:257:ASP:N	1:G:257:ASP:OD1	2.36	0.58
1:I:486:LYS:HG2	1:I:509:VAL:HG12	1.86	0.58
5:Q:10:GLY:C	5:Q:12:LEU:N	2.45	0.58
1:B:19:ASP:HA	1:B:48:PRO:HD2	1.86	0.58
1:D:360:ASP:O	1:D:361:ARG:HG3	2.04	0.58
1:E:239:GLN:HE21	1:E:240:ALA:H	1.52	0.58
1:H:134:GLN:HG3	1:H:155:LYS:HZ3	1.68	0.58
1:J:278:LYS:HZ1	1:L:428:ILE:HG22	1.68	0.58
1:K:22:GLU:O	6:V:176:SER:OG	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:253:ASP:OD1	1:K:254:LEU:N	2.31	0.58
1:A:262:ASP:OD2	1:A:279:ALA:N	2.36	0.58
1:B:695:PHE:H	2:N:72:GLN:HE22	1.52	0.58
1:F:681:THR:HG22	1:F:715:ASN:ND2	2.19	0.58
1:G:633:MET:O	1:G:639:HIS:NE2	2.37	0.58
1:H:825:ASN:O	1:H:825:ASN:ND2	2.37	0.58
1:A:379:ARG:NH1	1:B:789:ASP:OD2	2.33	0.58
1:E:96:MET:HG2	1:E:569:ILE:HG22	1.85	0.58
1:H:433:ASP:OD1	1:H:433:ASP:N	2.37	0.58
1:J:152:ASP:HA	1:L:444:ASP:HA	1.85	0.58
1:J:557:PRO:HD2	1:K:860:THR:HG21	1.85	0.58
1:K:151:LYS:HB3	1:K:154:THR:HG21	1.85	0.58
1:B:436:GLU:O	1:B:437:GLU:HB2	2.03	0.58
1:D:887:ASP:OD1	1:D:887:ASP:N	2.37	0.58
1:G:548:MET:HE2	1:H:523:ARG:HG2	1.86	0.58
1:K:151:LYS:O	1:K:154:THR:OG1	2.21	0.58
4:M:141:LEU:HD22	4:M:170:VAL:HG21	1.86	0.58
1:C:214:ARG:NH2	1:C:286:GLU:OE2	2.37	0.57
1:D:447:SER:HB2	1:E:264:PRO:HB3	1.85	0.57
1:D:836:MET:HE1	1:F:414:LEU:HD13	1.85	0.57
1:F:731:TRP:O	1:F:733:GLY:N	2.36	0.57
1:H:480:TYR:OH	1:H:538:PRO:HD3	2.03	0.57
1:L:480:TYR:OH	1:L:538:PRO:HD3	2.04	0.57
1:A:433:ASP:OD2	1:B:169:ASN:N	2.35	0.57
1:B:107:LEU:HG	1:B:608:VAL:HG12	1.86	0.57
1:F:483:ASP:OD1	1:F:507:ARG:NH1	2.37	0.57
1:F:603:VAL:HA	5:R:40:PRO:HB3	1.86	0.57
1:H:681:THR:OG1	1:H:682:ARG:N	2.37	0.57
1:H:769:GLN:HE21	1:H:872:ARG:H	1.50	0.57
1:I:723:ILE:HG12	1:I:903:MET:HE3	1.86	0.57
1:J:804:GLN:HE22	1:L:551:GLY:HA3	1.70	0.57
2:N:130:PHE:HB3	2:N:248:LEU:HD12	1.85	0.57
6:V:3:LYS:H	6:V:3:LYS:HD2	1.69	0.57
1:E:329:ASN:OD1	1:E:377:ARG:NH2	2.37	0.57
1:H:33:ARG:NH1	7:5:20:GLY:O	2.37	0.57
1:I:651:ASN:ND2	1:I:917:TYR:OH	2.37	0.57
1:K:569:ILE:HA	1:K:572:LEU:HD22	1.86	0.57
1:L:135:TRP:CZ3	1:L:156:THR:HB	2.39	0.57
1:L:298:VAL:HB	1:L:317:MET:HG2	1.86	0.57
1:A:831:TYR:HB3	1:A:838:GLN:NE2	2.20	0.57
1:D:239:GLN:HE21	1:D:240:ALA:H	1.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:622:MET:HG3	1:D:627:ALA:HB2	1.85	0.57
1:D:731:TRP:CG	1:D:732:PRO:HD3	2.39	0.57
1:E:653:LEU:HD23	1:E:915:LEU:HG	1.85	0.57
1:H:670:ARG:NH1	1:H:944:PRO:O	2.36	0.57
1:J:360:ASP:OD1	1:J:361:ARG:N	2.36	0.57
1:K:771:LEU:HD13	1:K:777:GLY:HA3	1.86	0.57
1:B:161:ALA:HB3	1:B:198:GLN:HB3	1.84	0.57
1:B:384:TRP:NE1	1:C:781:PHE:O	2.28	0.57
1:C:637:ASP:OD1	1:C:637:ASP:N	2.37	0.57
1:D:137:THR:HG22	1:D:152:ASP:HB2	1.87	0.57
1:F:202:GLU:O	1:F:203:ASN:C	2.46	0.57
1:G:377:ARG:HB3	1:G:388:VAL:HG11	1.85	0.57
1:H:155:LYS:HG3	1:H:261:PHE:CZ	2.39	0.57
1:H:405:ASP:OD2	1:H:463:ASN:ND2	2.38	0.57
1:I:132:PRO:HB3	1:I:158:GLY:HA2	1.86	0.57
1:L:405:ASP:OD2	1:L:463:ASN:ND2	2.35	0.57
1:G:319:ASN:H	1:G:319:ASN:HD22	1.53	0.57
1:H:253:ASP:OD1	1:H:254:LEU:N	2.36	0.57
2:N:414:GLU:OE2	2:N:472:THR:OG1	2.23	0.57
7:6:12:ARG:NH2	7:6:15:THR:O	2.37	0.57
1:A:433:ASP:N	1:A:433:ASP:OD1	2.37	0.57
1:A:604:ASP:OD1	1:A:604:ASP:N	2.37	0.57
1:C:152:ASP:O	1:C:154:THR:N	2.38	0.57
1:E:333:LEU:HD23	1:E:562:VAL:HG11	1.86	0.57
1:G:135:TRP:NE1	1:G:156:THR:OG1	2.38	0.57
1:I:113:PHE:HE2	1:I:553:GLY:H	1.53	0.57
1:J:4:PRO:HG2	6:U:58:GLN:HE21	1.70	0.57
1:J:327:ARG:NH1	1:J:591:MET:O	2.36	0.57
1:K:389:ASP:OD1	1:K:540:ASN:ND2	2.27	0.57
1:K:590:ASN:HB2	1:K:602:ARG:HG3	1.87	0.57
1:L:364:GLU:HB2	1:L:708:LEU:HB2	1.86	0.57
1:D:138:LYS:HA	1:D:149:GLN:HA	1.85	0.57
1:E:731:TRP:N	1:E:732:PRO:HD2	2.19	0.57
1:H:744:GLU:OE2	1:H:747:ARG:NH1	2.38	0.57
1:I:483:ASP:OD1	1:I:507:ARG:NH1	2.38	0.57
1:J:423:TYR:HE1	1:K:263:VAL:HG22	1.69	0.57
1:K:755:ASN:O	1:K:763:LYS:NZ	2.35	0.57
2:N:70:ASN:HB2	2:N:73:ASN:HB2	1.85	0.57
2:N:385:VAL:HG13	2:N:416:MET:HG2	1.87	0.57
1:D:911:ASP:OD1	1:D:911:ASP:N	2.29	0.57
1:E:726:ASP:N	1:E:726:ASP:OD1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:417:THR:HG22	1:F:457:VAL:HG13	1.87	0.57
1:A:445:ALA:N	1:B:152:ASP:O	2.37	0.57
1:A:771:LEU:HD13	1:A:777:GLY:HA3	1.87	0.57
1:B:121:TYR:HA	1:C:824:ASN:OD1	2.05	0.57
1:C:644:ASN:HB3	1:C:925:VAL:HG12	1.87	0.57
1:C:726:ASP:OD1	1:C:726:ASP:N	2.32	0.57
1:E:167:ILE:HD13	1:E:282:ILE:HB	1.86	0.57
1:F:107:LEU:HD11	1:F:593:LEU:HD11	1.85	0.57
1:H:162:THR:HG23	1:H:193:PHE:CE2	2.40	0.57
1:H:230:ALA:O	1:H:239:GLN:NE2	2.37	0.57
1:H:916:LEU:HD22	1:H:917:TYR:H	1.69	0.57
1:B:728:SER:OG	1:B:729:VAL:N	2.38	0.56
1:D:486:LYS:HG2	1:D:509:VAL:HG22	1.86	0.56
1:E:198:GLN:NE2	1:F:839:GLY:O	2.23	0.56
1:E:561:GLN:NE2	1:F:756:VAL:O	2.37	0.56
1:L:614:ASN:N	1:L:614:ASN:OD1	2.37	0.56
5:P:40:PRO:O	5:P:41:VAL:C	2.48	0.56
1:B:235:GLU:OE1	1:B:235:GLU:N	2.37	0.56
1:D:639:HIS:HD2	1:F:25:SER:H	1.53	0.56
1:H:352:LEU:HB3	6:V:110:GLY:HA2	1.87	0.56
1:H:423:TYR:O	1:H:449:GLN:NE2	2.38	0.56
1:I:134:GLN:HG2	1:I:155:LYS:HD3	1.87	0.56
1:I:480:TYR:OH	1:I:538:PRO:HD3	2.05	0.56
1:I:765:TRP:O	1:I:766:PHE:C	2.43	0.56
1:J:590:ASN:OD1	1:J:602:ARG:NE	2.36	0.56
5:Q:74:ALA:HA	5:Q:77:LEU:HB3	1.86	0.56
1:A:135:TRP:CH2	1:A:309:GLU:HB2	2.40	0.56
1:A:450:ASN:HD21	1:B:154:THR:HG23	1.70	0.56
1:D:648:SER:OG	1:D:922:VAL:O	2.21	0.56
1:G:294:ASP:O	1:G:319:ASN:ND2	2.37	0.56
1:G:410:TYR:HE1	1:H:414:LEU:HD21	1.69	0.56
1:K:198:GLN:HG3	1:K:199:VAL:N	2.18	0.56
1:L:602:ARG:HD2	5:Q:80:SER:HB2	1.87	0.56
5:P:16:TYR:HB3	5:P:18:THR:HG22	1.86	0.56
5:P:56:ASN:N	5:P:56:ASN:OD1	2.36	0.56
1:F:415:ASN:O	1:F:417:THR:N	2.38	0.56
1:F:427:LYS:HB2	1:F:442:LYS:HD2	1.88	0.56
1:I:257:ASP:OD1	1:I:285:THR:OG1	2.23	0.56
1:J:682:ARG:NH2	1:J:910:MET:SD	2.79	0.56
2:N:326:VAL:HG23	3:O:7:VAL:HG23	1.87	0.56
4:M:116:LEU:O	4:M:120:VAL:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:U:2:SER:OG	6:U:3:LYS:O	2.23	0.56
1:D:339:THR:OG1	1:D:359:GLN:NE2	2.33	0.56
1:D:711:THR:O	1:D:711:THR:OG1	2.22	0.56
1:H:661:THR:OG1	1:H:662:ASN:N	2.36	0.56
1:I:762:THR:HG22	1:I:763:LYS:H	1.69	0.56
1:J:602:ARG:HG2	5:P:35:THR:HG23	1.88	0.56
1:J:635:ARG:NH1	1:J:932:HIS:O	2.39	0.56
5:R:60:ASP:N	5:R:60:ASP:OD1	2.37	0.56
1:C:151:LYS:HG2	1:C:154:THR:HG21	1.87	0.56
1:C:801:MET:HE1	1:C:863:LYS:HE3	1.88	0.56
1:E:389:ASP:OD1	1:E:540:ASN:ND2	2.31	0.56
1:G:804:GLN:NE2	1:I:552:ASN:O	2.39	0.56
1:J:711:THR:O	1:J:711:THR:OG1	2.18	0.56
1:J:825:ASN:HD21	1:L:124:LEU:HB2	1.70	0.56
1:L:150:GLU:C	1:L:152:ASP:N	2.63	0.56
1:L:234:ASN:HD21	1:L:238:GLY:HA3	1.69	0.56
7:5:12:ARG:NH2	7:5:15:THR:O	2.38	0.56
1:C:470:LYS:NZ	1:C:515:ASP:OD1	2.34	0.56
1:C:724:MET:HG2	1:C:729:VAL:HG23	1.88	0.56
1:F:456:ASN:OD1	1:F:457:VAL:N	2.38	0.56
1:G:94:LEU:HD21	1:G:617:ALA:HB1	1.88	0.56
1:J:360:ASP:OD1	1:J:942:ARG:NH2	2.38	0.56
1:B:676:ARG:NH2	1:B:921:GLU:OE1	2.39	0.56
1:G:194:GLN:HB3	1:G:197:PRO:CD	2.31	0.56
1:G:328:ASP:O	1:G:330:PHE:N	2.39	0.56
1:K:485:TYR:HB3	1:K:513:LEU:HD21	1.88	0.56
1:L:93:VAL:HG21	1:L:630:LEU:HD23	1.86	0.56
1:B:486:LYS:HG2	1:B:509:VAL:HG12	1.86	0.56
1:C:538:PRO:O	1:C:544:ARG:NH1	2.39	0.56
1:F:463:ASN:O	1:F:467:ASN:ND2	2.30	0.56
1:H:158:GLY:O	1:H:159:VAL:C	2.49	0.56
1:J:663:VAL:HG13	1:J:905:PHE:HB2	1.88	0.56
1:L:188:TYR:HA	1:L:192:THR:HG23	1.87	0.56
1:L:388:VAL:HG11	1:L:791:MET:HE1	1.88	0.56
1:B:523:ARG:NH2	1:B:799:GLN:OE1	2.36	0.56
1:G:793:SER:O	1:G:797:ASN:ND2	2.39	0.56
1:K:450:ASN:CB	1:L:156:THR:HA	2.36	0.56
1:K:636:ASN:HB3	1:K:639:HIS:CE1	2.41	0.56
1:L:320:ARG:NH2	1:L:479:LEU:O	2.38	0.56
1:A:152:ASP:O	1:A:154:THR:N	2.37	0.55
1:D:150:GLU:HB3	1:F:443:ASP:HB3	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:474:TYR:O	1:D:475:SER:C	2.46	0.55
1:H:349:ALA:O	1:L:933:ARG:NH2	2.39	0.55
1:H:489:PRO:HD3	1:H:508:VAL:HG12	1.88	0.55
1:J:296:HIS:CE1	1:J:317:MET:HG2	2.42	0.55
1:B:5:SER:HA	6:U:185:THR:HB	1.87	0.55
1:B:424:GLN:NE2	1:C:276:GLU:OE2	2.39	0.55
1:C:399:GLU:OE2	1:C:401:HIS:NE2	2.35	0.55
1:D:151:LYS:O	1:F:444:ASP:HA	2.07	0.55
1:D:163:GLY:N	1:D:199:VAL:HB	2.21	0.55
1:D:842:TYR:HE2	1:F:239:GLN:HG2	1.71	0.55
1:G:152:ASP:N	1:G:152:ASP:OD1	2.34	0.55
1:G:239:GLN:HE21	1:G:240:ALA:H	1.54	0.55
1:H:684:LYS:NZ	1:H:713:TYR:OH	2.40	0.55
1:I:715:ASN:O	1:I:871:TRP:NE1	2.36	0.55
2:N:60:ASP:OD1	2:N:60:ASP:N	2.37	0.55
5:Q:8:PHE:CD1	5:R:28:ARG:HG2	2.41	0.55
1:A:169:ASN:OD1	1:C:432:ASN:ND2	2.39	0.55
1:C:752:GLU:OE1	1:C:753:GLY:N	2.40	0.55
1:B:192:THR:OG1	1:B:214:ARG:NH1	2.39	0.55
1:B:230:ALA:HB3	1:B:239:GLN:HE22	1.71	0.55
1:B:327:ARG:NH1	1:B:703:GLY:O	2.40	0.55
1:C:141:GLN:O	1:C:146:GLY:N	2.33	0.55
1:E:651:ASN:N	1:E:651:ASN:OD1	2.40	0.55
1:H:588:ASP:OD2	1:H:602:ARG:NH2	2.40	0.55
1:H:761:MET:HE2	1:H:765:TRP:HD1	1.70	0.55
1:I:609:ARG:NH1	1:I:611:ASP:OD1	2.40	0.55
1:L:588:ASP:OD1	1:L:591:MET:N	2.39	0.55
2:N:185:TYR:O	2:N:186:LEU:C	2.45	0.55
1:C:489:PRO:HG2	1:C:492:VAL:HG21	1.87	0.55
1:H:327:ARG:HH21	1:H:705:ILE:HG12	1.71	0.55
1:J:427:LYS:N	1:J:439:GLU:O	2.39	0.55
1:J:480:TYR:OH	1:J:538:PRO:HD3	2.07	0.55
1:L:648:SER:OG	1:L:676:ARG:NH2	2.39	0.55
2:N:186:LEU:O	2:N:187:GLN:C	2.46	0.55
1:B:360:ASP:OD1	1:B:361:ARG:N	2.39	0.55
1:D:437:GLU:OE1	1:D:437:GLU:N	2.39	0.55
1:D:538:PRO:O	1:D:544:ARG:NH2	2.39	0.55
1:E:320:ARG:HG2	1:E:505:ASN:OD1	2.07	0.55
1:F:178:GLU:OE1	1:F:179:THR:OG1	2.19	0.55
1:J:73:ARG:NH2	1:J:611:ASP:O	2.38	0.55
1:J:313:VAL:HG21	1:L:202:GLU:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:748:SER:OG	1:J:749:VAL:N	2.39	0.55
1:K:327:ARG:HH21	1:K:705:ILE:HG13	1.72	0.55
1:B:535:PHE:O	1:B:536:ASN:ND2	2.39	0.55
1:B:680:PHE:HB3	1:B:918:LEU:HD13	1.88	0.55
1:D:199:VAL:HG11	1:D:211:TYR:CE2	2.42	0.55
1:D:396:ARG:NH1	1:D:867:ASP:OD2	2.40	0.55
1:E:308:SER:OG	1:E:311:ASN:OD1	2.24	0.55
1:E:497:ASN:OD1	1:E:500:THR:OG1	2.21	0.55
1:F:46:ARG:NH2	7:4:28:SER:H	2.05	0.55
1:F:389:ASP:N	1:F:389:ASP:OD1	2.40	0.55
1:F:931:PRO:O	1:F:932:HIS:ND1	2.40	0.55
1:E:609:ARG:HH12	5:P:62:THR:HG21	1.71	0.55
1:G:135:TRP:N	1:G:154:THR:OG1	2.34	0.55
1:G:811:TYR:HD2	1:G:814:TYR:HB2	1.72	0.55
1:B:43:ASN:OD1	1:B:44:LYS:NZ	2.35	0.55
1:B:362:ASN:OD1	1:B:651:ASN:ND2	2.40	0.55
1:D:168:THR:OG1	1:D:185:LYS:NZ	2.39	0.55
1:D:731:TRP:CD2	1:D:732:PRO:HD3	2.41	0.55
1:F:277:TYR:HD1	1:F:277:TYR:H	1.55	0.55
1:G:228:SER:HB2	1:G:290:LEU:HD11	1.88	0.55
1:J:117:SER:HA	1:J:321:PRO:HG3	1.87	0.55
1:J:398:ILE:HD11	1:J:477:VAL:HG21	1.89	0.55
1:J:592:ILE:HG13	1:J:593:LEU:HD22	1.89	0.55
1:K:566:PHE:O	1:K:570:LYS:HB2	2.07	0.55
1:L:361:ARG:NH2	1:L:924:ASP:OD1	2.40	0.55
6:V:146:LEU:HG	6:V:148:PRO:HD3	1.89	0.55
1:A:87:ALA:HA	1:A:578:SER:HA	1.88	0.55
1:A:414:LEU:HD21	1:C:410:TYR:HE2	1.72	0.55
1:A:681:THR:HG21	1:A:712:PHE:HB3	1.89	0.55
1:B:377:ARG:NH1	1:B:386:SER:OG	2.40	0.55
1:E:173:LEU:HD13	1:E:185:LYS:HZ3	1.72	0.55
1:F:320:ARG:HH11	1:F:479:LEU:HB3	1.72	0.55
1:H:151:LYS:HB3	1:H:154:THR:CG2	2.37	0.55
1:I:151:LYS:HB3	1:I:154:THR:HG21	1.88	0.55
1:I:306:ASN:O	1:I:311:ASN:ND2	2.39	0.55
1:I:759:CYS:HB3	1:I:800:PRO:HB3	1.87	0.55
1:J:327:ARG:NH1	1:J:593:LEU:O	2.39	0.55
1:K:155:LYS:HD3	1:K:283:LEU:HD13	1.87	0.55
1:L:20:ALA:H	1:L:47:ASN:HB3	1.71	0.55
1:L:161:ALA:H	1:L:198:GLN:HE22	1.53	0.55
1:B:250:GLN:NE2	1:B:251:PRO:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:456:ASN:OD1	1:D:456:ASN:N	2.37	0.54
1:F:140:LYS:HA	1:F:147:VAL:HA	1.88	0.54
1:F:298:VAL:HB	1:F:317:MET:HG2	1.87	0.54
1:H:666:SER:HB3	5:Q:16:TYR:CE1	2.43	0.54
1:H:688:THR:O	5:Q:28:ARG:NH2	2.40	0.54
1:K:193:PHE:O	1:K:194:GLN:C	2.46	0.54
1:K:306:ASN:O	1:K:311:ASN:ND2	2.40	0.54
1:D:199:VAL:HG11	1:D:211:TYR:HE2	1.73	0.54
1:H:403:VAL:HG23	1:H:465:GLN:HB3	1.89	0.54
1:I:462:ILE:HG12	1:I:463:ASN:H	1.70	0.54
1:J:257:ASP:N	1:J:257:ASP:OD1	2.41	0.54
1:J:550:LEU:HB3	1:J:556:VAL:HG11	1.87	0.54
1:K:497:ASN:OD1	1:K:500:THR:OG1	2.25	0.54
1:A:277:TYR:HD1	1:A:277:TYR:H	1.54	0.54
1:C:134:GLN:HA	1:C:155:LYS:H	1.70	0.54
1:G:156:THR:HG22	1:G:157:PHE:HD1	1.71	0.54
1:G:456:ASN:ND2	1:I:839:GLY:H	2.04	0.54
1:J:433:ASP:OD1	1:J:434:GLY:N	2.41	0.54
1:K:196:GLU:CG	1:L:823:HIS:HB3	2.31	0.54
1:B:223:LYS:HE2	1:B:292:THR:HG21	1.90	0.54
1:F:480:TYR:OH	1:F:538:PRO:HD3	2.07	0.54
1:F:682:ARG:NH1	1:F:910:MET:SD	2.81	0.54
1:F:756:VAL:HG11	1:F:766:PHE:HB2	1.88	0.54
1:G:427:LYS:O	1:G:439:GLU:N	2.37	0.54
1:L:161:ALA:H	1:L:198:GLN:NE2	2.05	0.54
5:Q:12:LEU:HG	5:Q:15:PRO:CD	2.38	0.54
1:A:139:GLU:HG2	1:A:152:ASP:CG	2.33	0.54
1:A:377:ARG:HB3	1:A:791:MET:HE3	1.89	0.54
1:C:633:MET:HE3	6:U:171:LEU:HD13	1.89	0.54
1:C:837:ARG:O	1:C:837:ARG:NE	2.34	0.54
1:H:189:ALA:O	1:H:241:LYS:NZ	2.39	0.54
1:H:486:LYS:HG2	1:H:509:VAL:HG12	1.89	0.54
1:H:818:THR:HB	1:H:820:PRO:HD2	1.90	0.54
1:L:155:LYS:HG3	1:L:261:PHE:CZ	2.33	0.54
1:A:384:TRP:NE1	1:B:781:PHE:O	2.36	0.54
1:A:823:HIS:NE2	1:C:239:GLN:OE1	2.40	0.54
1:C:153:VAL:O	1:C:156:THR:OG1	2.24	0.54
1:C:172:LEU:HD13	1:C:193:PHE:HZ	1.71	0.54
1:D:480:TYR:OH	1:D:538:PRO:HD3	2.08	0.54
1:H:590:ASN:HD21	1:H:601:LEU:H	1.55	0.54
1:J:410:TYR:HE1	1:K:414:LEU:HD21	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:135:TRP:CH2	1:K:309:GLU:HB2	2.43	0.54
1:K:217:LYS:N	1:K:286:GLU:O	2.34	0.54
5:P:12:LEU:HD22	5:P:15:PRO:HD3	1.89	0.54
1:A:539:ARG:NH2	1:B:404:GLU:OE2	2.34	0.54
1:D:401:HIS:CE1	1:F:544:ARG:HD3	2.42	0.54
1:E:648:SER:O	1:E:648:SER:OG	2.25	0.54
1:F:661:THR:HG22	1:F:909:PRO:HG3	1.90	0.54
1:F:908:ASP:OD1	1:F:908:ASP:N	2.36	0.54
1:J:190:ASP:HB3	1:J:236:LYS:HB3	1.90	0.54
1:K:161:ALA:HB1	1:K:198:GLN:HB2	1.89	0.54
1:K:443:ASP:HB3	1:L:151:LYS:H	1.71	0.54
1:L:667:ILE:HG22	1:L:668:PRO:O	2.08	0.54
1:A:244:PRO:HD3	1:A:255:ASP:N	2.23	0.54
1:B:8:PRO:HB3	6:U:18:GLY:HA3	1.89	0.54
1:C:485:TYR:CZ	1:C:528:PRO:HB3	2.43	0.54
1:C:662:ASN:HA	1:C:906:GLU:HA	1.89	0.54
1:E:135:TRP:CH2	1:E:309:GLU:HB2	2.43	0.54
1:F:172:LEU:HD22	1:F:193:PHE:HZ	1.72	0.54
1:G:400:ASN:ND2	1:G:518:ILE:O	2.41	0.54
1:C:607:SER:O	1:C:607:SER:OG	2.20	0.54
1:G:277:TYR:OH	1:G:280:ASP:OD2	2.20	0.54
1:K:445:ALA:HB3	1:K:449:GLN:HE21	1.73	0.54
1:A:835:THR:OG1	1:C:201:GLU:OE2	2.22	0.54
1:A:842:TYR:HE2	1:C:239:GLN:HG2	1.72	0.54
1:B:651:ASN:N	1:B:651:ASN:OD1	2.39	0.54
1:D:730:SER:O	1:D:733:GLY:N	2.41	0.54
1:D:825:ASN:HD21	1:F:124:LEU:H	1.56	0.54
1:E:151:LYS:HB3	1:E:154:THR:HG21	1.90	0.54
1:H:113:PHE:HE1	1:H:324:ILE:H	1.55	0.54
1:I:188:TYR:HB2	1:I:256:ILE:HG21	1.88	0.54
1:J:670:ARG:HG3	1:J:671:ASN:N	2.22	0.54
1:J:821:PHE:HD1	1:L:194:GLN:HE22	1.53	0.54
1:K:354:ALA:O	1:K:940:TYR:OH	2.24	0.54
1:K:473:LEU:O	1:K:477:VAL:HG12	2.08	0.54
1:K:649:ALA:HA	1:K:922:VAL:HG22	1.89	0.54
1:K:825:ASN:O	1:K:825:ASN:ND2	2.40	0.54
1:A:88:VAL:HG23	1:A:619:PHE:HE2	1.73	0.53
1:A:417:THR:HG22	1:A:419:THR:H	1.72	0.53
1:D:12:TYR:OH	6:U:161:SER:OG	2.23	0.53
1:E:440:TRP:CZ2	1:F:276:GLU:HG3	2.43	0.53
1:E:460:MET:HE1	1:F:460:MET:HG2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:341:ASN:OD1	1:I:341:ASN:N	2.41	0.53
1:K:186:ASP:HB3	1:K:191:LYS:O	2.08	0.53
1:K:427:LYS:HD3	1:K:442:LYS:HG2	1.89	0.53
1:B:47:ASN:HD21	7:1:25:ILE:HG12	1.71	0.53
1:D:200:GLY:HA3	1:D:206:GLU:CD	2.32	0.53
1:H:19:ASP:OD1	1:H:19:ASP:N	2.41	0.53
1:I:789:ASP:O	1:I:796:ARG:NH2	2.33	0.53
1:J:655:PRO:HG2	5:P:17:LEU:HD22	1.89	0.53
1:K:58:THR:HG23	1:L:736:ARG:NH2	2.23	0.53
1:K:237:GLY:HA3	1:L:821:PHE:HB3	1.90	0.53
1:K:331:VAL:HG13	1:K:364:GLU:HG2	1.90	0.53
2:N:185:TYR:HE1	2:N:194:VAL:HG23	1.72	0.53
1:A:676:ARG:NH2	1:A:921:GLU:OE1	2.41	0.53
1:E:18:GLN:HB3	1:E:22:GLU:HB2	1.88	0.53
1:G:152:ASP:HA	1:I:444:ASP:HA	1.90	0.53
1:J:793:SER:O	1:J:797:ASN:ND2	2.40	0.53
1:K:241:LYS:NZ	1:K:286:GLU:OE1	2.39	0.53
1:D:676:ARG:HE	1:D:921:GLU:HB3	1.73	0.53
1:D:837:ARG:HD2	1:E:457:VAL:CG2	2.37	0.53
1:E:52:PRO:HD3	7:3:11:PRO:HA	1.89	0.53
1:F:198:GLN:C	1:F:200:GLY:N	2.64	0.53
1:H:636:ASN:HB2	1:H:639:HIS:NE2	2.23	0.53
1:I:537:HIS:CD2	1:I:538:PRO:HD2	2.43	0.53
1:I:575:LEU:HB3	1:I:576:PRO:HD2	1.90	0.53
1:K:425:GLY:HA3	1:K:444:ASP:HB2	1.89	0.53
1:A:752:GLU:OE1	1:A:753:GLY:N	2.41	0.53
1:B:315:GLN:HE22	1:B:835:THR:HA	1.73	0.53
1:D:478:ALA:C	1:D:480:TYR:N	2.56	0.53
1:D:922:VAL:HB	1:D:944:PRO:HD2	1.91	0.53
1:G:135:TRP:CH2	1:G:309:GLU:HB2	2.43	0.53
1:G:240:ALA:HB3	1:G:288:VAL:HG23	1.91	0.53
1:G:842:TYR:HE2	1:I:239:GLN:HG2	1.73	0.53
1:I:134:GLN:HA	1:I:154:THR:O	2.07	0.53
1:K:214:ARG:HH12	1:K:241:LYS:HZ1	1.56	0.53
1:K:728:SER:OG	1:K:729:VAL:N	2.41	0.53
1:L:76:THR:HG22	1:L:77:THR:H	1.74	0.53
1:L:813:ASP:N	1:L:813:ASP:OD1	2.39	0.53
5:P:10:GLY:HA2	5:P:13:PHE:HD1	1.74	0.53
5:Q:5:GLY:C	5:Q:7:ALA:N	2.63	0.53
1:A:152:ASP:C	1:A:154:THR:H	2.15	0.53
1:A:239:GLN:HE21	1:A:240:ALA:H	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:TYR:CZ	1:A:279:ALA:HB2	2.44	0.53
1:C:914:THR:OG1	1:C:915:LEU:N	2.38	0.53
1:E:192:THR:HB	1:E:214:ARG:HD2	1.89	0.53
1:E:449:GLN:HG3	1:E:450:ASN:H	1.73	0.53
1:G:584:ASN:N	1:G:584:ASN:OD1	2.41	0.53
1:I:277:TYR:CZ	1:I:279:ALA:HB2	2.44	0.53
1:L:190:ASP:OD1	1:L:191:LYS:N	2.42	0.53
1:A:457:VAL:O	1:C:837:ARG:NH1	2.42	0.53
1:C:167:ILE:HD13	1:C:282:ILE:HG23	1.89	0.53
1:C:480:TYR:OH	1:C:538:PRO:HD3	2.09	0.53
1:G:761:MET:HE2	1:G:765:TRP:HD1	1.74	0.53
1:I:396:ARG:NH1	1:I:867:ASP:OD2	2.40	0.53
1:I:445:ALA:HB3	1:I:450:ASN:HB2	1.91	0.53
1:K:83:ARG:HG3	1:K:582:GLU:HB2	1.90	0.53
1:K:379:ARG:NH2	1:L:789:ASP:OD2	2.40	0.53
1:L:135:TRP:HZ3	1:L:156:THR:HG21	1.74	0.53
5:P:9:GLU:OE2	5:P:10:GLY:N	2.42	0.53
6:V:36:ALA:HB1	6:V:40:MET:HB2	1.91	0.53
1:B:135:TRP:CZ3	1:B:137:THR:HB	2.43	0.53
1:B:436:GLU:HG2	1:C:270:ALA:HB1	1.89	0.53
1:C:172:LEU:HD22	1:C:193:PHE:CE1	2.44	0.53
1:C:481:LEU:HD23	1:C:529:MET:HE3	1.91	0.53
1:D:441:GLU:HG2	1:D:443:ASP:H	1.72	0.53
1:E:135:TRP:N	1:E:154:THR:OG1	2.38	0.53
1:F:186:ASP:OD1	1:F:187:ILE:N	2.42	0.53
1:H:13:MET:HG3	1:I:941:LEU:HD22	1.90	0.53
1:I:653:LEU:HB3	1:I:915:LEU:HD12	1.90	0.53
1:I:813:ASP:OD1	1:I:813:ASP:N	2.41	0.53
1:J:202:GLU:HG3	1:J:206:GLU:HB2	1.89	0.53
1:L:552:ASN:O	1:L:552:ASN:ND2	2.41	0.53
2:N:40:ASN:O	2:N:40:ASN:ND2	2.41	0.53
1:D:414:LEU:HD21	1:F:410:TYR:HE1	1.74	0.53
1:F:711:THR:O	1:F:711:THR:OG1	2.20	0.53
1:G:715:ASN:HB2	1:G:871:TRP:NE1	2.24	0.53
1:K:51:ALA:HB1	1:L:882:MET:HG3	1.91	0.53
1:K:190:ASP:O	1:K:192:THR:HG22	2.09	0.53
4:M:178:VAL:HG21	6:U:207:LEU:HD21	1.91	0.53
1:B:8:PRO:HG2	1:B:11:ALA:HB3	1.90	0.53
1:G:817:VAL:HG12	1:I:237:GLY:HA2	1.90	0.53
5:P:35:THR:OG1	5:P:36:VAL:N	2.35	0.53
1:B:162:THR:HA	1:B:193:PHE:CE2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:461:GLU:OE1	1:B:461:GLU:N	2.43	0.52
1:C:723:ILE:HG12	1:C:903:MET:HE3	1.91	0.52
1:D:639:HIS:HB3	1:F:24:LEU:HD22	1.90	0.52
1:E:65:THR:HB	1:E:618:THR:HG22	1.90	0.52
1:E:194:GLN:O	1:E:197:PRO:HD2	2.09	0.52
1:F:135:TRP:CH2	1:F:309:GLU:HB3	2.44	0.52
1:G:825:ASN:HD21	1:I:124:LEU:HG	1.74	0.52
1:G:842:TYR:OH	1:I:286:GLU:OE2	2.27	0.52
1:I:531:ASN:HB2	1:I:714:LEU:HD11	1.91	0.52
1:J:153:VAL:HG12	1:J:156:THR:HG23	1.92	0.52
1:L:156:THR:HG23	1:L:157:PHE:N	2.24	0.52
4:M:228:PRO:HB2	6:U:4:GLU:HB3	1.91	0.52
5:Q:14:SER:O	5:R:15:PRO:HB2	2.09	0.52
1:A:599:ASN:O	1:A:702:SER:OG	2.22	0.52
1:B:445:ALA:C	1:B:449:GLN:HB2	2.34	0.52
1:C:234:ASN:HD21	1:C:238:GLY:HA3	1.74	0.52
1:D:836:MET:HA	1:E:410:TYR:OH	2.08	0.52
1:F:126:PRO:HG2	1:F:129:ALA:HB2	1.91	0.52
1:F:161:ALA:O	1:F:199:VAL:HG23	2.09	0.52
1:L:922:VAL:HB	1:L:944:PRO:HD2	1.90	0.52
4:M:227:THR:HG22	4:M:229:ASN:H	1.75	0.52
1:B:194:GLN:O	1:B:197:PRO:HD2	2.09	0.52
1:C:590:ASN:HB2	1:C:602:ARG:HE	1.73	0.52
1:D:152:ASP:C	1:D:154:THR:N	2.68	0.52
1:F:139:GLU:OE1	1:F:140:LYS:N	2.40	0.52
1:B:427:LYS:HD2	1:B:441:GLU:HG3	1.91	0.52
1:C:152:ASP:C	1:C:154:THR:N	2.67	0.52
1:D:433:ASP:OD1	1:D:434:GLY:N	2.33	0.52
1:D:833:ALA:C	1:D:835:THR:H	2.17	0.52
1:H:288:VAL:HG23	1:H:290:LEU:HB2	1.92	0.52
1:J:19:ASP:O	1:J:22:GLU:N	2.36	0.52
1:J:406:GLU:HG2	1:L:479:LEU:HD11	1.91	0.52
1:K:25:SER:OG	1:L:639:HIS:NE2	2.41	0.52
4:M:373:ALA:HA	6:U:100:ARG:HB2	1.92	0.52
1:C:256:ILE:HD13	1:C:286:GLU:HB3	1.91	0.52
1:C:693:SER:OG	1:K:750:ASP:OD2	2.27	0.52
1:F:134:GLN:OE1	1:F:155:LYS:NZ	2.32	0.52
1:G:758:GLN:HE21	1:I:549:LEU:HD21	1.74	0.52
1:H:389:ASP:OD1	1:H:540:ASN:ND2	2.34	0.52
1:H:498:THR:HG23	1:H:503:TYR:CE2	2.44	0.52
1:L:445:ALA:HB3	1:L:450:ASN:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:23:ASN:C	7:6:25:ILE:N	2.64	0.52
1:A:572:LEU:HD13	1:A:928:VAL:HG21	1.92	0.52
1:A:867:ASP:N	1:A:867:ASP:OD1	2.41	0.52
1:B:552:ASN:HB3	1:C:522:ALA:HB2	1.91	0.52
1:D:756:VAL:HG23	1:F:561:GLN:HE22	1.75	0.52
1:E:575:LEU:HB3	1:E:576:PRO:HD2	1.90	0.52
1:G:198:GLN:OE1	1:H:839:GLY:N	2.29	0.52
1:H:748:SER:HA	5:R:54:VAL:HG13	1.92	0.52
1:I:212:GLY:HA2	1:I:282:ILE:O	2.10	0.52
1:I:523:ARG:NH2	1:I:799:GLN:OE1	2.33	0.52
1:J:423:TYR:HB3	1:K:261:PHE:HB3	1.92	0.52
1:J:845:ASN:HB3	1:L:239:GLN:HE22	1.75	0.52
5:S:35:THR:HA	5:S:43:PRO:HG2	1.90	0.52
1:A:139:GLU:HB2	1:A:150:GLU:HB2	1.90	0.52
1:F:670:ARG:NH2	1:F:944:PRO:O	2.43	0.52
1:F:760:ASN:HB2	5:P:54:VAL:HG21	1.91	0.52
1:J:564:GLN:HE21	1:J:569:ILE:HB	1.74	0.52
1:J:662:ASN:ND2	5:Q:22:PRO:HG3	2.25	0.52
1:L:282:ILE:HD12	1:L:284:TYR:HE1	1.75	0.52
1:A:706:PRO:HA	1:A:711:THR:HG23	1.91	0.52
1:C:575:LEU:HB3	1:C:576:PRO:HD2	1.92	0.52
1:C:640:ASP:OD1	1:C:640:ASP:N	2.35	0.52
1:D:715:ASN:ND2	1:D:866:CYS:O	2.43	0.52
1:E:399:GLU:OE2	1:E:401:HIS:NE2	2.43	0.52
1:F:188:TYR:HA	1:F:192:THR:HA	1.91	0.52
1:F:241:LYS:HG2	1:F:286:GLU:HG3	1.92	0.52
1:G:319:ASN:OD1	1:G:501:TYR:OH	2.23	0.52
1:H:339:THR:HB	1:J:740:PRO:HG2	1.90	0.52
1:I:240:ALA:HB3	1:I:288:VAL:HB	1.92	0.52
1:K:539:ARG:NH2	1:L:404:GLU:OE2	2.34	0.52
1:A:662:ASN:HA	1:A:906:GLU:HA	1.92	0.52
1:B:214:ARG:NH2	1:B:286:GLU:OE2	2.43	0.52
1:G:821:PHE:HB3	1:I:237:GLY:HA3	1.91	0.52
1:I:588:ASP:OD2	1:I:602:ARG:NH2	2.43	0.52
1:J:523:ARG:NH2	1:J:799:GLN:OE1	2.43	0.52
1:J:735:ASP:OD1	1:L:63:ARG:NH1	2.43	0.52
1:L:417:THR:HG23	1:L:458:TYR:H	1.74	0.52
1:L:812:LYS:H	1:L:812:LYS:HD2	1.74	0.52
4:M:257:THR:HA	4:M:260:ARG:HH11	1.74	0.52
1:A:60:ARG:HD2	1:A:624:HIS:CE1	2.45	0.52
1:A:139:GLU:OE1	1:A:141:GLN:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:59:ASP:OD1	1:D:59:ASP:N	2.43	0.52
1:D:478:ALA:C	1:D:480:TYR:H	2.17	0.52
1:E:720:LYS:HG2	1:E:906:GLU:HB3	1.92	0.52
1:F:167:ILE:HD13	1:F:282:ILE:HG23	1.92	0.52
1:L:608:VAL:HG21	5:Q:69:ALA:HB1	1.91	0.52
1:L:608:VAL:HG22	1:L:609:ARG:HG3	1.92	0.52
1:C:417:THR:HG21	1:C:453:CYS:HB2	1.91	0.51
1:F:111:PRO:HD2	1:F:604:ASP:HB3	1.93	0.51
1:G:231:ARG:O	1:G:240:ALA:HB2	2.10	0.51
1:G:651:ASN:HB3	1:G:919:LEU:HD12	1.92	0.51
1:H:241:LYS:HB2	1:H:254:LEU:HD22	1.92	0.51
1:K:172:LEU:CD1	1:K:193:PHE:CZ	2.92	0.51
1:L:94:LEU:HG	1:L:95:ASP:N	2.25	0.51
1:A:640:ASP:OD1	1:A:640:ASP:N	2.43	0.51
1:B:388:VAL:HG21	1:B:791:MET:HE1	1.91	0.51
1:D:468:LEU:HD21	1:E:464:LEU:HD22	1.92	0.51
1:G:515:ASP:OD1	1:G:516:ALA:N	2.38	0.51
1:H:13:MET:HB3	1:I:925:VAL:HG21	1.93	0.51
1:H:214:ARG:NH2	1:H:286:GLU:OE2	2.43	0.51
1:I:328:ASP:O	1:I:329:ASN:C	2.52	0.51
1:K:196:GLU:HG2	1:L:823:HIS:CB	2.29	0.51
1:K:731:TRP:N	1:K:732:PRO:HD2	2.25	0.51
1:C:320:ARG:NH2	1:C:479:LEU:O	2.43	0.51
1:D:738:LEU:HD23	1:D:738:LEU:H	1.75	0.51
1:F:96:MET:HG2	1:F:574:LEU:HD22	1.91	0.51
1:F:757:ALA:O	1:F:759:CYS:N	2.42	0.51
1:G:428:ILE:HD12	1:H:169:ASN:HB3	1.91	0.51
1:I:329:ASN:O	1:I:330:PHE:C	2.51	0.51
1:J:188:TYR:HA	1:J:192:THR:HG23	1.92	0.51
1:L:47:ASN:OD1	7:9:27:THR:OG1	2.27	0.51
5:Q:5:GLY:HA3	5:Q:8:PHE:O	2.09	0.51
1:B:217:LYS:NZ	1:B:257:ASP:OD2	2.39	0.51
1:B:277:TYR:CE2	1:B:279:ALA:HB2	2.45	0.51
1:C:135:TRP:NE1	1:C:156:THR:OG1	2.41	0.51
1:C:922:VAL:HG23	1:C:944:PRO:HG2	1.93	0.51
1:D:924:ASP:HB3	1:D:942:ARG:HG3	1.93	0.51
1:E:731:TRP:O	1:E:733:GLY:N	2.44	0.51
1:F:720:LYS:HG3	1:F:744:GLU:HG3	1.92	0.51
1:G:240:ALA:HB3	1:G:288:VAL:CG2	2.39	0.51
1:G:761:MET:HE2	1:G:765:TRP:CD1	2.45	0.51
1:H:590:ASN:HB2	1:H:602:ARG:HE	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:495:PRO:HG3	1:J:502:GLU:HG3	1.93	0.51
1:K:731:TRP:O	1:K:733:GLY:N	2.44	0.51
1:L:319:ASN:ND2	1:L:505:ASN:OD1	2.42	0.51
1:L:536:ASN:HB3	1:L:596:SER:O	2.10	0.51
1:L:720:LYS:HG2	1:L:906:GLU:HB3	1.92	0.51
7:5:17:PRO:HB2	7:5:19:MET:HG2	1.92	0.51
1:B:151:LYS:HE2	1:B:218:LYS:HD3	1.91	0.51
1:B:339:THR:OG1	1:B:359:GLN:OE1	2.21	0.51
1:B:644:ASN:HB3	1:B:925:VAL:HG12	1.91	0.51
1:B:842:TYR:CG	1:B:843:PRO:HD2	2.45	0.51
1:D:152:ASP:C	1:D:154:THR:H	2.19	0.51
1:D:494:LEU:HD11	1:D:506:GLY:HA3	1.91	0.51
1:D:657:PRO:HG2	1:D:660:ALA:HB2	1.93	0.51
1:E:239:GLN:HG2	1:F:842:TYR:HE2	1.74	0.51
1:E:336:TYR:CZ	1:E:565:LYS:HG3	2.46	0.51
1:H:107:LEU:HD23	1:H:108:ASP:N	2.25	0.51
1:K:785:GLU:OE1	1:K:785:GLU:N	2.43	0.51
1:L:173:LEU:HG	1:L:185:LYS:HZ3	1.76	0.51
1:L:199:VAL:HG22	1:L:206:GLU:HG2	1.93	0.51
1:A:263:VAL:HG22	1:C:423:TYR:HE1	1.75	0.51
1:B:438:SER:HB2	1:C:278:LYS:HB3	1.91	0.51
1:B:446:ILE:N	1:B:449:GLN:HB2	2.26	0.51
1:C:631:GLU:C	1:C:633:MET:H	2.19	0.51
1:D:495:PRO:HG3	1:D:502:GLU:HB3	1.92	0.51
1:D:640:ASP:OD1	1:D:640:ASP:N	2.41	0.51
1:F:315:GLN:N	1:F:315:GLN:OE1	2.44	0.51
1:I:705:ILE:O	1:I:709:ASP:HB2	2.10	0.51
1:J:134:GLN:OE1	1:J:155:LYS:NZ	2.31	0.51
1:J:345:LEU:HD23	1:J:569:ILE:HD12	1.93	0.51
1:L:114:LYS:HE2	1:L:116:TYR:O	2.11	0.51
1:L:759:CYS:SG	1:L:760:ASN:N	2.82	0.51
1:A:190:ASP:OD1	1:A:191:LYS:N	2.41	0.51
1:C:486:LYS:HB2	1:C:507:ARG:HH11	1.76	0.51
1:C:897:SER:OG	1:C:899:HIS:NE2	2.25	0.51
1:D:552:ASN:HD22	1:E:522:ALA:HB2	1.74	0.51
1:D:639:HIS:CD2	1:F:25:SER:H	2.28	0.51
1:E:50:VAL:HG22	7:3:12:ARG:HB2	1.91	0.51
1:H:756:VAL:HG13	1:H:763:LYS:HG2	1.93	0.51
1:J:107:LEU:HD23	1:J:556:VAL:HB	1.93	0.51
2:N:454:CYS:SG	2:N:455:ARG:N	2.84	0.51
5:R:45:ASN:O	5:R:46:SER:OG	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:514:VAL:HA	1:A:518:ILE:HG21	1.93	0.51
1:A:590:ASN:HB2	1:A:602:ARG:HG3	1.91	0.51
1:A:663:VAL:HG13	1:A:905:PHE:HB2	1.93	0.51
1:C:489:PRO:HD3	1:C:508:VAL:HG12	1.92	0.51
1:D:83:ARG:HG3	1:D:582:GLU:HB3	1.93	0.51
1:D:119:THR:OG1	1:D:120:ALA:N	2.42	0.51
1:D:234:ASN:HD21	1:D:238:GLY:HA3	1.75	0.51
1:D:358:LEU:HD21	1:D:947:ALA:HB2	1.93	0.51
1:J:240:ALA:O	1:J:241:LYS:HD3	2.11	0.51
1:A:696:ASP:OD1	1:A:696:ASP:N	2.43	0.51
1:C:596:SER:C	1:C:598:GLY:N	2.62	0.51
1:C:827:GLY:HA2	1:C:839:GLY:C	2.36	0.51
1:E:812:LYS:H	1:E:812:LYS:HD2	1.75	0.51
1:F:194:GLN:O	1:F:197:PRO:HD2	2.11	0.51
1:G:789:ASP:OD2	1:I:379:ARG:NH2	2.30	0.51
1:K:302:GLY:O	1:K:491:ASN:ND2	2.44	0.51
1:L:358:LEU:HD23	1:L:361:ARG:HH12	1.76	0.51
1:A:7:MET:HG3	1:A:12:TYR:HB2	1.93	0.51
1:D:379:ARG:NH2	1:E:789:ASP:OD2	2.34	0.51
1:E:676:ARG:NH2	1:E:921:GLU:OE1	2.44	0.51
1:F:932:HIS:C	1:F:934:GLY:H	2.18	0.51
1:G:239:GLN:HB3	1:G:241:LYS:HZ1	1.76	0.51
1:G:539:ARG:NH2	1:H:404:GLU:OE2	2.44	0.51
1:J:922:VAL:HG12	1:J:944:PRO:HG2	1.93	0.51
2:N:237:PRO:HA	2:N:268:TYR:CG	2.46	0.51
1:A:330:PHE:CZ	1:A:385:ASN:HB2	2.46	0.50
1:B:33:ARG:HH22	7:1:22:TRP:NE1	2.09	0.50
1:B:119:THR:OG1	1:B:120:ALA:N	2.44	0.50
1:B:480:TYR:OH	1:B:538:PRO:HD3	2.11	0.50
1:C:103:ILE:H	1:C:103:ILE:HD12	1.75	0.50
1:C:651:ASN:HB3	1:C:919:LEU:HB3	1.93	0.50
1:C:711:THR:O	1:C:711:THR:OG1	2.29	0.50
1:H:426:VAL:HG12	1:H:440:TRP:HB3	1.93	0.50
1:I:188:TYR:HA	1:I:192:THR:HG23	1.93	0.50
1:J:134:GLN:HA	1:J:154:THR:O	2.11	0.50
1:A:99:THR:HB	1:A:615:LEU:HD11	1.94	0.50
1:A:308:SER:OG	1:A:311:ASN:OD1	2.29	0.50
1:D:392:ASP:HB3	1:D:395:VAL:HG12	1.92	0.50
1:G:103:ILE:HG23	1:G:613:VAL:HG22	1.94	0.50
1:H:135:TRP:HE1	1:H:156:THR:HG23	1.76	0.50
1:J:446:ILE:HG23	1:J:447:SER:H	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:923:PHE:O	1:J:942:ARG:HA	2.11	0.50
1:L:102:ASP:OD1	1:L:559:HIS:NE2	2.44	0.50
5:Q:14:SER:C	5:R:15:PRO:CB	2.85	0.50
1:A:427:LYS:HD2	1:A:441:GLU:HB3	1.92	0.50
1:D:286:GLU:OE2	1:E:842:TYR:OH	2.30	0.50
1:D:415:ASN:HD21	1:D:418:GLY:HA2	1.77	0.50
1:F:785:GLU:OE1	1:F:785:GLU:N	2.42	0.50
1:H:269:PRO:HD2	1:H:273:SER:HB3	1.94	0.50
1:H:761:MET:HE2	1:H:765:TRP:CD1	2.45	0.50
1:I:83:ARG:HA	1:I:582:GLU:HB2	1.92	0.50
1:K:914:THR:OG1	1:K:915:LEU:N	2.44	0.50
1:L:94:LEU:HB2	1:L:619:PHE:CE2	2.46	0.50
1:L:187:ILE:HG12	1:L:189:ALA:H	1.76	0.50
1:A:804:GLN:HE22	1:C:551:GLY:HA3	1.76	0.50
1:E:531:ASN:HB2	1:E:714:LEU:HD11	1.93	0.50
1:F:931:PRO:HD2	1:F:935:VAL:HG13	1.93	0.50
1:G:114:LYS:NZ	1:G:116:TYR:O	2.30	0.50
1:G:240:ALA:O	1:G:288:VAL:HG23	2.11	0.50
1:H:155:LYS:HG3	1:H:261:PHE:HZ	1.76	0.50
1:H:589:VAL:HG21	1:H:606:ALA:HB1	1.92	0.50
1:H:685:THR:O	5:Q:28:ARG:NH1	2.44	0.50
1:K:813:ASP:OD1	1:K:813:ASP:N	2.44	0.50
1:L:698:TYR:O	1:L:700:VAL:HG22	2.12	0.50
6:V:11:TRP:HZ2	6:V:69:LEU:HD12	1.77	0.50
1:A:385:ASN:OD1	1:A:546:ARG:HD2	2.12	0.50
1:A:456:ASN:HD21	1:C:838:GLN:HA	1.76	0.50
1:A:575:LEU:HD21	1:A:634:LEU:HD23	1.92	0.50
1:B:237:GLY:HA3	1:C:821:PHE:HB3	1.92	0.50
1:B:417:THR:HA	1:B:457:VAL:HG12	1.94	0.50
1:C:671:ASN:OD1	1:C:672:TRP:N	2.44	0.50
1:D:173:LEU:HB2	1:D:185:LYS:HD3	1.92	0.50
1:D:714:LEU:HD21	1:D:910:MET:HE1	1.92	0.50
1:H:191:LYS:C	1:H:193:PHE:H	2.19	0.50
1:H:721:VAL:HG22	1:H:905:PHE:HD1	1.76	0.50
1:I:476:ASN:HB2	1:I:537:HIS:HE1	1.77	0.50
6:U:2:SER:HB3	6:U:199:ASN:HA	1.92	0.50
1:B:20:ALA:HA	1:B:23:TYR:CE2	2.47	0.50
1:B:102:ASP:OD2	1:C:763:LYS:NZ	2.45	0.50
1:F:662:ASN:ND2	5:P:22:PRO:HG2	2.26	0.50
1:G:196:GLU:HG2	1:H:823:HIS:HB3	1.93	0.50
1:H:527:ASP:HA	1:H:530:ASP:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:684:LYS:NZ	1:I:713:TYR:OH	2.34	0.50
1:J:203:ASN:N	1:J:203:ASN:OD1	2.44	0.50
1:K:230:ALA:O	1:K:239:GLN:NE2	2.44	0.50
5:Q:41:VAL:HG22	5:Q:43:PRO:HG3	1.92	0.50
1:B:103:ILE:HG12	1:B:613:VAL:HG22	1.94	0.50
1:B:426:VAL:HG12	1:B:440:TRP:HB3	1.93	0.50
1:B:604:ASP:OD1	1:B:604:ASP:N	2.35	0.50
1:D:137:THR:CG2	1:D:152:ASP:HB2	2.41	0.50
1:F:289:ASN:N	1:F:289:ASN:OD1	2.44	0.50
1:F:827:GLY:HA2	1:F:839:GLY:C	2.36	0.50
1:I:429:THR:HG22	1:I:430:ASN:H	1.76	0.50
1:I:771:LEU:HD21	1:I:778:TYR:CZ	2.47	0.50
1:L:83:ARG:HA	1:L:582:GLU:HB2	1.92	0.50
5:P:10:GLY:HA2	5:P:13:PHE:CD1	2.46	0.50
1:B:246:ASN:ND2	1:B:247:GLU:O	2.45	0.50
1:C:447:SER:O	1:C:449:GLN:HG2	2.12	0.50
1:E:67:ARG:HG3	1:E:616:TYR:CZ	2.46	0.50
1:F:371:LEU:HB3	1:F:377:ARG:HD3	1.94	0.50
1:G:719:LYS:NZ	1:G:908:ASP:OD1	2.29	0.50
1:I:38:TYR:OH	7:6:9:LEU:O	2.30	0.50
1:I:510:ALA:HA	1:I:832:LEU:O	2.12	0.50
1:J:198:GLN:HE22	1:K:840:GLN:HB3	1.75	0.50
1:K:392:ASP:OD2	1:K:395:VAL:N	2.44	0.50
1:L:711:THR:O	1:L:711:THR:OG1	2.26	0.50
1:B:122:ASN:HA	1:C:825:ASN:HD22	1.76	0.50
1:B:479:LEU:HD11	1:C:406:GLU:HG2	1.93	0.50
1:D:731:TRP:H	1:D:731:TRP:CD1	2.30	0.50
1:E:91:ASN:OD1	1:E:628:SER:OG	2.30	0.50
1:H:485:TYR:CE2	1:H:528:PRO:HB3	2.46	0.50
1:J:234:ASN:HD21	1:J:238:GLY:HA3	1.76	0.50
1:J:277:TYR:OH	1:J:280:ASP:OD2	2.27	0.50
1:K:424:GLN:NE2	1:L:276:GLU:OE2	2.44	0.50
1:K:513:LEU:HD13	1:K:819:LEU:HD22	1.94	0.50
1:K:696:ASP:OD1	1:K:696:ASP:N	2.45	0.50
1:L:656:ILE:HD13	1:L:682:ARG:HH12	1.75	0.50
5:P:34:SER:OG	5:P:35:THR:HG22	2.11	0.50
1:A:752:GLU:O	1:C:104:ARG:NH1	2.45	0.49
1:B:121:TYR:CE2	1:C:847:PRO:HG2	2.47	0.49
1:B:328:ASP:OD2	1:B:377:ARG:NH2	2.45	0.49
1:C:203:ASN:OD1	1:C:203:ASN:N	2.38	0.49
1:F:152:ASP:C	1:F:154:THR:N	2.69	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:620:PHE:CD2	1:H:622:MET:HG2	2.47	0.49
1:I:304:SER:OG	1:I:306:ASN:OD1	2.30	0.49
1:I:442:LYS:HG2	1:I:443:ASP:H	1.76	0.49
1:K:203:ASN:OD1	1:K:203:ASN:N	2.45	0.49
1:L:132:PRO:HB3	1:L:157:PHE:O	2.12	0.49
1:L:165:ILE:HD11	1:L:173:LEU:HD22	1.94	0.49
1:B:96:MET:HG2	1:B:569:ILE:HG22	1.93	0.49
1:B:422:THR:HG23	1:B:449:GLN:O	2.12	0.49
1:D:96:MET:O	1:D:99:THR:OG1	2.31	0.49
1:D:320:ARG:NH1	1:D:479:LEU:O	2.41	0.49
1:G:278:LYS:HA	1:I:438:SER:HB3	1.95	0.49
1:G:730:SER:OG	1:G:732:PRO:HD2	2.12	0.49
1:H:397:ILE:HG21	1:H:801:MET:HE1	1.94	0.49
1:I:187:ILE:HG22	1:I:189:ALA:H	1.76	0.49
1:L:714:LEU:HD21	1:L:910:MET:HE1	1.93	0.49
2:N:77:ASN:HD21	2:N:488:ARG:HE	1.58	0.49
2:N:189:GLY:HA3	2:N:194:VAL:HG22	1.94	0.49
2:N:245:GLU:N	2:N:245:GLU:OE1	2.45	0.49
1:A:80:TYR:O	1:A:585:PHE:N	2.44	0.49
1:A:263:VAL:HG22	1:C:423:TYR:CE1	2.47	0.49
1:B:943:THR:HG23	1:B:944:PRO:HD3	1.94	0.49
1:C:20:ALA:HA	1:C:23:TYR:CE2	2.47	0.49
1:C:189:ALA:O	1:C:241:LYS:NZ	2.36	0.49
1:E:480:TYR:OH	1:E:538:PRO:HD3	2.11	0.49
1:F:396:ARG:HD3	1:F:534:PRO:HB3	1.94	0.49
1:H:119:THR:OG1	1:H:120:ALA:N	2.45	0.49
1:K:190:ASP:CG	1:K:191:LYS:H	2.19	0.49
1:L:150:GLU:HB2	1:L:152:ASP:OD1	2.12	0.49
1:B:214:ARG:HH22	1:B:241:LYS:HE2	1.77	0.49
1:C:419:THR:HB	1:C:453:CYS:HA	1.95	0.49
1:D:193:PHE:CD2	1:D:213:GLY:HA2	2.48	0.49
1:D:526:LEU:HD13	1:D:528:PRO:HD2	1.93	0.49
1:D:824:ASN:OD1	1:F:121:TYR:HA	2.11	0.49
1:F:153:VAL:O	1:F:156:THR:OG1	2.20	0.49
1:F:664:PRO:O	5:R:17:LEU:HB2	2.12	0.49
1:G:150:GLU:HB3	1:I:443:ASP:HB2	1.94	0.49
1:H:72:ASP:OD1	1:H:72:ASP:N	2.45	0.49
7:2:30:LEU:O	7:2:31:ASN:C	2.52	0.49
1:A:159:VAL:HG21	1:B:841:PRO:HD2	1.94	0.49
1:B:204:TRP:CZ2	1:B:415:ASN:HA	2.47	0.49
1:E:771:LEU:HD21	1:E:778:TYR:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:764:ASP:OD1	1:F:765:TRP:N	2.45	0.49
1:H:664:PRO:HB3	5:R:19:THR:HG23	1.95	0.49
1:I:33:ARG:HD3	7:6:22:TRP:NE1	2.26	0.49
1:I:590:ASN:O	1:I:590:ASN:ND2	2.46	0.49
1:J:804:GLN:OE1	1:L:556:VAL:HG12	2.13	0.49
1:K:684:LYS:HB3	1:K:687:GLU:HG2	1.95	0.49
1:L:676:ARG:NH2	1:L:921:GLU:OE1	2.44	0.49
1:B:224:PRO:HG2	1:B:316:SER:HB3	1.94	0.49
1:C:71:VAL:HG12	1:E:72:ASP:HB3	1.94	0.49
1:D:460:MET:SD	1:E:460:MET:HE2	2.53	0.49
1:E:202:GLU:HB3	1:F:313:VAL:HG11	1.93	0.49
1:G:500:THR:HG23	1:G:503:TYR:H	1.77	0.49
1:I:33:ARG:HD3	7:6:22:TRP:HE1	1.77	0.49
1:I:98:SER:HB2	1:I:618:THR:HG23	1.94	0.49
1:J:211:TYR:HE2	1:L:454:LYS:HE2	1.78	0.49
1:J:665:ILE:HG12	1:J:903:MET:HB2	1.95	0.49
1:K:112:SER:O	1:K:322:ASN:ND2	2.46	0.49
1:C:65:THR:HB	1:C:618:THR:HG22	1.95	0.49
1:D:443:ASP:N	1:D:443:ASP:OD1	2.43	0.49
1:G:328:ASP:C	1:G:330:PHE:N	2.68	0.49
1:H:441:GLU:HG2	1:H:442:LYS:HB2	1.95	0.49
1:I:155:LYS:HG3	1:I:261:PHE:CZ	2.48	0.49
1:J:198:GLN:NE2	1:K:840:GLN:HB3	2.28	0.49
1:K:141:GLN:O	1:K:145:GLY:HA3	2.13	0.49
2:N:131:LYS:NZ	2:N:245:GLU:OE2	2.33	0.49
5:R:18:THR:O	5:R:20:ARG:N	2.42	0.49
1:A:243:LYS:HA	1:A:254:LEU:HA	1.95	0.49
1:B:527:ASP:OD1	1:B:863:LYS:NZ	2.45	0.49
1:B:620:PHE:CE2	1:C:880:MET:HE1	2.48	0.49
1:C:69:VAL:HG21	1:E:74:GLU:HB3	1.93	0.49
1:C:134:GLN:HE21	1:C:218:LYS:H	1.60	0.49
1:D:130:PRO:HG3	1:F:204:TRP:CZ2	2.47	0.49
1:D:771:LEU:HD13	1:D:777:GLY:HA3	1.94	0.49
1:E:387:ALA:HB3	1:E:546:ARG:HG3	1.94	0.49
1:F:491:ASN:N	1:F:491:ASN:OD1	2.46	0.49
1:G:328:ASP:O	1:G:329:ASN:C	2.55	0.49
1:H:46:ARG:NE	1:I:644:ASN:OD1	2.41	0.49
1:H:396:ARG:NH1	1:H:867:ASP:OD2	2.46	0.49
1:I:513:LEU:HD13	1:I:819:LEU:HD22	1.95	0.49
1:J:538:PRO:O	1:J:544:ARG:NE	2.45	0.49
1:K:426:VAL:HG12	1:K:440:TRP:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:456:ASN:HD22	1:F:838:GLN:HA	1.77	0.49
1:G:19:ASP:OD1	1:G:20:ALA:N	2.45	0.49
1:H:700:VAL:HG13	5:Q:34:SER:HB2	1.94	0.49
1:J:4:PRO:HG2	6:U:58:GLN:NE2	2.28	0.49
1:J:573:LEU:HB3	1:J:641:GLN:HE21	1.78	0.49
1:K:190:ASP:C	1:K:192:THR:H	2.21	0.49
1:K:588:ASP:OD2	1:K:602:ARG:NH2	2.37	0.49
1:L:219:ASP:OD2	1:L:287:ASN:ND2	2.45	0.49
1:L:392:ASP:HB3	1:L:395:VAL:HG22	1.95	0.49
4:M:221:THR:OG1	4:M:222:VAL:N	2.45	0.49
1:A:194:GLN:NE2	1:A:237:GLY:O	2.44	0.49
1:A:644:ASN:HD21	7:2:29:GLN:HE21	1.61	0.49
1:B:333:LEU:HA	1:B:586:ARG:HB3	1.94	0.49
1:G:256:ILE:HG13	1:G:286:GLU:HB3	1.94	0.49
1:H:760:ASN:HB3	5:R:54:VAL:HG11	1.95	0.49
1:I:888:LEU:HD12	1:I:888:LEU:HA	1.66	0.49
1:J:842:TYR:CG	1:J:843:PRO:HD2	2.47	0.49
1:K:275:GLU:HG3	1:K:276:GLU:HG3	1.94	0.49
1:L:199:VAL:HG21	1:L:211:TYR:HE1	1.78	0.49
1:L:417:THR:HG21	1:L:453:CYS:SG	2.53	0.49
1:B:173:LEU:HD11	1:B:183:GLY:HA3	1.94	0.48
1:D:620:PHE:CD2	1:D:622:MET:HB3	2.47	0.48
1:E:222:MET:HG2	1:E:307:SER:HA	1.95	0.48
1:E:691:LEU:HD12	1:E:707:TYR:HE2	1.77	0.48
1:F:119:THR:OG1	1:F:120:ALA:N	2.46	0.48
1:F:152:ASP:C	1:F:154:THR:H	2.21	0.48
1:F:836:MET:HE3	1:F:837:ARG:HH21	1.77	0.48
1:G:239:GLN:HG2	1:H:842:TYR:HE2	1.78	0.48
1:G:378:THR:O	1:G:378:THR:OG1	2.31	0.48
1:G:527:ASP:HA	1:G:530:ASP:HB2	1.95	0.48
1:H:549:LEU:HG	1:I:758:GLN:HG3	1.94	0.48
1:K:109:ARG:NH2	1:K:550:LEU:HB2	2.28	0.48
1:K:419:THR:HB	1:K:453:CYS:HB2	1.95	0.48
1:K:715:ASN:O	1:K:871:TRP:NE1	2.44	0.48
1:L:96:MET:N	1:L:572:LEU:O	2.46	0.48
1:L:513:LEU:HD13	1:L:819:LEU:HD22	1.95	0.48
1:L:794:PHE:HA	1:L:869:VAL:HG11	1.95	0.48
5:P:72:MET:HG2	5:P:76:ARG:HE	1.77	0.48
1:A:515:ASP:OD1	1:A:516:ALA:N	2.40	0.48
1:B:476:ASN:O	1:B:478:ALA:N	2.46	0.48
1:D:327:ARG:HD3	1:D:594:GLN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:19:ASP:HB3	7:3:14:GLY:HA3	1.94	0.48
1:G:106:VAL:HG21	1:G:609:ARG:HH21	1.77	0.48
1:G:133:SER:OG	1:G:134:GLN:N	2.45	0.48
1:G:847:PRO:HG2	1:I:121:TYR:CE1	2.48	0.48
1:H:42:GLY:HA2	7:5:24:GLU:HG2	1.95	0.48
1:J:657:PRO:HG2	1:J:660:ALA:HB2	1.95	0.48
5:S:16:TYR:O	5:S:18:THR:N	2.39	0.48
1:B:162:THR:H	1:B:211:TYR:HD1	1.60	0.48
1:B:385:ASN:HD21	1:B:546:ARG:HG3	1.78	0.48
1:B:663:VAL:HG13	1:B:905:PHE:HB2	1.95	0.48
1:C:842:TYR:CG	1:C:843:PRO:HD2	2.48	0.48
1:D:214:ARG:HD3	1:D:284:TYR:HB2	1.94	0.48
1:D:353:ASN:OD1	1:D:355:VAL:HG12	2.13	0.48
1:D:941:LEU:HD22	1:F:13:MET:HG3	1.95	0.48
1:E:94:LEU:HB2	1:E:619:PHE:CE2	2.48	0.48
1:E:807:ASP:OD2	1:E:810:ASN:ND2	2.37	0.48
1:F:172:LEU:HD13	1:F:193:PHE:HE2	1.77	0.48
1:F:539:ARG:HA	1:F:544:ARG:NH2	2.29	0.48
1:H:204:TRP:HH2	1:I:130:PRO:HG3	1.78	0.48
1:H:731:TRP:N	1:H:732:PRO:HD2	2.28	0.48
4:M:388:TRP:CZ2	4:M:391:PRO:HD3	2.47	0.48
5:S:72:MET:O	5:S:73:THR:C	2.57	0.48
1:A:173:LEU:HA	1:A:185:LYS:HA	1.94	0.48
1:A:217:LYS:HG2	1:A:285:THR:HG22	1.95	0.48
1:A:837:ARG:HH11	1:B:457:VAL:HG23	1.78	0.48
1:C:696:ASP:N	1:C:696:ASP:OD1	2.46	0.48
1:D:427:LYS:HG2	1:D:441:GLU:HB2	1.95	0.48
1:E:119:THR:OG1	1:E:120:ALA:N	2.46	0.48
1:G:93:VAL:HG21	1:G:622:MET:HE3	1.95	0.48
1:G:233:THR:O	1:H:815:LYS:NZ	2.32	0.48
1:H:107:LEU:HD22	1:H:109:ARG:HD2	1.95	0.48
1:I:514:VAL:HA	1:I:518:ILE:HG21	1.95	0.48
1:I:635:ARG:HG3	1:I:930:GLN:O	2.14	0.48
1:J:20:ALA:HA	1:J:23:TYR:CE2	2.49	0.48
1:J:198:GLN:HG3	1:K:839:GLY:HA2	1.96	0.48
1:K:190:ASP:C	1:K:192:THR:N	2.71	0.48
1:K:243:LYS:HG2	1:K:251:PRO:HB2	1.95	0.48
1:L:396:ARG:HD3	1:L:534:PRO:HB3	1.95	0.48
2:N:113:ILE:HG13	2:N:471:LEU:HG	1.94	0.48
1:B:203:ASN:HD21	1:B:415:ASN:HB3	1.78	0.48
1:D:377:ARG:NH2	1:D:388:VAL:HG12	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:663:VAL:HG13	1:E:905:PHE:HB2	1.95	0.48
1:F:719:LYS:HE3	1:F:908:ASP:HB3	1.95	0.48
1:G:608:VAL:HG12	1:G:609:ARG:HD3	1.95	0.48
1:H:631:GLU:OE1	1:H:635:ARG:NH1	2.46	0.48
1:I:191:LYS:O	1:I:193:PHE:N	2.43	0.48
1:J:449:GLN:HB3	1:K:153:VAL:HG13	1.95	0.48
1:J:633:MET:C	1:J:639:HIS:HE2	2.21	0.48
1:K:188:TYR:HD1	1:K:188:TYR:H	1.59	0.48
1:K:193:PHE:CE2	1:K:212:GLY:HA3	2.48	0.48
1:K:460:MET:HE1	1:L:460:MET:HB3	1.93	0.48
1:L:222:MET:HE2	1:L:307:SER:HA	1.94	0.48
1:L:510:ALA:HA	1:L:832:LEU:O	2.13	0.48
4:M:388:TRP:CH2	4:M:391:PRO:HD3	2.48	0.48
1:A:372:ASP:OD2	1:A:790:ARG:HB3	2.13	0.48
1:B:219:ASP:OD2	1:B:287:ASN:ND2	2.45	0.48
1:B:890:GLN:HG3	4:M:50:ALA:HB2	1.95	0.48
1:C:441:GLU:HB2	1:C:446:ILE:HG23	1.95	0.48
1:G:476:ASN:O	1:G:478:ALA:N	2.47	0.48
1:G:676:ARG:NH2	7:6:31:ASN:H	2.11	0.48
1:K:400:ASN:HD22	1:K:469:TRP:HZ2	1.62	0.48
1:L:878:ASN:HD21	1:L:882:MET:HE1	1.78	0.48
2:N:426:ASP:OD1	2:N:426:ASP:N	2.47	0.48
1:A:278:LYS:HD2	1:C:437:GLU:O	2.14	0.48
1:B:3:THR:OG1	1:B:4:PRO:HD2	2.14	0.48
1:C:791:MET:SD	1:C:868:ARG:NH1	2.86	0.48
1:D:196:GLU:HG3	1:E:823:HIS:HB3	1.96	0.48
1:E:130:PRO:HG3	1:E:312:LEU:HG	1.96	0.48
1:F:172:LEU:HD13	1:F:193:PHE:CE2	2.49	0.48
1:F:203:ASN:ND2	1:F:203:ASN:H	2.11	0.48
1:F:684:LYS:NZ	1:F:713:TYR:OH	2.47	0.48
1:G:219:ASP:HB2	1:G:287:ASN:HD21	1.78	0.48
1:H:154:THR:O	1:H:156:THR:N	2.47	0.48
1:I:135:TRP:NE1	1:I:156:THR:OG1	2.47	0.48
1:J:498:THR:O	1:J:498:THR:OG1	2.26	0.48
1:L:135:TRP:HE1	1:L:137:THR:HG23	1.79	0.48
1:L:296:HIS:CE1	1:L:317:MET:HG3	2.49	0.48
1:A:64:LEU:HB2	1:B:736:ARG:O	2.14	0.48
1:B:112:SER:OG	1:B:322:ASN:ND2	2.47	0.48
1:C:88:VAL:HB	1:C:576:PRO:HA	1.96	0.48
1:C:714:LEU:HD13	1:C:910:MET:HE1	1.95	0.48
1:D:130:PRO:HG3	1:F:204:TRP:HZ2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:257:ASP:OD1	1:H:285:THR:OG1	2.29	0.48
1:H:538:PRO:O	1:H:544:ARG:NH2	2.43	0.48
1:H:640:ASP:OD1	1:H:640:ASP:N	2.41	0.48
1:I:76:THR:HG22	1:I:77:THR:H	1.79	0.48
1:I:476:ASN:HB2	1:I:537:HIS:CE1	2.48	0.48
1:I:878:ASN:HD21	1:I:882:MET:HE1	1.79	0.48
1:J:134:GLN:CD	1:J:155:LYS:HZ3	2.17	0.48
1:J:637:ASP:N	1:J:637:ASP:OD1	2.46	0.48
1:J:774:TYR:HB2	1:J:776:ILE:HG12	1.95	0.48
1:K:192:THR:OG1	1:K:193:PHE:N	2.43	0.48
1:K:328:ASP:OD2	1:K:368:GLN:NE2	2.46	0.48
1:L:725:PHE:HD2	1:L:731:TRP:HB2	1.78	0.48
4:M:215:PRO:HG2	4:M:221:THR:HG21	1.95	0.48
5:Q:14:SER:HB3	5:R:15:PRO:HB3	1.94	0.48
1:A:682:ARG:NH2	1:A:910:MET:HG3	2.28	0.48
1:D:170:GLN:CD	1:D:185:LYS:HG3	2.38	0.48
1:F:680:PHE:HB3	1:F:918:LEU:HD12	1.96	0.48
1:G:246:ASN:ND2	1:G:250:GLN:O	2.40	0.48
1:I:204:TRP:CD1	1:I:204:TRP:H	2.32	0.48
1:J:808:GLU:OE1	1:J:808:GLU:N	2.46	0.48
1:K:443:ASP:HB3	1:L:150:GLU:HB3	1.95	0.48
1:K:526:LEU:HD13	1:K:528:PRO:HD2	1.95	0.48
1:C:152:ASP:O	1:C:154:THR:HG22	2.13	0.48
1:D:804:GLN:NE2	1:F:556:VAL:HG12	2.28	0.48
1:G:140:LYS:HA	1:G:147:VAL:HA	1.95	0.48
1:I:336:TYR:CZ	1:I:565:LYS:HG2	2.49	0.48
1:D:313:VAL:HG11	1:F:202:GLU:HA	1.95	0.47
1:E:201:GLU:H	1:E:201:GLU:HG2	1.50	0.47
1:E:253:ASP:OD1	1:E:254:LEU:N	2.37	0.47
1:F:657:PRO:HD2	5:R:12:LEU:HD22	1.94	0.47
1:G:52:PRO:HD3	7:6:11:PRO:HA	1.96	0.47
1:G:309:GLU:OE2	1:I:205:GLN:NE2	2.41	0.47
1:G:456:ASN:HD21	1:I:839:GLY:H	1.61	0.47
1:I:151:LYS:HB3	1:I:154:THR:CB	2.44	0.47
1:I:193:PHE:HE2	1:I:284:TYR:CG	2.32	0.47
1:J:72:ASP:N	1:J:72:ASP:OD1	2.46	0.47
1:J:443:ASP:OD1	1:J:443:ASP:N	2.43	0.47
1:J:836:MET:HE3	1:J:836:MET:HB3	1.74	0.47
1:K:169:ASN:OD1	1:K:169:ASN:N	2.47	0.47
1:K:336:TYR:HE1	1:K:566:PHE:HB2	1.78	0.47
1:L:308:SER:O	1:L:310:ILE:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:13:PHE:CD2	5:P:14:SER:N	2.82	0.47
5:P:39:ARG:HH21	5:P:41:VAL:HG21	1.79	0.47
1:A:355:VAL:HB	1:A:569:ILE:HD11	1.95	0.47
1:A:651:ASN:HB3	1:A:919:LEU:HD12	1.95	0.47
1:A:831:TYR:H	1:A:838:GLN:HE21	1.62	0.47
1:B:403:VAL:HG11	1:B:466:ALA:HA	1.96	0.47
1:B:426:VAL:HA	1:B:440:TRP:HA	1.95	0.47
1:C:152:ASP:C	1:C:154:THR:H	2.22	0.47
1:D:200:GLY:HA3	1:D:206:GLU:OE1	2.14	0.47
1:D:207:ASN:OD1	1:D:207:ASN:N	2.47	0.47
1:D:288:VAL:HG13	1:D:290:LEU:H	1.80	0.47
1:E:449:GLN:HG3	1:E:450:ASN:N	2.30	0.47
1:F:134:GLN:HG2	1:F:155:LYS:HG2	1.96	0.47
1:H:187:ILE:O	1:H:191:LYS:N	2.45	0.47
1:I:20:ALA:HA	1:I:23:TYR:CE2	2.49	0.47
1:J:264:PRO:HD3	1:L:423:TYR:HA	1.95	0.47
1:K:629:THR:O	1:K:633:MET:HG2	2.13	0.47
1:K:767:LEU:O	1:K:771:LEU:HB2	2.14	0.47
1:K:952:THR:H	6:U:33:TRP:HZ2	1.60	0.47
2:N:280:LEU:HD11	2:N:285:TYR:HB2	1.96	0.47
2:N:281:ASP:OD1	2:N:281:ASP:N	2.47	0.47
1:A:244:PRO:HD3	1:A:254:LEU:C	2.38	0.47
1:B:96:MET:HE1	1:B:574:LEU:HD22	1.96	0.47
1:B:230:ALA:HB3	1:B:239:GLN:NE2	2.27	0.47
1:B:678:TRP:HE1	1:B:901:LEU:HD21	1.79	0.47
1:C:770:MET:HE3	1:C:776:ILE:HD11	1.96	0.47
1:D:427:LYS:HG3	1:D:439:GLU:HB2	1.95	0.47
1:E:334:MET:HE3	1:E:336:TYR:CE2	2.50	0.47
1:F:20:ALA:HA	1:F:23:TYR:CE2	2.49	0.47
1:H:813:ASP:OD1	1:H:813:ASP:N	2.46	0.47
1:J:38:TYR:HB2	1:L:880:MET:HE1	1.96	0.47
1:J:122:ASN:HA	1:K:825:ASN:HA	1.95	0.47
1:J:426:VAL:HG12	1:J:440:TRP:HD1	1.79	0.47
1:J:764:ASP:OD1	1:J:765:TRP:N	2.46	0.47
4:M:86:ARG:HB2	4:M:89:GLU:HG3	1.96	0.47
5:S:72:MET:O	5:S:74:ALA:N	2.47	0.47
6:U:2:SER:HB2	6:U:200:PRO:HD3	1.96	0.47
6:U:26:ASP:OD2	6:U:29:THR:OG1	2.31	0.47
1:E:322:ASN:ND2	1:E:597:LEU:H	2.13	0.47
1:E:872:ARG:NH2	7:3:30:LEU:O	2.45	0.47
1:F:513:LEU:HD13	1:F:819:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:102:ASP:OD1	1:H:559:HIS:NE2	2.48	0.47
1:H:217:LYS:HD2	1:H:287:ASN:HD21	1.79	0.47
1:H:676:ARG:HD3	1:H:923:PHE:CE2	2.50	0.47
1:I:267:SER:HB3	1:I:277:TYR:CD1	2.50	0.47
1:I:495:PRO:HG2	1:I:502:GLU:HG3	1.96	0.47
1:I:842:TYR:CG	1:I:843:PRO:HD2	2.49	0.47
1:J:589:VAL:HG23	1:J:593:LEU:HD23	1.96	0.47
1:J:693:SER:OG	5:P:25:ALA:N	2.37	0.47
1:J:804:GLN:OE1	1:J:860:THR:HB	2.14	0.47
1:K:452:ILE:HG23	1:L:158:GLY:O	2.13	0.47
1:L:429:THR:HG22	1:L:430:ASN:H	1.79	0.47
1:L:684:LYS:HE2	1:L:713:TYR:OH	2.14	0.47
5:P:39:ARG:HB3	5:P:41:VAL:HG23	1.96	0.47
6:U:24:SER:O	6:U:25:GLN:C	2.56	0.47
1:A:622:MET:HG3	1:A:627:ALA:HB2	1.97	0.47
1:B:49:THR:HG21	7:1:27:THR:HG21	1.96	0.47
1:E:172:LEU:HD11	1:E:282:ILE:HG21	1.95	0.47
1:G:548:MET:SD	1:H:401:HIS:NE2	2.88	0.47
1:G:561:GLN:HE22	1:H:756:VAL:HA	1.80	0.47
1:J:819:LEU:HA	1:J:822:GLN:CD	2.38	0.47
1:L:135:TRP:CD1	1:L:135:TRP:C	2.93	0.47
5:S:34:SER:OG	5:S:35:THR:N	2.47	0.47
1:D:344:VAL:HG22	1:D:582:GLU:HG2	1.97	0.47
1:D:696:ASP:OD1	1:D:696:ASP:N	2.45	0.47
1:H:526:LEU:HD13	1:H:528:PRO:HD2	1.95	0.47
1:H:715:ASN:HB2	1:H:871:TRP:NE1	2.29	0.47
1:J:590:ASN:OD1	1:J:602:ARG:HB2	2.14	0.47
1:B:907:VAL:HG23	1:B:908:ASP:H	1.79	0.47
1:C:58:THR:HB	1:C:623:ALA:HA	1.97	0.47
1:D:112:SER:O	1:D:322:ASN:ND2	2.47	0.47
1:D:217:LYS:NZ	1:D:257:ASP:OD2	2.43	0.47
1:D:924:ASP:N	1:D:924:ASP:OD1	2.47	0.47
1:F:228:SER:HB2	1:F:290:LEU:HD11	1.97	0.47
1:F:681:THR:CG2	1:F:715:ASN:HD21	2.27	0.47
1:F:886:THR:HG23	1:F:889:GLY:H	1.79	0.47
1:G:88:VAL:HG22	1:G:576:PRO:HA	1.97	0.47
1:G:137:THR:OG1	1:G:138:LYS:N	2.46	0.47
1:G:234:ASN:HD21	1:G:238:GLY:HA3	1.80	0.47
1:G:341:ASN:O	1:G:341:ASN:ND2	2.44	0.47
1:G:457:VAL:O	1:I:837:ARG:NH1	2.48	0.47
1:G:485:TYR:CZ	1:G:528:PRO:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:193:PHE:HE1	1:H:198:GLN:HB3	1.79	0.47
1:H:198:GLN:NE2	1:I:838:GLN:HB2	2.30	0.47
1:H:240:ALA:O	1:H:288:VAL:HG12	2.15	0.47
1:H:656:ILE:HG12	1:H:663:VAL:HG21	1.97	0.47
1:H:760:ASN:CG	5:R:54:VAL:HG21	2.39	0.47
1:I:767:LEU:O	1:I:771:LEU:HB2	2.14	0.47
1:I:872:ARG:NH1	7:5:31:ASN:O	2.48	0.47
1:J:44:LYS:NZ	1:K:95:ASP:OD2	2.41	0.47
1:J:639:HIS:CD2	1:L:28:LEU:HD12	2.50	0.47
1:K:214:ARG:HH22	1:K:241:LYS:HZ3	1.62	0.47
1:K:514:VAL:HA	1:K:518:ILE:HG21	1.96	0.47
2:N:341:ASN:ND2	2:N:341:ASN:O	2.48	0.47
5:Q:127:GLU:HG2	5:Q:128:GLN:HG3	1.96	0.47
1:A:923:PHE:O	1:A:942:ARG:HA	2.15	0.47
1:C:266:GLY:HA3	1:C:277:TYR:CE1	2.50	0.47
1:E:113:PHE:HE1	1:E:324:ILE:H	1.61	0.47
1:F:442:LYS:HG2	1:F:443:ASP:H	1.79	0.47
1:G:383:MET:HA	1:H:757:ALA:HA	1.96	0.47
1:G:771:LEU:HD21	1:G:778:TYR:CE2	2.50	0.47
1:H:237:GLY:HA3	1:I:821:PHE:HB3	1.95	0.47
1:H:682:ARG:NH2	1:H:910:MET:HE3	2.30	0.47
1:J:52:PRO:HB2	1:J:56:VAL:HG21	1.97	0.47
1:J:419:THR:HB	1:J:453:CYS:HB2	1.97	0.47
1:K:138:LYS:HA	1:K:149:GLN:HA	1.96	0.47
1:K:204:TRP:CD1	1:K:415:ASN:HB3	2.50	0.47
1:L:287:ASN:OD1	1:L:287:ASN:N	2.47	0.47
1:L:597:LEU:HD12	1:L:597:LEU:HA	1.70	0.47
1:L:811:TYR:CD1	1:L:857:PRO:HD2	2.50	0.47
5:S:98:GLU:H	5:S:98:GLU:CD	2.23	0.47
1:A:237:GLY:HA3	1:B:821:PHE:HB2	1.97	0.47
1:B:638:THR:HG23	1:B:639:HIS:ND1	2.30	0.47
1:D:152:ASP:O	1:D:154:THR:HG22	2.15	0.47
1:D:765:TRP:O	1:D:766:PHE:C	2.53	0.47
1:E:756:VAL:HG13	1:E:763:LYS:HG2	1.95	0.47
1:F:548:MET:HE2	1:F:548:MET:HB3	1.78	0.47
1:F:657:PRO:HG2	1:F:660:ALA:HB2	1.96	0.47
1:G:636:ASN:OD1	1:G:637:ASP:N	2.47	0.47
1:G:640:ASP:HB2	1:G:928:VAL:O	2.14	0.47
1:H:148:GLN:HG3	1:H:150:GLU:OE1	2.15	0.47
5:R:12:LEU:HD11	5:R:17:LEU:HD21	1.96	0.47
1:A:3:THR:HG23	1:A:4:PRO:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:ASP:OD2	1:D:790:ARG:HB3	2.15	0.47
1:G:216:LEU:HB3	1:G:220:THR:HG21	1.96	0.47
1:I:244:PRO:HD3	1:I:253:ASP:O	2.15	0.47
1:J:59:ASP:OD1	1:J:59:ASP:N	2.47	0.47
1:J:438:SER:HB3	1:K:278:LYS:HD2	1.96	0.47
4:M:42:GLU:HG3	4:M:45:ARG:NH1	2.30	0.47
5:P:35:THR:O	5:P:36:VAL:C	2.53	0.47
1:A:244:PRO:HD2	1:A:253:ASP:C	2.39	0.46
1:B:64:LEU:HD21	1:B:621:PRO:HG3	1.97	0.46
1:C:263:VAL:O	1:C:277:TYR:OH	2.23	0.46
1:C:328:ASP:O	1:C:329:ASN:C	2.56	0.46
1:D:299:TYR:OH	1:F:202:GLU:HG2	2.15	0.46
1:D:451:GLN:HB2	1:E:156:THR:O	2.15	0.46
1:D:825:ASN:OD1	1:F:124:LEU:HB2	2.15	0.46
1:E:675:PHE:HE1	1:E:920:PHE:HB3	1.79	0.46
1:F:154:THR:HG23	1:F:155:LYS:HG3	1.96	0.46
1:G:640:ASP:OD1	1:G:640:ASP:N	2.44	0.46
1:H:827:GLY:HA2	1:H:839:GLY:C	2.40	0.46
1:I:74:GLU:HB3	1:I:81:LYS:HB3	1.97	0.46
1:I:204:TRP:CD2	1:I:415:ASN:HB3	2.50	0.46
1:J:591:MET:HE2	1:J:591:MET:HB2	1.87	0.46
1:J:746:LYS:HZ3	5:Q:54:VAL:HG21	1.80	0.46
1:J:824:ASN:HD22	1:J:825:ASN:HB2	1.80	0.46
1:K:191:LYS:HA	1:K:191:LYS:HD2	1.54	0.46
1:K:503:TYR:OH	1:K:507:ARG:NH1	2.47	0.46
1:L:34:ALA:HA	7:9:19:MET:HG2	1.97	0.46
7:9:22:TRP:CD1	7:9:22:TRP:H	2.33	0.46
1:A:842:TYR:OH	1:C:286:GLU:OE2	2.33	0.46
1:G:367:TYR:CD2	1:G:565:LYS:HE2	2.50	0.46
1:G:429:THR:HG22	1:G:439:GLU:HB2	1.97	0.46
1:H:195:PRO:HG2	1:I:823:HIS:CD2	2.50	0.46
1:I:79:LEU:HD21	1:I:341:ASN:HD22	1.80	0.46
1:I:151:LYS:C	1:I:154:THR:HB	2.40	0.46
1:I:160:ALA:HB1	1:I:212:GLY:C	2.40	0.46
1:I:590:ASN:HB3	1:I:602:ARG:HH21	1.81	0.46
1:I:676:ARG:NH2	1:I:921:GLU:OE1	2.47	0.46
1:J:113:PHE:CG	1:J:113:PHE:O	2.69	0.46
1:L:189:ALA:C	1:L:241:LYS:HZ2	2.20	0.46
5:S:49:MET:SD	5:S:50:THR:N	2.89	0.46
1:A:564:GLN:HE22	1:A:569:ILE:HD12	1.80	0.46
1:A:759:CYS:HB3	1:A:800:PRO:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:ASN:OD1	1:B:418:GLY:N	2.37	0.46
1:C:204:TRP:HE1	1:C:415:ASN:HB2	1.80	0.46
1:D:724:MET:HG3	1:D:728:SER:O	2.16	0.46
1:E:773:HIS:CE1	1:E:872:ARG:HH11	2.34	0.46
1:E:801:MET:HE2	1:E:801:MET:HB3	1.86	0.46
1:F:731:TRP:N	1:F:732:PRO:HD2	2.31	0.46
1:G:575:LEU:HB3	1:G:576:PRO:HD2	1.97	0.46
1:H:121:TYR:O	1:H:122:ASN:C	2.58	0.46
1:J:392:ASP:HB3	1:J:395:VAL:HG12	1.97	0.46
1:J:670:ARG:NH2	1:J:946:SER:H	2.13	0.46
1:L:575:LEU:HB3	1:L:576:PRO:HD2	1.96	0.46
1:A:255:ASP:O	1:A:286:GLU:HB3	2.14	0.46
1:C:6:MET:HE2	1:C:6:MET:HA	1.96	0.46
1:D:162:THR:HB	1:D:193:PHE:CD1	2.50	0.46
1:D:239:GLN:HG2	1:E:842:TYR:HE2	1.80	0.46
1:E:754:TYR:O	1:E:763:LYS:N	2.46	0.46
1:F:759:CYS:SG	1:F:760:ASN:N	2.88	0.46
1:G:28:LEU:HD12	1:H:639:HIS:ND1	2.31	0.46
1:G:237:GLY:HA3	1:H:821:PHE:HB3	1.97	0.46
1:H:64:LEU:HD13	1:I:736:ARG:HD2	1.96	0.46
1:H:913:PRO:HB2	5:P:8:PHE:HB2	1.98	0.46
1:I:161:ALA:HB3	1:I:198:GLN:NE2	2.29	0.46
1:J:266:GLY:HA3	1:J:276:GLU:HA	1.96	0.46
1:J:831:TYR:HD1	1:L:196:GLU:HB2	1.80	0.46
1:K:292:THR:O	1:K:292:THR:OG1	2.34	0.46
1:L:423:TYR:N	1:L:450:ASN:O	2.31	0.46
5:Q:4:THR:HB	5:Q:13:PHE:CE1	2.50	0.46
5:Q:101:LEU:HD22	5:S:96:ILE:HG13	1.97	0.46
1:A:423:TYR:HE1	1:B:263:VAL:HG22	1.80	0.46
1:A:495:PRO:HG3	1:A:502:GLU:HB3	1.96	0.46
1:B:403:VAL:HG22	1:B:465:GLN:HB3	1.98	0.46
1:B:449:GLN:HE21	1:B:449:GLN:HA	1.80	0.46
1:D:56:VAL:HG21	1:E:882:MET:HE3	1.97	0.46
1:D:237:GLY:HA3	1:E:821:PHE:HB3	1.98	0.46
1:D:256:ILE:HA	1:D:286:GLU:HB3	1.97	0.46
1:D:401:HIS:NE2	1:F:544:ARG:HD3	2.30	0.46
1:D:414:LEU:HD21	1:F:410:TYR:CE1	2.50	0.46
1:D:475:SER:O	1:D:476:ASN:C	2.58	0.46
1:G:449:GLN:HG2	1:H:153:VAL:HG22	1.97	0.46
1:H:44:LYS:HE3	1:I:573:LEU:HB2	1.97	0.46
1:H:573:LEU:HD23	1:H:634:LEU:HD21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:836:MET:HE3	1:H:837:ARG:HH21	1.81	0.46
1:I:155:LYS:HG3	1:I:261:PHE:HZ	1.79	0.46
1:J:18:GLN:O	1:J:22:GLU:HB2	2.15	0.46
1:J:241:LYS:HD2	1:J:256:ILE:HD11	1.97	0.46
1:J:747:ARG:NH2	1:J:752:GLU:OE2	2.41	0.46
4:M:254:HIS:O	4:M:257:THR:OG1	2.26	0.46
1:A:737:LEU:O	1:C:63:ARG:NH1	2.48	0.46
1:D:223:LYS:HD3	1:D:292:THR:HG23	1.97	0.46
1:E:767:LEU:O	1:E:771:LEU:HB2	2.15	0.46
1:F:392:ASP:HB3	1:F:395:VAL:HG22	1.98	0.46
1:H:115:PRO:HD2	1:H:116:TYR:HD1	1.81	0.46
1:J:162:THR:H	1:J:211:TYR:HD1	1.64	0.46
1:J:762:THR:OG1	1:J:763:LYS:N	2.48	0.46
1:K:310:ILE:HD12	1:K:311:ASN:H	1.80	0.46
1:L:150:GLU:O	1:L:152:ASP:N	2.43	0.46
1:A:275:GLU:OE1	1:A:276:GLU:N	2.47	0.46
1:A:438:SER:HB3	1:B:278:LYS:HD2	1.97	0.46
1:A:475:SER:OG	1:B:406:GLU:OE1	2.21	0.46
1:B:651:ASN:ND2	1:B:917:TYR:OH	2.49	0.46
1:B:767:LEU:O	1:B:771:LEU:HB2	2.15	0.46
1:C:19:ASP:HB2	7:1:14:GLY:HA3	1.96	0.46
1:C:761:MET:HE2	1:C:765:TRP:HD1	1.80	0.46
1:D:138:LYS:HG2	1:D:147:VAL:HG12	1.97	0.46
1:F:364:GLU:HB2	1:F:708:LEU:HB2	1.96	0.46
1:G:239:GLN:HG2	1:H:842:TYR:CE2	2.51	0.46
1:G:771:LEU:HD12	1:G:775:ASN:HA	1.98	0.46
1:H:61:SER:HA	1:I:734:ASN:HB2	1.97	0.46
1:H:604:ASP:OD1	1:H:605:GLY:N	2.39	0.46
1:H:752:GLU:CD	1:H:752:GLU:H	2.24	0.46
1:I:512:SER:HA	1:I:515:ASP:HB2	1.98	0.46
1:J:135:TRP:CZ3	1:J:137:THR:HB	2.50	0.46
1:J:261:PHE:O	1:J:280:ASP:N	2.45	0.46
1:K:49:THR:HG22	1:L:884:ALA:H	1.81	0.46
1:K:269:PRO:HG3	1:K:277:TYR:HB3	1.98	0.46
1:L:109:ARG:HH21	1:L:556:VAL:HG11	1.81	0.46
1:A:573:LEU:HD23	1:A:634:LEU:HD21	1.98	0.46
1:A:728:SER:OG	1:A:729:VAL:N	2.49	0.46
1:B:162:THR:HG23	1:B:193:PHE:CD1	2.50	0.46
1:B:198:GLN:HB2	1:C:838:GLN:O	2.16	0.46
1:B:573:LEU:HD23	1:B:573:LEU:HA	1.79	0.46
1:B:595:SER:HB2	1:B:601:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:GLY:HA2	1:C:211:TYR:HA	1.97	0.46
1:C:476:ASN:O	1:C:537:HIS:NE2	2.29	0.46
1:F:369:LEU:HD12	1:F:647:LEU:HD13	1.97	0.46
1:G:151:LYS:HD3	1:G:154:THR:HG21	1.97	0.46
1:G:775:ASN:N	1:G:775:ASN:OD1	2.48	0.46
1:I:201:GLU:CD	1:I:202:GLU:H	2.24	0.46
1:I:361:ARG:HG2	1:I:363:THR:HG23	1.97	0.46
1:I:766:PHE:O	1:I:767:LEU:C	2.58	0.46
1:J:350:SER:O	1:J:352:LEU:N	2.48	0.46
1:J:399:GLU:HB3	1:J:523:ARG:HB3	1.96	0.46
1:K:527:ASP:HA	1:K:530:ASP:HB2	1.98	0.46
1:K:808:GLU:OE1	1:K:808:GLU:N	2.49	0.46
1:L:650:ALA:HB2	1:L:942:ARG:HE	1.80	0.46
4:M:40:ASN:OD1	4:M:40:ASN:N	2.49	0.46
1:B:320:ARG:O	1:B:501:TYR:OH	2.32	0.46
1:D:422:THR:HA	1:D:450:ASN:O	2.16	0.46
1:D:575:LEU:HB3	1:D:635:ARG:NH2	2.31	0.46
1:D:785:GLU:H	1:D:785:GLU:HG2	1.61	0.46
1:E:239:GLN:HG2	1:F:842:TYR:CE2	2.51	0.46
1:F:360:ASP:OD1	1:F:942:ARG:NH1	2.37	0.46
1:F:771:LEU:HD13	1:F:879:PHE:HB2	1.98	0.46
1:G:441:GLU:OE1	1:G:443:ASP:N	2.29	0.46
1:G:822:GLN:HE21	1:G:822:GLN:C	2.23	0.46
1:G:836:MET:HA	1:H:410:TYR:OH	2.16	0.46
1:H:51:ALA:HB2	1:I:883:GLY:HA3	1.98	0.46
1:K:888:LEU:HD12	1:K:888:LEU:HA	1.79	0.46
1:L:377:ARG:HH12	1:L:386:SER:HB2	1.81	0.46
7:3:21:THR:O	7:3:23:ASN:N	2.48	0.46
1:A:76:THR:HG22	1:A:77:THR:H	1.80	0.46
1:A:575:LEU:HD11	1:A:634:LEU:HB3	1.98	0.46
1:B:372:ASP:O	1:B:790:ARG:NH1	2.49	0.46
1:B:486:LYS:O	1:B:507:ARG:NH1	2.49	0.46
1:C:537:HIS:CG	1:C:538:PRO:HD2	2.51	0.46
1:C:807:ASP:HB3	1:C:859:VAL:HB	1.97	0.46
1:E:296:HIS:CE1	1:E:317:MET:HG2	2.51	0.46
1:F:168:THR:OG1	1:F:169:ASN:N	2.44	0.46
1:H:728:SER:O	1:H:728:SER:OG	2.33	0.46
1:I:151:LYS:HB3	1:I:154:THR:CG2	2.46	0.46
1:I:734:ASN:OD1	1:I:736:ARG:NH1	2.46	0.46
1:I:772:SER:OG	1:I:872:ARG:HG2	2.16	0.46
1:K:7:MET:HE3	1:K:12:TYR:HD1	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:124:TYR:CD2	2:N:125:MET:HG3	2.51	0.46
1:A:52:PRO:HD3	7:2:11:PRO:HA	1.96	0.45
1:A:823:HIS:HB3	1:C:196:GLU:CD	2.41	0.45
1:B:423:TYR:CE1	1:C:263:VAL:HG22	2.51	0.45
1:C:328:ASP:C	1:C:330:PHE:N	2.72	0.45
1:D:66:LEU:HD23	1:D:66:LEU:HA	1.82	0.45
1:D:151:LYS:HD3	1:D:151:LYS:HA	1.83	0.45
1:E:19:ASP:O	1:E:23:TYR:HE1	1.99	0.45
1:E:336:TYR:CE2	1:E:565:LYS:HG3	2.51	0.45
1:F:69:VAL:HG23	1:F:70:PRO:HD2	1.97	0.45
1:G:407:LEU:HD11	1:I:474:TYR:HB3	1.98	0.45
1:G:473:LEU:HD12	1:G:473:LEU:HA	1.84	0.45
1:G:733:GLY:C	1:G:735:ASP:H	2.24	0.45
1:H:135:TRP:CZ2	1:H:309:GLU:HB2	2.51	0.45
1:I:350:SER:O	1:I:352:LEU:N	2.47	0.45
1:J:315:GLN:HE22	1:J:836:MET:H	1.64	0.45
2:N:170:GLU:OE2	2:N:462:THR:OG1	2.28	0.45
1:A:410:TYR:OH	1:C:836:MET:HA	2.16	0.45
1:B:423:TYR:HA	1:C:264:PRO:HD3	1.97	0.45
1:E:58:THR:OG1	1:E:59:ASP:N	2.49	0.45
1:E:421:SER:OG	1:E:452:ILE:O	2.34	0.45
1:G:210:PHE:HD1	1:G:280:ASP:HA	1.81	0.45
1:I:696:ASP:OD1	1:I:696:ASP:N	2.46	0.45
1:J:68:PHE:HB2	1:J:615:LEU:HD23	1.98	0.45
1:J:137:THR:OG1	1:J:138:LYS:N	2.46	0.45
1:J:327:ARG:NH2	1:J:702:SER:O	2.49	0.45
1:J:514:VAL:HA	1:J:518:ILE:HG21	1.98	0.45
1:K:208:GLU:HB2	1:K:211:TYR:CZ	2.51	0.45
1:L:519:ASN:OD1	1:L:803:ARG:NH1	2.50	0.45
1:L:693:SER:OG	1:L:694:GLY:N	2.48	0.45
1:A:156:THR:O	1:A:157:PHE:C	2.59	0.45
1:B:233:THR:OG1	1:B:240:ALA:HA	2.15	0.45
1:B:328:ASP:O	1:B:331:VAL:HG22	2.16	0.45
1:B:392:ASP:HB3	1:B:395:VAL:HG12	1.98	0.45
1:B:825:ASN:O	1:B:829:THR:HG22	2.16	0.45
1:C:514:VAL:HA	1:C:518:ILE:HG21	1.97	0.45
1:C:678:TRP:HD1	1:C:918:LEU:HD11	1.81	0.45
1:D:167:ILE:HG22	1:D:172:LEU:HA	1.98	0.45
1:D:764:ASP:OD1	1:D:764:ASP:N	2.35	0.45
1:E:126:PRO:HG2	1:E:129:ALA:HB2	1.97	0.45
1:E:135:TRP:HE1	1:E:156:THR:HG22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:757:ALA:C	1:F:759:CYS:N	2.75	0.45
1:F:870:MET:HE1	1:F:919:LEU:HD13	1.99	0.45
1:G:449:GLN:CB	1:H:153:VAL:HG13	2.37	0.45
1:G:644:ASN:HB3	1:G:925:VAL:HG12	1.97	0.45
1:I:20:ALA:O	1:I:24:LEU:HG	2.16	0.45
1:I:50:VAL:HG13	7:5:12:ARG:HB2	1.98	0.45
1:I:809:ILE:HD12	1:I:810:ASN:H	1.82	0.45
1:K:731:TRP:HE1	1:K:888:LEU:HD23	1.81	0.45
1:L:884:ALA:HB1	7:8:29:GLN:NE2	2.31	0.45
2:N:189:GLY:O	2:N:190:ARG:C	2.58	0.45
4:M:145:LEU:HD23	4:M:145:LEU:HA	1.76	0.45
1:A:412:PHE:CE2	1:A:459:ALA:HB2	2.50	0.45
1:A:417:THR:HG21	1:A:453:CYS:HB2	1.99	0.45
1:A:607:SER:O	1:A:607:SER:OG	2.28	0.45
1:B:124:LEU:HB2	1:C:825:ASN:HD21	1.82	0.45
1:C:620:PHE:HD2	1:C:622:MET:HB2	1.82	0.45
1:D:201:GLU:H	1:D:201:GLU:CD	2.24	0.45
1:D:336:TYR:CZ	1:D:565:LYS:HG2	2.51	0.45
1:E:320:ARG:CZ	1:E:597:LEU:HD11	2.47	0.45
1:E:770:MET:HE3	1:E:776:ILE:HD11	1.97	0.45
1:F:531:ASN:HB2	1:F:714:LEU:HD11	1.98	0.45
1:G:18:GLN:HA	7:6:15:THR:HG23	1.99	0.45
1:G:20:ALA:HA	1:G:23:TYR:CE2	2.51	0.45
1:G:249:GLU:HG3	1:G:250:GLN:HG2	1.99	0.45
1:H:198:GLN:HE22	1:I:838:GLN:HB2	1.80	0.45
1:H:536:ASN:HB3	1:H:596:SER:O	2.16	0.45
1:J:196:GLU:CD	1:K:823:HIS:HB3	2.41	0.45
1:K:950:ALA:HA	6:U:48:ARG:HH12	1.82	0.45
1:L:172:LEU:HD12	1:L:282:ILE:HD11	1.98	0.45
5:P:42:LEU:HB2	5:P:43:PRO:CD	2.47	0.45
1:A:201:GLU:H	1:A:201:GLU:CD	2.21	0.45
1:A:738:LEU:HD23	1:A:738:LEU:HA	1.75	0.45
1:B:94:LEU:HB2	1:B:619:PHE:CE2	2.51	0.45
1:D:172:LEU:HD11	1:D:212:GLY:HA3	1.99	0.45
1:D:639:HIS:CD2	1:F:25:SER:HG	2.33	0.45
1:E:59:ASP:N	1:E:59:ASP:OD1	2.48	0.45
1:E:586:ARG:NH1	1:E:591:MET:HG2	2.32	0.45
1:G:698:TYR:HA	5:R:81:TYR:HB2	1.98	0.45
1:H:152:ASP:C	1:H:154:THR:N	2.62	0.45
1:H:189:ALA:HB1	1:H:234:ASN:ND2	2.31	0.45
1:H:239:GLN:HE21	1:H:240:ALA:H	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:451:GLN:HE21	1:I:157:PHE:HE1	1.63	0.45
1:I:503:TYR:CZ	1:I:507:ARG:HD2	2.51	0.45
1:K:397:ILE:HG21	1:K:801:MET:HE1	1.97	0.45
5:P:17:LEU:HD23	5:R:14:SER:HA	1.97	0.45
5:Q:20:ARG:O	5:Q:21:LEU:C	2.59	0.45
1:A:240:ALA:HB3	1:A:288:VAL:HG23	1.98	0.45
1:A:357:ASP:HB3	1:A:566:PHE:HE1	1.81	0.45
1:B:261:PHE:O	1:B:280:ASP:HA	2.15	0.45
1:B:620:PHE:HE2	1:C:880:MET:HE1	1.80	0.45
1:E:25:SER:H	1:F:639:HIS:HE1	1.60	0.45
1:E:155:LYS:HD2	1:E:261:PHE:CZ	2.52	0.45
1:E:192:THR:HG22	1:E:193:PHE:CD1	2.52	0.45
1:E:684:LYS:HB2	1:E:684:LYS:HE3	1.71	0.45
1:F:172:LEU:HD22	1:F:193:PHE:CZ	2.50	0.45
1:G:139:GLU:HB3	1:G:152:ASP:OD2	2.17	0.45
1:G:202:GLU:HB2	1:G:205:GLN:HB2	1.98	0.45
1:G:204:TRP:CE3	1:H:313:VAL:HG22	2.51	0.45
1:G:595:SER:HB3	1:G:702:SER:OG	2.17	0.45
1:H:636:ASN:HB2	1:H:639:HIS:HE2	1.81	0.45
1:K:25:SER:H	1:L:639:HIS:HE1	1.59	0.45
1:L:946:SER:O	1:L:947:ALA:C	2.58	0.45
6:V:143:SER:HB2	6:V:170:THR:O	2.17	0.45
1:A:239:GLN:HG2	1:B:842:TYR:HE2	1.82	0.45
1:A:421:SER:OG	1:A:452:ILE:O	2.35	0.45
1:A:438:SER:HB3	1:B:278:LYS:HB3	1.98	0.45
1:A:649:ALA:HA	1:A:922:VAL:HG22	1.99	0.45
1:A:735:ASP:N	1:A:735:ASP:OD1	2.48	0.45
1:B:424:GLN:HA	1:B:449:GLN:HG2	1.97	0.45
1:C:923:PHE:HB2	1:C:943:THR:HG1	1.81	0.45
1:D:383:MET:HA	1:E:757:ALA:HA	1.99	0.45
1:F:26:PRO:HA	1:F:29:VAL:HG12	1.99	0.45
1:F:739:THR:O	1:F:741:ASN:N	2.41	0.45
1:G:193:PHE:CG	1:G:194:GLN:N	2.85	0.45
1:G:410:TYR:OH	1:I:836:MET:HA	2.16	0.45
1:G:676:ARG:NH2	1:G:921:GLU:OE1	2.50	0.45
1:H:426:VAL:O	1:I:260:TYR:HB2	2.17	0.45
1:H:657:PRO:HG3	5:Q:12:LEU:HD22	1.99	0.45
1:L:309:GLU:C	1:L:312:LEU:H	2.22	0.45
2:N:195:LEU:HD12	2:N:195:LEU:HA	1.80	0.45
4:M:322:TYR:OH	4:M:348:ASN:O	2.24	0.45
1:C:162:THR:HB	1:C:193:PHE:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:631:GLU:OE2	1:C:632:ALA:N	2.50	0.45
1:D:684:LYS:HB3	1:D:687:GLU:HG2	1.99	0.45
1:E:237:GLY:HA3	1:F:821:PHE:HB3	1.98	0.45
1:F:947:ALA:HA	1:H:728:SER:HA	1.98	0.45
1:G:315:GLN:NE2	1:I:203:ASN:OD1	2.50	0.45
1:H:138:LYS:HD3	1:H:149:GLN:HB2	1.99	0.45
1:I:186:ASP:OD1	1:I:187:ILE:N	2.49	0.45
1:J:263:VAL:HG22	1:L:423:TYR:CE1	2.52	0.45
1:J:300:LYS:NZ	1:J:305:ASP:OD1	2.46	0.45
1:J:503:TYR:C	1:J:505:ASN:H	2.25	0.45
1:K:10:TRP:CZ2	1:L:674:ALA:HB2	2.52	0.45
1:K:730:SER:OG	1:K:741:ASN:OD1	2.21	0.45
1:L:52:PRO:HD3	7:8:11:PRO:HA	1.99	0.45
1:L:387:ALA:HB3	1:L:546:ARG:HE	1.81	0.45
2:N:173:THR:O	2:N:177:MET:HG3	2.17	0.45
1:A:715:ASN:ND2	1:A:869:VAL:HG13	2.32	0.45
1:B:290:LEU:HD12	1:B:290:LEU:HA	1.81	0.45
1:B:524:TRP:CH2	1:B:863:LYS:HG2	2.52	0.45
1:D:515:ASP:H	1:D:518:ILE:HG12	1.82	0.45
1:D:811:TYR:CD1	1:D:857:PRO:HD2	2.52	0.45
1:E:56:VAL:HG13	1:E:57:THR:HG22	1.99	0.45
1:E:633:MET:C	1:E:639:HIS:HE2	2.24	0.45
1:E:813:ASP:OD1	1:E:813:ASP:N	2.47	0.45
1:G:456:ASN:HD22	1:G:456:ASN:HA	1.63	0.45
1:H:214:ARG:NH2	1:H:241:LYS:HE2	2.30	0.45
1:H:589:VAL:HG21	1:H:606:ALA:CB	2.47	0.45
1:I:651:ASN:OD1	1:I:651:ASN:N	2.50	0.45
1:I:759:CYS:HB2	1:I:864:PHE:HB3	1.99	0.45
1:J:76:THR:HG22	1:J:77:THR:H	1.82	0.45
1:K:58:THR:OG1	1:K:59:ASP:N	2.47	0.45
5:P:15:PRO:HG3	5:R:14:SER:CB	2.47	0.45
5:R:81:TYR:CD2	5:R:82:MET:HG3	2.52	0.45
5:S:4:THR:HB	5:S:13:PHE:HE1	1.82	0.45
5:S:72:MET:C	5:S:74:ALA:N	2.75	0.45
1:A:595:SER:OG	1:A:596:SER:N	2.49	0.45
1:A:721:VAL:CG1	1:A:743:PHE:HB2	2.40	0.45
1:C:141:GLN:HG3	1:C:142:GLY:H	1.82	0.45
1:C:400:ASN:ND2	1:C:518:ILE:O	2.42	0.45
1:D:73:ARG:NH1	1:D:80:TYR:OH	2.50	0.45
1:E:485:TYR:CZ	1:E:528:PRO:HB3	2.52	0.45
1:E:714:LEU:HG	1:E:910:MET:HE1	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:113:PHE:HE1	1:F:324:ILE:H	1.65	0.45
1:F:239:GLN:HE21	1:F:240:ALA:H	1.63	0.45
1:F:337:ASN:ND2	1:F:361:ARG:O	2.50	0.45
1:F:346:ALA:O	1:F:580:THR:HG22	2.16	0.45
1:H:134:GLN:HA	1:H:154:THR:O	2.16	0.45
1:I:591:MET:HE2	1:I:591:MET:HB2	1.87	0.45
1:I:640:ASP:OD1	1:I:640:ASP:N	2.46	0.45
1:J:240:ALA:O	1:J:288:VAL:HG12	2.17	0.45
1:J:456:ASN:HB2	1:L:837:ARG:HH22	1.82	0.45
1:K:755:ASN:H	1:K:763:LYS:NZ	2.16	0.45
1:L:489:PRO:HD3	1:L:508:VAL:HG12	1.99	0.45
5:P:12:LEU:HA	5:P:12:LEU:HD23	1.64	0.45
1:A:170:GLN:HG2	1:A:185:LYS:HG3	1.98	0.44
1:A:204:TRP:CZ2	1:A:415:ASN:HA	2.52	0.44
1:A:890:GLN:OE1	1:C:53:THR:OG1	2.35	0.44
1:B:323:TYR:H	1:B:596:SER:HB3	1.82	0.44
1:B:922:VAL:HB	1:B:944:PRO:HD2	1.98	0.44
1:F:152:ASP:O	1:F:154:THR:HG22	2.17	0.44
1:F:188:TYR:HB2	1:F:192:THR:HG23	1.98	0.44
1:G:480:TYR:OH	1:G:538:PRO:HD3	2.17	0.44
1:G:529:MET:HE2	1:G:529:MET:HB2	1.72	0.44
1:G:657:PRO:HG2	1:G:660:ALA:HB2	1.99	0.44
1:H:924:ASP:OD1	1:H:924:ASP:N	2.49	0.44
1:J:298:VAL:HG21	1:J:317:MET:HB3	1.98	0.44
1:J:546:ARG:NH2	1:J:594:GLN:OE1	2.48	0.44
5:S:74:ALA:O	5:S:75:THR:C	2.57	0.44
1:C:733:GLY:O	1:C:736:ARG:HG2	2.17	0.44
1:F:681:THR:HG21	1:F:715:ASN:HD21	1.81	0.44
1:G:280:ASP:OD1	1:G:280:ASP:N	2.49	0.44
1:J:152:ASP:O	1:L:445:ALA:N	2.50	0.44
1:J:155:LYS:HG3	1:J:261:PHE:CZ	2.52	0.44
1:J:452:ILE:HG21	1:K:281:ILE:HD11	1.99	0.44
1:K:445:ALA:HB2	1:L:152:ASP:HB3	2.00	0.44
1:L:747:ARG:HE	1:L:750:ASP:HB3	1.82	0.44
2:N:291:LYS:HB3	2:N:291:LYS:HZ3	1.81	0.44
5:Q:5:GLY:C	5:Q:7:ALA:H	2.26	0.44
1:A:761:MET:HE3	1:A:761:MET:HB3	1.89	0.44
1:A:840:GLN:O	1:A:841:PRO:C	2.57	0.44
1:B:240:ALA:O	1:B:241:LYS:HG3	2.17	0.44
1:C:574:LEU:HD23	1:C:574:LEU:HA	1.77	0.44
1:J:20:ALA:O	1:J:24:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:10:TRP:HZ2	1:L:674:ALA:HB2	1.83	0.44
1:K:177:ASP:HB2	1:K:184:LYS:HE3	1.99	0.44
1:K:423:TYR:C	1:K:449:GLN:HG2	2.43	0.44
1:K:763:LYS:HZ3	1:K:763:LYS:HB2	1.81	0.44
1:L:94:LEU:O	1:L:95:ASP:HB2	2.17	0.44
1:A:198:GLN:HG3	1:A:199:VAL:O	2.17	0.44
1:B:667:ILE:HD12	1:B:901:LEU:HD23	2.00	0.44
1:C:172:LEU:HD22	1:C:193:PHE:HE1	1.83	0.44
1:C:178:GLU:HG2	1:C:179:THR:N	2.33	0.44
1:C:922:VAL:HG23	1:C:944:PRO:HD2	1.97	0.44
1:D:842:TYR:CE2	1:F:239:GLN:HG2	2.51	0.44
1:E:423:TYR:HA	1:F:264:PRO:HD3	2.00	0.44
1:E:609:ARG:HH22	5:P:62:THR:HG21	1.82	0.44
1:F:512:SER:HA	1:F:515:ASP:HB2	1.99	0.44
1:F:657:PRO:HD3	5:Q:13:PHE:CE2	2.47	0.44
1:F:684:LYS:HD3	1:F:912:GLU:CD	2.43	0.44
1:F:725:PHE:O	1:F:901:LEU:HA	2.17	0.44
1:H:162:THR:HA	1:H:193:PHE:CZ	2.52	0.44
1:I:88:VAL:HG23	1:I:577:GLY:H	1.83	0.44
1:I:277:TYR:CE1	1:I:279:ALA:HB2	2.53	0.44
1:I:746:LYS:HE3	1:I:746:LYS:HB3	1.72	0.44
1:J:383:MET:HA	1:K:757:ALA:HA	1.98	0.44
1:J:575:LEU:HB3	1:J:576:PRO:HD2	2.00	0.44
1:K:391:TYR:H	1:K:391:TYR:HD1	1.65	0.44
1:L:202:GLU:HB3	1:L:206:GLU:HB2	1.99	0.44
5:P:8:PHE:O	5:Q:29:GLN:HB2	2.17	0.44
1:A:313:VAL:HG11	1:C:202:GLU:HB2	1.99	0.44
1:A:932:HIS:CG	1:A:933:ARG:H	2.35	0.44
1:B:517:TYR:HA	1:B:520:ILE:HG23	1.99	0.44
1:C:652:MET:HE3	1:C:652:MET:HB3	1.91	0.44
1:D:747:ARG:NE	1:D:750:ASP:HB2	2.31	0.44
1:E:537:HIS:CG	1:E:538:PRO:HD2	2.52	0.44
1:E:933:ARG:NH2	1:J:349:ALA:O	2.50	0.44
1:F:520:ILE:H	1:F:520:ILE:HG13	1.46	0.44
1:G:172:LEU:HD11	1:G:212:GLY:HA3	2.00	0.44
1:H:103:ILE:HG23	1:H:613:VAL:HG12	1.99	0.44
1:H:189:ALA:HB1	1:H:234:ASN:HD21	1.83	0.44
1:I:135:TRP:CH2	1:I:309:GLU:HB3	2.51	0.44
1:J:28:LEU:HD12	1:K:639:HIS:CD2	2.52	0.44
1:J:167:ILE:HD11	1:J:260:TYR:HD1	1.81	0.44
1:J:730:SER:OG	1:J:741:ASN:O	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:155:LYS:HD3	1:K:283:LEU:HD22	1.99	0.44
1:K:194:GLN:O	1:K:195:PRO:C	2.56	0.44
1:K:514:VAL:HG23	1:K:518:ILE:HG12	2.00	0.44
1:K:590:ASN:HD21	1:K:701:TYR:H	1.66	0.44
1:L:722:SER:HG	1:L:904:THR:HG1	1.62	0.44
1:A:204:TRP:CE3	1:B:313:VAL:HG13	2.53	0.44
1:A:360:ASP:OD1	1:A:360:ASP:N	2.48	0.44
1:C:635:ARG:HE	1:C:635:ARG:HB3	1.46	0.44
1:D:74:GLU:OE1	1:D:74:GLU:N	2.51	0.44
1:D:481:LEU:HD23	1:D:529:MET:HG2	1.98	0.44
1:F:286:GLU:OE1	1:F:286:GLU:N	2.51	0.44
1:G:770:MET:HE1	1:G:795:PHE:CD1	2.51	0.44
1:H:242:PHE:HD1	1:H:242:PHE:HA	1.72	0.44
1:H:731:TRP:O	1:H:732:PRO:C	2.60	0.44
1:I:119:THR:OG1	1:I:120:ALA:N	2.51	0.44
1:I:524:TRP:CH2	1:I:863:LYS:HE3	2.53	0.44
1:I:665:ILE:HG12	1:I:903:MET:HB2	1.98	0.44
1:K:385:ASN:OD1	1:K:546:ARG:HG2	2.18	0.44
1:K:676:ARG:NH1	1:K:922:VAL:O	2.50	0.44
1:L:236:LYS:HE2	1:L:236:LYS:HB3	1.82	0.44
2:N:254:ILE:HG22	2:N:264:PHE:CZ	2.52	0.44
4:M:144:PHE:HZ	4:M:203:PHE:CE1	2.36	0.44
1:B:638:THR:HG21	4:M:16:SER:O	2.17	0.44
1:C:137:THR:HG23	1:C:152:ASP:HB2	1.99	0.44
1:H:43:ASN:OD1	1:I:571:ASN:ND2	2.51	0.44
1:H:573:LEU:HD12	1:H:573:LEU:HA	1.84	0.44
1:H:948:GLY:O	6:V:105:GLY:HA2	2.18	0.44
1:I:635:ARG:NH2	1:I:932:HIS:O	2.51	0.44
1:J:644:ASN:OD1	1:L:46:ARG:NE	2.43	0.44
1:K:101:PHE:HB2	1:K:562:VAL:HG23	1.99	0.44
1:K:341:ASN:O	1:K:341:ASN:ND2	2.47	0.44
1:L:309:GLU:HA	1:L:312:LEU:HB2	1.98	0.44
1:L:644:ASN:HB3	1:L:925:VAL:HG12	1.99	0.44
5:Q:45:ASN:O	5:Q:46:SER:OG	2.28	0.44
1:A:135:TRP:CH2	1:A:153:VAL:HB	2.48	0.44
1:B:262:ASP:OD2	1:B:279:ALA:N	2.49	0.44
1:B:912:GLU:OE1	1:B:912:GLU:N	2.51	0.44
1:C:721:VAL:HG23	1:C:743:PHE:HB2	2.00	0.44
1:D:64:LEU:HB2	1:E:736:ARG:O	2.17	0.44
1:D:116:TYR:HB2	1:E:402:GLY:HA3	1.98	0.44
1:D:137:THR:OG1	1:D:138:LYS:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:432:ASN:O	1:E:168:THR:OG1	2.31	0.44
1:D:644:ASN:OD1	1:F:46:ARG:NE	2.51	0.44
1:F:19:ASP:OD1	1:F:47:ASN:ND2	2.51	0.44
1:F:280:ASP:OD1	1:F:280:ASP:N	2.51	0.44
1:F:720:LYS:HB3	1:F:742:GLU:HG3	2.00	0.44
1:G:332:GLY:O	1:G:586:ARG:NH1	2.46	0.44
1:H:445:ALA:HB2	1:I:152:ASP:HB3	2.00	0.44
1:H:503:TYR:CE2	1:H:507:ARG:HD2	2.52	0.44
1:H:620:PHE:HD2	1:H:622:MET:HG2	1.82	0.44
1:J:347:GLY:O	1:J:350:SER:N	2.35	0.44
1:J:517:TYR:HA	1:J:520:ILE:HG23	1.99	0.44
1:K:190:ASP:CG	1:K:191:LYS:N	2.76	0.44
1:K:730:SER:HB2	1:K:732:PRO:HD2	2.00	0.44
1:K:752:GLU:H	1:K:752:GLU:HG3	1.54	0.44
1:L:239:GLN:O	1:L:241:LYS:HG3	2.17	0.44
1:L:400:ASN:HB3	1:L:469:TRP:HZ2	1.82	0.44
1:L:442:LYS:HG2	1:L:443:ASP:H	1.82	0.44
5:Q:13:PHE:CD1	5:Q:13:PHE:N	2.86	0.44
6:U:19:LEU:HD11	6:U:74:TRP:HE1	1.82	0.44
1:A:135:TRP:CZ2	1:A:309:GLU:HB2	2.51	0.44
1:A:473:LEU:HD12	1:A:473:LEU:HA	1.84	0.44
1:A:485:TYR:CZ	1:A:528:PRO:HB3	2.53	0.44
1:B:193:PHE:O	1:B:198:GLN:NE2	2.46	0.44
1:B:444:ASP:HB3	1:B:449:GLN:OE1	2.17	0.44
1:B:726:ASP:N	1:B:900:ALA:O	2.31	0.44
1:C:687:GLU:OE2	1:C:713:TYR:OH	2.27	0.44
1:D:98:SER:HB3	1:E:780:GLY:H	1.83	0.44
1:D:526:LEU:HA	1:D:526:LEU:HD22	1.81	0.44
1:D:847:PRO:HG2	1:F:121:TYR:CE2	2.53	0.44
1:E:263:VAL:O	1:E:265:GLY:N	2.50	0.44
1:E:344:VAL:HB	1:E:353:ASN:HB2	2.00	0.44
1:F:344:VAL:HG22	1:F:582:GLU:HG2	2.00	0.44
1:K:446:ILE:HG13	1:K:447:SER:H	1.83	0.44
1:K:573:LEU:HD12	1:K:573:LEU:HA	1.84	0.44
1:K:836:MET:HE3	1:K:836:MET:HB3	1.70	0.44
1:K:917:TYR:CG	1:K:917:TYR:O	2.68	0.44
1:L:277:TYR:CE2	1:L:279:ALA:HB2	2.52	0.44
1:L:397:ILE:HD12	1:L:801:MET:HE1	2.00	0.44
5:P:15:PRO:HG3	5:R:14:SER:OG	2.18	0.44
5:Q:8:PHE:HE1	5:R:28:ARG:HH11	1.65	0.44
1:A:530:ASP:OD2	1:A:863:LYS:NZ	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:PHE:HB3	1:A:745:ILE:HG13	2.00	0.43
1:B:336:TYR:HE2	1:B:565:LYS:HD2	1.82	0.43
1:B:656:ILE:HD11	1:B:916:LEU:HB2	1.99	0.43
1:C:655:PRO:HA	1:C:915:LEU:HB3	2.00	0.43
1:E:230:ALA:O	1:E:239:GLN:NE2	2.51	0.43
1:E:323:TYR:H	1:E:596:SER:HB3	1.83	0.43
1:E:456:ASN:H	1:E:456:ASN:HD22	1.66	0.43
1:F:47:ASN:HA	1:F:48:PRO:HD2	1.84	0.43
1:F:398:ILE:HG22	1:F:524:TRP:O	2.18	0.43
1:H:445:ALA:O	1:H:449:GLN:HB2	2.18	0.43
1:K:65:THR:HG23	1:L:738:LEU:HD13	1.99	0.43
5:P:42:LEU:O	5:P:43:PRO:C	2.55	0.43
1:A:473:LEU:O	1:A:477:VAL:HG12	2.17	0.43
1:A:825:ASN:HA	1:C:122:ASN:HA	2.00	0.43
1:B:204:TRP:CE3	1:C:313:VAL:HG22	2.53	0.43
1:B:526:LEU:HB3	1:B:528:PRO:HD2	2.00	0.43
1:C:398:ILE:HD12	1:C:473:LEU:HD11	1.99	0.43
1:C:524:TRP:CD2	1:C:803:ARG:HG2	2.53	0.43
1:C:686:LYS:HE3	1:C:686:LYS:HB2	1.90	0.43
1:D:756:VAL:HB	1:D:763:LYS:HG3	2.00	0.43
1:E:192:THR:HG22	1:E:193:PHE:CE1	2.53	0.43
1:E:604:ASP:OD1	1:E:605:GLY:N	2.44	0.43
1:G:66:LEU:HA	1:G:66:LEU:HD23	1.80	0.43
1:G:357:ASP:HB3	1:G:566:PHE:HE1	1.83	0.43
1:G:414:LEU:HD23	1:G:414:LEU:HA	1.83	0.43
1:G:440:TRP:HE1	1:H:277:TYR:HA	1.83	0.43
1:H:113:PHE:CE2	1:H:115:PRO:HG3	2.52	0.43
1:H:479:LEU:HD11	1:I:406:GLU:HG2	2.00	0.43
1:I:151:LYS:HB3	1:I:154:THR:HB	2.00	0.43
1:J:17:GLY:H	1:J:48:PRO:CG	2.29	0.43
1:J:114:LYS:NZ	1:J:118:GLY:O	2.48	0.43
1:J:278:LYS:NZ	1:L:438:SER:HB3	2.33	0.43
1:J:417:THR:HA	1:J:457:VAL:HG13	2.00	0.43
1:J:573:LEU:HB3	1:J:641:GLN:NE2	2.34	0.43
1:J:687:GLU:OE2	1:J:713:TYR:OH	2.32	0.43
1:K:146:GLY:C	1:K:148:GLN:H	2.26	0.43
1:K:277:TYR:CZ	1:K:279:ALA:HB2	2.53	0.43
1:K:633:MET:HB3	1:K:633:MET:HE2	1.44	0.43
1:K:886:THR:HG23	1:K:889:GLY:H	1.83	0.43
1:L:531:ASN:HB2	1:L:714:LEU:HD11	2.00	0.43
5:Q:76:ARG:HB3	5:Q:76:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:28:ARG:HD3	5:S:31:VAL:HG11	2.00	0.43
1:A:411:CYS:SG	1:C:460:MET:HG3	2.58	0.43
1:A:718:PHE:CD1	1:A:907:VAL:HG12	2.53	0.43
1:A:744:GLU:O	1:A:762:THR:OG1	2.29	0.43
1:B:109:ARG:NH1	1:B:324:ILE:O	2.51	0.43
1:C:327:ARG:HD2	1:C:331:VAL:HG23	1.98	0.43
1:C:677:GLY:H	1:C:875:PHE:HB2	1.83	0.43
1:D:825:ASN:HD21	1:F:124:LEU:HG	1.83	0.43
1:G:130:PRO:HG3	1:G:312:LEU:HG	1.99	0.43
1:I:69:VAL:HG22	1:I:70:PRO:HD2	1.99	0.43
1:I:369:LEU:HD12	1:I:647:LEU:HD13	2.00	0.43
1:J:640:ASP:OD1	1:J:640:ASP:N	2.47	0.43
1:J:706:PRO:HB3	1:J:711:THR:O	2.18	0.43
1:J:894:TYR:HD1	1:L:4:PRO:HD2	1.82	0.43
1:K:58:THR:HG23	1:L:736:ARG:HH22	1.82	0.43
1:K:134:GLN:HE21	1:K:154:THR:HB	1.84	0.43
4:M:203:PHE:HB2	4:M:206:LEU:HD13	1.99	0.43
5:Q:9:GLU:OE2	5:Q:10:GLY:N	2.51	0.43
6:V:69:LEU:HD23	6:V:69:LEU:H	1.83	0.43
1:A:151:LYS:O	1:C:445:ALA:N	2.51	0.43
1:A:194:GLN:O	1:A:197:PRO:HD2	2.18	0.43
1:A:231:ARG:O	1:A:240:ALA:HB2	2.18	0.43
1:A:368:GLN:NE2	1:A:709:ASP:OD1	2.51	0.43
1:B:3:THR:HG23	1:B:5:SER:H	1.83	0.43
1:B:67:ARG:HB2	1:B:616:TYR:CE2	2.54	0.43
1:B:138:LYS:HG2	1:B:149:GLN:HB3	2.00	0.43
1:D:162:THR:HG22	1:D:212:GLY:O	2.19	0.43
1:D:230:ALA:O	1:E:845:ASN:HB3	2.18	0.43
1:D:428:ILE:HD11	1:E:169:ASN:HB3	2.00	0.43
1:E:198:GLN:HB2	1:F:838:GLN:O	2.19	0.43
1:G:169:ASN:HB3	1:I:428:ILE:HD13	1.99	0.43
1:G:524:TRP:CD2	1:G:803:ARG:HG2	2.54	0.43
1:H:109:ARG:H	1:H:109:ARG:HG2	1.64	0.43
1:H:372:ASP:OD2	1:H:790:ARG:HB3	2.18	0.43
1:H:785:GLU:HG3	1:H:787:TYR:CE1	2.54	0.43
1:I:193:PHE:HZ	1:I:284:TYR:CZ	2.36	0.43
1:K:480:TYR:OH	1:K:538:PRO:HD3	2.19	0.43
1:K:524:TRP:CD2	1:K:803:ARG:HG2	2.54	0.43
1:L:228:SER:HA	1:L:292:THR:HG22	2.00	0.43
5:Q:51:TYR:O	5:Q:54:VAL:HG13	2.18	0.43
1:A:114:LYS:NZ	1:A:116:TYR:O	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:835:THR:O	1:C:410:TYR:OH	2.36	0.43
1:D:738:LEU:HA	1:F:63:ARG:NH1	2.32	0.43
1:E:437:GLU:O	1:F:278:LYS:HD2	2.17	0.43
1:E:795:PHE:O	1:E:796:ARG:C	2.57	0.43
1:F:732:PRO:HB3	1:F:743:PHE:CE1	2.54	0.43
1:F:761:MET:HE3	1:F:761:MET:HB2	1.75	0.43
1:G:520:ILE:H	1:G:520:ILE:HG13	1.46	0.43
1:G:759:CYS:SG	1:G:761:MET:HB3	2.59	0.43
1:H:153:VAL:O	1:H:154:THR:C	2.56	0.43
1:I:746:LYS:HG2	1:I:864:PHE:HE1	1.83	0.43
1:L:90:ASP:OD1	1:L:91:ASN:N	2.52	0.43
5:Q:49:MET:HG3	5:Q:50:THR:H	1.82	0.43
1:A:414:LEU:HD21	1:C:410:TYR:CE2	2.52	0.43
1:A:725:PHE:HE1	1:A:731:TRP:HB2	1.83	0.43
1:A:842:TYR:CE2	1:C:239:GLN:HG2	2.52	0.43
1:C:34:ALA:HB1	7:2:10:ALA:HB2	2.00	0.43
1:D:536:ASN:HB3	1:D:596:SER:O	2.18	0.43
1:I:462:ILE:HG12	1:I:463:ASN:N	2.34	0.43
1:J:193:PHE:HZ	1:J:284:TYR:CZ	2.37	0.43
1:K:593:LEU:O	1:K:594:GLN:C	2.62	0.43
1:L:309:GLU:C	1:L:311:ASN:N	2.75	0.43
4:M:234:LEU:HD11	4:M:252:LEU:HD22	2.01	0.43
5:Q:42:LEU:N	5:Q:43:PRO:HD3	2.34	0.43
7:4:4:ILE:HG13	7:4:7:ALA:HB2	1.99	0.43
1:A:80:TYR:HD2	1:A:585:PHE:HB2	1.82	0.43
1:A:241:LYS:HE2	1:A:286:GLU:HG2	2.01	0.43
1:A:738:LEU:HG	1:C:65:THR:HG23	1.99	0.43
1:B:172:LEU:HD21	1:B:212:GLY:HA3	2.00	0.43
1:B:379:ARG:H	1:B:379:ARG:HG2	1.60	0.43
1:C:922:VAL:HG22	1:C:923:PHE:N	2.34	0.43
1:F:308:SER:OG	1:F:311:ASN:ND2	2.44	0.43
1:F:911:ASP:OD1	1:F:911:ASP:N	2.50	0.43
1:G:320:ARG:CZ	1:G:597:LEU:HD11	2.49	0.43
1:G:328:ASP:C	1:G:330:PHE:H	2.27	0.43
1:H:764:ASP:O	1:H:768:VAL:HG12	2.19	0.43
1:I:771:LEU:HD13	1:I:777:GLY:HA3	2.01	0.43
1:K:239:GLN:NE2	1:K:240:ALA:H	2.15	0.43
1:K:537:HIS:ND1	1:K:538:PRO:HD2	2.33	0.43
1:L:47:ASN:OD1	1:L:47:ASN:N	2.50	0.43
5:Q:14:SER:C	5:R:15:PRO:HB3	2.43	0.43
6:U:31:MET:HE1	6:U:44:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:U:81:GLN:NE2	6:U:179:ARG:O	2.52	0.43
1:B:135:TRP:NE1	1:B:156:THR:OG1	2.52	0.43
1:B:423:TYR:HE1	1:C:263:VAL:HG22	1.84	0.43
1:B:440:TRP:CD1	1:B:440:TRP:H	2.37	0.43
1:B:824:ASN:O	1:B:825:ASN:C	2.61	0.43
1:C:679:SER:HB2	1:C:919:LEU:HG	2.01	0.43
1:D:158:GLY:O	1:F:452:ILE:HA	2.19	0.43
1:F:46:ARG:HH12	7:4:27:THR:HG23	1.83	0.43
1:G:838:GLN:HB3	1:I:200:GLY:HA3	2.00	0.43
1:I:684:LYS:HG2	1:I:914:THR:HG22	2.01	0.43
1:I:748:SER:HA	5:S:54:VAL:HG23	2.00	0.43
1:I:803:ARG:HH21	1:I:805:VAL:HG11	1.84	0.43
1:J:440:TRP:NE1	1:K:276:GLU:O	2.50	0.43
1:J:763:LYS:HE3	1:J:763:LYS:HB2	1.83	0.43
1:L:824:ASN:OD1	1:L:825:ASN:N	2.52	0.43
2:N:198:ASP:HA	2:N:236:LEU:HD11	2.01	0.43
5:P:16:TYR:C	5:P:18:THR:N	2.73	0.43
5:Q:13:PHE:C	5:Q:15:PRO:HD2	2.44	0.43
1:B:320:ARG:NH2	1:B:479:LEU:O	2.52	0.43
1:B:736:ARG:HA	1:B:736:ARG:HD3	1.84	0.43
1:C:114:LYS:NZ	1:C:116:TYR:O	2.33	0.43
1:C:413:PRO:HD3	1:C:458:TYR:O	2.19	0.43
1:D:230:ALA:HB3	1:D:239:GLN:NE2	2.34	0.43
1:D:388:VAL:HG21	1:D:791:MET:HE1	2.01	0.43
1:D:483:ASP:O	1:D:484:SER:C	2.57	0.43
1:D:923:PHE:O	1:D:942:ARG:HA	2.19	0.43
1:E:155:LYS:HZ3	1:E:283:LEU:HB3	1.83	0.43
1:E:631:GLU:OE2	1:E:635:ARG:NH1	2.45	0.43
1:E:846:PHE:HB3	1:E:847:PRO:HD3	2.00	0.43
1:G:76:THR:HG22	1:G:77:THR:H	1.83	0.43
1:G:396:ARG:NH2	1:G:865:LEU:HD11	2.34	0.43
1:H:231:ARG:O	1:H:240:ALA:HB2	2.19	0.43
1:H:513:LEU:HD13	1:H:819:LEU:HD22	2.00	0.43
1:I:327:ARG:HH21	1:I:705:ILE:HG12	1.84	0.43
1:J:160:ALA:HB1	1:J:212:GLY:C	2.44	0.43
1:J:372:ASP:OD2	1:J:790:ARG:HB3	2.19	0.43
1:J:738:LEU:HB3	1:J:754:TYR:CE2	2.52	0.43
4:M:257:THR:O	4:M:261:GLU:HG2	2.17	0.43
6:V:197:TYR:OH	6:V:200:PRO:O	2.32	0.43
1:A:537:HIS:ND1	1:A:538:PRO:HD2	2.34	0.43
1:B:387:ALA:HB3	1:B:546:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:222:MET:HE3	1:C:307:SER:HA	2.00	0.43
1:D:407:LEU:HD11	1:F:474:TYR:HB3	2.00	0.43
1:D:478:ALA:O	1:D:479:LEU:C	2.53	0.43
1:E:842:TYR:CD1	1:E:843:PRO:HD2	2.54	0.43
1:F:6:MET:HE3	1:F:10:TRP:HE1	1.82	0.43
1:F:794:PHE:HA	1:F:869:VAL:HG11	2.01	0.43
1:F:808:GLU:OE1	1:F:808:GLU:N	2.34	0.43
1:G:198:GLN:HB2	1:H:839:GLY:N	2.34	0.43
1:G:336:TYR:OH	1:G:565:LYS:HG2	2.19	0.43
1:G:867:ASP:OD1	1:G:867:ASP:N	2.52	0.43
1:H:192:THR:HG22	1:H:284:TYR:CG	2.54	0.43
1:I:737:LEU:HD11	1:I:743:PHE:CE2	2.53	0.43
1:J:732:PRO:HG3	1:J:743:PHE:CZ	2.54	0.43
1:K:161:ALA:N	1:K:212:GLY:O	2.47	0.43
1:K:836:MET:HA	1:L:410:TYR:OH	2.18	0.43
1:L:731:TRP:O	1:L:732:PRO:C	2.61	0.43
4:M:207:ARG:HA	4:M:210:TRP:CD1	2.54	0.43
5:P:16:TYR:HB3	5:P:18:THR:CG2	2.49	0.43
6:V:87:THR:HG23	6:V:173:SER:HB3	2.00	0.43
1:A:836:MET:HG2	1:A:837:ARG:H	1.84	0.42
1:C:676:ARG:O	1:C:921:GLU:HB2	2.19	0.42
1:D:204:TRP:CZ2	1:D:415:ASN:HA	2.54	0.42
1:D:372:ASP:HB2	1:D:377:ARG:HD3	2.01	0.42
1:D:682:ARG:CZ	1:D:910:MET:HE2	2.49	0.42
1:F:160:ALA:HB1	1:F:212:GLY:C	2.44	0.42
1:F:500:THR:HG23	1:F:503:TYR:H	1.84	0.42
1:F:744:GLU:CD	1:F:747:ARG:HE	2.27	0.42
1:F:790:ARG:H	1:F:793:SER:HB3	1.84	0.42
1:G:261:PHE:HB3	1:I:423:TYR:HB3	2.01	0.42
1:G:385:ASN:OD1	1:G:546:ARG:HD2	2.19	0.42
1:G:943:THR:HB	1:G:944:PRO:HD3	2.01	0.42
1:H:126:PRO:HG2	1:H:129:ALA:HB2	2.01	0.42
1:I:19:ASP:HB2	7:5:14:GLY:HA3	2.01	0.42
1:J:109:ARG:NH1	1:J:324:ILE:O	2.52	0.42
1:K:117:SER:HA	1:K:321:PRO:HB3	2.01	0.42
1:L:923:PHE:O	1:L:942:ARG:HA	2.18	0.42
2:N:189:GLY:CA	2:N:194:VAL:HG22	2.49	0.42
1:A:114:LYS:HE2	1:A:116:TYR:CE1	2.54	0.42
1:A:206:GLU:O	1:A:211:TYR:OH	2.37	0.42
1:A:520:ILE:H	1:A:520:ILE:HG12	1.53	0.42
1:B:162:THR:HG23	1:B:193:PHE:CG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:668:PRO:HG3	1:K:664:PRO:HG3	2.00	0.42
1:D:473:LEU:HD12	1:D:473:LEU:HA	1.78	0.42
1:E:101:PHE:CZ	1:E:581:TYR:HE2	2.37	0.42
1:E:114:LYS:HE2	1:E:319:ASN:O	2.20	0.42
1:E:198:GLN:HB2	1:F:838:GLN:HB2	2.01	0.42
1:E:450:ASN:HD22	1:F:155:LYS:HB2	1.85	0.42
1:E:456:ASN:H	1:E:456:ASN:ND2	2.17	0.42
1:E:629:THR:O	1:E:633:MET:HG2	2.19	0.42
1:F:661:THR:HA	1:F:907:VAL:O	2.18	0.42
1:G:31:PHE:O	1:G:35:THR:HG22	2.19	0.42
1:G:111:PRO:HG3	1:G:554:ARG:HH12	1.84	0.42
1:H:666:SER:CB	5:Q:16:TYR:HE1	2.32	0.42
1:L:685:THR:HG21	1:L:913:PRO:HG2	2.00	0.42
2:N:146:GLU:H	2:N:146:GLU:HG3	1.52	0.42
5:P:10:GLY:C	5:P:12:LEU:N	2.76	0.42
1:A:137:THR:OG1	1:A:138:LYS:N	2.52	0.42
1:A:138:LYS:HA	1:A:149:GLN:HA	2.00	0.42
1:A:486:LYS:O	1:A:507:ARG:NH1	2.52	0.42
1:B:520:ILE:H	1:B:520:ILE:HG12	1.46	0.42
1:E:58:THR:HB	1:E:623:ALA:HA	2.01	0.42
1:H:460:MET:HE1	1:I:460:MET:HE2	2.00	0.42
1:I:353:ASN:OD1	1:I:355:VAL:HG12	2.19	0.42
1:J:778:TYR:HD2	1:J:880:MET:HE3	1.84	0.42
1:K:589:VAL:O	1:K:593:LEU:HB2	2.19	0.42
1:L:310:ILE:HD12	1:L:310:ILE:HA	1.88	0.42
1:L:337:ASN:ND2	1:L:357:ASP:OD1	2.52	0.42
1:L:422:THR:HA	1:L:451:GLN:HA	2.00	0.42
1:L:642:SER:HA	1:L:926:VAL:O	2.19	0.42
1:B:334:MET:O	1:B:583:TRP:NE1	2.49	0.42
1:B:389:ASP:OD2	1:B:594:GLN:NE2	2.40	0.42
1:B:745:ILE:HG23	1:B:765:TRP:CD1	2.55	0.42
1:C:7:MET:C	1:C:9:GLN:H	2.22	0.42
1:C:228:SER:HB2	1:C:290:LEU:HD11	2.01	0.42
1:C:377:ARG:NH2	1:C:388:VAL:HG22	2.34	0.42
1:D:187:ILE:O	1:D:192:THR:N	2.52	0.42
1:E:924:ASP:HB3	1:E:942:ARG:HG3	2.01	0.42
1:F:396:ARG:NH2	1:F:865:LEU:HD11	2.34	0.42
1:G:552:ASN:HB3	1:H:522:ALA:HB2	2.00	0.42
1:G:734:ASN:HB3	1:I:61:SER:HA	2.01	0.42
1:H:537:HIS:ND1	1:H:538:PRO:HD2	2.34	0.42
1:H:950:ALA:C	1:J:892:MET:HE1	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:745:ILE:HG23	1:I:765:TRP:CD1	2.54	0.42
1:I:885:LEU:HB3	1:I:886:THR:H	1.60	0.42
1:J:135:TRP:CH2	1:J:309:GLU:HB2	2.54	0.42
1:J:136:GLU:OE2	1:J:151:LYS:HE2	2.19	0.42
1:J:214:ARG:HH22	1:J:241:LYS:CE	2.32	0.42
1:K:58:THR:HG22	1:K:621:PRO:O	2.19	0.42
1:L:574:LEU:HD12	1:L:574:LEU:HA	1.85	0.42
1:L:715:ASN:HD21	1:L:869:VAL:HG23	1.84	0.42
8:X:8:UNK:O	8:X:12:UNK:N	2.52	0.42
1:A:198:GLN:CD	1:B:838:GLN:HA	2.44	0.42
1:A:480:TYR:OH	1:A:538:PRO:HD3	2.19	0.42
1:A:559:HIS:HE1	1:B:753:GLY:HA2	1.85	0.42
1:A:809:ILE:HG21	5:P:78:ALA:HB1	2.01	0.42
1:B:385:ASN:OD1	1:B:546:ARG:HD2	2.19	0.42
1:B:920:PHE:O	1:B:922:VAL:HG13	2.20	0.42
1:C:286:GLU:OE1	1:C:286:GLU:N	2.52	0.42
1:D:239:GLN:HG2	1:E:842:TYR:CE2	2.55	0.42
1:E:128:GLY:HA2	1:E:314:GLN:O	2.18	0.42
1:E:524:TRP:CD1	1:E:803:ARG:HD3	2.54	0.42
1:F:912:GLU:HG3	1:F:913:PRO:HD2	2.01	0.42
1:G:597:LEU:HD12	1:G:597:LEU:HA	1.89	0.42
1:G:620:PHE:O	1:G:622:MET:N	2.49	0.42
1:H:394:ASP:OD1	1:H:394:ASP:N	2.29	0.42
1:H:801:MET:HE2	1:H:801:MET:HB3	1.83	0.42
1:H:811:TYR:CD1	1:H:857:PRO:HD2	2.54	0.42
1:H:870:MET:O	1:H:871:TRP:C	2.60	0.42
1:J:6:MET:HE1	6:U:51:ARG:HH22	1.85	0.42
1:J:310:ILE:H	1:J:310:ILE:HG13	1.58	0.42
1:L:193:PHE:HZ	1:L:284:TYR:CG	2.38	0.42
7:9:5:ASN:OD1	7:9:5:ASN:N	2.52	0.42
1:A:487:TYR:OH	1:A:832:LEU:O	2.26	0.42
1:B:20:ALA:HA	1:B:23:TYR:CD2	2.54	0.42
1:B:140:LYS:HA	1:B:146:GLY:O	2.20	0.42
1:B:341:ASN:OD1	1:B:341:ASN:N	2.52	0.42
1:C:42:GLY:HA2	7:2:25:ILE:HG23	2.01	0.42
1:C:358:LEU:HD22	1:C:942:ARG:NH1	2.34	0.42
1:C:575:LEU:HD22	1:C:631:GLU:HB3	2.01	0.42
1:C:893:LEU:HD13	6:U:225:GLY:HA3	2.01	0.42
1:D:388:VAL:O	1:D:542:GLY:HA3	2.19	0.42
1:D:476:ASN:OD1	1:D:476:ASN:N	2.52	0.42
1:D:731:TRP:C	1:D:733:GLY:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:520:ILE:H	1:E:520:ILE:HG12	1.53	0.42
1:E:937:GLU:HA	6:U:110:GLY:HA3	2.01	0.42
1:F:327:ARG:HB3	1:F:331:VAL:HG22	2.02	0.42
1:F:745:ILE:HG23	1:F:765:TRP:CD1	2.55	0.42
1:G:440:TRP:HH2	1:H:275:GLU:H	1.67	0.42
1:G:446:ILE:HG12	1:G:447:SER:H	1.85	0.42
1:G:546:ARG:NH2	1:G:594:GLN:OE1	2.48	0.42
1:G:770:MET:HE3	1:G:776:ILE:HD11	2.02	0.42
1:H:423:TYR:HB3	1:I:261:PHE:HB3	2.01	0.42
1:H:485:TYR:HE2	1:H:528:PRO:HB3	1.85	0.42
1:H:724:MET:HE1	5:R:20:ARG:HH12	1.85	0.42
1:H:744:GLU:O	1:H:762:THR:OG1	2.36	0.42
1:I:167:ILE:HD13	1:I:282:ILE:HB	2.00	0.42
1:I:474:TYR:OH	1:I:834:PRO:HG3	2.19	0.42
1:J:751:GLY:O	1:L:104:ARG:NH2	2.53	0.42
1:K:47:ASN:ND2	7:8:25:ILE:HG22	2.31	0.42
1:K:262:ASP:HA	1:K:280:ASP:HA	2.02	0.42
1:K:444:ASP:OD1	1:K:444:ASP:N	2.49	0.42
1:K:745:ILE:HG23	1:K:765:TRP:CD1	2.55	0.42
1:L:155:LYS:NZ	1:L:215:ALA:HB3	2.34	0.42
1:L:738:LEU:HD12	1:L:738:LEU:HA	1.75	0.42
2:N:80:THR:OG1	2:N:81:THR:N	2.53	0.42
5:P:8:PHE:HD1	5:Q:28:ARG:HD3	1.84	0.42
5:Q:13:PHE:O	5:Q:14:SER:C	2.59	0.42
5:S:77:LEU:O	5:S:78:ALA:C	2.62	0.42
1:A:18:GLN:HB3	1:A:22:GLU:HG3	2.01	0.42
1:A:423:TYR:CE1	1:B:263:VAL:HG22	2.54	0.42
1:B:13:MET:HE1	1:C:939:VAL:HB	2.02	0.42
1:B:364:GLU:HB3	1:B:708:LEU:HB2	2.00	0.42
1:B:533:ASN:OD1	1:B:533:ASN:N	2.53	0.42
1:D:198:GLN:HB3	1:E:838:GLN:HB2	2.02	0.42
1:D:446:ILE:HG13	1:E:141:GLN:HB3	2.02	0.42
1:E:135:TRP:CH2	1:E:153:VAL:HB	2.55	0.42
1:G:683:LEU:O	1:G:915:LEU:N	2.45	0.42
1:G:738:LEU:HD12	1:G:738:LEU:HA	1.85	0.42
1:G:842:TYR:CE2	1:I:239:GLN:HG2	2.53	0.42
1:H:107:LEU:HB3	1:H:556:VAL:HG13	2.01	0.42
1:H:715:ASN:HB2	1:H:871:TRP:HE1	1.85	0.42
1:I:151:LYS:O	1:I:154:THR:HB	2.19	0.42
1:I:534:PRO:HG2	1:I:535:PHE:CD1	2.55	0.42
1:J:162:THR:HG22	1:J:212:GLY:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:714:LEU:HD12	1:J:714:LEU:HA	1.85	0.42
1:K:360:ASP:OD1	1:K:361:ARG:N	2.53	0.42
1:K:750:ASP:N	1:K:750:ASP:OD1	2.49	0.42
1:L:372:ASP:OD2	1:L:790:ARG:HB3	2.20	0.42
1:L:495:PRO:HG2	1:L:503:TYR:HB2	2.00	0.42
2:N:169:SER:O	2:N:172:MET:N	2.41	0.42
2:N:225:THR:HG22	2:N:227:GLU:H	1.84	0.42
5:P:45:ASN:O	5:P:46:SER:CB	2.67	0.42
5:P:49:MET:HB3	5:P:50:THR:H	1.73	0.42
5:Q:2:ASN:HA	5:Q:6:GLY:HA3	2.02	0.42
6:V:2:SER:HB3	6:V:200:PRO:HD2	2.02	0.42
6:V:211:GLU:H	6:V:211:GLU:HG2	1.67	0.42
1:A:357:ASP:HB3	1:A:566:PHE:CE1	2.55	0.42
1:B:495:PRO:HG3	1:B:502:GLU:HB3	2.02	0.42
1:B:514:VAL:HA	1:B:518:ILE:HG21	2.02	0.42
1:B:575:LEU:O	1:B:577:GLY:N	2.52	0.42
1:D:312:LEU:HB3	1:F:204:TRP:CH2	2.55	0.42
1:F:108:ASP:HA	1:F:554:ARG:O	2.20	0.42
1:F:353:ASN:OD1	1:F:354:ALA:N	2.53	0.42
1:G:191:LYS:HB2	1:G:191:LYS:HE2	1.57	0.42
1:G:514:VAL:HA	1:G:518:ILE:HG21	2.01	0.42
1:J:683:LEU:O	1:J:915:LEU:N	2.46	0.42
1:K:197:PRO:HG3	1:L:831:TYR:CE1	2.55	0.42
1:K:234:ASN:HD21	1:K:238:GLY:HA3	1.85	0.42
5:Q:8:PHE:HD1	5:R:28:ARG:HG2	1.83	0.42
1:A:83:ARG:NH1	1:A:582:GLU:OE1	2.53	0.42
1:A:159:VAL:HG11	1:B:840:GLN:HB2	2.02	0.42
1:A:838:GLN:HB2	1:C:198:GLN:HG2	2.00	0.42
1:B:233:THR:O	1:C:815:LYS:HE3	2.19	0.42
1:B:530:ASP:OD1	1:B:531:ASN:N	2.53	0.42
1:D:662:ASN:HB3	1:D:906:GLU:HG2	2.02	0.42
1:E:19:ASP:N	1:E:19:ASP:OD1	2.47	0.42
1:F:334:MET:HG3	1:F:336:TYR:CE2	2.55	0.42
1:F:524:TRP:CD2	1:F:803:ARG:HG2	2.54	0.42
1:G:313:VAL:HB	1:I:203:ASN:HB2	2.00	0.42
1:G:572:LEU:HD11	1:G:928:VAL:HG11	2.02	0.42
1:G:823:HIS:HB3	1:I:196:GLU:CD	2.44	0.42
1:H:240:ALA:O	1:H:241:LYS:HD3	2.19	0.42
1:I:256:ILE:HD13	1:I:286:GLU:HB3	2.02	0.42
1:I:337:ASN:ND2	1:I:361:ARG:HB3	2.34	0.42
1:I:747:ARG:HG3	1:I:748:SER:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:748:SER:O	1:I:749:VAL:C	2.63	0.42
1:I:764:ASP:OD1	1:I:764:ASP:N	2.52	0.42
1:J:635:ARG:HG3	1:J:930:GLN:O	2.20	0.42
1:K:172:LEU:HD11	1:K:193:PHE:CZ	2.54	0.42
1:L:599:ASN:O	1:L:702:SER:HB3	2.20	0.42
1:L:783:VAL:HG12	1:L:795:PHE:CZ	2.54	0.42
1:L:837:ARG:H	1:L:837:ARG:HG3	1.29	0.42
2:N:241:VAL:HG22	2:N:266:ILE:HB	2.01	0.42
5:P:36:VAL:O	5:P:37:ASP:C	2.59	0.42
1:A:360:ASP:O	1:A:361:ARG:HG3	2.20	0.42
1:B:320:ARG:N	1:B:505:ASN:OD1	2.43	0.42
1:B:600:ASP:OD1	1:B:602:ARG:N	2.53	0.42
1:B:668:PRO:HB2	2:N:88:PHE:CE1	2.55	0.42
1:B:808:GLU:HG3	1:B:814:TYR:CE2	2.54	0.42
1:D:513:LEU:O	1:D:514:VAL:C	2.63	0.42
1:D:652:MET:N	1:D:652:MET:SD	2.93	0.42
1:D:888:LEU:HA	1:D:888:LEU:HD23	1.87	0.42
1:E:176:THR:HA	1:E:183:GLY:HA2	2.01	0.42
1:E:240:ALA:O	1:E:288:VAL:HG12	2.20	0.42
1:E:442:LYS:HD3	1:E:442:LYS:HA	1.90	0.42
1:F:594:GLN:HG3	1:F:703:GLY:O	2.20	0.42
1:F:726:ASP:H	1:F:729:VAL:HG13	1.84	0.42
1:F:759:CYS:HG	1:F:761:MET:H	1.68	0.42
1:G:202:GLU:HB3	1:H:313:VAL:HG21	2.02	0.42
1:G:649:ALA:HA	1:G:922:VAL:HG22	2.02	0.42
1:G:801:MET:HB2	1:G:801:MET:HE2	1.62	0.42
1:I:231:ARG:O	1:I:240:ALA:HB2	2.20	0.42
1:K:486:LYS:HB3	1:K:509:VAL:HG22	2.02	0.42
6:U:97:ALA:HB2	6:U:163:THR:HG21	2.02	0.42
1:A:677:GLY:HA3	1:A:874:PRO:HA	2.02	0.41
1:B:505:ASN:O	1:B:505:ASN:ND2	2.50	0.41
1:B:706:PRO:HB3	1:B:711:THR:O	2.19	0.41
1:C:172:LEU:HD23	1:C:174:LEU:HD23	2.01	0.41
1:C:199:VAL:O	1:C:201:GLU:N	2.51	0.41
1:C:530:ASP:OD1	1:C:865:LEU:HD21	2.20	0.41
1:C:573:LEU:HD23	1:C:634:LEU:HD21	2.02	0.41
1:C:763:LYS:HE3	1:C:763:LYS:HB2	1.93	0.41
1:D:231:ARG:O	1:D:240:ALA:HB2	2.20	0.41
1:D:265:GLY:HA2	1:D:276:GLU:CD	2.44	0.41
1:E:358:LEU:HD21	1:E:947:ALA:HB2	2.01	0.41
1:E:641:GLN:HB3	1:E:643:PHE:CZ	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:836:MET:HE3	1:E:837:ARG:HH21	1.85	0.41
1:G:166:ASN:O	1:G:173:LEU:HB3	2.20	0.41
1:G:288:VAL:HG13	1:G:290:LEU:H	1.84	0.41
1:H:130:PRO:HG3	1:H:312:LEU:HG	2.02	0.41
1:H:200:GLY:O	1:I:836:MET:HE1	2.20	0.41
1:H:234:ASN:OD1	1:H:234:ASN:N	2.53	0.41
1:H:403:VAL:CG2	1:H:465:GLN:HB3	2.50	0.41
1:I:170:GLN:HB3	1:I:185:LYS:HE2	2.01	0.41
1:I:437:GLU:OE1	1:I:438:SER:N	2.53	0.41
1:J:401:HIS:CE1	1:L:544:ARG:HD2	2.55	0.41
1:J:752:GLU:C	1:L:104:ARG:HH22	2.28	0.41
1:K:652:MET:HE2	1:K:652:MET:HB3	1.89	0.41
2:N:129:LYS:HA	2:N:161:PHE:O	2.20	0.41
5:R:16:TYR:HD1	5:R:16:TYR:HA	1.65	0.41
1:A:202:GLU:HA	1:B:313:VAL:CG1	2.48	0.41
1:A:924:ASP:OD1	1:A:924:ASP:N	2.47	0.41
1:B:336:TYR:CE2	1:B:565:LYS:HB2	2.55	0.41
1:B:429:THR:HB	1:B:430:ASN:H	1.39	0.41
1:C:623:ALA:HB3	1:C:626:THR:HG23	2.02	0.41
1:C:865:LEU:HA	1:C:865:LEU:HD23	1.83	0.41
1:D:95:ASP:OD2	1:F:44:LYS:NZ	2.50	0.41
1:D:134:GLN:HA	1:D:155:LYS:H	1.84	0.41
1:D:641:GLN:HE21	1:D:641:GLN:H	1.67	0.41
1:E:642:SER:HA	1:E:926:VAL:O	2.20	0.41
1:E:845:ASN:N	1:E:845:ASN:OD1	2.53	0.41
1:F:705:ILE:H	1:F:705:ILE:HG12	1.61	0.41
1:G:94:LEU:HD23	1:G:619:PHE:CE2	2.54	0.41
1:G:731:TRP:CG	1:G:732:PRO:HD3	2.55	0.41
1:H:194:GLN:O	1:H:197:PRO:HD2	2.19	0.41
1:H:352:LEU:HD23	1:H:352:LEU:HA	1.96	0.41
1:H:943:THR:HG23	1:H:944:PRO:HD3	2.02	0.41
1:I:328:ASP:HB2	1:I:546:ARG:NH1	2.35	0.41
1:I:427:LYS:HB2	1:I:442:LYS:HD2	2.02	0.41
1:I:878:ASN:HD21	1:I:882:MET:CE	2.33	0.41
1:J:103:ILE:HA	1:J:613:VAL:HA	2.02	0.41
1:K:304:SER:OG	1:K:306:ASN:OD1	2.37	0.41
1:L:135:TRP:HZ3	1:L:156:THR:CG2	2.33	0.41
5:Q:13:PHE:CG	5:Q:14:SER:N	2.88	0.41
1:A:503:TYR:CZ	1:A:507:ARG:HD2	2.55	0.41
1:A:941:LEU:HB3	1:C:13:MET:HG2	2.03	0.41
1:B:86:LEU:HD23	1:B:581:TYR:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:GLY:HA2	1:B:174:LEU:HA	2.01	0.41
1:B:456:ASN:CG	1:C:198:GLN:OE1	2.63	0.41
1:B:566:PHE:HD2	1:B:569:ILE:HG13	1.85	0.41
1:C:260:TYR:CD2	1:C:282:ILE:HG22	2.55	0.41
1:C:328:ASP:O	1:C:330:PHE:N	2.52	0.41
1:D:88:VAL:HG13	1:D:577:GLY:H	1.86	0.41
1:D:114:LYS:HE3	1:D:116:TYR:O	2.21	0.41
1:F:481:LEU:O	1:F:486:LYS:NZ	2.53	0.41
1:G:230:ALA:HB1	1:G:288:VAL:HG22	2.02	0.41
1:G:410:TYR:CE1	1:H:414:LEU:HD21	2.52	0.41
1:H:262:ASP:OD2	1:H:279:ALA:N	2.54	0.41
1:H:429:THR:HG22	1:H:430:ASN:H	1.84	0.41
1:H:495:PRO:HG3	1:H:502:GLU:HB2	2.00	0.41
1:I:150:GLU:HB2	1:I:152:ASP:OD1	2.19	0.41
1:I:202:GLU:HB2	1:I:206:GLU:HB2	2.01	0.41
1:I:346:ALA:O	1:I:580:THR:HG22	2.19	0.41
1:J:739:THR:O	1:J:739:THR:OG1	2.33	0.41
1:L:327:ARG:HB3	1:L:331:VAL:HG22	2.03	0.41
1:L:419:THR:HG22	1:L:451:GLN:HB2	2.01	0.41
1:L:460:MET:HE3	1:L:460:MET:HB2	1.92	0.41
2:N:271:LEU:O	2:N:352:ARG:HD3	2.20	0.41
4:M:361:ILE:O	4:M:365:MET:HG2	2.20	0.41
1:B:236:LYS:HD2	1:B:236:LYS:HA	1.97	0.41
1:B:293:PRO:O	1:B:295:THR:OG1	2.36	0.41
1:B:771:LEU:HD12	1:B:771:LEU:HA	1.75	0.41
1:D:880:MET:HE3	1:D:880:MET:HB2	1.84	0.41
1:E:172:LEU:HD22	1:E:193:PHE:HE2	1.85	0.41
1:E:463:ASN:O	1:E:467:ASN:ND2	2.43	0.41
1:E:524:TRP:CG	1:E:803:ARG:HD3	2.55	0.41
1:F:589:VAL:HG23	1:F:593:LEU:HD12	2.02	0.41
1:G:294:ASP:N	1:G:294:ASP:OD1	2.52	0.41
1:H:765:TRP:O	1:H:766:PHE:C	2.57	0.41
1:H:808:GLU:H	1:H:808:GLU:CD	2.28	0.41
1:I:48:PRO:HG2	7:5:14:GLY:HA2	2.01	0.41
1:I:428:ILE:HD11	1:I:432:ASN:HA	2.03	0.41
1:J:684:LYS:HD2	1:J:686:LYS:HE2	2.01	0.41
1:J:801:MET:HG2	1:J:863:LYS:O	2.20	0.41
1:K:717:THR:HB	1:K:908:ASP:HB2	2.02	0.41
1:L:151:LYS:HE2	1:L:218:LYS:HD2	2.02	0.41
4:M:138:LEU:O	4:M:139:VAL:C	2.60	0.41
5:Q:16:TYR:CG	5:R:18:THR:OG1	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:13:PHE:CG	5:R:14:SER:N	2.88	0.41
5:S:99:GLU:H	5:S:99:GLU:CD	2.26	0.41
6:U:211:GLU:H	6:U:211:GLU:HG2	1.61	0.41
1:A:278:LYS:HD2	1:C:437:GLU:HG3	2.03	0.41
1:A:377:ARG:NH1	1:A:386:SER:OG	2.52	0.41
1:A:396:ARG:NH1	1:A:534:PRO:HG3	2.35	0.41
1:A:415:ASN:HD22	1:B:157:PHE:HZ	1.68	0.41
1:A:837:ARG:NH1	1:B:456:ASN:CG	2.78	0.41
1:B:24:LEU:HG	1:C:639:HIS:HB3	2.01	0.41
1:C:60:ARG:NH2	6:U:98:GLU:OE2	2.54	0.41
1:C:683:LEU:C	1:C:914:THR:HG1	2.25	0.41
1:D:446:ILE:O	1:D:447:SER:OG	2.34	0.41
1:E:135:TRP:HE1	1:E:156:THR:CG2	2.33	0.41
1:E:369:LEU:HD23	7:3:30:LEU:HD13	2.01	0.41
1:F:536:ASN:HB3	1:F:596:SER:O	2.20	0.41
1:F:803:ARG:NH1	1:F:861:GLN:OE1	2.53	0.41
1:F:859:VAL:HG23	5:P:58:SER:HA	2.01	0.41
1:F:894:TYR:OH	1:J:949:ASN:OD1	2.37	0.41
1:I:88:VAL:HG12	1:I:619:PHE:CE2	2.49	0.41
1:I:346:ALA:HB2	1:I:353:ASN:HA	2.03	0.41
1:J:543:LEU:O	1:J:546:ARG:N	2.53	0.41
1:K:198:GLN:HG2	1:L:839:GLY:H	1.83	0.41
1:K:342:MET:HE1	1:K:357:ASP:H	1.85	0.41
5:P:20:ARG:O	5:P:21:LEU:C	2.61	0.41
6:U:41:ILE:HD13	6:U:41:ILE:HG21	1.85	0.41
6:U:213:ILE:HB	6:U:216:PHE:HB2	2.02	0.41
1:A:107:LEU:HA	1:A:607:SER:HB2	2.01	0.41
1:A:588:ASP:O	1:A:592:ILE:HG12	2.20	0.41
1:B:135:TRP:HE1	1:B:156:THR:HG21	1.86	0.41
1:B:942:ARG:O	1:B:946:SER:HA	2.21	0.41
1:C:513:LEU:O	1:C:514:VAL:C	2.63	0.41
1:C:596:SER:O	1:C:597:LEU:C	2.59	0.41
1:C:724:MET:HB3	1:C:729:VAL:HA	2.03	0.41
1:D:166:ASN:HA	1:D:210:PHE:CD2	2.56	0.41
1:D:276:GLU:HB2	1:F:440:TRP:CE3	2.54	0.41
1:D:470:LYS:HE2	1:F:124:LEU:HD11	2.02	0.41
1:F:204:TRP:HD1	1:F:204:TRP:H	1.58	0.41
1:F:698:TYR:CZ	5:R:47:SER:HB2	2.56	0.41
1:G:190:ASP:CG	1:G:191:LYS:H	2.29	0.41
1:G:559:HIS:CE1	1:H:753:GLY:HA2	2.55	0.41
1:I:731:TRP:O	1:I:732:PRO:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:923:PHE:O	1:K:942:ARG:HA	2.21	0.41
1:L:334:MET:HB2	1:L:336:TYR:CE2	2.55	0.41
1:L:634:LEU:HD12	1:L:634:LEU:HA	1.82	0.41
1:L:808:GLU:H	1:L:808:GLU:CD	2.28	0.41
2:N:184:ASN:O	2:N:185:TYR:C	2.63	0.41
5:R:54:VAL:HG12	5:R:55:GLY:N	2.31	0.41
1:A:1:MET:HG3	1:B:931:PRO:HG2	2.02	0.41
1:A:718:PHE:HB2	1:A:745:ILE:HG21	2.03	0.41
1:A:763:LYS:HE3	1:A:763:LYS:HB2	1.87	0.41
1:D:122:ASN:OD1	1:D:122:ASN:N	2.54	0.41
1:D:173:LEU:HA	1:D:185:LYS:HA	2.02	0.41
1:D:824:ASN:HA	1:D:844:ALA:CB	2.51	0.41
1:D:896:ASN:ND2	1:F:3:THR:O	2.49	0.41
1:D:931:PRO:HD2	1:D:935:VAL:HG23	2.03	0.41
1:E:724:MET:HG3	1:E:728:SER:O	2.20	0.41
1:F:721:VAL:HG13	1:F:743:PHE:HB2	2.03	0.41
1:G:211:TYR:HE2	1:I:454:LYS:HE2	1.85	0.41
1:H:322:ASN:HA	1:H:596:SER:OG	2.21	0.41
1:H:422:THR:HA	1:H:450:ASN:O	2.21	0.41
1:H:715:ASN:ND2	1:H:869:VAL:O	2.54	0.41
1:I:631:GLU:O	1:I:635:ARG:HB2	2.21	0.41
1:J:119:THR:OG1	1:J:120:ALA:N	2.53	0.41
1:J:444:ASP:HA	1:K:152:ASP:HA	2.02	0.41
1:J:471:SER:HA	1:K:407:LEU:HD11	2.02	0.41
1:J:485:TYR:CZ	1:J:528:PRO:HB3	2.55	0.41
1:K:243:LYS:HG3	1:K:253:ASP:O	2.21	0.41
1:K:529:MET:HG2	1:K:532:VAL:HG11	2.02	0.41
1:K:714:LEU:HD23	1:K:714:LEU:HA	1.91	0.41
1:K:731:TRP:O	1:K:732:PRO:C	2.64	0.41
1:K:863:LYS:HG2	1:K:864:PHE:H	1.86	0.41
5:R:10:GLY:O	5:R:12:LEU:N	2.53	0.41
6:U:36:ALA:HB1	6:U:40:MET:HB2	2.02	0.41
7:4:17:PRO:HB2	7:4:19:MET:HG3	2.02	0.41
1:B:567:PHE:HA	1:B:570:LYS:HE2	2.03	0.41
1:B:685:THR:HG21	1:B:913:PRO:HB2	2.02	0.41
1:B:835:THR:HG22	1:B:836:MET:H	1.86	0.41
1:C:527:ASP:N	1:C:528:PRO:HD2	2.36	0.41
1:D:473:LEU:O	1:D:474:TYR:C	2.58	0.41
1:D:717:THR:HB	1:D:908:ASP:HB2	2.03	0.41
1:D:773:HIS:CE1	1:D:872:ARG:HD3	2.55	0.41
1:D:943:THR:OG1	1:D:944:PRO:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:GLN:HA	1:E:155:LYS:H	1.86	0.41
1:E:254:LEU:HD22	1:E:254:LEU:HA	1.83	0.41
1:E:443:ASP:HB2	1:F:150:GLU:HB3	2.02	0.41
1:H:74:GLU:HG2	1:H:81:LYS:HB3	2.02	0.41
1:H:785:GLU:OE1	1:H:785:GLU:N	2.54	0.41
1:H:790:ARG:H	1:H:793:SER:HB3	1.86	0.41
1:H:870:MET:HE3	1:H:870:MET:HB2	1.93	0.41
1:I:88:VAL:HG23	1:I:577:GLY:N	2.36	0.41
1:I:102:ASP:OD2	1:I:559:HIS:NE2	2.45	0.41
1:I:836:MET:HE3	1:I:837:ARG:O	2.21	0.41
1:J:212:GLY:HA2	1:J:282:ILE:O	2.20	0.41
1:J:761:MET:HE2	1:J:765:TRP:HD1	1.86	0.41
1:J:801:MET:HE2	1:J:801:MET:HB3	1.30	0.41
1:K:132:PRO:HB2	1:K:215:ALA:HA	2.03	0.41
1:K:146:GLY:C	1:K:148:GLN:N	2.79	0.41
1:L:261:PHE:O	1:L:280:ASP:HA	2.21	0.41
5:Q:36:VAL:O	5:Q:39:ARG:N	2.53	0.41
1:A:88:VAL:HG13	1:A:576:PRO:HA	2.01	0.41
1:A:498:THR:HG23	1:A:503:TYR:CE2	2.56	0.41
1:A:513:LEU:HD13	1:A:513:LEU:HA	1.88	0.41
1:A:821:PHE:HB3	1:C:237:GLY:HA3	2.03	0.41
1:B:134:GLN:HE22	1:B:217:LYS:HG3	1.85	0.41
1:B:396:ARG:NH1	1:B:867:ASP:OD2	2.54	0.41
1:B:636:ASN:C	1:B:638:THR:H	2.29	0.41
1:B:771:LEU:HD21	1:B:778:TYR:CE2	2.56	0.41
1:B:811:TYR:CD1	1:B:857:PRO:HD2	2.56	0.41
1:B:924:ASP:HB3	1:B:942:ARG:HG2	2.02	0.41
1:C:488:THR:HG22	1:C:507:ARG:HG2	2.03	0.41
1:C:615:LEU:HD23	1:C:615:LEU:HA	1.84	0.41
1:D:16:ALA:HA	1:D:48:PRO:HB3	2.03	0.41
1:D:410:TYR:OH	1:F:836:MET:HA	2.21	0.41
1:D:472:PHE:O	1:D:473:LEU:C	2.62	0.41
1:D:485:TYR:CZ	1:D:528:PRO:HB3	2.56	0.41
1:D:546:ARG:NH2	1:D:594:GLN:OE1	2.53	0.41
1:E:330:PHE:CZ	1:E:560:ILE:HB	2.55	0.41
1:E:731:TRP:O	1:E:732:PRO:C	2.64	0.41
1:E:872:ARG:NH2	7:3:30:LEU:HG	2.36	0.41
1:F:46:ARG:HH22	7:4:28:SER:H	1.66	0.41
1:F:185:LYS:HE3	1:F:185:LYS:HB2	1.85	0.41
1:F:190:ASP:OD1	1:F:191:LYS:N	2.54	0.41
1:F:214:ARG:HH12	1:F:241:LYS:HE2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:319:ASN:OD1	1:F:505:ASN:ND2	2.46	0.41
1:F:760:ASN:CB	5:P:54:VAL:HG21	2.50	0.41
1:G:313:VAL:HG12	1:I:204:TRP:CE2	2.54	0.41
1:G:417:THR:HG21	1:G:453:CYS:SG	2.61	0.41
1:G:460:MET:HG3	1:I:460:MET:HE2	2.02	0.41
1:G:839:GLY:HA2	1:I:198:GLN:HG3	2.03	0.41
1:H:168:THR:OG1	1:H:169:ASN:N	2.54	0.41
1:H:368:GLN:HG2	1:H:709:ASP:O	2.21	0.41
1:H:529:MET:HE3	1:H:529:MET:HB2	1.85	0.41
1:H:681:THR:HG21	1:H:712:PHE:CD1	2.56	0.41
1:H:892:MET:HA	1:H:895:ALA:HB3	2.02	0.41
1:I:599:ASN:O	1:I:702:SER:OG	2.34	0.41
1:I:771:LEU:HD21	1:I:778:TYR:CE2	2.56	0.41
1:I:771:LEU:HD12	1:I:771:LEU:HA	1.87	0.41
1:J:79:LEU:HD22	1:J:335:TYR:HE2	1.86	0.41
1:J:158:GLY:HA3	1:J:283:LEU:HD11	2.01	0.41
1:J:396:ARG:NH2	1:J:865:LEU:HD11	2.36	0.41
1:J:539:ARG:HB2	1:J:539:ARG:HH11	1.86	0.41
1:J:825:ASN:HA	1:L:122:ASN:HA	2.01	0.41
1:K:599:ASN:O	1:K:702:SER:OG	2.30	0.41
1:L:240:ALA:O	1:L:288:VAL:HG12	2.20	0.41
1:L:282:ILE:HD12	1:L:284:TYR:CE1	2.55	0.41
1:L:290:LEU:HD12	1:L:290:LEU:HA	1.87	0.41
1:L:350:SER:O	1:L:352:LEU:N	2.53	0.41
1:L:904:THR:O	1:L:904:THR:OG1	2.38	0.41
2:N:140:HIS:ND1	2:N:141:PRO:HD2	2.36	0.41
2:N:182:LEU:HD21	2:N:446:ARG:HD2	2.02	0.41
4:M:98:LEU:HD23	4:M:98:LEU:HA	1.88	0.41
1:A:640:ASP:HB2	1:A:928:VAL:O	2.20	0.41
1:B:288:VAL:HG23	1:B:290:LEU:HB2	2.03	0.41
1:C:109:ARG:NH2	1:C:550:LEU:HB2	2.35	0.41
1:C:789:ASP:N	1:C:789:ASP:OD1	2.54	0.41
1:D:193:PHE:HE2	1:E:840:GLN:CD	2.29	0.41
1:D:203:ASN:HD21	1:D:415:ASN:HB3	1.86	0.41
1:E:85:THR:O	1:E:85:THR:OG1	2.37	0.41
1:E:108:ASP:HB3	1:E:606:ALA:HB3	2.04	0.41
1:E:323:TYR:OH	1:F:401:HIS:HB3	2.21	0.41
1:E:477:VAL:HG11	1:E:514:VAL:HG21	2.03	0.41
1:E:566:PHE:O	1:E:570:LYS:N	2.53	0.41
1:F:135:TRP:CZ3	1:F:137:THR:HB	2.56	0.41
1:F:163:GLY:HA2	1:F:210:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:445:ALA:HB2	1:H:152:ASP:C	2.45	0.41
1:H:471:SER:HA	1:I:407:LEU:HD11	2.02	0.41
1:H:526:LEU:HD22	1:H:526:LEU:HA	1.91	0.41
1:I:309:GLU:H	1:I:309:GLU:HG3	1.70	0.41
1:J:198:GLN:CG	1:K:839:GLY:HA2	2.51	0.41
1:J:231:ARG:O	1:J:240:ALA:HB2	2.21	0.41
1:J:696:ASP:OD1	1:J:696:ASP:N	2.50	0.41
1:J:771:LEU:HG	1:J:777:GLY:HA3	2.02	0.41
1:K:20:ALA:HA	1:K:23:TYR:CE2	2.56	0.41
1:K:62:GLN:HE21	1:K:62:GLN:HB2	1.61	0.41
1:K:943:THR:HB	1:K:944:PRO:HD3	2.03	0.41
5:Q:8:PHE:CE1	5:R:28:ARG:HG2	2.56	0.41
5:Q:10:GLY:O	5:Q:11:GLY:C	2.54	0.41
6:U:59:ALA:O	6:U:60:ALA:C	2.62	0.41
1:A:20:ALA:HA	1:A:23:TYR:CE2	2.56	0.40
1:A:99:THR:HA	1:A:616:TYR:O	2.21	0.40
1:A:429:THR:HG22	1:A:430:ASN:H	1.87	0.40
1:A:556:VAL:HG12	1:B:804:GLN:NE2	2.36	0.40
1:B:461:GLU:OE2	1:C:414:LEU:HA	2.21	0.40
1:B:630:LEU:O	1:B:634:LEU:HB2	2.21	0.40
1:B:637:ASP:OD1	1:B:929:HIS:ND1	2.29	0.40
1:C:764:ASP:O	1:C:768:VAL:HG12	2.21	0.40
1:D:801:MET:HE2	1:D:801:MET:HB3	1.33	0.40
1:E:61:SER:HA	1:F:734:ASN:HB2	2.02	0.40
1:E:155:LYS:HD2	1:E:261:PHE:CE1	2.56	0.40
1:E:842:TYR:CG	1:E:843:PRO:HD2	2.55	0.40
1:E:875:PHE:O	1:E:888:LEU:HB2	2.21	0.40
1:F:901:LEU:HD13	1:F:903:MET:HG3	2.02	0.40
1:G:167:ILE:HD11	1:G:260:TYR:CD1	2.56	0.40
1:G:588:ASP:O	1:G:592:ILE:HG12	2.20	0.40
1:G:807:ASP:OD2	1:G:810:ASN:ND2	2.54	0.40
1:H:162:THR:HA	1:H:193:PHE:CE1	2.56	0.40
1:I:676:ARG:HH12	7:5:31:ASN:H	1.69	0.40
1:J:785:GLU:HB2	1:J:788:LYS:HB2	2.03	0.40
1:K:575:LEU:HB3	1:K:576:PRO:HD2	2.03	0.40
1:K:779:GLN:HE22	1:L:39:PHE:HA	1.86	0.40
1:L:31:PHE:HD2	7:9:6:PHE:HD1	1.68	0.40
1:L:155:LYS:O	1:L:156:THR:C	2.62	0.40
1:L:518:ILE:H	1:L:518:ILE:HG13	1.74	0.40
2:N:377:ASP:N	2:N:377:ASP:OD1	2.54	0.40
2:N:462:THR:OG1	2:N:463:THR:N	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:10:GLY:O	5:R:13:PHE:N	2.53	0.40
5:S:38:GLY:C	5:S:40:PRO:HD3	2.46	0.40
6:U:75:PRO:HD2	6:U:78:LEU:HD12	2.03	0.40
7:4:4:ILE:H	7:4:4:ILE:HG12	1.70	0.40
1:A:283:LEU:HD23	1:A:283:LEU:HA	1.92	0.40
1:A:388:VAL:O	1:A:542:GLY:HA3	2.21	0.40
1:A:922:VAL:HA	1:A:944:PRO:HG2	2.04	0.40
1:B:392:ASP:O	1:B:395:VAL:HG12	2.22	0.40
1:C:277:TYR:CD1	1:C:277:TYR:N	2.89	0.40
1:D:203:ASN:H	1:E:313:VAL:CG1	2.35	0.40
1:D:725:PHE:O	1:D:726:ASP:C	2.64	0.40
1:E:208:GLU:OE1	1:E:208:GLU:N	2.54	0.40
1:E:240:ALA:O	1:E:241:LYS:HD3	2.21	0.40
1:E:588:ASP:OD1	1:E:591:MET:N	2.41	0.40
1:E:597:LEU:HD12	1:E:597:LEU:HA	1.93	0.40
1:E:924:ASP:OD1	1:E:924:ASP:N	2.53	0.40
1:F:89:GLY:O	1:F:576:PRO:HB3	2.21	0.40
1:F:227:GLY:HA3	1:F:295:THR:HG21	2.03	0.40
1:F:560:ILE:H	1:F:560:ILE:HG13	1.77	0.40
1:G:415:ASN:OD1	1:G:417:THR:N	2.53	0.40
1:G:696:ASP:OD1	1:G:696:ASP:N	2.44	0.40
1:G:823:HIS:CD2	1:I:195:PRO:HG2	2.57	0.40
1:H:499:ASN:O	1:H:599:ASN:HB2	2.21	0.40
1:H:590:ASN:HD22	1:H:602:ARG:HG3	1.87	0.40
1:H:696:ASP:OD1	1:H:696:ASP:N	2.48	0.40
1:H:724:MET:HE2	1:H:724:MET:HB3	2.00	0.40
1:I:397:ILE:HG21	1:I:523:ARG:HG2	2.03	0.40
1:I:620:PHE:O	1:I:622:MET:N	2.52	0.40
1:J:174:LEU:HD13	1:J:191:LYS:HE2	2.03	0.40
1:K:498:THR:HG23	1:K:503:TYR:CE2	2.56	0.40
1:K:593:LEU:HD23	1:K:593:LEU:HA	1.74	0.40
2:N:54:THR:HG22	2:N:55:ARG:H	1.86	0.40
5:Q:9:GLU:HG3	5:R:21:LEU:HD12	2.03	0.40
6:U:14:GLN:O	6:U:15:PRO:C	2.64	0.40
7:4:29:GLN:O	7:4:30:LEU:C	2.64	0.40
1:A:918:LEU:HD23	1:A:919:LEU:N	2.37	0.40
1:A:943:THR:OG1	1:A:944:PRO:HD3	2.21	0.40
1:B:753:GLY:O	1:B:763:LYS:NZ	2.53	0.40
1:B:851:ILE:H	1:B:851:ILE:HD13	1.86	0.40
1:C:52:PRO:HG3	7:1:11:PRO:HG3	2.04	0.40
1:E:634:LEU:HD12	1:E:634:LEU:HA	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:359:GLN:NE2	1:F:692:GLY:HA2	2.35	0.40
1:G:202:GLU:OE2	1:H:299:TYR:OH	2.39	0.40
1:G:771:LEU:HD12	1:G:771:LEU:HA	1.89	0.40
1:G:771:LEU:HD13	1:G:777:GLY:HA3	2.04	0.40
1:H:442:LYS:HG2	1:H:443:ASP:H	1.85	0.40
1:H:630:LEU:O	1:H:634:LEU:HB2	2.21	0.40
1:H:634:LEU:HD12	1:H:634:LEU:HA	1.88	0.40
1:H:682:ARG:NH2	1:H:914:THR:HG21	2.36	0.40
1:H:942:ARG:O	1:H:946:SER:HA	2.21	0.40
1:J:57:THR:HG21	1:K:877:SER:OG	2.21	0.40
1:J:574:LEU:HA	1:J:574:LEU:HD23	1.87	0.40
1:J:763:LYS:HD3	1:L:100:TYR:OH	2.22	0.40
1:J:911:ASP:OD1	1:J:911:ASP:N	2.47	0.40
1:K:109:ARG:NH1	1:K:553:GLY:O	2.55	0.40
1:K:722:SER:O	1:K:903:MET:HA	2.20	0.40
1:L:74:GLU:HG3	1:L:81:LYS:HE3	2.03	0.40
1:L:589:VAL:HB	1:L:606:ALA:HA	2.02	0.40
2:N:112:THR:HB	2:N:387:TRP:CZ2	2.55	0.40
2:N:332:GLU:H	2:N:332:GLU:HG3	1.77	0.40
2:N:383:GLU:CD	2:N:383:GLU:H	2.28	0.40
5:Q:49:MET:C	5:Q:51:TYR:H	2.30	0.40
1:A:313:VAL:HG22	1:C:204:TRP:CE3	2.51	0.40
1:A:513:LEU:O	1:A:514:VAL:C	2.65	0.40
1:A:566:PHE:O	1:A:570:LYS:HB2	2.21	0.40
1:A:589:VAL:O	1:A:593:LEU:HB2	2.21	0.40
1:A:647:LEU:HD11	1:A:919:LEU:HD21	2.04	0.40
1:C:192:THR:HG21	1:C:214:ARG:HH11	1.85	0.40
1:D:67:ARG:HB2	1:D:616:TYR:CE1	2.56	0.40
1:E:651:ASN:HB3	1:E:917:TYR:HE1	1.87	0.40
1:F:663:VAL:HG13	5:R:17:LEU:HD12	2.04	0.40
1:F:870:MET:HE2	1:F:870:MET:HB3	1.85	0.40
1:I:199:VAL:HB	1:I:206:GLU:HG2	2.02	0.40
1:J:47:ASN:OD1	1:J:47:ASN:N	2.53	0.40
1:J:138:LYS:HG2	1:J:149:GLN:HG3	2.02	0.40
1:J:152:ASP:C	1:J:154:THR:H	2.29	0.40
1:J:194:GLN:HB2	1:J:196:GLU:OE1	2.21	0.40
1:J:411:CYS:HB3	1:L:462:ILE:HB	2.02	0.40
1:J:761:MET:HE2	1:J:765:TRP:CD1	2.56	0.40
1:K:725:PHE:CD1	1:K:731:TRP:HB2	2.56	0.40
1:K:752:GLU:OE1	1:K:753:GLY:N	2.55	0.40
2:N:39:ARG:NH1	2:N:516:SER:OG	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:102:LEU:HD12	5:S:102:LEU:HA	1.91	0.40
1:A:426:VAL:HG23	1:B:260:TYR:HB2	2.03	0.40
1:B:76:THR:HG22	1:B:77:THR:H	1.85	0.40
1:B:159:VAL:HG21	1:C:841:PRO:HD2	2.04	0.40
1:B:193:PHE:HZ	1:B:199:VAL:HG23	1.86	0.40
1:C:721:VAL:HG12	1:C:905:PHE:HD2	1.86	0.40
1:D:574:LEU:HD12	1:D:574:LEU:HA	1.97	0.40
1:D:620:PHE:HD2	1:D:622:MET:HB3	1.87	0.40
1:F:94:LEU:HD23	1:F:574:LEU:HD21	2.03	0.40
1:F:423:TYR:OH	1:F:454:LYS:HG3	2.22	0.40
1:F:427:LYS:HD2	1:F:442:LYS:HE3	2.02	0.40
1:G:46:ARG:HB2	1:G:46:ARG:HH11	1.85	0.40
1:G:127:LYS:HE2	1:G:127:LYS:HB2	1.92	0.40
1:G:358:LEU:HD22	1:G:942:ARG:NH1	2.36	0.40
1:I:283:LEU:HD23	1:I:283:LEU:HA	1.83	0.40
1:J:942:ARG:HD2	1:J:945:PHE:O	2.21	0.40
1:K:71:VAL:HG21	1:K:85:THR:HG23	2.04	0.40
1:L:154:THR:HG23	1:L:155:LYS:HG2	2.03	0.40
1:L:192:THR:HG21	1:L:214:ARG:HH11	1.87	0.40
1:L:750:ASP:OD1	1:L:750:ASP:N	2.55	0.40
5:Q:41:VAL:H	5:Q:43:PRO:HD3	1.86	0.40
5:R:34:SER:OG	5:R:35:THR:N	2.54	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	A	949/952 (100%)	825 (87%)	121 (13%)	3 (0%)	36	64
1	B	947/952 (100%)	843 (89%)	101 (11%)	3 (0%)	36	64
1	C	944/952 (99%)	803 (85%)	139 (15%)	2 (0%)	43	70

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	945/952 (99%)	821 (87%)	122 (13%)	2 (0%)	43	70
1	E	945/952 (99%)	841 (89%)	104 (11%)	0	100	100
1	F	947/952 (100%)	815 (86%)	129 (14%)	3 (0%)	36	64
1	G	945/952 (99%)	817 (86%)	123 (13%)	5 (0%)	24	53
1	H	945/952 (99%)	817 (86%)	127 (13%)	1 (0%)	48	77
1	I	947/952 (100%)	818 (86%)	128 (14%)	1 (0%)	48	77
1	J	949/952 (100%)	830 (88%)	118 (12%)	1 (0%)	48	77
1	K	948/952 (100%)	833 (88%)	115 (12%)	0	100	100
1	L	945/952 (99%)	821 (87%)	120 (13%)	4 (0%)	30	58
2	N	467/519 (90%)	434 (93%)	32 (7%)	1 (0%)	43	70
3	O	15/374 (4%)	13 (87%)	2 (13%)	0	100	100
4	M	358/560 (64%)	344 (96%)	14 (4%)	0	100	100
5	P	118/134 (88%)	96 (81%)	19 (16%)	3 (2%)	4	21
5	Q	110/134 (82%)	84 (76%)	24 (22%)	2 (2%)	6	26
5	R	131/134 (98%)	109 (83%)	22 (17%)	0	100	100
5	S	118/134 (88%)	98 (83%)	18 (15%)	2 (2%)	7	27
6	U	184/227 (81%)	172 (94%)	12 (6%)	0	100	100
6	V	182/227 (80%)	167 (92%)	15 (8%)	0	100	100
7	1	28/234 (12%)	20 (71%)	8 (29%)	0	100	100
7	2	24/234 (10%)	16 (67%)	8 (33%)	0	100	100
7	3	25/234 (11%)	20 (80%)	5 (20%)	0	100	100
7	4	27/234 (12%)	18 (67%)	9 (33%)	0	100	100
7	5	26/234 (11%)	21 (81%)	5 (19%)	0	100	100
7	6	25/234 (11%)	21 (84%)	4 (16%)	0	100	100
7	7	25/234 (11%)	20 (80%)	5 (20%)	0	100	100
7	8	27/234 (12%)	24 (89%)	3 (11%)	0	100	100
7	9	26/234 (11%)	20 (77%)	6 (23%)	0	100	100
All	All	13272/15973 (83%)	11581 (87%)	1658 (12%)	33 (0%)	44	70

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	ASP

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Mol	Chain	Res	Type
1	C	153	VAL
1	D	153	VAL
1	F	153	VAL
1	F	203	ASN
1	G	193	PHE
1	I	885	LEU
1	L	152	ASP
5	P	15	PRO
5	P	46	SER
5	Q	9	GLU
5	S	78	ALA
1	G	329	ASN
1	L	95	ASP
1	L	309	GLU
5	Q	10	GLY
1	A	248	GLY
1	G	727	SER
1	L	94	LEU
1	D	152	ASP
1	F	152	ASP
5	S	73	THR
1	C	152	ASP
1	H	845	ASN
1	J	20	ALA
5	P	40	PRO
1	B	429	THR
1	B	456	ASN
1	G	196	GLU
2	N	390	PRO
1	A	153	VAL
1	B	477	VAL
1	G	477	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	A	817/818 (100%)	732 (90%)	85 (10%)	7	24
1	B	815/818 (100%)	723 (89%)	92 (11%)	5	21
1	C	814/818 (100%)	718 (88%)	96 (12%)	5	20
1	D	814/818 (100%)	719 (88%)	95 (12%)	5	20
1	E	814/818 (100%)	716 (88%)	98 (12%)	5	20
1	F	816/818 (100%)	721 (88%)	95 (12%)	5	21
1	G	814/818 (100%)	712 (88%)	102 (12%)	4	18
1	H	814/818 (100%)	698 (86%)	116 (14%)	3	13
1	I	815/818 (100%)	712 (87%)	103 (13%)	4	18
1	J	817/818 (100%)	718 (88%)	99 (12%)	5	19
1	K	817/818 (100%)	714 (87%)	103 (13%)	4	18
1	L	814/818 (100%)	710 (87%)	104 (13%)	4	17
2	N	426/462 (92%)	382 (90%)	44 (10%)	7	25
3	O	15/324 (5%)	12 (80%)	3 (20%)	1	4
4	M	304/472 (64%)	290 (95%)	14 (5%)	24	50
5	P	91/102 (89%)	80 (88%)	11 (12%)	5	19
5	Q	83/102 (81%)	72 (87%)	11 (13%)	4	16
5	R	101/102 (99%)	89 (88%)	12 (12%)	5	20
5	S	91/102 (89%)	82 (90%)	9 (10%)	7	27
6	U	162/190 (85%)	152 (94%)	10 (6%)	16	43
6	V	160/190 (84%)	149 (93%)	11 (7%)	14	40
7	1	25/195 (13%)	22 (88%)	3 (12%)	5	20
7	2	21/195 (11%)	11 (52%)	10 (48%)	0	0
7	3	22/195 (11%)	22 (100%)	0	100	100
7	4	24/195 (12%)	22 (92%)	2 (8%)	10	35
7	5	23/195 (12%)	22 (96%)	1 (4%)	26	51
7	6	22/195 (11%)	20 (91%)	2 (9%)	9	30
7	7	22/195 (11%)	19 (86%)	3 (14%)	3	15
7	8	24/195 (12%)	22 (92%)	2 (8%)	10	35
7	9	23/195 (12%)	21 (91%)	2 (9%)	9	32
All	All	11420/13617 (84%)	10082 (88%)	1338 (12%)	7	20

All (1338) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	A	57	THR
1	A	76	THR
1	A	85	THR
1	A	93	VAL
1	A	106	VAL
1	A	107	LEU
1	A	109	ARG
1	A	134	GLN
1	A	147	VAL
1	A	148	GLN
1	A	153	VAL
1	A	154	THR
1	A	156	THR
1	A	169	ASN
1	A	172	LEU
1	A	192	THR
1	A	193	PHE
1	A	235	GLU
1	A	242	PHE
1	A	245	VAL
1	A	247	GLU
1	A	275	GLU
1	A	277	TYR
1	A	282	ILE
1	A	286	GLU
1	A	287	ASN
1	A	313	VAL
1	A	341	ASN
1	A	344	VAL
1	A	355	VAL
1	A	356	VAL
1	A	360	ASP
1	A	361	ARG
1	A	372	ASP
1	A	388	VAL
1	A	406	GLU
1	A	426	VAL
1	A	428	ILE
1	A	429	THR
1	A	433	ASP
1	A	457	VAL
1	A	462	ILE

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Mol	Chain	Res	Type
1	A	477	VAL
1	A	508	VAL
1	A	513	LEU
1	A	514	VAL
1	A	520	ILE
1	A	527	ASP
1	A	537	HIS
1	A	561	GLN
1	A	565	LYS
1	A	582	GLU
1	A	589	VAL
1	A	604	ASP
1	A	608	VAL
1	A	626	THR
1	A	631	GLU
1	A	639	HIS
1	A	643	PHE
1	A	663	VAL
1	A	683	LEU
1	A	711	THR
1	A	714	LEU
1	A	728	SER
1	A	735	ASP
1	A	739	THR
1	A	740	PRO
1	A	744	GLU
1	A	752	GLU
1	A	758	GLN
1	A	760	ASN
1	A	761	MET
1	A	805	VAL
1	A	837	ARG
1	A	840	GLN
1	A	853	GLN
1	A	866	CYS
1	A	869	VAL
1	A	919	LEU
1	A	925	VAL
1	A	928	VAL
1	A	939	VAL
1	A	943	THR
1	A	951	THR

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Mol	Chain	Res	Type
1	B	3	THR
1	B	9	GLN
1	B	49	THR
1	B	58	THR
1	B	66	LEU
1	B	69	VAL
1	B	76	THR
1	B	78	TYR
1	B	86	LEU
1	B	88	VAL
1	B	109	ARG
1	B	119	THR
1	B	131	ASN
1	B	141	GLN
1	B	149	GLN
1	B	154	THR
1	B	156	THR
1	B	166	ASN
1	B	186	ASP
1	B	188	TYR
1	B	196	GLU
1	B	203	ASN
1	B	206	GLU
1	B	214	ARG
1	B	231	ARG
1	B	239	GLN
1	B	241	LYS
1	B	262	ASP
1	B	278	LYS
1	B	292	THR
1	B	295	THR
1	B	311	ASN
1	B	339	THR
1	B	341	ASN
1	B	344	VAL
1	B	345	LEU
1	B	355	VAL
1	B	364	GLU
1	B	372	ASP
1	B	379	ARG
1	B	396	ARG
1	B	422	THR

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Mol	Chain	Res	Type
1	B	433	ASP
1	B	443	ASP
1	B	446	ILE
1	B	449	GLN
1	B	450	ASN
1	B	456	ASN
1	B	457	VAL
1	B	462	ILE
1	B	464	LEU
1	B	500	THR
1	B	509	VAL
1	B	514	VAL
1	B	518	ILE
1	B	520	ILE
1	B	537	HIS
1	B	548	MET
1	B	556	VAL
1	B	561	GLN
1	B	573	LEU
1	B	574	LEU
1	B	589	VAL
1	B	626	THR
1	B	651	ASN
1	B	652	MET
1	B	661	THR
1	B	663	VAL
1	B	691	LEU
1	B	696	ASP
1	B	708	LEU
1	B	734	ASN
1	B	741	ASN
1	B	746	LYS
1	B	771	LEU
1	B	774	TYR
1	B	790	ARG
1	B	813	ASP
1	B	818	THR
1	B	821	PHE
1	B	826	SER
1	B	835	THR
1	B	837	ARG
1	B	851	ILE

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Mol	Chain	Res	Type
1	B	863	LYS
1	B	868	ARG
1	B	887	ASP
1	B	893	LEU
1	B	907	VAL
1	B	908	ASP
1	B	926	VAL
1	B	943	THR
1	C	13	MET
1	C	35	THR
1	C	47	ASN
1	C	65	THR
1	C	69	VAL
1	C	72	ASP
1	C	79	LEU
1	C	88	VAL
1	C	90	ASP
1	C	104	ARG
1	C	106	VAL
1	C	107	LEU
1	C	136	GLU
1	C	144	THR
1	C	149	GLN
1	C	173	LEU
1	C	192	THR
1	C	203	ASN
1	C	222	MET
1	C	236	LYS
1	C	277	TYR
1	C	287	ASN
1	C	311	ASN
1	C	314	GLN
1	C	341	ASN
1	C	357	ASP
1	C	363	THR
1	C	372	ASP
1	C	378	THR
1	C	384	TRP
1	C	396	ARG
1	C	398	ILE
1	C	403	VAL
1	C	414	LEU

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Mol	Chain	Res	Type
1	C	429	THR
1	C	456	ASN
1	C	461	GLU
1	C	462	ILE
1	C	467	ASN
1	C	468	LEU
1	C	473	LEU
1	C	477	VAL
1	C	505	ASN
1	C	513	LEU
1	C	514	VAL
1	C	520	ILE
1	C	556	VAL
1	C	570	LYS
1	C	582	GLU
1	C	589	VAL
1	C	590	ASN
1	C	613	VAL
1	C	615	LEU
1	C	626	THR
1	C	630	LEU
1	C	631	GLU
1	C	635	ARG
1	C	639	HIS
1	C	640	ASP
1	C	641	GLN
1	C	651	ASN
1	C	652	MET
1	C	663	VAL
1	C	665	ILE
1	C	683	LEU
1	C	708	LEU
1	C	711	THR
1	C	724	MET
1	C	729	VAL
1	C	739	THR
1	C	752	GLU
1	C	762	THR
1	C	767	LEU
1	C	768	VAL
1	C	779	GLN
1	C	783	VAL

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Mol	Chain	Res	Type
1	C	790	ARG
1	C	791	MET
1	C	796	ARG
1	C	801	MET
1	C	804	GLN
1	C	837	ARG
1	C	840	GLN
1	C	851	ILE
1	C	853	GLN
1	C	866	CYS
1	C	885	LEU
1	C	886	THR
1	C	887	ASP
1	C	902	ASP
1	C	908	ASP
1	C	914	THR
1	C	928	VAL
1	C	935	VAL
1	C	936	ILE
1	C	943	THR
1	D	9	GLN
1	D	10	TRP
1	D	49	THR
1	D	76	THR
1	D	85	THR
1	D	88	VAL
1	D	99	THR
1	D	108	ASP
1	D	109	ARG
1	D	131	ASN
1	D	157	PHE
1	D	166	ASN
1	D	168	THR
1	D	172	LEU
1	D	186	ASP
1	D	188	TYR
1	D	192	THR
1	D	196	GLU
1	D	199	VAL
1	D	276	GLU
1	D	281	ILE
1	D	282	ILE

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Mol	Chain	Res	Type
1	D	286	GLU
1	D	300	LYS
1	D	310	ILE
1	D	344	VAL
1	D	352	LEU
1	D	356	VAL
1	D	368	GLN
1	D	372	ASP
1	D	388	VAL
1	D	403	VAL
1	D	404	GLU
1	D	427	LYS
1	D	429	THR
1	D	443	ASP
1	D	456	ASN
1	D	462	ILE
1	D	464	LEU
1	D	473	LEU
1	D	488	THR
1	D	498	THR
1	D	502	GLU
1	D	513	LEU
1	D	514	VAL
1	D	518	ILE
1	D	520	ILE
1	D	526	LEU
1	D	527	ASP
1	D	529	MET
1	D	537	HIS
1	D	561	GLN
1	D	565	LYS
1	D	570	LYS
1	D	575	LEU
1	D	588	ASP
1	D	589	VAL
1	D	590	ASN
1	D	625	ASN
1	D	638	THR
1	D	639	HIS
1	D	641	GLN
1	D	643	PHE
1	D	663	VAL

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Mol	Chain	Res	Type
1	D	665	ILE
1	D	667	ILE
1	D	711	THR
1	D	721	VAL
1	D	726	ASP
1	D	738	LEU
1	D	739	THR
1	D	750	ASP
1	D	758	GLN
1	D	762	THR
1	D	764	ASP
1	D	767	LEU
1	D	769	GLN
1	D	774	TYR
1	D	783	VAL
1	D	791	MET
1	D	804	GLN
1	D	805	VAL
1	D	806	VAL
1	D	819	LEU
1	D	836	MET
1	D	863	LYS
1	D	865	LEU
1	D	868	ARG
1	D	885	LEU
1	D	911	ASP
1	D	912	GLU
1	D	918	LEU
1	D	925	VAL
1	D	943	THR
1	D	951	THR
1	E	47	ASN
1	E	50	VAL
1	E	54	HIS
1	E	56	VAL
1	E	57	THR
1	E	64	LEU
1	E	65	THR
1	E	92	ARG
1	E	144	THR
1	E	153	VAL
1	E	154	THR

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Mol	Chain	Res	Type
1	E	174	LEU
1	E	176	THR
1	E	186	ASP
1	E	193	PHE
1	E	196	GLU
1	E	198	GLN
1	E	201	GLU
1	E	207	ASN
1	E	235	GLU
1	E	254	LEU
1	E	257	ASP
1	E	262	ASP
1	E	278	LYS
1	E	283	LEU
1	E	285	THR
1	E	286	GLU
1	E	288	VAL
1	E	292	THR
1	E	300	LYS
1	E	319	ASN
1	E	321	PRO
1	E	338	SER
1	E	353	ASN
1	E	368	GLN
1	E	374	LEU
1	E	377	ARG
1	E	395	VAL
1	E	396	ARG
1	E	398	ILE
1	E	407	LEU
1	E	417	THR
1	E	429	THR
1	E	440	TRP
1	E	454	LYS
1	E	461	GLU
1	E	462	ILE
1	E	464	LEU
1	E	473	LEU
1	E	500	THR
1	E	508	VAL
1	E	518	ILE
1	E	520	ILE

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Mol	Chain	Res	Type
1	E	537	HIS
1	E	550	LEU
1	E	552	ASN
1	E	556	VAL
1	E	561	GLN
1	E	571	ASN
1	E	572	LEU
1	E	573	LEU
1	E	575	LEU
1	E	593	LEU
1	E	608	VAL
1	E	626	THR
1	E	634	LEU
1	E	635	ARG
1	E	636	ASN
1	E	643	PHE
1	E	651	ASN
1	E	659	LYS
1	E	663	VAL
1	E	665	ILE
1	E	670	ARG
1	E	683	LEU
1	E	708	LEU
1	E	709	ASP
1	E	711	THR
1	E	714	LEU
1	E	739	THR
1	E	742	GLU
1	E	756	VAL
1	E	771	LEU
1	E	774	TYR
1	E	809	ILE
1	E	825	ASN
1	E	837	ARG
1	E	851	ILE
1	E	854	THR
1	E	877	SER
1	E	885	LEU
1	E	902	ASP
1	E	915	LEU
1	E	919	LEU
1	E	926	VAL

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Mol	Chain	Res	Type
1	E	930	GLN
1	E	936	ILE
1	E	943	THR
1	F	1	MET
1	F	35	THR
1	F	47	ASN
1	F	50	VAL
1	F	64	LEU
1	F	65	THR
1	F	69	VAL
1	F	71	VAL
1	F	72	ASP
1	F	76	THR
1	F	86	LEU
1	F	88	VAL
1	F	109	ARG
1	F	137	THR
1	F	153	VAL
1	F	156	THR
1	F	172	LEU
1	F	179	THR
1	F	185	LYS
1	F	188	TYR
1	F	193	PHE
1	F	203	ASN
1	F	204	TRP
1	F	218	LYS
1	F	233	THR
1	F	277	TYR
1	F	288	VAL
1	F	289	ASN
1	F	313	VAL
1	F	341	ASN
1	F	344	VAL
1	F	363	THR
1	F	371	LEU
1	F	372	ASP
1	F	389	ASP
1	F	407	LEU
1	F	409	ASN
1	F	428	ILE
1	F	461	GLU

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Mol	Chain	Res	Type
1	F	462	ILE
1	F	470	LYS
1	F	473	LEU
1	F	476	ASN
1	F	491	ASN
1	F	502	GLU
1	F	507	ARG
1	F	509	VAL
1	F	518	ILE
1	F	520	ILE
1	F	543	LEU
1	F	562	VAL
1	F	565	LYS
1	F	570	LYS
1	F	582	GLU
1	F	615	LEU
1	F	626	THR
1	F	633	MET
1	F	635	ARG
1	F	636	ASN
1	F	640	ASP
1	F	652	MET
1	F	656	ILE
1	F	672	TRP
1	F	683	LEU
1	F	684	LYS
1	F	686	LYS
1	F	705	ILE
1	F	711	THR
1	F	721	VAL
1	F	729	VAL
1	F	734	ASN
1	F	739	THR
1	F	754	TYR
1	F	762	THR
1	F	767	LEU
1	F	769	GLN
1	F	771	LEU
1	F	774	TYR
1	F	783	VAL
1	F	803	ARG
1	F	804	GLN

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Mol	Chain	Res	Type
1	F	806	VAL
1	F	813	ASP
1	F	832	LEU
1	F	837	ARG
1	F	877	SER
1	F	885	LEU
1	F	890	GLN
1	F	902	ASP
1	F	915	LEU
1	F	925	VAL
1	F	926	VAL
1	F	935	VAL
1	F	936	ILE
1	F	943	THR
1	G	6	MET
1	G	9	GLN
1	G	10	TRP
1	G	13	MET
1	G	28	LEU
1	G	46	ARG
1	G	54	HIS
1	G	58	THR
1	G	72	ASP
1	G	76	THR
1	G	78	TYR
1	G	85	THR
1	G	88	VAL
1	G	93	VAL
1	G	147	VAL
1	G	152	ASP
1	G	153	VAL
1	G	154	THR
1	G	167	ILE
1	G	191	LYS
1	G	192	THR
1	G	196	GLU
1	G	199	VAL
1	G	202	GLU
1	G	222	MET
1	G	257	ASP
1	G	281	ILE
1	G	282	ILE

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Mol	Chain	Res	Type
1	G	286	GLU
1	G	291	GLU
1	G	310	ILE
1	G	319	ASN
1	G	320	ARG
1	G	327	ARG
1	G	341	ASN
1	G	344	VAL
1	G	355	VAL
1	G	361	ARG
1	G	372	ASP
1	G	378	THR
1	G	379	ARG
1	G	388	VAL
1	G	407	LEU
1	G	409	ASN
1	G	428	ILE
1	G	438	SER
1	G	443	ASP
1	G	461	GLU
1	G	462	ILE
1	G	477	VAL
1	G	508	VAL
1	G	514	VAL
1	G	518	ILE
1	G	520	ILE
1	G	529	MET
1	G	556	VAL
1	G	561	GLN
1	G	565	LYS
1	G	575	LEU
1	G	580	THR
1	G	582	GLU
1	G	584	ASN
1	G	590	ASN
1	G	607	SER
1	G	631	GLU
1	G	638	THR
1	G	651	ASN
1	G	653	LEU
1	G	663	VAL
1	G	665	ILE

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Mol	Chain	Res	Type
1	G	681	THR
1	G	688	THR
1	G	700	VAL
1	G	720	LYS
1	G	721	VAL
1	G	726	ASP
1	G	728	SER
1	G	738	LEU
1	G	756	VAL
1	G	758	GLN
1	G	769	GLN
1	G	775	ASN
1	G	783	VAL
1	G	801	MET
1	G	822	GLN
1	G	836	MET
1	G	840	GLN
1	G	850	LEU
1	G	859	VAL
1	G	860	THR
1	G	865	LEU
1	G	872	ARG
1	G	880	MET
1	G	887	ASP
1	G	912	GLU
1	G	919	LEU
1	G	923	PHE
1	G	926	VAL
1	G	930	GLN
1	G	935	VAL
1	G	937	GLU
1	G	943	THR
1	H	50	VAL
1	H	59	ASP
1	H	65	THR
1	H	72	ASP
1	H	79	LEU
1	H	109	ARG
1	H	134	GLN
1	H	137	THR
1	H	147	VAL
1	H	154	THR

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Mol	Chain	Res	Type
1	H	156	THR
1	H	157	PHE
1	H	172	LEU
1	H	174	LEU
1	H	176	THR
1	H	188	TYR
1	H	190	ASP
1	H	192	THR
1	H	196	GLU
1	H	198	GLN
1	H	199	VAL
1	H	204	TRP
1	H	218	LYS
1	H	221	LYS
1	H	235	GLU
1	H	242	PHE
1	H	245	VAL
1	H	263	VAL
1	H	292	THR
1	H	300	LYS
1	H	317	MET
1	H	327	ARG
1	H	339	THR
1	H	341	ASN
1	H	348	GLN
1	H	351	GLN
1	H	353	ASN
1	H	357	ASP
1	H	364	GLU
1	H	369	LEU
1	H	372	ASP
1	H	394	ASP
1	H	395	VAL
1	H	396	ARG
1	H	398	ILE
1	H	403	VAL
1	H	407	LEU
1	H	409	ASN
1	H	415	ASN
1	H	417	THR
1	H	428	ILE
1	H	429	THR

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Mol	Chain	Res	Type
1	H	433	ASP
1	H	450	ASN
1	H	461	GLU
1	H	462	ILE
1	H	465	GLN
1	H	470	LYS
1	H	477	VAL
1	H	488	THR
1	H	509	VAL
1	H	514	VAL
1	H	520	ILE
1	H	526	LEU
1	H	537	HIS
1	H	556	VAL
1	H	565	LYS
1	H	575	LEU
1	H	583	TRP
1	H	587	LYS
1	H	590	ASN
1	H	597	LEU
1	H	608	VAL
1	H	618	THR
1	H	626	THR
1	H	635	ARG
1	H	637	ASP
1	H	639	HIS
1	H	642	SER
1	H	659	LYS
1	H	661	THR
1	H	681	THR
1	H	684	LYS
1	H	700	VAL
1	H	708	LEU
1	H	711	THR
1	H	726	ASP
1	H	728	SER
1	H	734	ASN
1	H	739	THR
1	H	742	GLU
1	H	759	CYS
1	H	761	MET
1	H	767	LEU

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Mol	Chain	Res	Type
1	H	768	VAL
1	H	769	GLN
1	H	776	ILE
1	H	783	VAL
1	H	797	ASN
1	H	818	THR
1	H	825	ASN
1	H	837	ARG
1	H	851	ILE
1	H	853	GLN
1	H	867	ASP
1	H	877	SER
1	H	893	LEU
1	H	902	ASP
1	H	912	GLU
1	H	914	THR
1	H	923	PHE
1	H	928	VAL
1	H	930	GLN
1	H	939	VAL
1	H	942	ARG
1	H	943	THR
1	I	6	MET
1	I	28	LEU
1	I	49	THR
1	I	50	VAL
1	I	57	THR
1	I	64	LEU
1	I	65	THR
1	I	69	VAL
1	I	72	ASP
1	I	76	THR
1	I	79	LEU
1	I	86	LEU
1	I	109	ARG
1	I	131	ASN
1	I	136	GLU
1	I	137	THR
1	I	139	GLU
1	I	147	VAL
1	I	154	THR
1	I	156	THR

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Mol	Chain	Res	Type
1	I	157	PHE
1	I	173	LEU
1	I	193	PHE
1	I	194	GLN
1	I	196	GLU
1	I	201	GLU
1	I	217	LYS
1	I	218	LYS
1	I	245	VAL
1	I	247	GLU
1	I	249	GLU
1	I	277	TYR
1	I	287	ASN
1	I	289	ASN
1	I	295	THR
1	I	313	VAL
1	I	341	ASN
1	I	344	VAL
1	I	345	LEU
1	I	372	ASP
1	I	378	THR
1	I	383	MET
1	I	397	ILE
1	I	407	LEU
1	I	417	THR
1	I	426	VAL
1	I	429	THR
1	I	437	GLU
1	I	464	LEU
1	I	473	LEU
1	I	476	ASN
1	I	492	VAL
1	I	514	VAL
1	I	518	ILE
1	I	543	LEU
1	I	556	VAL
1	I	561	GLN
1	I	565	LYS
1	I	582	GLU
1	I	590	ASN
1	I	591	MET
1	I	601	LEU

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Mol	Chain	Res	Type
1	I	612	SER
1	I	618	THR
1	I	630	LEU
1	I	635	ARG
1	I	638	THR
1	I	640	ASP
1	I	641	GLN
1	I	642	SER
1	I	651	ASN
1	I	652	MET
1	I	656	ILE
1	I	665	ILE
1	I	670	ARG
1	I	681	THR
1	I	683	LEU
1	I	708	LEU
1	I	709	ASP
1	I	714	LEU
1	I	742	GLU
1	I	756	VAL
1	I	764	ASP
1	I	769	GLN
1	I	770	MET
1	I	771	LEU
1	I	774	TYR
1	I	783	VAL
1	I	790	ARG
1	I	807	ASP
1	I	809	ILE
1	I	837	ARG
1	I	848	TYR
1	I	859	VAL
1	I	868	ARG
1	I	885	LEU
1	I	886	THR
1	I	888	LEU
1	I	890	GLN
1	I	902	ASP
1	I	926	VAL
1	I	935	VAL
1	I	936	ILE
1	J	10	TRP

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Mol	Chain	Res	Type
1	J	28	LEU
1	J	47	ASN
1	J	57	THR
1	J	69	VAL
1	J	72	ASP
1	J	76	THR
1	J	90	ASP
1	J	103	ILE
1	J	106	VAL
1	J	107	LEU
1	J	108	ASP
1	J	109	ARG
1	J	153	VAL
1	J	154	THR
1	J	156	THR
1	J	167	ILE
1	J	169	ASN
1	J	188	TYR
1	J	192	THR
1	J	193	PHE
1	J	194	GLN
1	J	196	GLU
1	J	199	VAL
1	J	218	LYS
1	J	267	SER
1	J	281	ILE
1	J	282	ILE
1	J	285	THR
1	J	288	VAL
1	J	291	GLU
1	J	303	THR
1	J	310	ILE
1	J	312	LEU
1	J	317	MET
1	J	333	LEU
1	J	339	THR
1	J	356	VAL
1	J	365	LEU
1	J	371	LEU
1	J	372	ASP
1	J	379	ARG
1	J	391	TYR

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Mol	Chain	Res	Type
1	J	399	GLU
1	J	407	LEU
1	J	417	THR
1	J	429	THR
1	J	436	GLU
1	J	443	ASP
1	J	446	ILE
1	J	462	ILE
1	J	477	VAL
1	J	498	THR
1	J	518	ILE
1	J	520	ILE
1	J	525	SER
1	J	537	HIS
1	J	572	LEU
1	J	613	VAL
1	J	614	ASN
1	J	615	LEU
1	J	626	THR
1	J	651	ASN
1	J	663	VAL
1	J	670	ARG
1	J	681	THR
1	J	700	VAL
1	J	711	THR
1	J	728	SER
1	J	731	TRP
1	J	742	GLU
1	J	750	ASP
1	J	756	VAL
1	J	769	GLN
1	J	770	MET
1	J	783	VAL
1	J	804	GLN
1	J	805	VAL
1	J	806	VAL
1	J	809	ILE
1	J	818	THR
1	J	837	ARG
1	J	838	GLN
1	J	850	LEU
1	J	859	VAL

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Mol	Chain	Res	Type
1	J	861	GLN
1	J	862	LYS
1	J	863	LYS
1	J	865	LEU
1	J	869	VAL
1	J	916	LEU
1	J	918	LEU
1	J	919	LEU
1	J	927	ARG
1	J	928	VAL
1	J	930	GLN
1	J	935	VAL
1	J	939	VAL
1	J	943	THR
1	K	50	VAL
1	K	64	LEU
1	K	65	THR
1	K	72	ASP
1	K	93	VAL
1	K	107	LEU
1	K	131	ASN
1	K	139	GLU
1	K	144	THR
1	K	153	VAL
1	K	155	LYS
1	K	169	ASN
1	K	176	THR
1	K	178	GLU
1	K	188	TYR
1	K	191	LYS
1	K	195	PRO
1	K	196	GLU
1	K	198	GLN
1	K	199	VAL
1	K	201	GLU
1	K	203	ASN
1	K	204	TRP
1	K	280	ASP
1	K	282	ILE
1	K	283	LEU
1	K	310	ILE
1	K	333	LEU

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Mol	Chain	Res	Type
1	K	341	ASN
1	K	344	VAL
1	K	361	ARG
1	K	364	GLU
1	K	372	ASP
1	K	389	ASP
1	K	391	TYR
1	K	395	VAL
1	K	396	ARG
1	K	403	VAL
1	K	407	LEU
1	K	409	ASN
1	K	417	THR
1	K	449	GLN
1	K	454	LYS
1	K	461	GLU
1	K	462	ILE
1	K	464	LEU
1	K	470	LYS
1	K	488	THR
1	K	500	THR
1	K	513	LEU
1	K	514	VAL
1	K	520	ILE
1	K	526	LEU
1	K	532	VAL
1	K	537	HIS
1	K	556	VAL
1	K	580	THR
1	K	589	VAL
1	K	592	ILE
1	K	593	LEU
1	K	597	LEU
1	K	615	LEU
1	K	618	THR
1	K	626	THR
1	K	635	ARG
1	K	638	THR
1	K	639	HIS
1	K	640	ASP
1	K	641	GLN
1	K	643	PHE

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Mol	Chain	Res	Type
1	K	652	MET
1	K	659	LYS
1	K	663	VAL
1	K	700	VAL
1	K	720	LYS
1	K	728	SER
1	K	734	ASN
1	K	739	THR
1	K	752	GLU
1	K	756	VAL
1	K	761	MET
1	K	762	THR
1	K	763	LYS
1	K	769	GLN
1	K	770	MET
1	K	779	GLN
1	K	783	VAL
1	K	803	ARG
1	K	804	GLN
1	K	805	VAL
1	K	818	THR
1	K	825	ASN
1	K	837	ARG
1	K	843	PRO
1	K	854	THR
1	K	862	LYS
1	K	863	LYS
1	K	866	CYS
1	K	877	SER
1	K	914	THR
1	K	930	GLN
1	K	941	LEU
1	K	949	ASN
1	L	28	LEU
1	L	71	VAL
1	L	86	LEU
1	L	88	VAL
1	L	104	ARG
1	L	134	GLN
1	L	137	THR
1	L	154	THR
1	L	173	LEU

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Mol	Chain	Res	Type
1	L	187	ILE
1	L	196	GLU
1	L	199	VAL
1	L	217	LYS
1	L	235	GLU
1	L	242	PHE
1	L	247	GLU
1	L	256	ILE
1	L	277	TYR
1	L	280	ASP
1	L	285	THR
1	L	289	ASN
1	L	303	THR
1	L	309	GLU
1	L	313	VAL
1	L	333	LEU
1	L	341	ASN
1	L	345	LEU
1	L	355	VAL
1	L	356	VAL
1	L	371	LEU
1	L	372	ASP
1	L	388	VAL
1	L	399	GLU
1	L	403	VAL
1	L	407	LEU
1	L	429	THR
1	L	430	ASN
1	L	446	ILE
1	L	462	ILE
1	L	464	LEU
1	L	473	LEU
1	L	494	LEU
1	L	502	GLU
1	L	505	ASN
1	L	508	VAL
1	L	514	VAL
1	L	518	ILE
1	L	520	ILE
1	L	529	MET
1	L	537	HIS
1	L	543	LEU

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Mol	Chain	Res	Type
1	L	544	ARG
1	L	546	ARG
1	L	561	GLN
1	L	570	LYS
1	L	582	GLU
1	L	587	LYS
1	L	589	VAL
1	L	596	SER
1	L	597	LEU
1	L	601	LEU
1	L	608	VAL
1	L	613	VAL
1	L	614	ASN
1	L	631	GLU
1	L	634	LEU
1	L	635	ARG
1	L	641	GLN
1	L	656	ILE
1	L	659	LYS
1	L	665	ILE
1	L	700	VAL
1	L	711	THR
1	L	714	LEU
1	L	725	PHE
1	L	726	ASP
1	L	729	VAL
1	L	734	ASN
1	L	738	LEU
1	L	749	VAL
1	L	756	VAL
1	L	759	CYS
1	L	769	GLN
1	L	774	TYR
1	L	806	VAL
1	L	812	LYS
1	L	813	ASP
1	L	829	THR
1	L	837	ARG
1	L	853	GLN
1	L	859	VAL
1	L	867	ASP
1	L	869	VAL

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Mol	Chain	Res	Type
1	L	870	MET
1	L	877	SER
1	L	885	LEU
1	L	890	GLN
1	L	901	LEU
1	L	907	VAL
1	L	908	ASP
1	L	926	VAL
1	L	935	VAL
1	L	936	ILE
1	L	937	GLU
2	N	37	GLU
2	N	43	ARG
2	N	45	SER
2	N	54	THR
2	N	55	ARG
2	N	60	ASP
2	N	71	TYR
2	N	77	ASN
2	N	83	VAL
2	N	85	ASN
2	N	95	THR
2	N	98	ILE
2	N	109	ASP
2	N	131	LYS
2	N	136	VAL
2	N	146	GLU
2	N	175	ASP
2	N	186	LEU
2	N	223	VAL
2	N	252	LEU
2	N	282	VAL
2	N	289	LYS
2	N	291	LYS
2	N	297	LYS
2	N	326	VAL
2	N	327	GLU
2	N	334	ASP
2	N	342	LEU
2	N	346	THR
2	N	368	GLN
2	N	388	SER

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Mol	Chain	Res	Type
2	N	393	MET
2	N	405	VAL
2	N	426	ASP
2	N	440	LEU
2	N	449	ASP
2	N	461	ILE
2	N	486	VAL
2	N	491	VAL
2	N	492	THR
2	N	503	TYR
2	N	508	ILE
2	N	514	LEU
2	N	519	PHE
3	O	4	ARG
3	O	7	VAL
3	O	14	VAL
4	M	15	GLN
4	M	34	MET
4	M	45	ARG
4	M	92	LEU
4	M	101	VAL
4	M	107	THR
4	M	110	GLN
4	M	113	LEU
4	M	119	ASP
4	M	159	TYR
4	M	197	VAL
4	M	201	GLN
4	M	203	PHE
4	M	381	ASN
5	P	4	THR
5	P	9	GLU
5	P	13	PHE
5	P	14	SER
5	P	16	TYR
5	P	17	LEU
5	P	22	PRO
5	P	36	VAL
5	P	50	THR
5	P	54	VAL
5	P	56	ASN
5	Q	9	GLU

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Mol	Chain	Res	Type
5	Q	14	SER
5	Q	15	PRO
5	Q	16	TYR
5	Q	24	TRP
5	Q	27	VAL
5	Q	35	THR
5	Q	54	VAL
5	Q	108	LEU
5	Q	120	GLN
5	Q	127	GLU
5	R	16	TYR
5	R	19	THR
5	R	36	VAL
5	R	49	MET
5	R	53	THR
5	R	60	ASP
5	R	62	THR
5	R	104	LEU
5	R	108	LEU
5	R	124	GLU
5	R	125	LEU
5	R	134	LYS
5	S	17	LEU
5	S	18	THR
5	S	20	ARG
5	S	35	THR
5	S	41	VAL
5	S	53	THR
5	S	54	VAL
5	S	75	THR
5	S	81	TYR
6	U	2	SER
6	U	3	LYS
6	U	19	LEU
6	U	24	SER
6	U	28	SER
6	U	34	LEU
6	U	43	ARG
6	U	51	ARG
6	U	163	THR
6	U	211	GLU
6	V	1	MET

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Mol	Chain	Res	Type
6	V	3	LYS
6	V	28	SER
6	V	51	ARG
6	V	77	THR
6	V	89	VAL
6	V	144	ILE
6	V	163	THR
6	V	193	VAL
6	V	196	VAL
6	V	221	GLU
7	1	29	GLN
7	1	30	LEU
7	1	31	ASN
7	2	6	PHE
7	2	9	LEU
7	2	13	HIS
7	2	15	THR
7	2	19	MET
7	2	22	TRP
7	2	25	ILE
7	2	27	THR
7	2	30	LEU
7	2	31	ASN
7	4	4	ILE
7	4	24	GLU
7	5	27	THR
7	6	9	LEU
7	6	29	GLN
7	7	9	LEU
7	7	15	THR
7	7	27	THR
7	8	27	THR
7	8	31	ASN
7	9	4	ILE
7	9	22	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (145) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	207	ASN
1	A	531	ASN
1	A	571	ASN

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Mol	Chain	Res	Type
1	A	715	ASN
1	A	716	HIS
1	A	741	ASN
1	A	773	HIS
1	A	949	ASN
1	B	9	GLN
1	B	122	ASN
1	B	134	GLN
1	B	203	ASN
1	B	239	GLN
1	B	314	GLN
1	B	315	GLN
1	B	329	ASN
1	B	385	ASN
1	B	449	GLN
1	B	450	ASN
1	B	519	ASN
1	B	651	ASN
1	B	715	ASN
1	B	734	ASN
1	C	43	ASN
1	C	148	GLN
1	C	234	ASN
1	C	337	ASN
1	C	348	GLN
1	C	476	ASN
1	C	491	ASN
1	C	651	ASN
1	C	773	HIS
1	C	822	GLN
1	C	825	ASN
1	C	949	ASN
1	D	14	HIS
1	D	134	GLN
1	D	329	ASN
1	D	641	GLN
1	D	755	ASN
1	D	769	GLN
1	D	782	HIS
1	D	804	GLN
1	D	825	ASN
1	D	949	ASN

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Mol	Chain	Res	Type
1	E	311	ASN
1	E	314	GLN
1	E	319	ASN
1	E	322	ASN
1	E	337	ASN
1	E	351	GLN
1	E	476	ASN
1	E	561	GLN
1	E	599	ASN
1	E	715	ASN
1	E	769	GLN
1	E	929	HIS
1	F	43	ASN
1	F	91	ASN
1	F	203	ASN
1	F	322	ASN
1	F	451	GLN
1	F	499	ASN
1	F	536	ASN
1	F	584	ASN
1	F	599	ASN
1	F	636	ASN
1	F	644	ASN
1	F	662	ASN
1	F	671	ASN
1	F	715	ASN
1	F	760	ASN
1	G	14	HIS
1	G	43	ASN
1	G	122	ASN
1	G	287	ASN
1	G	329	ASN
1	G	456	ASN
1	G	651	ASN
1	G	734	ASN
1	G	810	ASN
1	G	822	GLN
1	H	122	ASN
1	H	134	GLN
1	H	198	GLN
1	H	409	ASN
1	H	432	ASN

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Mol	Chain	Res	Type
1	H	456	ASN
1	H	590	ASN
1	H	769	GLN
1	I	47	ASN
1	I	205	GLN
1	I	519	ASN
1	I	537	HIS
1	I	584	ASN
1	I	614	ASN
1	I	625	ASN
1	I	641	GLN
1	I	651	ASN
1	I	838	GLN
1	I	949	ASN
1	J	337	ASN
1	J	497	ASN
1	J	505	ASN
1	J	519	ASN
1	J	662	ASN
1	J	804	GLN
1	J	822	GLN
1	J	840	GLN
1	J	932	HIS
1	K	62	GLN
1	K	122	ASN
1	K	424	GLN
1	K	505	ASN
1	L	134	GLN
1	L	141	GLN
1	L	169	ASN
1	L	182	ASN
1	L	198	GLN
1	L	296	HIS
1	L	329	ASN
1	L	368	GLN
1	L	734	ASN
1	L	840	GLN
2	N	70	ASN
2	N	77	ASN
2	N	115	HIS
2	N	140	HIS
2	N	341	ASN

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Mol	Chain	Res	Type
2	N	344	GLN
2	N	394	GLN
4	M	17	GLN
4	M	66	ASN
4	M	110	GLN
4	M	357	ASN
5	S	56	ASN
6	U	165	ASN
6	U	187	GLN
6	V	166	GLN
6	V	215	ASN
7	1	31	ASN
7	2	29	GLN
7	2	31	ASN
7	8	5	ASN
7	8	31	ASN

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 ⓘ

There are no chain breaks in this entry.

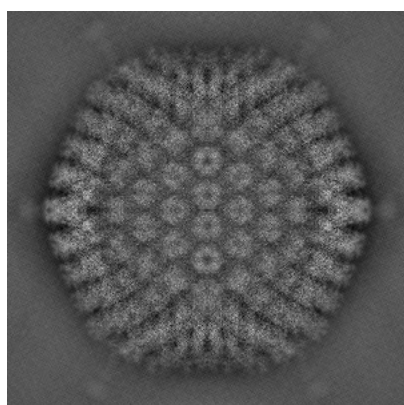
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25786. These allow visual inspection of the internal detail of the map and identification of artifacts.

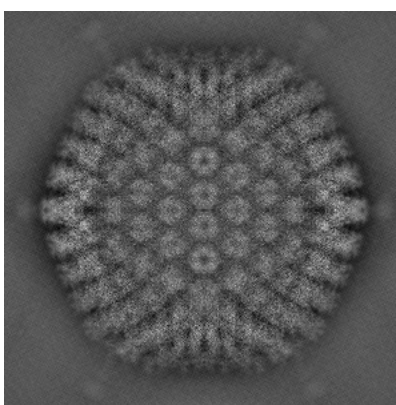
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

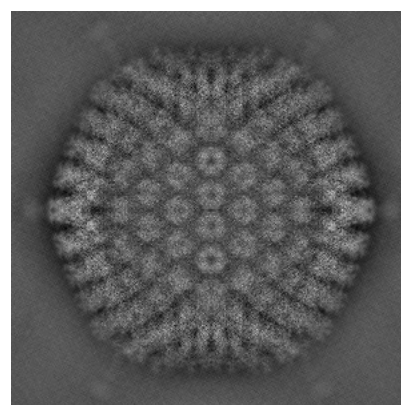
6.1.1 Primary map



X



Y

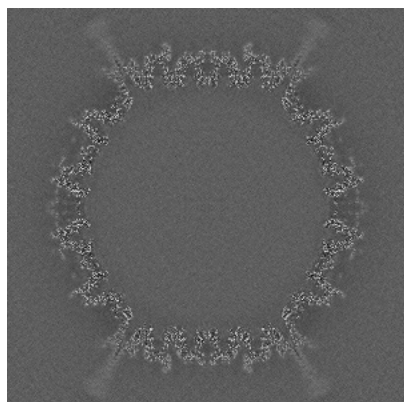


Z

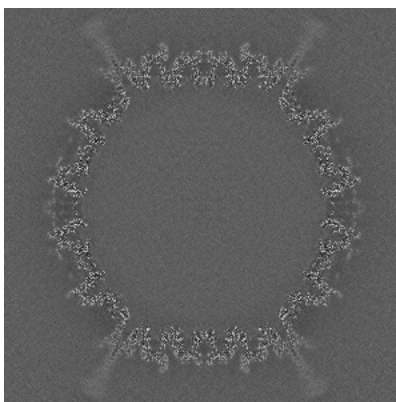
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

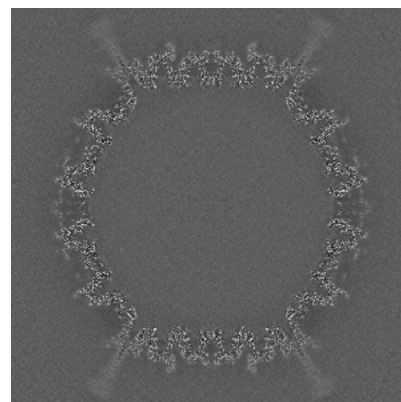
6.2.1 Primary map



X Index: 416



Y Index: 416

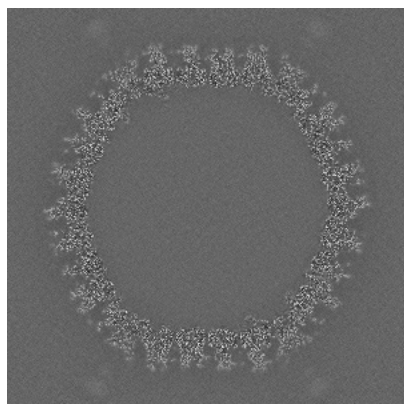


Z Index: 416

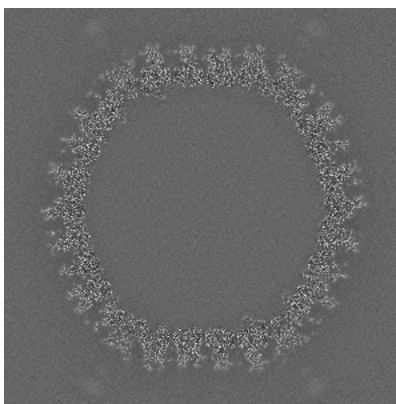
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

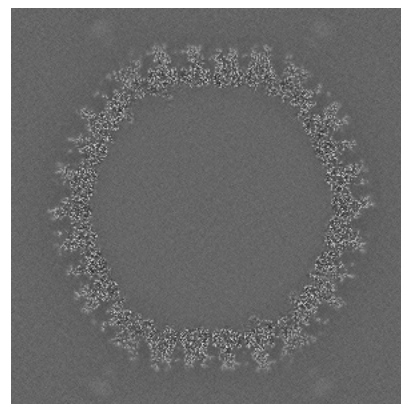
6.3.1 Primary map



X Index: 431



Y Index: 431

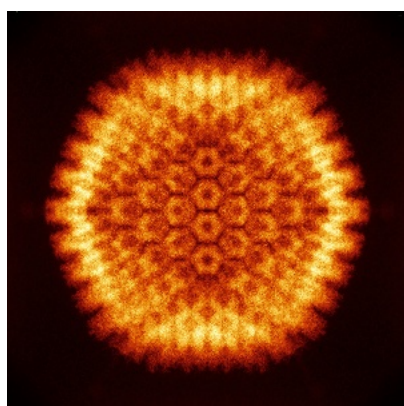


Z Index: 431

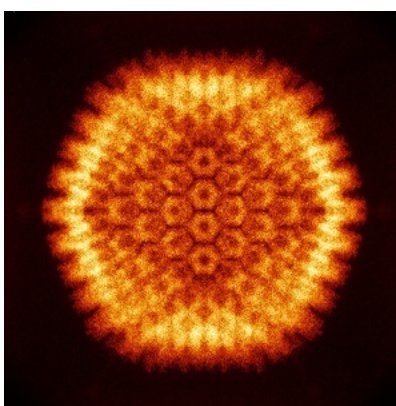
The images above show the largest variance slices of the map in three orthogonal directions.

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

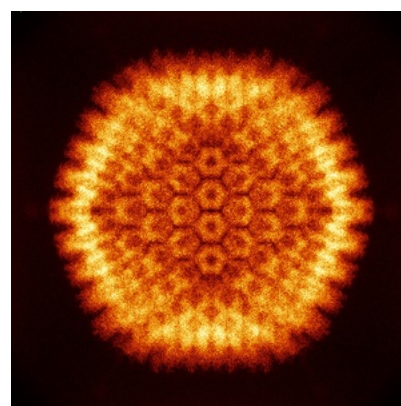
6.4.1 Primary map



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

This section was not generated.

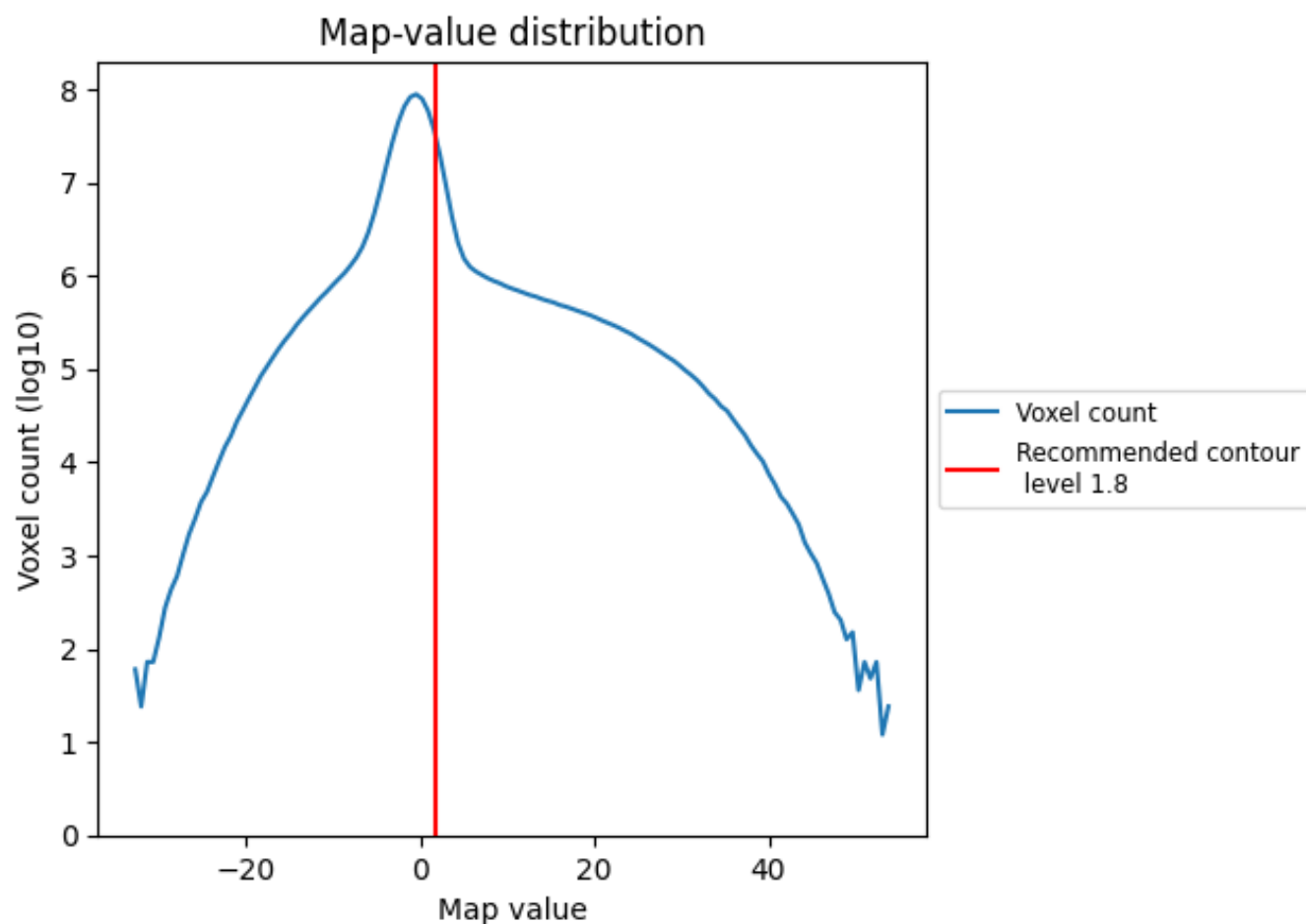
6.6 Mask visualisation

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

7 Map analysis [i](#)

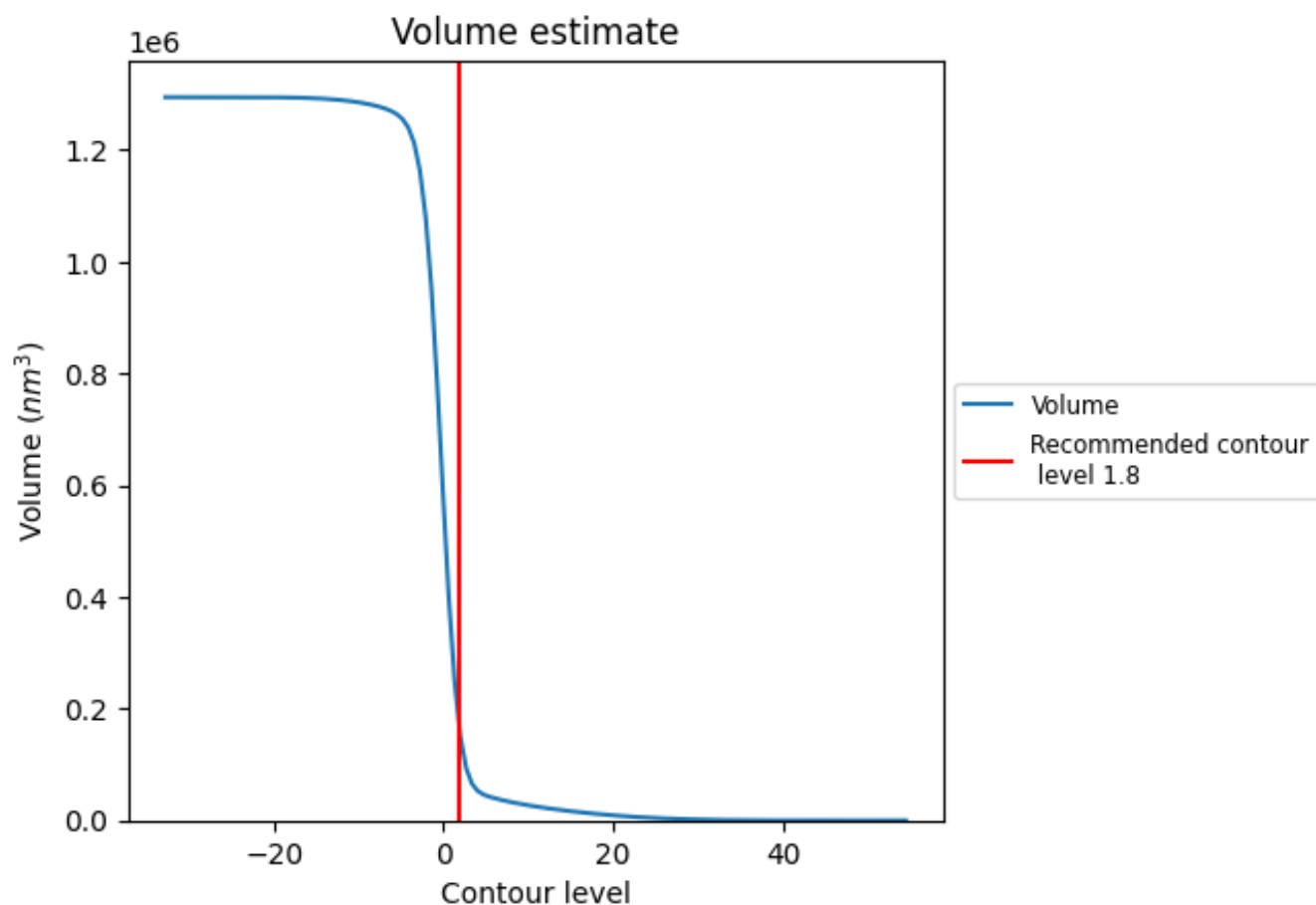
This section contains the results of statistical analysis of the map.

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.

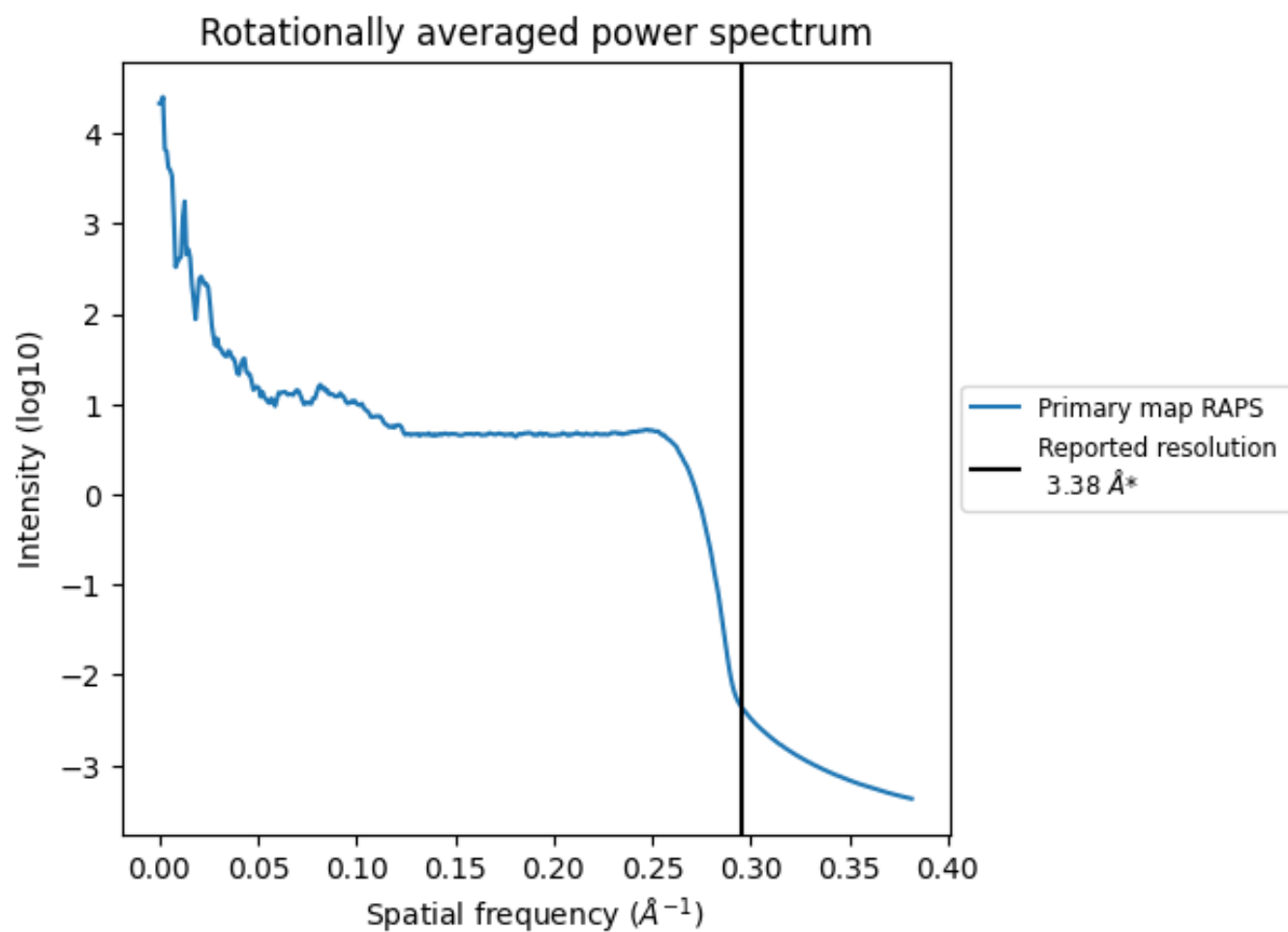
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 176024 nm³; this corresponds to an approximate mass of 159007 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 ⓘ

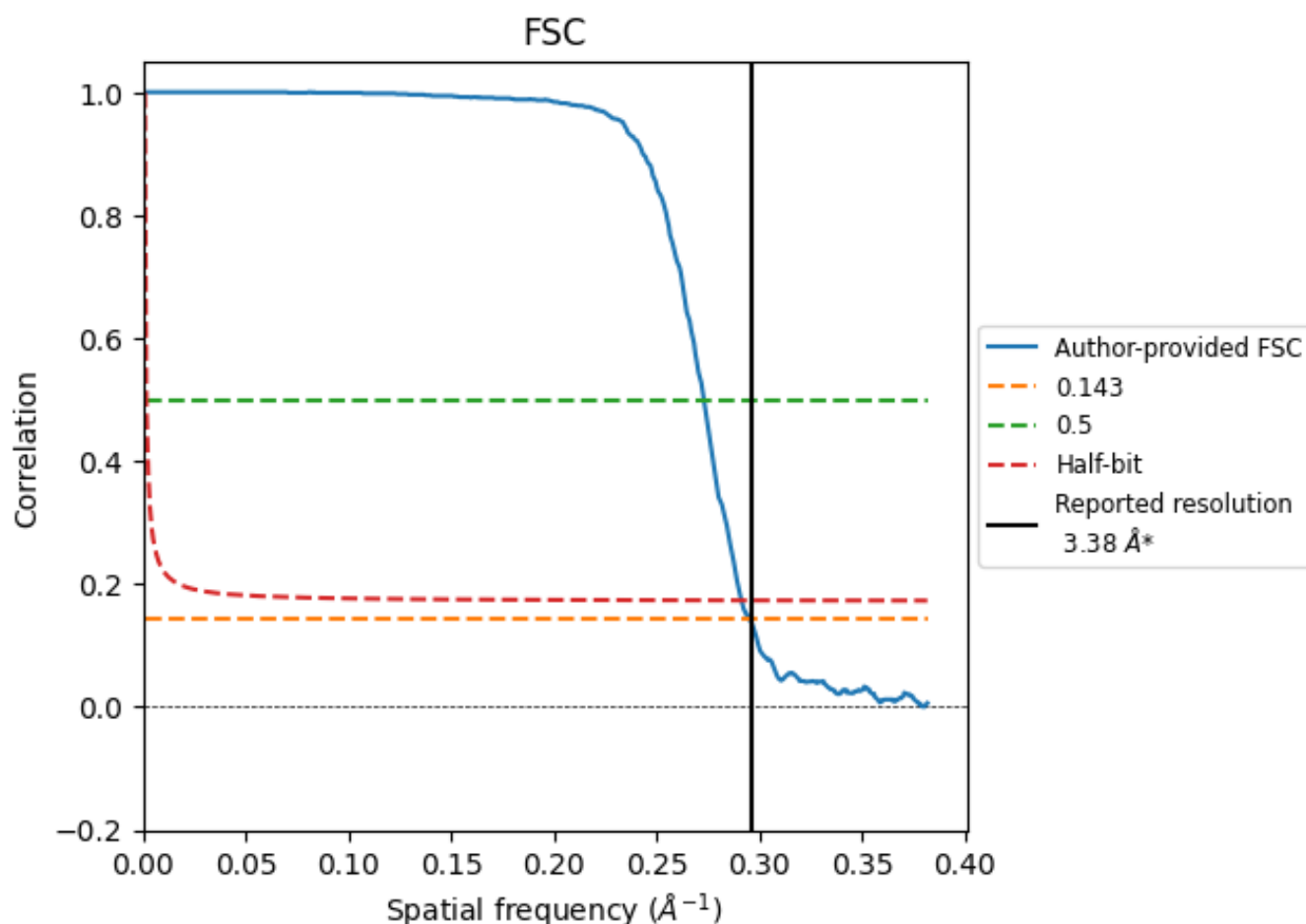


*Reported resolution corresponds to spatial frequency of 0.296 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.296 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.38	-	-
Author-provided FSC curve	3.39	3.66	3.43
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

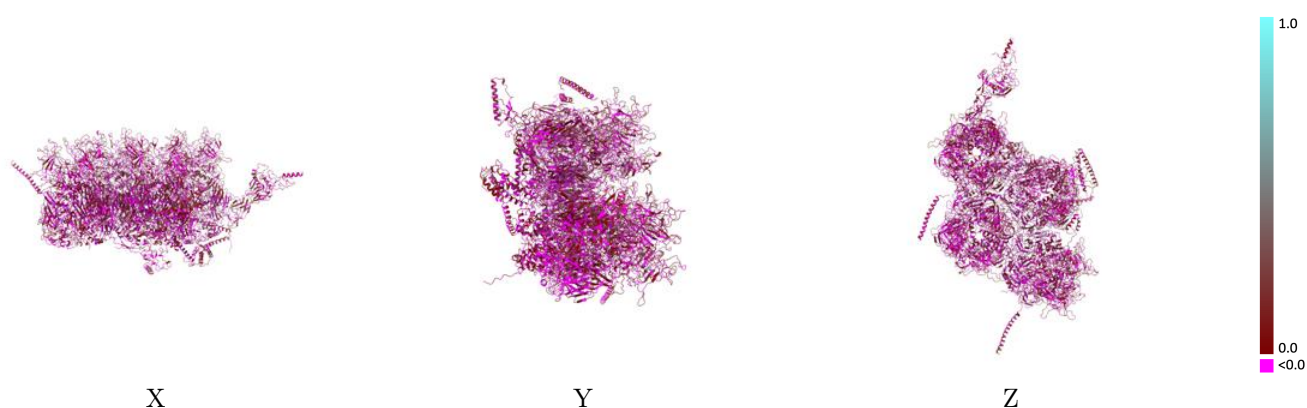
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25786 and PDB model 7TAU. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

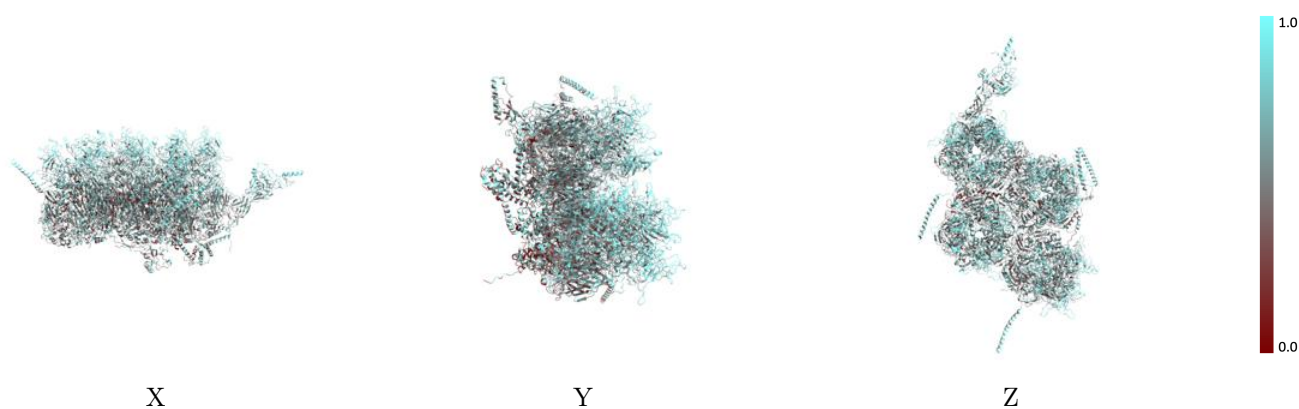
This section was not generated.

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



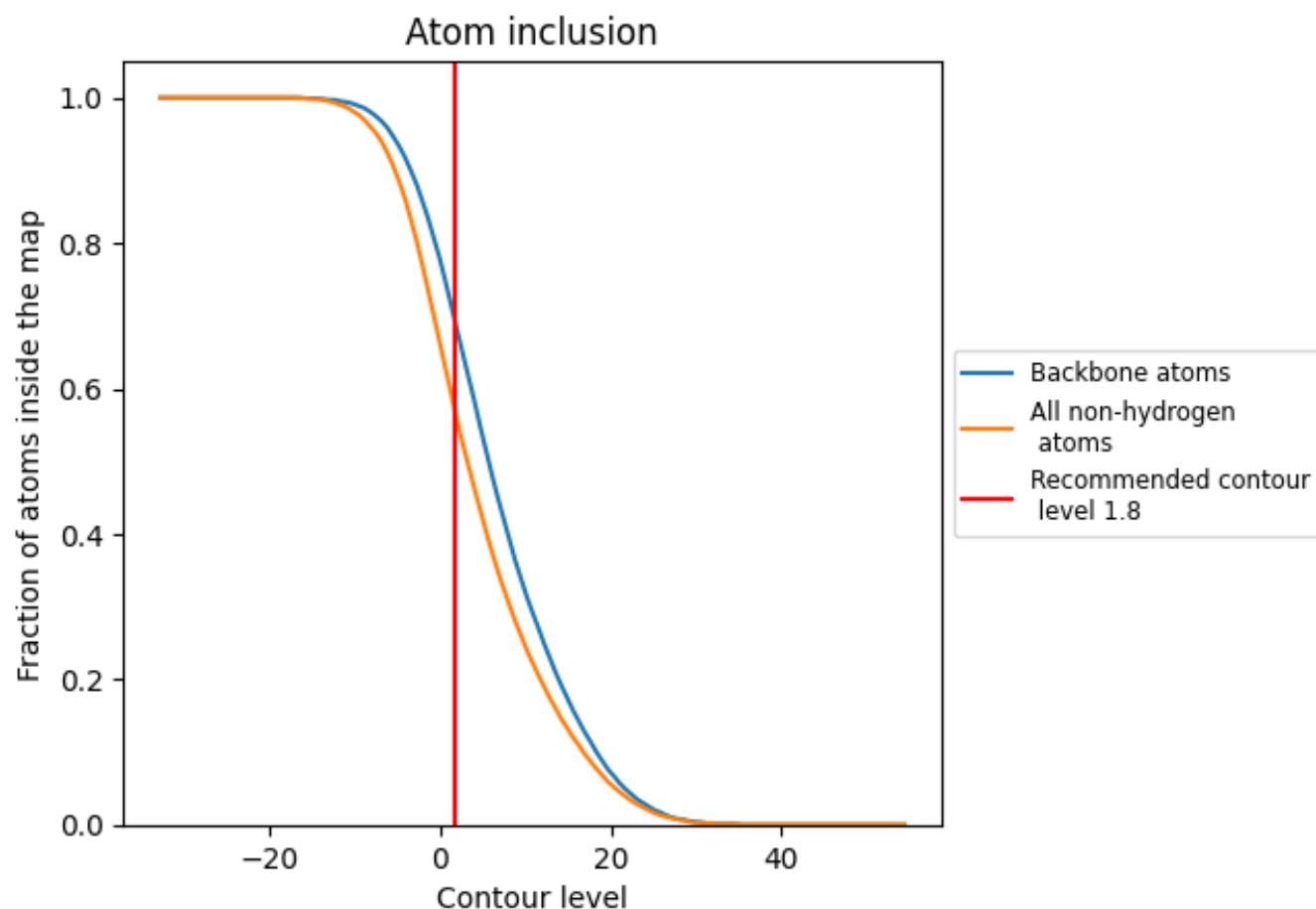
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 57% 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 (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5660	 0.0400
1	 0.4160	 0.0680
2	 0.5400	 0.0510
3	 0.3060	 0.0190
4	 0.4600	 0.0280
5	 0.4440	 0.1130
6	 0.2480	 -0.0080
7	 0.3110	 -0.0030
8	 0.4550	 0.0800
9	 0.2800	 0.0020
A	 0.5800	 0.0330
B	 0.6070	 0.0440
C	 0.6050	 0.0580
D	 0.5590	 0.0200
E	 0.5670	 0.0260
F	 0.5720	 0.0430
G	 0.5540	 0.0240
H	 0.5610	 0.0350
I	 0.5720	 0.0460
J	 0.5640	 0.0340
K	 0.5830	 0.0410
L	 0.5980	 0.0630
M	 0.4190	 0.0430
N	 0.6180	 0.0650
O	 0.6070	 0.0450
P	 0.4950	 0.0330
Q	 0.4980	 0.0410
R	 0.5910	 0.1010
S	 0.5320	 0.0800
U	 0.4880	 0.0120
V	 0.4940	 0.0190
X	 0.3600	 0.0470

