Full wwPDB X-ray Structure Validation Report ⓘ

Jun 11, 2024 – 10:40 PM EDT

PDB ID	:	1W8X
Title	:	Structural analysis of PRD1
Authors	:	Abrescia, N.G.A.; Cockburn, J.J.B.; Grimes, J.M.; Sutton, G.C.; Diprose, J.M.; Butcher, S.J.; Fuller, S.D.; San Martin, C.; Burnett, R.M.; Stuart, D.I.; Bamford, D.H.; Bamford, J.K.H.
Deposited on	:	2004-10-01
Resolution	:	4.20 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
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:

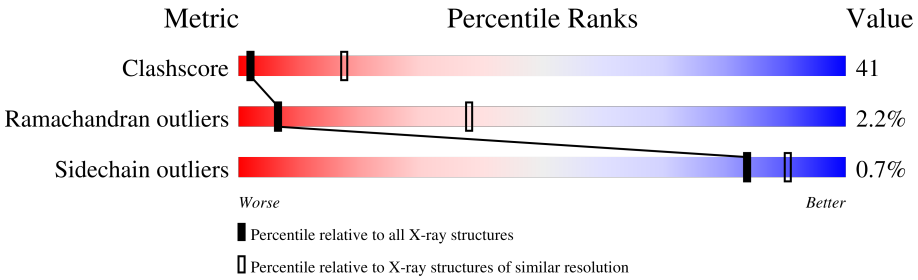
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1044 (4.60-3.80)
Ramachandran outliers	138981	1000 (4.60-3.80)
Sidechain outliers	138945	1007 (4.62-3.78)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	395	78% 13%
1	B	395	72% 21%
1	C	395	79% 15%
1	D	395	73% 20%
1	E	395	77% 16%
1	F	395	79% 17%
1	G	395	75% 16% 5%
1	H	395	76% 19%

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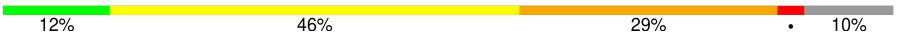
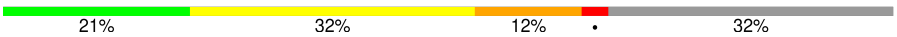
Mol	Chain	Length	Quality of chain
1	I	395	
1	J	395	
1	K	395	
1	L	395	
2	M	83	
3	N	126	
4	P	117	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 38116 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called MAJOR CAPSID PROTEIN (PROTEIN P3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	380	Total	C	N	O	S	0	0	0
			2956	1873	503	573	7			
1	B	392	Total	C	N	O	S	0	0	0
			3045	1929	517	592	7			
1	C	385	Total	C	N	O	S	0	0	0
			2999	1901	510	581	7			
1	D	392	Total	C	N	O	S	0	0	0
			3045	1929	517	592	7			
1	E	378	Total	C	N	O	S	0	0	0
			2944	1868	500	569	7			
1	F	388	Total	C	N	O	S	0	0	0
			3009	1908	510	584	7			
1	G	375	Total	C	N	O	S	0	0	0
			2926	1857	496	566	7			
1	H	392	Total	C	N	O	S	0	0	0
			3045	1929	517	592	7			
1	I	392	Total	C	N	O	S	0	0	0
			3045	1929	517	592	7			
1	J	390	Total	C	N	O	S	0	0	0
			3027	1919	514	587	7			
1	K	384	Total	C	N	O	S	0	0	0
			2992	1897	509	579	7			
1	L	379	Total	C	N	O	S	0	0	0
			2953	1873	502	571	7			

- Molecule 2 is a protein called PROTEIN P30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	83	Total	C	N	O	S	0	0	0
			638	408	113	114	3			

- Molecule 3 is a protein called PROTEIN P31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	114	Total	C	N	O	S	0	0	0
			872	552	147	169	4			

- Molecule 4 is a protein called PROTEIN P16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	P	80	Total	C	N	O	S	0	0	1
			620	401	103	114	2			

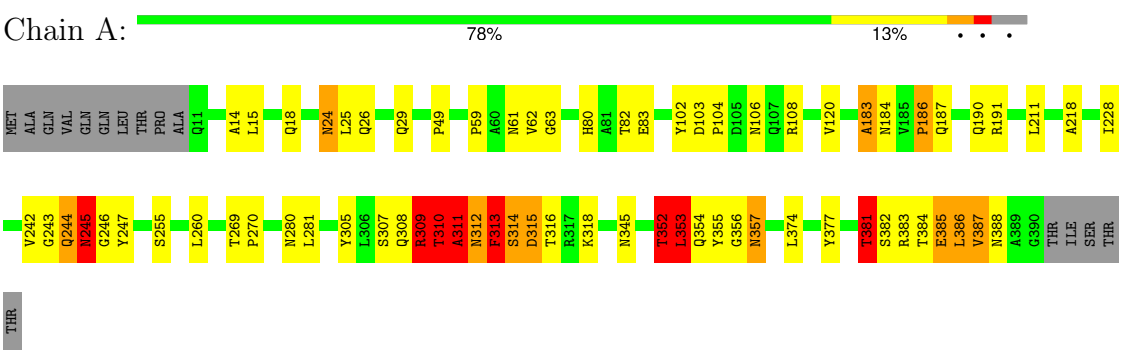
3 Residue-property plots

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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

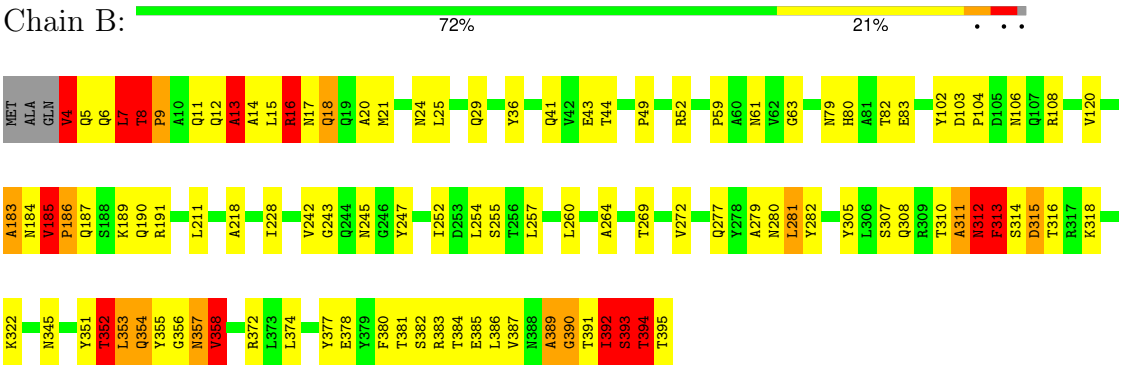
- Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain A:



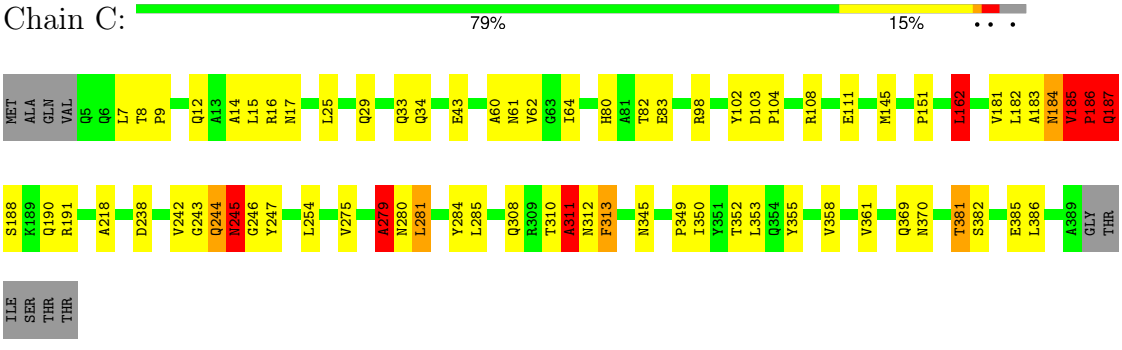
- Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain B:



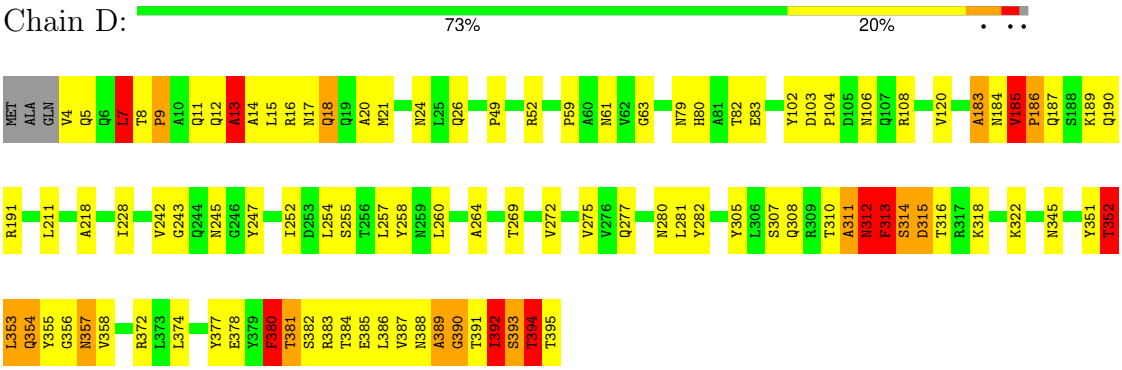
- Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain C:



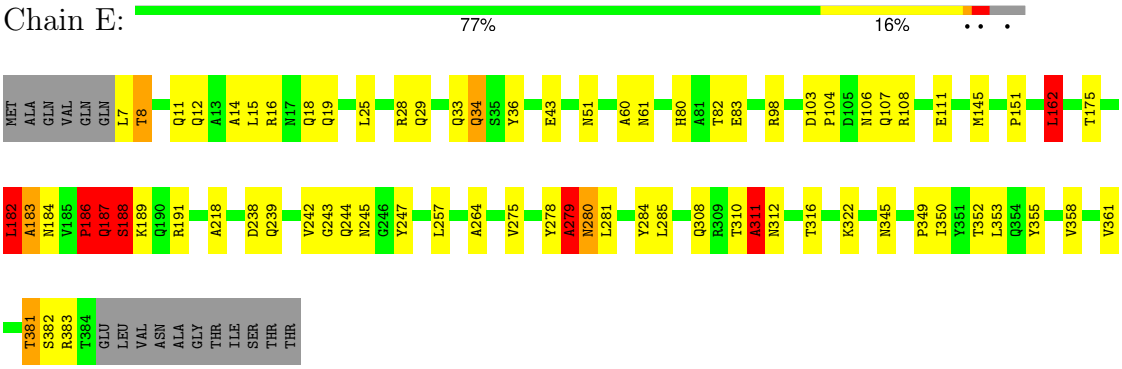
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain D:



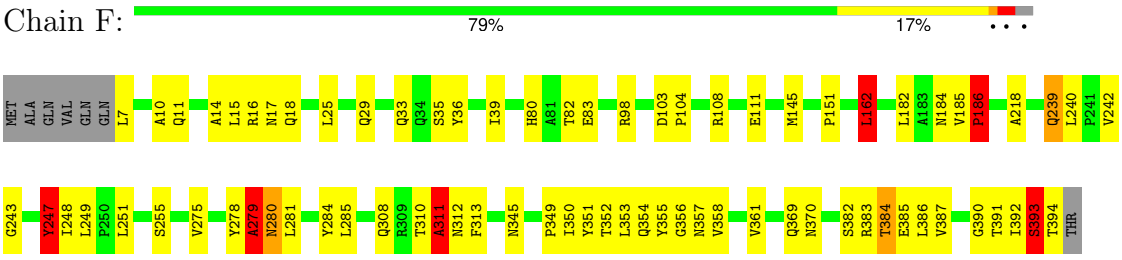
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain E:



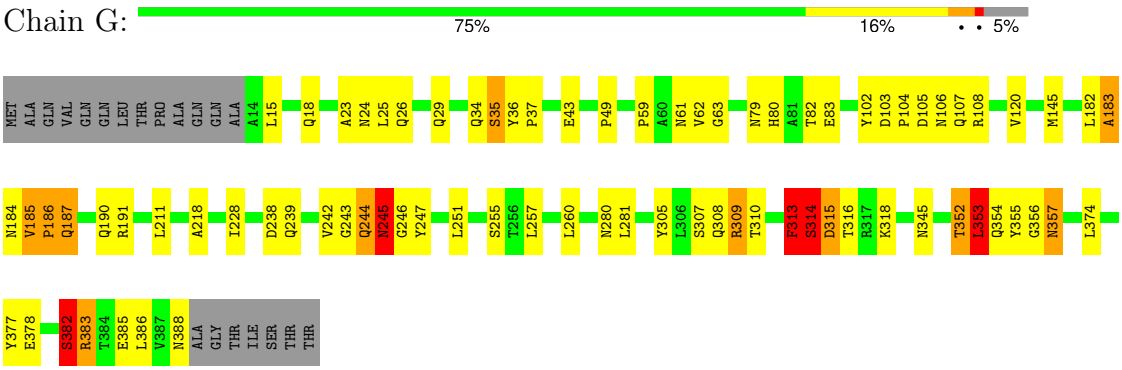
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain F:



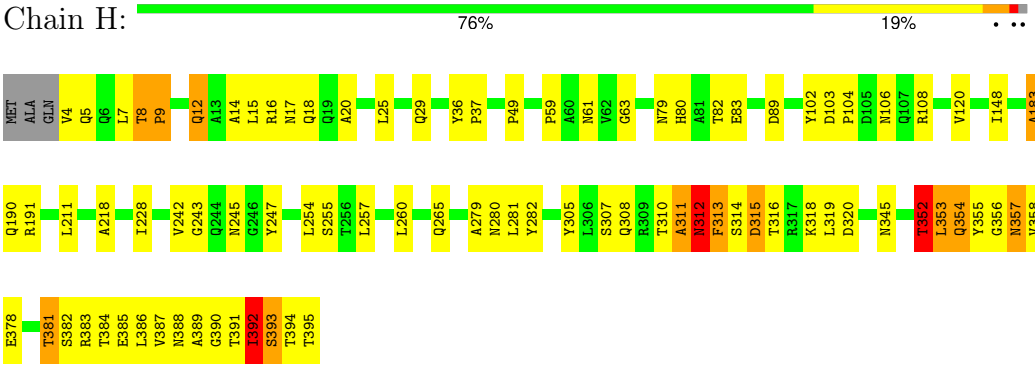
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain G:



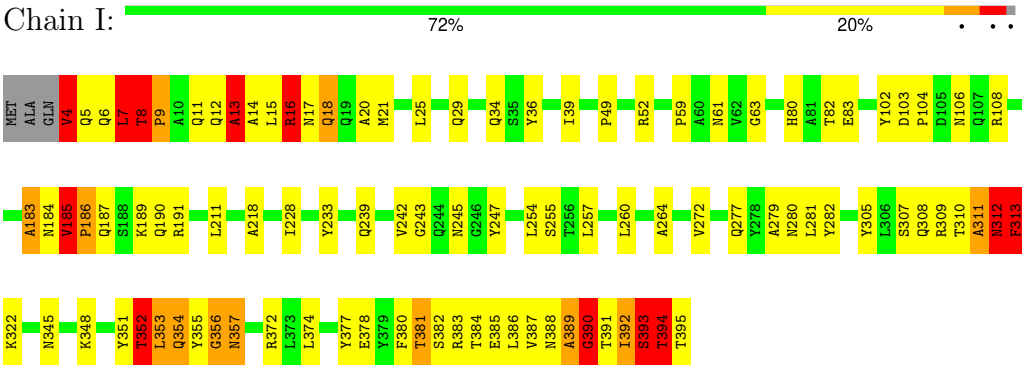
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain H:



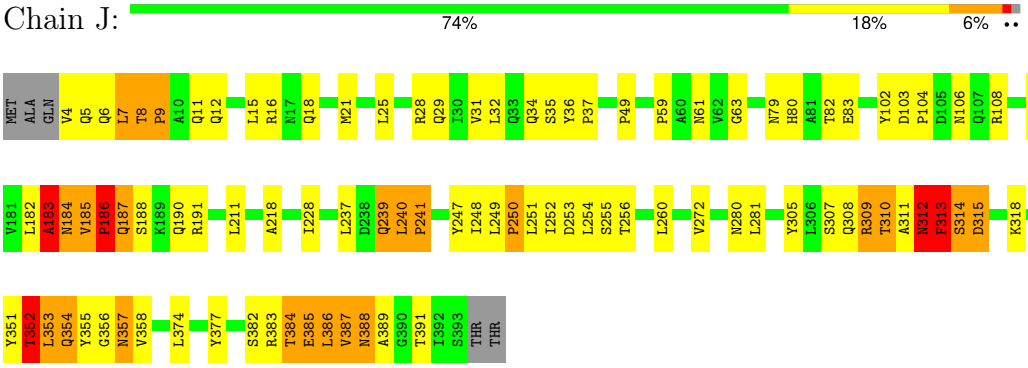
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain I:



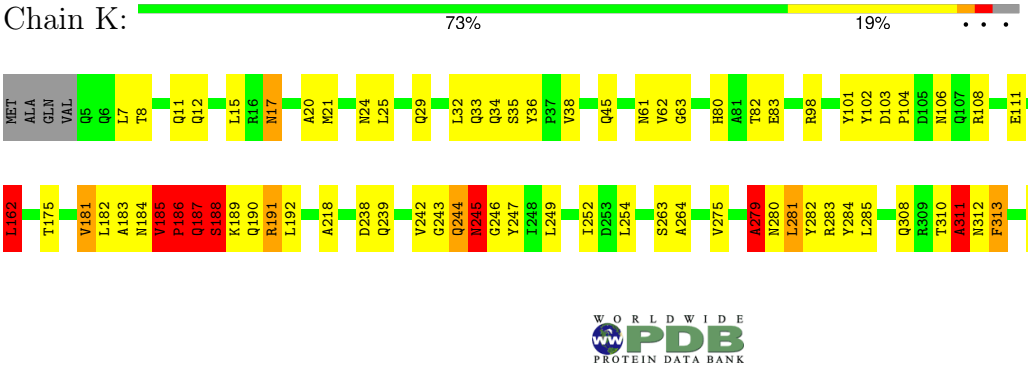
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

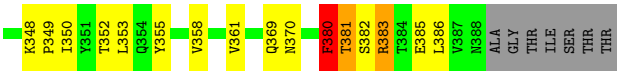
Chain J:



• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

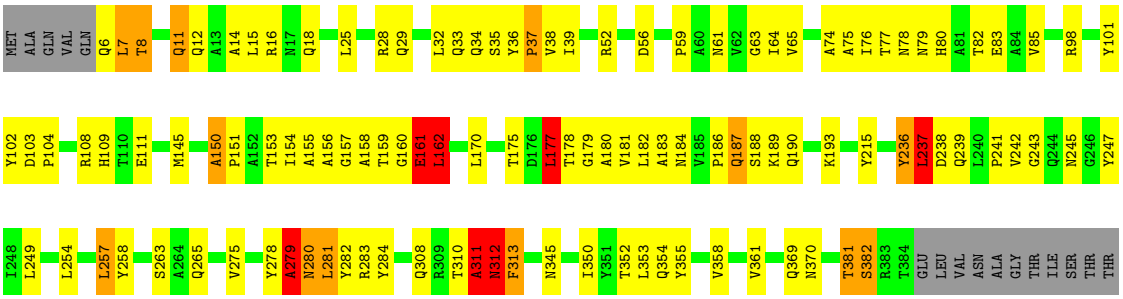
Chain K:





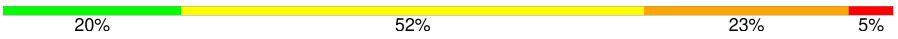
• Molecule 1: MAJOR CAPSID PROTEIN (PROTEIN P3)

Chain L:



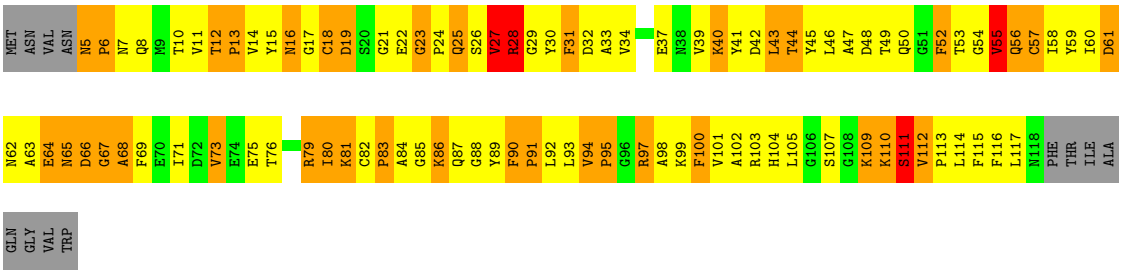
• Molecule 2: PROTEIN P30

Chain M:



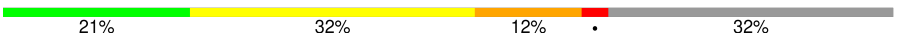
• Molecule 3: PROTEIN P31

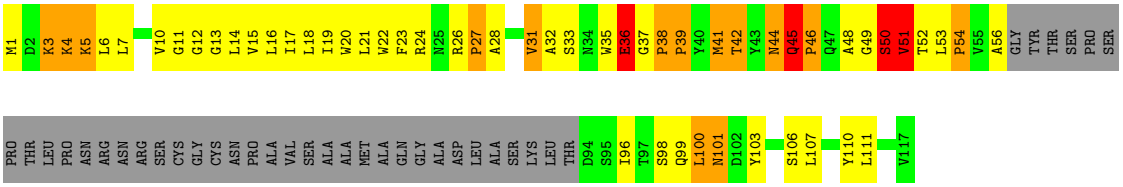
Chain N:



• Molecule 4: PROTEIN P16

Chain P:





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	903.00Å 920.60Å 926.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 4.20	Depositor
% Data completeness (in resolution range)	(Not available) (100.00-4.20)	Depositor
R_{merge}	0.33	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	38116	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

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	1.32	17/3021 (0.6%)	1.47	28/4128 (0.7%)
1	B	1.71	32/3110 (1.0%)	1.89	50/4250 (1.2%)
1	C	1.08	12/3064 (0.4%)	1.15	26/4186 (0.6%)
1	D	1.38	26/3111 (0.8%)	1.63	37/4253 (0.9%)
1	E	0.77	9/3011 (0.3%)	1.18	20/4117 (0.5%)
1	F	1.34	15/3074 (0.5%)	1.56	22/4201 (0.5%)
1	G	1.16	15/2991 (0.5%)	1.33	23/4087 (0.6%)
1	H	1.32	21/3112 (0.7%)	1.23	25/4256 (0.6%)
1	I	1.55	30/3110 (1.0%)	1.87	48/4250 (1.1%)
1	J	1.25	32/3092 (1.0%)	1.13	20/4225 (0.5%)
1	K	1.19	15/3058 (0.5%)	1.49	37/4179 (0.9%)
1	L	1.25	10/3018 (0.3%)	1.17	28/4123 (0.7%)
2	M	2.88	42/657 (6.4%)	2.16	27/898 (3.0%)
3	N	3.68	54/892 (6.1%)	2.82	46/1209 (3.8%)
4	P	2.89	37/637 (5.8%)	1.83	19/871 (2.2%)
All	All	1.48	367/38958 (0.9%)	1.52	456/53233 (0.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	13
1	C	0	7
1	D	0	10
1	E	0	5
1	F	0	6
1	G	0	5
1	H	0	5
1	I	0	10
1	J	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	K	0	10
1	L	0	5
3	N	0	3
All	All	0	91

All (367) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	111	SER	C-O	-43.65	0.40	1.23
1	F	391	THR	C-O	-43.51	0.40	1.23
3	N	27	VAL	C-O	-41.51	0.44	1.23
3	N	26	SER	C-O	-36.70	0.53	1.23
1	A	313	PHE	C-N	-35.91	0.51	1.34
1	L	312	ASN	C-O	-34.83	0.57	1.23
4	P	32	ALA	C-O	-33.88	0.58	1.23
1	B	358	VAL	CA-CB	-33.23	0.84	1.54
1	L	150	ALA	C-N	31.57	1.94	1.34
1	K	186	PRO	C-N	-30.73	0.63	1.34
2	M	64	GLY	C-O	-29.82	0.76	1.23
1	F	186	PRO	C-N	-28.84	0.67	1.34
4	P	31	VAL	C-O	-28.50	0.69	1.23
1	B	4	VAL	CA-CB	28.35	2.14	1.54
1	I	4	VAL	CA-CB	28.34	2.14	1.54
1	G	245	ASN	C-O	-28.21	0.69	1.23
1	A	245	ASN	C-O	-28.20	0.69	1.23
1	A	24	ASN	C-N	28.08	1.98	1.34
1	C	245	ASN	C-O	-27.64	0.70	1.23
1	K	245	ASN	C-O	-27.58	0.70	1.23
1	B	185	VAL	C-O	-27.44	0.71	1.23
1	D	185	VAL	C-O	-27.44	0.71	1.23
1	H	185	VAL	C-O	-27.43	0.71	1.23
1	I	185	VAL	C-O	-27.42	0.71	1.23
1	G	313	PHE	C-N	-27.14	0.71	1.34
1	L	381	THR	C-N	27.07	1.96	1.34
1	C	186	PRO	C-N	-27.03	0.71	1.34
1	D	313	PHE	C-O	-25.42	0.75	1.23
1	B	313	PHE	C-O	-25.41	0.75	1.23
1	H	313	PHE	C-O	-25.36	0.75	1.23
1	F	239	GLN	C-N	-24.86	0.76	1.34
1	I	313	PHE	C-O	-23.90	0.78	1.23
3	N	57	CYS	C-O	-23.56	0.78	1.23
1	J	313	PHE	C-O	-23.52	0.78	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	381	THR	C-N	21.65	1.83	1.34
3	N	54	GLY	C-O	-21.02	0.90	1.23
1	B	7	LEU	C-N	-20.91	0.85	1.34
1	D	7	LEU	C-N	-20.91	0.85	1.34
1	I	7	LEU	C-N	-20.88	0.86	1.34
1	J	184	ASN	C-O	-20.07	0.85	1.23
1	K	243	GLY	C-N	-19.86	0.88	1.34
1	C	243	GLY	C-N	-19.78	0.88	1.34
1	K	191	ARG	C-N	19.47	1.78	1.34
1	I	311	ALA	C-N	-18.98	0.90	1.34
1	B	313	PHE	C-N	-18.76	0.90	1.34
1	D	313	PHE	C-N	-18.73	0.91	1.34
1	H	313	PHE	C-N	-18.72	0.91	1.34
1	D	311	ALA	C-N	-18.67	0.91	1.34
1	H	311	ALA	C-N	-18.65	0.91	1.34
1	B	311	ALA	C-N	-18.63	0.91	1.34
1	G	35	SER	C-N	18.61	1.76	1.34
1	I	8	THR	C-N	18.54	1.69	1.34
1	B	8	THR	C-N	18.50	1.69	1.34
1	A	243	GLY	C-N	-18.44	0.91	1.34
1	G	243	GLY	C-N	-18.41	0.91	1.34
1	K	380	PHE	C-N	-18.24	0.92	1.34
1	B	389	ALA	C-O	-17.85	0.89	1.23
1	D	389	ALA	C-O	-17.84	0.89	1.23
1	H	389	ALA	C-O	-17.82	0.89	1.23
3	N	17	GLY	C-O	-17.80	0.95	1.23
1	I	389	ALA	C-O	-17.79	0.89	1.23
1	A	381	THR	C-N	-17.63	0.93	1.34
1	L	312	ASN	C-N	-17.29	0.94	1.34
1	J	256	THR	C-N	-16.99	0.94	1.34
1	E	381	THR	C-N	16.70	1.72	1.34
1	B	16	ARG	C-N	-16.69	0.95	1.34
1	I	16	ARG	C-N	-16.68	0.95	1.34
1	B	358	VAL	N-CA	16.31	1.78	1.46
1	I	392	ILE	C-N	16.28	1.71	1.34
1	L	257	LEU	C-N	16.19	1.71	1.34
2	M	11	GLY	C-O	-15.87	0.98	1.23
1	G	382	SER	C-N	15.66	1.70	1.34
1	B	185	VAL	C-N	-15.60	1.04	1.34
1	D	185	VAL	C-N	-15.60	1.04	1.34
1	E	311	ALA	C-N	-15.59	0.98	1.34
1	F	311	ALA	C-N	-15.59	0.98	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	185	VAL	C-N	-15.57	1.04	1.34
1	I	185	VAL	C-N	-15.56	1.04	1.34
1	I	313	PHE	C-N	-15.39	0.98	1.34
3	N	16	ASN	C-N	15.32	1.60	1.33
1	J	384	THR	C-N	15.21	1.69	1.34
1	B	358	VAL	CA-C	15.20	1.92	1.52
1	B	352	THR	C-N	-15.07	0.99	1.34
1	J	352	THR	C-N	-15.05	0.99	1.34
1	H	352	THR	C-N	-15.03	0.99	1.34
1	D	352	THR	C-N	-15.01	0.99	1.34
1	I	352	THR	C-N	-14.97	0.99	1.34
3	N	111	SER	C-N	-14.81	0.99	1.34
4	P	5	LYS	C-O	-14.67	0.95	1.23
1	B	394	THR	C-N	-14.59	1.00	1.34
1	D	394	THR	C-N	-14.57	1.00	1.34
1	I	394	THR	C-N	-14.55	1.00	1.34
3	N	55	VAL	C-N	14.15	1.66	1.34
2	M	46	PRO	N-CA	-14.06	1.23	1.47
3	N	57	CYS	C-N	-13.42	1.03	1.34
1	F	247	TYR	C-N	-13.39	1.03	1.34
1	G	183	ALA	C-N	-13.38	1.03	1.34
1	A	183	ALA	C-N	-13.35	1.03	1.34
3	N	65	ASN	C-O	-13.01	0.98	1.23
1	C	382	SER	C-O	-12.74	0.99	1.23
2	M	46	PRO	C-O	-12.70	0.97	1.23
3	N	56	GLN	N-CA	-12.68	1.21	1.46
1	F	390	GLY	CA-C	-12.60	1.31	1.51
2	M	66	GLY	CA-C	-12.55	1.31	1.51
3	N	110	LYS	C-O	-12.43	0.99	1.23
1	B	4	VAL	N-CA	12.36	1.71	1.46
1	I	4	VAL	N-CA	12.36	1.71	1.46
4	P	45	GLN	C-N	12.31	1.57	1.34
1	I	245	ASN	C-N	-12.26	1.10	1.33
1	J	9	PRO	C-O	-12.18	0.98	1.23
1	D	245	ASN	C-N	-12.15	1.11	1.33
1	H	245	ASN	C-N	-12.13	1.11	1.33
1	B	245	ASN	C-N	-12.13	1.11	1.33
1	J	187	GLN	C-N	12.03	1.61	1.34
3	N	68	ALA	N-CA	-11.89	1.22	1.46
1	F	393	SER	C-O	-11.88	1.00	1.23
1	C	244	GLN	C-O	-11.79	1.00	1.23
1	K	244	GLN	C-O	-11.72	1.01	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	18	CYS	C-O	-11.70	1.01	1.23
2	M	6	GLN	C-O	-11.68	1.01	1.23
1	J	313	PHE	C-N	-11.66	1.07	1.34
1	G	244	GLN	C-O	-11.65	1.01	1.23
4	P	49	GLY	C-O	-11.65	1.05	1.23
1	B	392	ILE	C-N	11.64	1.60	1.34
1	A	244	GLN	C-O	-11.61	1.01	1.23
3	N	44	THR	N-CA	-11.56	1.23	1.46
1	B	357	ASN	C-N	-11.56	1.07	1.34
3	N	61	ASP	C-O	-11.44	1.01	1.23
1	J	250	PRO	C-N	-11.39	1.07	1.34
2	M	9	TYR	C-N	11.35	1.60	1.34
1	E	187	GLN	N-CA	-11.33	1.23	1.46
1	J	388	ASN	C-O	-11.31	1.01	1.23
2	M	12	PRO	C-O	-11.28	1.00	1.23
1	D	392	ILE	C-N	-11.26	1.08	1.34
1	D	18	GLN	C-O	-11.25	1.01	1.23
1	I	18	GLN	C-O	-11.23	1.02	1.23
1	H	18	GLN	C-O	-11.21	1.02	1.23
1	B	18	GLN	C-O	-11.21	1.02	1.23
3	N	31	PHE	C-O	-11.14	1.02	1.23
4	P	4	LYS	N-CA	-10.95	1.24	1.46
1	C	187	GLN	C-O	-10.90	1.02	1.23
3	N	17	GLY	C-N	-10.90	1.08	1.34
2	M	49	GLN	N-CA	-10.83	1.24	1.46
2	M	24	MET	C-N	10.79	1.54	1.34
1	A	356	GLY	C-N	-10.73	1.09	1.34
1	G	356	GLY	C-N	-10.73	1.09	1.34
2	M	15	ILE	C-O	-10.66	1.03	1.23
2	M	64	GLY	C-N	-10.53	1.09	1.34
4	P	41	MET	C-O	-10.52	1.03	1.23
1	E	279	ALA	C-N	-10.49	1.09	1.34
1	F	279	ALA	C-N	-10.49	1.09	1.34
3	N	19	ASP	C-O	-10.48	1.03	1.23
4	P	99	GLN	C-O	-10.47	1.03	1.23
1	I	389	ALA	C-N	-10.39	1.14	1.33
1	D	389	ALA	C-N	-10.38	1.14	1.33
1	H	389	ALA	C-N	-10.37	1.14	1.33
3	N	109	LYS	C-O	-10.36	1.03	1.23
1	B	389	ALA	C-N	-10.35	1.14	1.33
2	M	64	GLY	CA-C	-10.33	1.35	1.51
3	N	65	ASN	C-N	-10.28	1.10	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	391	THR	CA-C	-10.18	1.26	1.52
3	N	27	VAL	CA-CB	10.16	1.76	1.54
3	N	112	VAL	C-N	10.16	1.53	1.34
1	D	354	GLN	C-O	-10.14	1.04	1.23
1	H	354	GLN	C-O	-10.14	1.04	1.23
1	B	354	GLN	C-O	-10.13	1.04	1.23
1	I	354	GLN	C-O	-10.12	1.04	1.23
1	J	354	GLN	C-O	-10.12	1.04	1.23
1	H	392	ILE	C-N	10.11	1.57	1.34
2	M	24	MET	CA-C	-10.08	1.26	1.52
3	N	26	SER	CA-CB	10.05	1.68	1.52
4	P	36	GLU	CA-C	-9.98	1.27	1.52
2	M	46	PRO	C-N	-9.90	1.11	1.34
1	B	381	THR	C-N	9.70	1.56	1.34
1	I	381	THR	C-N	9.70	1.56	1.34
1	K	17	ASN	C-N	9.69	1.56	1.34
1	D	381	THR	C-N	9.68	1.56	1.34
3	N	17	GLY	N-CA	-9.67	1.31	1.46
1	L	382	SER	C-O	-9.55	1.05	1.23
3	N	22	GLU	C-O	-9.54	1.05	1.23
1	J	184	ASN	N-CA	-9.51	1.27	1.46
3	N	27	VAL	C-N	-9.44	1.12	1.34
3	N	76	THR	C-N	9.38	1.50	1.33
1	L	311	ALA	C-N	-9.31	1.12	1.34
1	A	314	SER	N-CA	-9.29	1.27	1.46
2	M	69	MET	C-O	-9.26	1.05	1.23
1	D	357	ASN	C-O	-9.23	1.05	1.23
1	I	357	ASN	C-O	-9.22	1.05	1.23
1	C	311	ALA	C-N	-9.21	1.12	1.34
4	P	31	VAL	C-N	-9.20	1.12	1.34
1	J	357	ASN	C-O	-9.20	1.05	1.23
1	K	311	ALA	C-N	-9.19	1.12	1.34
4	P	36	GLU	C-O	-9.18	1.05	1.23
1	H	357	ASN	C-O	-9.17	1.05	1.23
1	G	314	SER	C-N	9.16	1.55	1.34
3	N	65	ASN	N-CA	-9.14	1.28	1.46
4	P	54	PRO	C-O	-9.14	1.04	1.23
1	A	353	LEU	N-CA	-9.11	1.28	1.46
4	P	48	ALA	C-O	-9.10	1.06	1.23
1	G	353	LEU	N-CA	-9.08	1.28	1.46
4	P	32	ALA	N-CA	-9.06	1.28	1.46
1	L	161	GLU	C-N	-9.05	1.13	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	67	ILE	C-O	-9.03	1.06	1.23
1	J	356	GLY	C-N	-8.88	1.13	1.34
1	B	357	ASN	C-O	-8.88	1.06	1.23
1	H	356	GLY	C-N	-8.88	1.13	1.34
4	P	48	ALA	C-N	8.88	1.49	1.33
4	P	33	SER	C-O	-8.85	1.06	1.23
1	D	356	GLY	C-N	-8.83	1.13	1.34
1	I	356	GLY	C-N	-8.82	1.13	1.34
1	B	390	GLY	C-O	-8.81	1.09	1.23
1	I	390	GLY	C-O	-8.79	1.09	1.23
1	H	390	GLY	C-O	-8.79	1.09	1.23
1	D	390	GLY	C-O	-8.78	1.09	1.23
1	B	390	GLY	C-N	8.73	1.54	1.34
1	I	390	GLY	C-N	8.73	1.54	1.34
1	D	390	GLY	C-N	8.72	1.54	1.34
4	P	42	THR	C-O	-8.67	1.06	1.23
1	D	12	GLN	C-O	-8.63	1.06	1.23
1	J	186	PRO	CA-C	-8.61	1.35	1.52
1	H	12	GLN	C-O	-8.59	1.07	1.23
1	B	12	GLN	C-O	-8.59	1.07	1.23
1	I	12	GLN	C-O	-8.55	1.07	1.23
3	N	44	THR	C-O	-8.53	1.07	1.23
2	M	21	THR	C-N	8.48	1.53	1.34
4	P	98	SER	C-O	-8.40	1.07	1.23
1	L	245	ASN	C-N	8.35	1.48	1.33
1	C	16	ARG	C-N	8.34	1.53	1.34
2	M	67	ILE	N-CA	-8.26	1.29	1.46
1	J	18	GLN	C-O	-8.22	1.07	1.23
2	M	10	ALA	N-CA	-8.18	1.29	1.46
1	J	385	GLU	N-CA	-8.16	1.30	1.46
3	N	73	VAL	C-O	-8.13	1.07	1.23
1	K	382	SER	CA-C	-8.05	1.32	1.52
1	H	9	PRO	C-O	-8.03	1.07	1.23
1	C	187	GLN	C-N	8.03	1.52	1.34
1	B	9	PRO	C-O	-8.02	1.07	1.23
1	I	9	PRO	C-O	-8.01	1.07	1.23
1	D	9	PRO	C-O	-7.99	1.07	1.23
2	M	41	ALA	C-O	-7.98	1.08	1.23
1	G	309	ARG	C-N	7.95	1.52	1.34
4	P	32	ALA	C-N	-7.91	1.15	1.34
1	J	389	ALA	C-O	-7.88	1.08	1.23
1	J	188	SER	N-CA	7.88	1.62	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	27	VAL	N-CA	-7.88	1.30	1.46
1	A	314	SER	CA-C	-7.84	1.32	1.52
4	P	32	ALA	CA-CB	7.83	1.69	1.52
1	F	391	THR	C-N	-7.80	1.16	1.34
3	N	67	GLY	C-N	7.76	1.51	1.34
2	M	11	GLY	C-N	-7.75	1.19	1.34
2	M	41	ALA	C-N	-7.67	1.16	1.34
1	F	390	GLY	C-O	-7.52	1.11	1.23
3	N	43	LEU	C-O	-7.51	1.09	1.23
3	N	28	ARG	CA-CB	7.49	1.70	1.53
1	J	183	ALA	C-N	7.47	1.51	1.34
4	P	49	GLY	CA-C	-7.44	1.40	1.51
1	A	387	VAL	C-O	-7.34	1.09	1.23
1	D	380	PHE	C-N	-7.33	1.17	1.34
2	M	17	GLY	C-O	-7.33	1.11	1.23
1	J	184	ASN	C-N	-7.32	1.17	1.34
1	B	393	SER	C-N	7.25	1.50	1.34
1	H	393	SER	C-N	7.24	1.50	1.34
1	I	393	SER	C-N	7.24	1.50	1.34
1	E	187	GLN	C-O	-7.22	1.09	1.23
1	D	393	SER	C-N	7.22	1.50	1.34
1	H	357	ASN	C-N	-7.20	1.17	1.34
1	J	357	ASN	C-N	-7.20	1.17	1.34
1	D	357	ASN	C-N	-7.18	1.17	1.34
1	I	357	ASN	C-N	-7.18	1.17	1.34
1	F	391	THR	CA-CB	7.17	1.72	1.53
1	B	4	VAL	CA-C	7.16	1.71	1.52
3	N	97	ARG	C-O	-7.15	1.09	1.23
1	I	4	VAL	CA-C	7.14	1.71	1.52
3	N	66	ASP	C-O	-7.05	1.09	1.23
3	N	33	ALA	C-O	-6.99	1.10	1.23
3	N	66	ASP	C-N	-6.95	1.20	1.33
3	N	26	SER	CA-C	-6.91	1.34	1.52
1	E	244	GLN	N-CA	-6.90	1.32	1.46
1	B	281	LEU	N-CA	6.85	1.60	1.46
3	N	22	GLU	C-N	6.85	1.45	1.33
4	P	33	SER	C-N	-6.82	1.18	1.34
3	N	79	ARG	C-N	6.75	1.49	1.34
4	P	4	LYS	C-O	-6.72	1.10	1.23
4	P	4	LYS	C-N	-6.68	1.18	1.34
1	F	387	VAL	C-N	6.67	1.49	1.34
1	F	384	THR	C-O	-6.63	1.10	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	38	PRO	C-O	-6.61	1.10	1.23
2	M	7	PHE	C-N	-6.56	1.21	1.34
1	K	187	GLN	C-O	-6.50	1.10	1.23
1	A	309	ARG	C-N	6.48	1.49	1.34
1	J	12	GLN	C-O	-6.45	1.11	1.23
4	P	42	THR	C-N	6.43	1.48	1.34
4	P	32	ALA	CA-C	-6.40	1.36	1.52
1	K	381	THR	C-O	-6.39	1.11	1.23
1	A	187	GLN	C-O	-6.37	1.11	1.23
4	P	31	VAL	CA-C	-6.37	1.36	1.52
2	M	65	THR	N-CA	-6.36	1.33	1.46
1	F	393	SER	C-N	-6.35	1.19	1.34
1	D	26	GLN	C-N	-6.34	1.19	1.34
1	G	187	GLN	C-O	-6.33	1.11	1.23
2	M	54	ALA	C-O	-6.28	1.11	1.23
2	M	7	PHE	N-CA	-6.26	1.33	1.46
4	P	100	LEU	C-O	-6.26	1.11	1.23
4	P	49	GLY	N-CA	-6.25	1.36	1.46
1	G	245	ASN	C-N	6.24	1.44	1.33
1	A	245	ASN	C-N	6.19	1.44	1.33
4	P	27	PRO	C-N	6.17	1.48	1.34
2	M	51	PRO	C-O	-6.16	1.10	1.23
1	C	279	ALA	C-N	-6.16	1.19	1.34
1	K	279	ALA	C-N	-6.13	1.20	1.34
2	M	47	PHE	C-O	-6.13	1.11	1.23
1	J	386	LEU	N-CA	6.13	1.58	1.46
1	J	312	ASN	C-O	-6.12	1.11	1.23
3	N	27	VAL	CA-C	-6.11	1.37	1.52
3	N	18	CYS	C-N	-6.10	1.20	1.34
1	C	185	VAL	N-CA	-6.08	1.34	1.46
2	M	67	ILE	C-N	-6.04	1.20	1.34
2	M	22	GLU	N-CA	-6.03	1.34	1.46
3	N	86	LYS	N-CA	-6.00	1.34	1.46
1	J	387	VAL	C-N	5.98	1.47	1.34
3	N	44	THR	CA-CB	5.96	1.68	1.53
3	N	54	GLY	C-N	-5.94	1.20	1.34
2	M	65	THR	CA-CB	5.89	1.68	1.53
2	M	12	PRO	CA-C	-5.86	1.41	1.52
3	N	19	ASP	CA-C	-5.85	1.37	1.52
1	E	183	ALA	N-CA	-5.82	1.34	1.46
1	E	34	GLN	C-N	-5.81	1.20	1.34
1	J	7	LEU	C-O	-5.81	1.12	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	51	VAL	C-O	-5.81	1.12	1.23
4	P	50	SER	N-CA	-5.81	1.34	1.46
1	D	183	ALA	C-N	-5.75	1.20	1.34
1	I	183	ALA	C-N	-5.75	1.20	1.34
1	K	187	GLN	C-N	-5.75	1.20	1.34
2	M	36	ALA	CA-CB	5.74	1.64	1.52
1	B	183	ALA	C-N	-5.73	1.20	1.34
1	H	183	ALA	C-N	-5.71	1.21	1.34
3	N	25	GLN	C-N	5.70	1.47	1.34
4	P	50	SER	CA-CB	5.68	1.61	1.52
2	M	46	PRO	N-CD	5.65	1.55	1.47
1	J	310	THR	N-CA	-5.64	1.35	1.46
1	J	384	THR	N-CA	5.60	1.57	1.46
4	P	50	SER	C-O	-5.59	1.12	1.23
1	K	383	ARG	C-O	-5.56	1.12	1.23
3	N	81	LYS	C-O	-5.44	1.13	1.23
1	G	383	ARG	C-O	-5.43	1.13	1.23
1	I	309	ARG	C-N	5.43	1.46	1.34
1	C	381	THR	C-N	5.42	1.46	1.34
1	A	386	LEU	C-O	-5.41	1.13	1.23
1	L	313	PHE	C-N	5.40	1.46	1.34
1	J	385	GLU	CA-C	5.38	1.67	1.52
1	K	385	GLU	C-O	-5.36	1.13	1.23
3	N	34	VAL	C-O	-5.34	1.13	1.23
3	N	81	LYS	C-N	-5.33	1.21	1.34
1	J	8	THR	C-N	5.32	1.44	1.34
3	N	84	ALA	C-N	-5.32	1.23	1.33
2	M	4	ASN	C-O	-5.28	1.13	1.23
2	M	58	GLN	C-O	-5.26	1.13	1.23
4	P	44	ASN	C-O	-5.18	1.13	1.23
2	M	65	THR	CA-C	-5.13	1.39	1.52
4	P	100	LEU	C-N	-5.10	1.22	1.34
2	M	47	PHE	CA-C	-5.08	1.39	1.52
1	J	185	VAL	N-CA	-5.06	1.36	1.46
1	E	245	ASN	C-N	-5.05	1.24	1.33
1	G	357	ASN	C-N	-5.05	1.22	1.34
2	M	36	ALA	C-N	-5.03	1.24	1.33
2	M	18	PRO	C-N	5.02	1.45	1.34
1	A	357	ASN	C-N	-5.02	1.22	1.34

All (456) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	24	ASN	O-C-N	-53.44	37.20	122.70
1	F	247	TYR	O-C-N	-45.14	50.48	122.70
1	G	313	PHE	O-C-N	-44.62	51.31	122.70
1	B	16	ARG	O-C-N	-42.15	55.26	122.70
1	I	16	ARG	O-C-N	-42.14	55.28	122.70
3	N	5	ASN	C-N-CD	-41.75	28.75	120.60
1	I	7	LEU	O-C-N	-38.43	61.21	122.70
1	D	7	LEU	O-C-N	-38.42	61.22	122.70
1	B	7	LEU	O-C-N	-38.40	61.26	122.70
1	K	380	PHE	O-C-N	-36.95	63.58	122.70
1	D	394	THR	O-C-N	-36.40	64.46	122.70
1	B	394	THR	O-C-N	-36.37	64.50	122.70
1	I	394	THR	O-C-N	-36.37	64.51	122.70
2	M	11	GLY	C-N-CD	-34.88	43.86	120.60
1	F	186	PRO	O-C-N	-31.58	72.17	122.70
1	K	187	GLN	O-C-N	-31.41	72.45	122.70
1	E	186	PRO	O-C-N	-31.31	72.60	122.70
1	I	313	PHE	O-C-N	-29.87	74.91	122.70
1	F	391	THR	CA-C-O	-28.70	59.84	120.10
1	F	239	GLN	O-C-N	26.55	165.17	122.70
1	H	185	VAL	C-N-CD	-25.41	64.69	120.60
1	B	185	VAL	C-N-CD	-25.41	64.70	120.60
1	D	185	VAL	C-N-CD	-25.39	64.73	120.60
1	I	185	VAL	C-N-CD	-25.39	64.73	120.60
1	L	312	ASN	O-C-N	-25.27	82.28	122.70
1	B	7	LEU	CA-C-N	24.87	171.91	117.20
1	I	7	LEU	CA-C-N	24.83	171.83	117.20
3	N	111	SER	O-C-N	-24.82	82.99	122.70
1	D	7	LEU	CA-C-N	24.81	171.79	117.20
1	H	313	PHE	O-C-N	-24.07	84.20	122.70
1	D	313	PHE	O-C-N	-24.04	84.23	122.70
1	B	313	PHE	O-C-N	-24.01	84.28	122.70
1	G	314	SER	O-C-N	-23.39	85.28	122.70
1	I	16	ARG	CA-C-N	23.01	167.82	117.20
1	B	16	ARG	CA-C-N	22.97	167.73	117.20
1	K	380	PHE	CA-C-N	22.89	167.56	117.20
1	F	186	PRO	CA-C-N	22.33	166.32	117.20
1	F	239	GLN	C-N-CA	-22.16	66.29	121.70
1	E	381	THR	O-C-N	21.82	157.62	122.70
1	G	352	THR	O-C-N	-21.49	88.31	122.70
1	I	16	ARG	C-N-CA	21.48	175.41	121.70
1	A	352	THR	O-C-N	-21.48	88.33	122.70
1	B	16	ARG	C-N-CA	21.47	175.36	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	K	187	GLN	CA-C-N	20.56	162.44	117.20
1	A	314	SER	CA-C-N	-20.23	72.69	117.20
1	E	186	PRO	CA-C-N	20.12	161.48	117.20
1	F	239	GLN	CA-C-N	-20.04	73.12	117.20
1	C	186	PRO	O-C-N	-19.91	90.85	122.70
1	I	313	PHE	CA-C-N	19.83	160.83	117.20
1	A	313	PHE	O-C-N	-19.82	90.98	122.70
3	N	27	VAL	CA-C-N	19.37	159.82	117.20
1	F	391	THR	CA-C-N	19.25	159.55	117.20
1	D	392	ILE	O-C-N	-18.80	92.62	122.70
1	K	245	ASN	O-C-N	-18.33	92.03	123.20
1	C	245	ASN	O-C-N	-18.31	92.08	123.20
1	J	313	PHE	O-C-N	-18.16	93.64	122.70
1	B	7	LEU	C-N-CA	17.98	166.65	121.70
1	I	7	LEU	C-N-CA	17.96	166.59	121.70
1	D	7	LEU	C-N-CA	17.92	166.50	121.70
3	N	26	SER	C-N-CA	17.72	166.00	121.70
1	D	313	PHE	CA-C-N	17.68	156.09	117.20
1	B	313	PHE	CA-C-N	17.67	156.07	117.20
1	H	313	PHE	CA-C-N	17.67	156.07	117.20
1	I	352	THR	O-C-N	-17.43	94.81	122.70
1	H	352	THR	O-C-N	-17.41	94.84	122.70
1	J	352	THR	O-C-N	-17.37	94.90	122.70
1	D	352	THR	O-C-N	-17.37	94.91	122.70
1	B	352	THR	O-C-N	-17.36	94.93	122.70
1	K	245	ASN	CA-C-N	17.22	150.65	116.20
1	C	245	ASN	CA-C-N	17.21	150.61	116.20
3	N	111	SER	C-N-CA	16.91	163.98	121.70
1	B	392	ILE	O-C-N	-16.82	95.79	122.70
1	K	187	GLN	C-N-CA	16.46	162.86	121.70
1	E	381	THR	CA-C-N	-16.28	81.38	117.20
3	N	111	SER	CA-C-N	16.18	152.81	117.20
1	L	312	ASN	CA-C-N	16.06	152.52	117.20
1	B	381	THR	O-C-N	15.82	148.01	122.70
1	D	381	THR	O-C-N	15.80	147.98	122.70
1	I	381	THR	O-C-N	15.79	147.97	122.70
1	B	311	ALA	O-C-N	-15.74	97.51	122.70
1	H	311	ALA	O-C-N	-15.73	97.53	122.70
1	A	352	THR	C-N-CA	15.73	161.02	121.70
1	D	311	ALA	O-C-N	-15.72	97.55	122.70
1	G	352	THR	C-N-CA	15.72	160.99	121.70
1	G	382	SER	CA-C-N	-15.67	82.72	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	352	THR	CA-C-N	15.54	151.38	117.20
1	A	352	THR	CA-C-N	15.52	151.34	117.20
1	B	4	VAL	CB-CA-C	-15.41	82.11	111.40
1	I	4	VAL	CB-CA-C	-15.41	82.11	111.40
1	J	250	PRO	O-C-N	-15.28	98.25	122.70
1	A	311	ALA	O-C-N	-14.91	98.85	122.70
1	B	4	VAL	N-CA-CB	-14.84	78.85	111.50
3	N	26	SER	CA-C-N	14.84	149.85	117.20
1	I	4	VAL	N-CA-CB	-14.84	78.86	111.50
1	F	186	PRO	C-N-CA	14.69	158.43	121.70
3	N	90	PHE	C-N-CD	-14.65	88.36	120.60
3	N	57	CYS	O-C-N	-14.63	99.28	122.70
1	L	161	GLU	O-C-N	-14.52	99.47	122.70
1	H	381	THR	O-C-N	14.20	145.43	122.70
1	A	314	SER	O-C-N	13.79	144.76	122.70
1	E	186	PRO	C-N-CA	13.77	156.13	121.70
1	H	352	THR	C-N-CA	13.68	155.90	121.70
1	D	352	THR	C-N-CA	13.67	155.88	121.70
1	J	352	THR	C-N-CA	13.66	155.85	121.70
1	B	352	THR	C-N-CA	13.65	155.83	121.70
1	I	352	THR	C-N-CA	13.64	155.80	121.70
1	D	380	PHE	O-C-N	-13.63	100.89	122.70
1	L	312	ASN	C-N-CA	13.62	155.75	121.70
1	D	392	ILE	CA-C-N	13.62	147.15	117.20
3	N	27	VAL	O-C-N	-13.45	101.18	122.70
1	C	184	ASN	C-N-CA	-13.34	88.36	121.70
1	K	279	ALA	O-C-N	-13.30	101.42	122.70
1	C	279	ALA	O-C-N	-13.20	101.57	122.70
3	N	17	GLY	O-C-N	-13.13	101.69	122.70
1	D	390	GLY	O-C-N	-13.09	101.76	122.70
1	I	390	GLY	O-C-N	-13.08	101.78	122.70
1	B	390	GLY	O-C-N	-13.06	101.80	122.70
1	A	24	ASN	CA-C-N	-13.05	88.49	117.20
1	F	279	ALA	C-N-CA	12.83	153.77	121.70
1	E	279	ALA	C-N-CA	12.82	153.75	121.70
3	N	27	VAL	N-CA-C	12.80	145.57	111.00
4	P	31	VAL	CA-C-N	12.80	145.36	117.20
1	K	186	PRO	O-C-N	-12.69	102.40	122.70
1	I	380	PHE	O-C-N	12.65	142.94	122.70
1	B	380	PHE	O-C-N	12.63	142.91	122.70
4	P	45	GLN	C-N-CD	-12.58	92.93	120.60
3	N	94	VAL	C-N-CD	-12.47	93.17	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	358	VAL	N-CA-CB	12.45	138.90	111.50
1	C	186	PRO	CA-N-CD	-12.45	94.07	111.50
1	B	311	ALA	C-N-CA	12.37	152.63	121.70
1	H	311	ALA	C-N-CA	12.37	152.62	121.70
1	D	311	ALA	C-N-CA	12.36	152.61	121.70
1	B	381	THR	CA-C-N	-12.36	90.02	117.20
1	D	381	THR	CA-C-N	-12.34	90.05	117.20
1	I	381	THR	CA-C-N	-12.34	90.06	117.20
1	F	247	TYR	C-N-CA	12.20	152.21	121.70
1	A	381	THR	O-C-N	-11.93	103.62	122.70
1	L	150	ALA	O-C-N	11.90	143.71	121.10
4	P	32	ALA	C-N-CA	11.85	151.32	121.70
4	P	31	VAL	C-N-CA	11.81	151.23	121.70
1	F	391	THR	C-N-CA	11.79	151.19	121.70
1	H	352	THR	CA-C-N	11.68	142.89	117.20
1	B	352	THR	CA-C-N	11.67	142.87	117.20
1	D	352	THR	CA-C-N	11.65	142.84	117.20
1	J	352	THR	CA-C-N	11.65	142.83	117.20
1	I	352	THR	CA-C-N	11.64	142.81	117.20
1	H	381	THR	CA-C-N	-11.60	91.69	117.20
1	J	185	VAL	C-N-CD	-11.58	95.13	120.60
1	I	313	PHE	C-N-CA	11.54	150.54	121.70
3	N	27	VAL	C-N-CA	11.43	150.28	121.70
1	K	311	ALA	O-C-N	-11.34	104.55	122.70
1	C	243	GLY	O-C-N	-11.28	104.65	122.70
1	I	392	ILE	C-N-CA	-11.28	93.50	121.70
1	A	313	PHE	C-N-CA	11.27	149.87	121.70
1	C	311	ALA	O-C-N	-11.25	104.70	122.70
1	K	243	GLY	O-C-N	-11.25	104.70	122.70
1	L	177	LEU	C-N-CA	-11.25	93.58	121.70
1	K	380	PHE	C-N-CA	11.22	149.76	121.70
1	F	391	THR	O-C-N	11.19	140.61	122.70
3	N	28	ARG	N-CA-C	11.11	141.00	111.00
1	K	188	SER	C-N-CA	11.09	149.42	121.70
1	B	8	THR	O-C-N	11.01	142.01	121.10
1	I	8	THR	O-C-N	11.00	142.01	121.10
1	H	311	ALA	CA-C-N	10.81	140.99	117.20
1	I	311	ALA	O-C-N	-10.81	105.40	122.70
1	B	311	ALA	CA-C-N	10.81	140.97	117.20
1	D	311	ALA	CA-C-N	10.79	140.94	117.20
4	P	32	ALA	CA-C-N	10.77	140.90	117.20
1	G	185	VAL	C-N-CD	-10.73	97.00	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	314	SER	CA-C-O	10.69	142.54	120.10
3	N	26	SER	CA-C-O	-10.67	97.70	120.10
3	N	40	LYS	O-C-N	-10.65	105.66	122.70
1	I	4	VAL	CA-CB-CG1	10.63	126.84	110.90
1	B	4	VAL	CA-CB-CG1	10.62	126.83	110.90
1	I	185	VAL	O-C-N	-10.62	100.93	121.10
1	H	185	VAL	O-C-N	-10.62	100.93	121.10
1	B	185	VAL	O-C-N	-10.61	100.95	121.10
4	P	31	VAL	O-C-N	-10.59	105.75	122.70
1	D	185	VAL	O-C-N	-10.57	101.01	121.10
1	C	186	PRO	CA-C-N	10.50	140.29	117.20
1	F	311	ALA	O-C-N	-10.43	106.01	122.70
1	E	311	ALA	O-C-N	-10.41	106.04	122.70
2	M	64	GLY	CA-C-N	10.38	140.05	117.20
3	N	25	GLN	O-C-N	-10.21	106.36	122.70
1	C	243	GLY	C-N-CA	10.17	147.13	121.70
1	K	243	GLY	C-N-CA	10.17	147.12	121.70
1	C	381	THR	CA-C-N	-10.16	94.85	117.20
4	P	36	GLU	CA-C-N	10.15	136.51	116.20
3	N	27	VAL	CA-C-O	-10.14	98.80	120.10
1	B	358	VAL	N-CA-C	-10.10	83.72	111.00
1	K	186	PRO	CA-C-N	10.10	139.42	117.20
1	G	35	SER	O-C-N	9.91	138.55	122.70
4	P	36	GLU	O-C-N	-9.89	106.38	123.20
1	C	245	ASN	C-N-CA	9.83	142.94	122.30
1	K	245	ASN	C-N-CA	9.82	142.92	122.30
1	A	313	PHE	CA-C-N	9.80	138.77	117.20
1	J	313	PHE	CA-C-N	9.80	138.76	117.20
1	C	279	ALA	C-N-CA	9.79	146.19	121.70
1	K	279	ALA	C-N-CA	9.78	146.15	121.70
1	G	313	PHE	CA-C-N	9.68	138.50	117.20
3	N	43	LEU	O-C-N	-9.66	107.23	122.70
1	L	381	THR	CA-C-N	-9.62	96.03	117.20
1	L	177	LEU	CA-C-N	-9.57	96.15	117.20
3	N	12	THR	C-N-CD	-9.53	99.63	120.60
1	L	177	LEU	O-C-N	9.45	137.83	122.70
3	N	26	SER	N-CA-C	9.26	136.01	111.00
4	P	32	ALA	N-CA-C	9.24	135.96	111.00
1	L	243	GLY	O-C-N	-9.24	107.91	122.70
1	I	380	PHE	CA-C-N	-9.22	96.92	117.20
1	B	380	PHE	CA-C-N	-9.21	96.94	117.20
1	K	186	PRO	CA-N-CD	-9.18	98.65	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	M	41	ALA	O-C-N	-9.15	108.06	122.70
1	A	243	GLY	C-N-CA	9.13	144.52	121.70
1	G	243	GLY	C-N-CA	9.12	144.49	121.70
1	K	185	VAL	C-N-CD	-8.85	101.13	120.60
3	N	17	GLY	CA-C-N	8.85	136.67	117.20
1	A	245	ASN	CA-C-N	8.81	133.81	116.20
1	G	245	ASN	CA-C-N	8.79	133.78	116.20
1	H	392	ILE	O-C-N	-8.77	108.66	122.70
2	M	64	GLY	O-C-N	-8.77	108.67	122.70
1	I	389	ALA	CA-C-N	8.76	133.73	116.20
1	D	389	ALA	CA-C-N	8.74	133.68	116.20
1	F	279	ALA	O-C-N	-8.74	108.71	122.70
1	H	389	ALA	CA-C-N	8.74	133.68	116.20
1	E	279	ALA	O-C-N	-8.72	108.74	122.70
1	B	389	ALA	CA-C-N	8.72	133.64	116.20
1	K	185	VAL	CB-CA-C	-8.70	94.87	111.40
1	J	187	GLN	O-C-N	-8.62	108.90	122.70
1	L	150	ALA	C-N-CD	8.60	146.46	128.40
1	L	279	ALA	C-N-CA	8.53	143.03	121.70
4	P	36	GLU	C-N-CA	8.47	140.08	122.30
1	K	244	GLN	O-C-N	-8.46	109.16	122.70
1	I	311	ALA	C-N-CA	8.44	142.79	121.70
2	M	36	ALA	C-N-CA	8.43	139.99	122.30
1	C	244	GLN	O-C-N	-8.42	109.22	122.70
2	M	46	PRO	O-C-N	-8.38	109.30	122.70
1	J	250	PRO	CA-C-N	8.36	135.60	117.20
3	N	25	GLN	CA-C-N	8.36	135.60	117.20
3	N	19	ASP	O-C-N	-8.34	109.36	122.70
1	D	313	PHE	C-N-CA	8.30	142.45	121.70
1	H	313	PHE	C-N-CA	8.28	142.41	121.70
1	B	313	PHE	C-N-CA	8.28	142.39	121.70
1	L	381	THR	O-C-N	-8.26	109.49	122.70
1	K	17	ASN	O-C-N	8.19	135.81	122.70
1	I	245	ASN	O-C-N	8.13	137.03	123.20
1	B	245	ASN	O-C-N	8.12	137.00	123.20
1	D	245	ASN	O-C-N	8.12	137.00	123.20
1	H	245	ASN	O-C-N	8.10	136.97	123.20
1	D	380	PHE	C-N-CA	8.09	141.93	121.70
1	L	236	TYR	CA-C-N	-8.07	99.44	117.20
1	J	310	THR	CA-C-N	-8.01	99.58	117.20
1	E	187	GLN	CA-C-N	-7.97	99.67	117.20
1	E	182	LEU	CA-C-N	-7.94	99.72	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	381	THR	C-N-CA	-7.93	101.88	121.70
1	I	381	THR	C-N-CA	-7.91	101.91	121.70
1	D	381	THR	C-N-CA	-7.90	101.95	121.70
1	A	243	GLY	O-C-N	-7.87	110.11	122.70
1	G	243	GLY	O-C-N	-7.85	110.14	122.70
1	H	389	ALA	O-C-N	-7.85	109.86	123.20
1	I	389	ALA	O-C-N	-7.85	109.86	123.20
1	I	380	PHE	C-N-CA	-7.83	102.12	121.70
1	B	389	ALA	O-C-N	-7.82	109.90	123.20
1	D	389	ALA	O-C-N	-7.82	109.91	123.20
1	B	380	PHE	C-N-CA	-7.82	102.15	121.70
3	N	28	ARG	O-C-N	-7.81	109.92	123.20
2	M	36	ALA	N-CA-C	7.77	131.98	111.00
1	K	244	GLN	CA-C-N	7.76	134.27	117.20
1	C	244	GLN	CA-C-N	7.72	134.19	117.20
1	L	150	ALA	CA-C-N	-7.67	95.64	117.10
1	J	184	ASN	O-C-N	-7.66	110.44	122.70
1	K	243	GLY	CA-C-N	7.65	134.03	117.20
1	H	392	ILE	CA-C-N	-7.61	100.45	117.20
1	C	243	GLY	CA-C-N	7.59	133.90	117.20
1	D	380	PHE	CA-C-N	7.58	133.87	117.20
3	N	109	LYS	C-N-CA	7.54	140.54	121.70
1	G	35	SER	CA-C-N	-7.51	100.69	117.20
1	I	185	VAL	CA-C-N	7.48	138.04	117.10
1	B	185	VAL	CA-C-N	7.47	138.03	117.10
1	H	185	VAL	CA-C-N	7.47	138.02	117.10
1	D	185	VAL	CA-C-N	7.46	138.00	117.10
4	P	32	ALA	O-C-N	-7.45	110.78	122.70
1	I	8	THR	C-N-CD	7.44	144.03	128.40
1	B	392	ILE	C-N-CA	-7.44	103.10	121.70
1	J	184	ASN	CA-C-N	7.43	133.54	117.20
1	B	8	THR	C-N-CD	7.43	144.00	128.40
1	J	309	ARG	C-N-CA	-7.43	103.13	121.70
1	L	257	LEU	CA-C-N	-7.39	100.93	117.20
1	B	394	THR	CA-C-N	7.35	133.38	117.20
1	K	244	GLN	C-N-CA	7.34	140.05	121.70
1	D	394	THR	CA-C-N	7.32	133.31	117.20
1	K	17	ASN	CA-C-N	-7.31	101.11	117.20
1	C	244	GLN	C-N-CA	7.30	139.96	121.70
1	E	186	PRO	CA-N-CD	-7.28	101.31	111.50
1	I	394	THR	CA-C-N	7.28	133.21	117.20
1	E	187	GLN	O-C-N	7.24	134.28	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	K	191	ARG	C-N-CA	-7.17	103.76	121.70
1	I	311	ALA	CA-C-N	7.17	132.98	117.20
1	J	250	PRO	C-N-CA	7.16	139.60	121.70
1	A	244	GLN	O-C-N	-7.11	111.32	122.70
3	N	54	GLY	O-C-N	-7.11	111.33	122.70
4	P	5	LYS	O-C-N	-7.10	111.34	122.70
1	G	244	GLN	O-C-N	-7.09	111.35	122.70
2	M	39	GLN	O-C-N	-7.07	111.38	122.70
3	N	57	CYS	C-N-CA	7.03	139.27	121.70
1	I	4	VAL	N-CA-C	-6.95	92.23	111.00
1	B	4	VAL	N-CA-C	-6.95	92.25	111.00
1	K	185	VAL	N-CA-C	6.93	129.72	111.00
1	K	186	PRO	C-N-CA	6.93	139.03	121.70
1	J	184	ASN	C-N-CA	6.93	139.02	121.70
1	F	391	THR	N-CA-C	6.92	129.69	111.00
1	I	8	THR	CA-C-N	-6.89	97.80	117.10
1	B	8	THR	CA-C-N	-6.88	97.84	117.10
1	F	393	SER	CA-C-O	6.87	134.52	120.10
1	G	245	ASN	O-C-N	-6.86	111.55	123.20
1	A	245	ASN	O-C-N	-6.85	111.55	123.20
1	A	310	THR	N-CA-CB	6.83	123.28	110.30
1	C	279	ALA	CA-C-N	6.80	132.16	117.20
1	G	35	SER	C-N-CA	-6.79	104.73	121.70
3	N	31	PHE	O-C-N	-6.76	111.88	122.70
1	B	358	VAL	CB-CA-C	6.75	124.23	111.40
3	N	40	LYS	C-N-CA	6.75	138.59	121.70
4	P	5	LYS	CA-C-N	6.75	132.05	117.20
1	K	279	ALA	CA-C-N	6.75	132.04	117.20
1	A	244	GLN	C-N-CA	6.68	138.40	121.70
1	G	244	GLN	C-N-CA	6.66	138.35	121.70
1	C	381	THR	O-C-N	6.65	133.34	122.70
1	B	4	VAL	C-N-CA	-6.65	105.07	121.70
1	I	4	VAL	C-N-CA	-6.64	105.09	121.70
1	L	313	PHE	O-C-N	6.61	133.27	122.70
4	P	101	ASN	O-C-N	-6.57	112.19	122.70
1	A	244	GLN	CA-C-N	6.53	131.57	117.20
1	I	312	ASN	O-C-N	-6.52	112.28	122.70
1	G	244	GLN	CA-C-N	6.51	131.52	117.20
3	N	23	GLY	C-N-CD	-6.50	106.31	120.60
3	N	57	CYS	CA-C-N	6.50	131.49	117.20
1	J	187	GLN	CA-C-N	6.48	131.45	117.20
2	M	64	GLY	C-N-CA	6.46	137.85	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	M	39	GLN	CA-C-N	6.46	131.40	117.20
1	A	314	SER	N-CA-C	6.40	128.29	111.00
1	K	181	VAL	C-N-CA	6.40	137.71	121.70
3	N	26	SER	O-C-N	-6.40	112.45	122.70
1	I	245	ASN	CA-C-N	-6.38	103.45	116.20
1	D	245	ASN	CA-C-N	-6.37	103.46	116.20
1	B	245	ASN	CA-C-N	-6.36	103.47	116.20
1	H	245	ASN	CA-C-N	-6.36	103.48	116.20
2	M	66	GLY	CA-C-N	6.36	131.19	117.20
1	I	13	ALA	C-N-CA	-6.36	105.81	121.70
1	G	314	SER	C-N-CA	-6.35	105.83	121.70
1	B	13	ALA	C-N-CA	-6.34	105.84	121.70
1	F	393	SER	CA-C-N	-6.32	103.31	117.20
1	D	13	ALA	C-N-CA	-6.31	105.92	121.70
3	N	40	LYS	CA-C-N	6.30	131.06	117.20
3	N	110	LYS	C-N-CA	6.29	137.42	121.70
1	L	243	GLY	CA-C-N	6.28	131.02	117.20
1	G	382	SER	O-C-N	-6.25	112.70	122.70
1	J	18	GLN	O-C-N	6.25	132.70	122.70
2	M	41	ALA	CA-C-N	6.24	130.92	117.20
1	D	312	ASN	O-C-N	-6.22	112.75	122.70
1	B	312	ASN	O-C-N	-6.21	112.76	122.70
1	H	312	ASN	O-C-N	-6.20	112.78	122.70
1	L	236	TYR	O-C-N	6.17	132.57	122.70
1	L	280	ASN	C-N-CA	6.15	137.08	121.70
1	H	381	THR	C-N-CA	-6.14	106.35	121.70
1	L	313	PHE	CA-C-N	-6.11	103.76	117.20
1	A	311	ALA	CA-C-N	6.10	130.62	117.20
1	C	185	VAL	CA-C-N	-6.09	100.06	117.10
1	A	186	PRO	N-CA-CB	6.03	110.53	103.30
1	F	243	GLY	O-C-N	-6.01	113.08	122.70
1	K	191	ARG	CA-C-N	-6.00	104.00	117.20
3	N	110	LYS	N-CA-C	6.00	127.20	111.00
3	N	25	GLN	C-N-CA	5.99	136.68	121.70
1	L	236	TYR	CA-CB-CG	5.99	124.78	113.40
1	K	162	LEU	CA-CB-CG	5.96	129.01	115.30
1	J	310	THR	O-C-N	5.95	132.22	122.70
3	N	61	ASP	O-C-N	-5.95	113.19	122.70
1	F	162	LEU	CA-CB-CG	5.93	128.95	115.30
1	L	161	GLU	CA-C-N	5.93	130.25	117.20
1	C	162	LEU	CA-CB-CG	5.92	128.91	115.30
1	L	162	LEU	CA-CB-CG	5.92	128.91	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	162	LEU	CA-CB-CG	5.91	128.90	115.30
1	I	389	ALA	C-N-CA	5.91	134.70	122.30
1	A	311	ALA	C-N-CA	5.90	136.45	121.70
3	N	65	ASN	CA-C-N	5.88	130.12	117.20
1	H	389	ALA	C-N-CA	5.87	134.63	122.30
1	J	256	THR	O-C-N	-5.87	113.31	122.70
1	D	389	ALA	C-N-CA	5.85	134.59	122.30
1	I	309	ARG	C-N-CA	5.85	136.34	121.70
1	B	389	ALA	C-N-CA	5.84	134.57	122.30
1	J	8	THR	CA-C-O	5.82	132.32	120.10
1	C	311	ALA	CA-C-N	5.79	129.94	117.20
2	M	76	PRO	CA-C-N	-5.79	104.47	117.20
1	K	311	ALA	CA-C-N	5.78	129.92	117.20
1	B	394	THR	C-N-CA	5.75	136.08	121.70
1	D	394	THR	C-N-CA	5.75	136.07	121.70
1	I	243	GLY	O-C-N	-5.71	113.56	122.70
3	N	65	ASN	O-C-N	-5.71	113.57	122.70
1	H	243	GLY	O-C-N	-5.70	113.58	122.70
1	I	394	THR	C-N-CA	5.70	135.94	121.70
1	B	243	GLY	O-C-N	-5.68	113.61	122.70
3	N	54	GLY	CA-C-N	5.68	129.70	117.20
1	D	243	GLY	O-C-N	-5.68	113.62	122.70
4	P	32	ALA	CA-C-O	-5.61	108.31	120.10
4	P	38	PRO	C-N-CD	-5.59	108.29	120.60
1	E	244	GLN	CA-C-O	-5.56	108.42	120.10
1	K	185	VAL	CA-C-N	-5.55	101.55	117.10
1	C	185	VAL	N-CA-C	-5.55	96.02	111.00
1	C	186	PRO	N-CA-C	5.54	126.51	112.10
1	C	185	VAL	O-C-N	5.54	131.62	121.10
2	M	60	TYR	C-N-CA	5.50	135.46	121.70
1	K	383	ARG	C-N-CA	5.50	135.44	121.70
2	M	76	PRO	CA-C-O	5.50	133.39	120.20
1	E	188	SER	CA-C-N	-5.49	105.12	117.20
3	N	18	CYS	CA-C-N	5.49	129.28	117.20
1	A	310	THR	N-CA-C	-5.48	96.20	111.00
1	G	313	PHE	C-N-CA	5.46	135.35	121.70
2	M	16	PRO	O-C-N	-5.44	113.95	123.20
1	H	185	VAL	C-N-CA	5.44	144.84	122.00
1	I	185	VAL	C-N-CA	5.44	144.84	122.00
1	B	185	VAL	C-N-CA	5.43	144.82	122.00
1	L	279	ALA	O-C-N	-5.43	114.01	122.70
1	C	313	PHE	O-C-N	5.43	131.38	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	185	VAL	C-N-CA	5.42	144.78	122.00
1	F	279	ALA	CA-C-N	5.42	129.12	117.20
2	M	46	PRO	CA-C-N	5.41	129.10	117.20
2	M	67	ILE	O-C-N	-5.40	114.06	122.70
1	E	279	ALA	CA-C-N	5.40	129.07	117.20
1	K	313	PHE	O-C-N	5.39	131.32	122.70
4	P	31	VAL	CA-C-O	-5.38	108.79	120.10
3	N	64	GLU	O-C-N	-5.38	114.09	122.70
1	L	161	GLU	C-N-CA	5.37	135.13	121.70
3	N	61	ASP	CA-C-N	5.33	128.93	117.20
4	P	98	SER	O-C-N	-5.30	114.22	122.70
1	E	311	ALA	CA-C-N	5.29	128.84	117.20
1	F	311	ALA	CA-C-N	5.27	128.80	117.20
1	L	237	LEU	N-CA-C	-5.25	96.82	111.00
2	M	48	LEU	CA-C-N	5.25	128.75	117.20
1	E	243	GLY	O-C-N	-5.23	114.33	122.70
2	M	15	ILE	C-N-CD	-5.23	109.09	120.60
2	M	64	GLY	CA-C-O	-5.20	111.24	120.60
1	G	314	SER	CA-C-N	5.19	128.61	117.20
4	P	3	LYS	C-N-CA	-5.18	108.74	121.70
1	L	236	TYR	N-CA-C	5.18	124.98	111.00
1	D	26	GLN	O-C-N	-5.17	114.42	122.70
1	A	310	THR	CB-CA-C	-5.17	97.64	111.60
2	M	36	ALA	N-CA-CB	-5.14	102.91	110.10
2	M	66	GLY	O-C-N	-5.12	114.50	122.70
2	M	65	THR	N-CA-C	5.11	124.81	111.00
1	A	243	GLY	CA-C-N	5.11	128.44	117.20
2	M	63	ILE	O-C-N	-5.10	114.53	123.20
2	M	13	VAL	N-CA-C	-5.09	97.26	111.00
1	G	243	GLY	CA-C-N	5.08	128.38	117.20
1	I	312	ASN	CA-C-N	5.08	128.37	117.20
2	M	48	LEU	O-C-N	-5.06	114.60	122.70
1	E	188	SER	C-N-CA	5.05	134.33	121.70
1	E	381	THR	C-N-CA	-5.04	109.09	121.70
3	N	44	THR	N-CA-C	5.02	124.56	111.00

There are no chirality outliers.

All (91) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	245	ASN	Mainchain
1	A	309	ARG	Mainchain

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Mol	Chain	Res	Type	Group
1	A	311	ALA	Mainchain
1	A	313	PHE	Mainchain
1	A	352	THR	Peptide
1	A	381	THR	Peptide,Mainchain
1	B	13	ALA	Mainchain
1	B	16	ARG	Peptide,Mainchain
1	B	313	PHE	Peptide,Mainchain
1	B	352	THR	Peptide,Mainchain
1	B	358	VAL	Mainchain
1	B	390	GLY	Mainchain
1	B	392	ILE	Peptide,Mainchain
1	B	394	THR	Mainchain
1	B	7	LEU	Mainchain
1	C	186	PRO	Peptide
1	C	245	ASN	Mainchain
1	C	279	ALA	Peptide,Mainchain
1	C	311	ALA	Peptide,Mainchain
1	C	381	THR	Mainchain
1	D	13	ALA	Mainchain
1	D	313	PHE	Peptide,Mainchain
1	D	352	THR	Peptide,Mainchain
1	D	380	PHE	Mainchain
1	D	390	GLY	Mainchain
1	D	392	ILE	Mainchain
1	D	394	THR	Mainchain
1	D	7	LEU	Mainchain
1	E	182	LEU	Mainchain
1	E	186	PRO	Mainchain
1	E	279	ALA	Mainchain
1	E	311	ALA	Peptide,Mainchain
1	F	186	PRO	Peptide,Mainchain
1	F	247	TYR	Mainchain
1	F	279	ALA	Mainchain
1	F	311	ALA	Peptide,Mainchain
1	G	245	ASN	Mainchain
1	G	313	PHE	Mainchain
1	G	314	SER	Peptide,Mainchain
1	G	352	THR	Peptide
1	H	313	PHE	Peptide,Mainchain
1	H	352	THR	Peptide,Mainchain
1	H	392	ILE	Mainchain
1	I	13	ALA	Mainchain

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Mol	Chain	Res	Type	Group
1	I	16	ARG	Peptide,Mainchain
1	I	313	PHE	Peptide,Mainchain
1	I	352	THR	Peptide,Mainchain
1	I	390	GLY	Mainchain
1	I	394	THR	Mainchain
1	I	7	LEU	Mainchain
1	J	183	ALA	Mainchain
1	J	250	PRO	Mainchain
1	J	313	PHE	Mainchain
1	J	352	THR	Peptide,Mainchain
1	K	181	VAL	Peptide
1	K	186	PRO	Mainchain
1	K	187	GLN	Mainchain
1	K	245	ASN	Mainchain
1	K	279	ALA	Peptide,Mainchain
1	K	311	ALA	Peptide,Mainchain
1	K	380	PHE	Peptide,Mainchain
1	L	11	GLN	Mainchain
1	L	161	GLU	Mainchain
1	L	177	LEU	Mainchain
1	L	279	ALA	Peptide,Mainchain
3	N	10	THR	Mainchain
3	N	111	SER	Peptide
3	N	52	PHE	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	2956	0	2851	116	0
1	B	3045	0	2937	307	0
1	C	2999	0	2903	129	0
1	D	3045	0	2939	334	0
1	E	2944	0	2846	212	0
1	F	3009	0	2912	268	0
1	G	2926	0	2832	196	0
1	H	3045	0	2951	197	0
1	I	3045	0	2931	337	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	3027	0	2927	210	0
1	K	2992	0	2880	234	0
1	L	2953	0	2854	329	0
2	M	638	0	620	405	0
3	N	872	0	814	459	0
4	P	620	0	598	161	0
All	All	38116	0	36795	3092	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 41.

All (3092) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:16:ARG:HD3	1:J:21:MET:SD	1.29	1.69
1:L:108:ARG:HH11	3:N:89:TYR:CB	0.99	1.62
1:A:255:SER:HA	1:A:383:ARG:CD	1.30	1.60
1:E:189:LYS:HZ2	1:K:61:ASN:CB	1.05	1.60
3:N:60:ILE:HD12	3:N:97:ARG:CD	1.23	1.59
1:H:281:LEU:CD1	1:H:385:GLU:HB3	1.26	1.59
3:N:80:ILE:CG2	3:N:116:PHE:CA	1.78	1.59
3:N:49:THR:CB	3:N:112:VAL:HG11	1.25	1.58
1:D:187:GLN:HB2	2:M:9:TYR:CE1	1.35	1.58
1:G:15:LEU:CD2	1:G:18:GLN:HE21	1.17	1.58
3:N:27:VAL:CA	3:N:27:VAL:CB	1.76	1.58
3:N:80:ILE:HG21	3:N:116:PHE:CA	1.28	1.58
1:J:384:THR:CG2	2:M:62:ALA:HB2	1.30	1.57
1:B:5:GLN:NE2	1:B:316:THR:CG2	1.68	1.57
1:B:108:ARG:NH2	1:D:314:SER:CA	1.68	1.56
1:D:187:GLN:CD	2:M:9:TYR:CD1	1.74	1.56
1:J:8:THR:CG2	1:J:9:PRO:HD2	1.13	1.55
1:C:8:THR:CG2	1:C:9:PRO:HD2	1.10	1.54
1:F:353:LEU:CD2	2:M:27:LEU:H	1.15	1.53
1:B:358:VAL:HA	1:B:358:VAL:CG2	1.39	1.53
1:B:281:LEU:CD1	1:B:385:GLU:HB3	1.38	1.51
1:I:5:GLN:CD	1:I:310:THR:HG21	1.15	1.51
1:H:281:LEU:HD11	1:H:385:GLU:CB	1.38	1.51
1:L:265:GLN:NE2	3:N:40:LYS:CE	1.71	1.51
3:N:81:LYS:CD	3:N:113:PRO:HG3	1.34	1.51
1:H:265:GLN:NE2	1:H:393:SER:HB2	1.24	1.50
1:I:4:VAL:N	1:I:4:VAL:CA	1.71	1.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:108:ARG:NH1	3:N:89:TYR:CA	1.73	1.49
1:A:255:SER:CA	1:A:383:ARG:HD2	1.02	1.49
1:F:239:GLN:CG	2:M:45:MET:CE	1.91	1.49
3:N:41:TYR:HA	3:N:45:TYR:CD2	1.44	1.49
3:N:112:VAL:HG23	3:N:113:PRO:CD	1.37	1.49
3:N:60:ILE:CD1	3:N:97:ARG:HH11	1.25	1.48
1:F:185:VAL:HG21	2:M:37:GLY:CA	1.40	1.48
1:L:182:LEU:HD11	1:L:184:ASN:ND2	1.22	1.48
3:N:41:TYR:CA	3:N:45:TYR:CD2	1.95	1.48
1:D:281:LEU:CD2	1:D:385:GLU:HB3	1.39	1.48
1:L:108:ARG:NH1	3:N:89:TYR:HA	1.18	1.48
4:P:96:ILE:HD12	4:P:100:LEU:CD2	1.43	1.48
1:L:312:ASN:ND2	2:M:73:PHE:CZ	1.81	1.47
3:N:64:GLU:CB	3:N:93:LEU:HB2	1.39	1.47
1:E:182:LEU:CD2	1:E:184:ASN:ND2	1.74	1.47
1:F:239:GLN:CB	2:M:45:MET:CE	1.92	1.46
1:H:281:LEU:CD1	1:H:385:GLU:CB	1.88	1.46
3:N:112:VAL:CG2	3:N:113:PRO:HD2	1.01	1.46
3:N:80:ILE:HG21	3:N:116:PHE:CB	1.46	1.45
1:B:358:VAL:N	1:B:358:VAL:CA	1.79	1.45
3:N:49:THR:HB	3:N:112:VAL:CG1	1.45	1.45
1:I:8:THR:C	1:I:9:PRO:N	1.69	1.45
1:G:382:SER:C	1:G:383:ARG:N	1.70	1.45
1:C:181:VAL:HG12	1:C:182:LEU:N	1.27	1.44
1:D:5:GLN:NE2	1:E:36:TYR:CE2	1.80	1.44
3:N:60:ILE:CD1	3:N:97:ARG:HD2	1.47	1.44
1:D:282:TYR:CE2	1:D:386:LEU:HG	1.52	1.44
3:N:61:ASP:HB2	3:N:75:GLU:CB	1.30	1.44
1:J:384:THR:C	1:J:385:GLU:N	1.69	1.43
3:N:68:ALA:H	3:N:87:GLN:CD	1.20	1.43
1:B:108:ARG:CZ	1:D:314:SER:CB	1.96	1.43
1:B:8:THR:C	1:B:9:PRO:N	1.69	1.43
1:G:239:GLN:HG3	1:I:4:VAL:CA	1.47	1.43
1:L:263:SER:OG	3:N:40:LYS:CE	1.66	1.43
3:N:49:THR:CG2	3:N:82:CYS:O	1.65	1.43
1:D:108:ARG:NH2	1:I:314:SER:N	1.64	1.42
3:N:49:THR:CG2	3:N:83:PRO:HA	1.49	1.42
1:G:23:ALA:HB3	1:G:24:ASN:N	1.20	1.42
1:G:185:VAL:CB	2:M:4:ASN:HB2	1.50	1.42
3:N:28:ARG:NH1	3:N:37:GLU:HG2	1.31	1.42
1:I:392:ILE:C	1:I:393:SER:N	1.71	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:49:THR:CB	3:N:112:VAL:CG1	1.96	1.41
1:B:108:ARG:NH2	1:D:314:SER:N	1.66	1.41
1:D:187:GLN:CD	2:M:9:TYR:HD1	0.88	1.40
1:E:189:LYS:NZ	1:K:61:ASN:CB	1.75	1.40
1:L:257:LEU:C	1:L:258:TYR:N	1.71	1.40
3:N:112:VAL:CG2	3:N:113:PRO:CD	1.91	1.40
4:P:96:ILE:CD1	4:P:100:LEU:CD2	1.97	1.40
1:D:372:ARG:NH1	1:I:272:VAL:CG2	1.83	1.40
4:P:103:TYR:O	4:P:107:LEU:CD1	1.68	1.40
2:M:45:MET:CB	2:M:48:LEU:HD11	1.49	1.39
3:N:49:THR:HG23	3:N:83:PRO:CA	1.52	1.39
1:B:108:ARG:NH1	1:D:314:SER:CB	1.86	1.39
1:B:277:GLN:CB	1:B:394:THR:OG1	1.67	1.39
3:N:28:ARG:NH1	3:N:37:GLU:CG	1.84	1.39
1:E:381:THR:C	1:E:382:SER:N	1.72	1.38
1:H:392:ILE:HG22	1:H:393:SER:N	1.38	1.38
1:E:8:THR:HG21	1:E:11:GLN:CG	1.54	1.38
1:G:35:SER:C	1:G:36:TYR:N	1.76	1.38
3:N:41:TYR:HB3	3:N:45:TYR:CB	1.50	1.38
3:N:79:ARG:NH2	3:N:104:HIS:HB2	1.37	1.38
1:D:281:LEU:CD2	1:D:385:GLU:CB	1.99	1.37
1:L:11:GLN:O	1:L:15:LEU:CD1	1.72	1.37
1:H:7:LEU:CD2	1:H:353:LEU:HD22	1.53	1.37
1:J:383:ARG:C	2:M:60:TYR:CD1	1.98	1.37
3:N:66:ASP:C	3:N:87:GLN:NE2	1.76	1.37
1:B:281:LEU:CD1	1:B:385:GLU:CB	1.94	1.37
1:F:382:SER:CB	1:F:383:ARG:N	1.84	1.37
1:D:17:ASN:CB	1:D:20:ALA:HB2	1.52	1.37
1:H:392:ILE:CG2	1:H:393:SER:H	1.33	1.37
1:L:111:GLU:OE1	3:N:89:TYR:CB	1.72	1.37
3:N:64:GLU:HB2	3:N:93:LEU:CB	1.55	1.37
1:D:108:ARG:NH2	1:I:314:SER:CA	1.81	1.36
1:F:239:GLN:CG	2:M:45:MET:HE2	1.49	1.36
1:I:17:ASN:CB	1:I:20:ALA:HB2	1.52	1.36
1:D:187:GLN:CB	2:M:9:TYR:HE1	1.35	1.36
1:G:34:GLN:HE22	1:I:9:PRO:CB	1.22	1.36
1:J:4:VAL:N	1:K:239:GLN:CG	1.88	1.36
4:P:107:LEU:O	4:P:111:LEU:CD1	1.72	1.36
1:B:4:VAL:O	1:B:313:PHE:CE1	1.77	1.36
1:F:353:LEU:HD22	2:M:27:LEU:N	1.06	1.36
1:D:187:GLN:CG	2:M:9:TYR:CD1	2.09	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:384:THR:O	2:M:33:GLY:CA	1.74	1.36
1:B:358:VAL:CA	1:B:358:VAL:CG1	2.03	1.35
1:A:313:PHE:CE1	1:K:383:ARG:CA	1.90	1.35
1:B:44:THR:H	1:K:191:ARG:CZ	1.36	1.35
1:B:358:VAL:CG2	1:B:358:VAL:CA	1.94	1.35
1:B:358:VAL:CA	1:B:358:VAL:C	1.92	1.35
3:N:68:ALA:N	3:N:87:GLN:NE2	1.70	1.35
1:C:8:THR:HG22	1:C:9:PRO:CD	1.57	1.34
1:G:239:GLN:CG	1:I:4:VAL:CA	2.02	1.34
1:A:63:GLY:H	1:A:184:ASN:ND2	1.25	1.34
1:B:108:ARG:CZ	1:D:314:SER:HB2	1.50	1.34
1:B:281:LEU:HD11	1:B:385:GLU:CB	1.31	1.34
3:N:81:LYS:HD3	3:N:113:PRO:CG	1.57	1.34
4:P:96:ILE:CG2	4:P:100:LEU:HD13	1.57	1.34
1:D:389:ALA:HB2	1:I:354:GLN:NE2	1.42	1.34
1:B:108:ARG:CZ	1:D:314:SER:CA	2.06	1.34
1:F:312:ASN:OD1	2:M:21:THR:HB	1.26	1.34
1:K:245:ASN:O	1:K:246:GLY:N	1.60	1.34
1:L:265:GLN:NE2	3:N:40:LYS:NZ	1.75	1.33
3:N:80:ILE:CG2	3:N:116:PHE:HA	0.87	1.33
1:J:8:THR:CG2	1:J:9:PRO:CD	2.06	1.33
1:G:239:GLN:HG3	1:I:4:VAL:N	1.41	1.33
1:L:108:ARG:NH1	3:N:89:TYR:CB	1.84	1.33
1:G:15:LEU:HD22	1:G:18:GLN:NE2	1.01	1.33
1:L:312:ASN:CG	2:M:73:PHE:CE2	2.00	1.33
3:N:67:GLY:N	3:N:87:GLN:HE22	1.25	1.33
1:K:191:ARG:C	1:K:192:LEU:N	1.78	1.32
3:N:82:CYS:SG	3:N:116:PHE:CE2	2.22	1.32
1:F:185:VAL:CG2	2:M:37:GLY:C	1.98	1.32
1:G:382:SER:CB	1:G:383:ARG:N	1.93	1.32
1:A:255:SER:CA	1:A:383:ARG:CD	1.93	1.32
1:B:108:ARG:NH2	1:D:314:SER:HA	1.25	1.32
1:L:78:ASN:O	1:L:156:ALA:HA	1.23	1.32
1:K:282:TYR:HA	1:K:381:THR:CB	1.60	1.31
3:N:41:TYR:HA	3:N:45:TYR:CE2	1.65	1.31
4:P:37:GLY:C	4:P:39:PRO:HD2	1.48	1.31
1:F:185:VAL:HG21	2:M:37:GLY:C	1.51	1.31
1:H:381:THR:C	1:H:382:SER:N	1.83	1.31
1:G:63:GLY:H	1:G:184:ASN:CG	1.34	1.31
1:G:63:GLY:H	1:G:184:ASN:ND2	1.25	1.31
1:G:251:LEU:CD1	1:G:388:ASN:OD1	1.76	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:41:TYR:CB	3:N:45:TYR:CD2	2.11	1.31
1:C:8:THR:CG2	1:C:9:PRO:CD	2.06	1.30
1:F:11:GLN:O	1:F:15:LEU:HD13	1.25	1.30
1:A:255:SER:O	1:A:383:ARG:CG	1.78	1.30
1:G:185:VAL:HB	2:M:4:ASN:CB	1.61	1.30
1:C:245:ASN:O	1:C:246:GLY:N	1.60	1.29
1:G:185:VAL:CG2	2:M:7:PHE:O	1.79	1.29
1:I:5:GLN:OE1	1:I:310:THR:HG21	1.20	1.29
1:A:63:GLY:H	1:A:184:ASN:CG	1.34	1.29
1:E:189:LYS:NZ	1:K:61:ASN:N	1.79	1.29
4:P:12:GLY:O	4:P:16:LEU:HD13	1.18	1.29
1:L:280:ASN:OD1	1:L:352:THR:HG21	1.33	1.29
1:G:62:VAL:CA	1:G:184:ASN:OD1	1.81	1.29
3:N:80:ILE:CD1	3:N:116:PHE:HB3	1.61	1.28
1:D:389:ALA:CB	1:I:354:GLN:HE22	1.46	1.28
1:H:5:GLN:NE2	1:I:36:TYR:CD2	1.99	1.28
3:N:49:THR:CG2	3:N:112:VAL:HG11	1.63	1.28
1:B:108:ARG:NH1	1:D:314:SER:OG	1.63	1.28
1:F:247:TYR:CE2	2:M:43:GLN:NE2	2.02	1.28
1:H:281:LEU:HD12	1:H:385:GLU:OE1	1.20	1.28
1:K:283:ARG:N	1:K:381:THR:OG1	1.66	1.28
1:B:9:PRO:HG3	1:C:34:GLN:OE1	1.31	1.28
1:G:382:SER:CB	1:G:383:ARG:H	1.47	1.28
1:L:282:TYR:CE1	3:N:42:ASP:OD2	1.86	1.28
1:A:62:VAL:CA	1:A:184:ASN:OD1	1.81	1.27
1:D:372:ARG:HH11	1:I:272:VAL:CG2	1.42	1.27
1:F:311:ALA:CB	2:M:23:THR:HB	1.63	1.27
1:F:351:TYR:OH	2:M:29:TYR:CE2	1.79	1.27
1:J:16:ARG:CD	1:J:21:MET:SD	2.22	1.27
1:L:311:ALA:O	2:M:73:PHE:HE2	1.02	1.27
3:N:91:PRO:C	3:N:92:LEU:HD12	1.54	1.27
1:L:353:LEU:HA	2:M:76:PRO:CG	1.64	1.27
3:N:81:LYS:CD	3:N:113:PRO:CG	2.12	1.27
1:E:182:LEU:HD21	1:E:184:ASN:CG	1.54	1.27
1:L:263:SER:CB	3:N:40:LYS:HE2	1.64	1.27
1:C:104:PRO:HB3	1:C:188:SER:O	1.34	1.27
1:D:9:PRO:HG3	1:E:34:GLN:OE1	1.22	1.27
1:D:17:ASN:HB3	1:D:20:ALA:CB	1.63	1.27
1:G:245:ASN:O	1:G:245:ASN:CA	1.81	1.27
4:P:52:THR:C	4:P:53:LEU:HD12	1.53	1.27
1:D:389:ALA:CB	1:I:354:GLN:NE2	1.98	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:7:LEU:HD22	1:H:353:LEU:CD2	1.63	1.27
3:N:60:ILE:CD1	3:N:97:ARG:NH1	1.96	1.27
3:N:81:LYS:HB3	3:N:113:PRO:CG	1.63	1.26
1:L:312:ASN:ND2	2:M:73:PHE:CE2	2.01	1.26
1:J:383:ARG:C	2:M:60:TYR:HD1	1.31	1.26
1:J:384:THR:HG22	2:M:62:ALA:CB	1.64	1.26
1:A:245:ASN:O	1:A:245:ASN:CA	1.82	1.26
1:B:4:VAL:CB	1:B:4:VAL:CA	2.14	1.26
1:I:17:ASN:HB3	1:I:20:ALA:CB	1.63	1.26
1:K:282:TYR:CA	1:K:381:THR:OG1	1.84	1.26
3:N:49:THR:HG22	3:N:82:CYS:O	1.10	1.26
1:D:187:GLN:CB	2:M:9:TYR:CE1	2.12	1.25
1:E:8:THR:CG2	1:E:11:GLN:HG3	1.65	1.25
1:I:5:GLN:CD	1:I:310:THR:CG2	2.04	1.25
3:N:81:LYS:CB	3:N:113:PRO:HG2	1.63	1.25
1:J:384:THR:CG2	2:M:62:ALA:CB	2.13	1.25
1:K:104:PRO:O	1:K:188:SER:HB3	1.36	1.25
1:E:189:LYS:HZ3	1:K:61:ASN:N	1.29	1.25
1:D:187:GLN:CG	2:M:9:TYR:HD1	1.44	1.25
1:F:239:GLN:CB	2:M:45:MET:HE1	1.52	1.25
1:L:353:LEU:O	2:M:76:PRO:HD2	1.32	1.25
3:N:65:ASN:ND2	3:N:71:ILE:HD12	1.51	1.25
2:M:14:PRO:C	2:M:16:PRO:HD2	1.55	1.25
1:G:251:LEU:HD11	1:G:388:ASN:OD1	1.22	1.24
1:A:255:SER:O	1:A:383:ARG:HG3	1.27	1.24
4:P:12:GLY:O	4:P:16:LEU:CD1	1.84	1.24
1:F:382:SER:HB3	1:F:383:ARG:N	0.92	1.24
1:K:245:ASN:O	1:K:245:ASN:CA	1.85	1.23
1:A:62:VAL:HA	1:A:184:ASN:OD1	1.11	1.23
3:N:64:GLU:OE1	3:N:93:LEU:HB3	1.38	1.23
1:D:17:ASN:CB	1:D:20:ALA:CB	2.15	1.23
1:G:62:VAL:HA	1:G:184:ASN:OD1	1.11	1.23
1:J:8:THR:HG22	1:J:9:PRO:CD	1.67	1.23
1:I:5:GLN:OE1	1:I:310:THR:CG2	1.86	1.23
1:D:5:GLN:N	1:E:239:GLN:NE2	1.85	1.23
1:E:189:LYS:NZ	1:K:61:ASN:HB2	1.43	1.23
1:I:355:TYR:OH	1:I:393:SER:O	1.58	1.22
3:N:25:GLN:CB	3:N:107:SER:OG	1.86	1.22
1:C:245:ASN:O	1:C:245:ASN:CA	1.85	1.22
1:F:239:GLN:HG2	2:M:45:MET:CE	1.54	1.22
1:F:239:GLN:HG2	2:M:45:MET:CG	1.68	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:79:ARG:HH22	3:N:104:HIS:CB	1.49	1.22
3:N:94:VAL:HG22	3:N:103:ARG:NH1	1.51	1.22
1:F:185:VAL:CG1	2:M:38:ILE:H	1.53	1.22
1:G:23:ALA:CB	1:G:24:ASN:N	2.02	1.22
1:F:11:GLN:O	1:F:15:LEU:CD1	1.87	1.21
3:N:41:TYR:HB3	3:N:45:TYR:CG	1.48	1.21
1:I:281:LEU:HD11	1:I:385:GLU:CB	1.61	1.21
1:A:313:PHE:CE1	1:K:383:ARG:HA	1.41	1.21
1:L:75:ALA:HA	1:L:160:GLY:O	1.39	1.21
1:K:104:PRO:O	1:K:188:SER:CB	1.87	1.21
1:L:108:ARG:HH11	3:N:89:TYR:CA	1.38	1.20
1:L:150:ALA:C	1:L:151:PRO:N	1.94	1.20
1:A:255:SER:C	1:A:383:ARG:HD2	1.59	1.20
1:B:7:LEU:HD22	1:B:353:LEU:CD2	1.70	1.20
2:M:41:ALA:O	2:M:42:ARG:HG3	1.36	1.20
4:P:107:LEU:O	4:P:111:LEU:HD13	1.07	1.20
1:F:35:SER:HB3	1:F:240:LEU:CD2	1.70	1.20
1:H:4:VAL:N	1:I:239:GLN:CD	1.93	1.20
1:D:187:GLN:NE2	2:M:9:TYR:HB3	1.57	1.19
1:L:311:ALA:O	2:M:73:PHE:CE2	1.95	1.19
4:P:96:ILE:CD1	4:P:100:LEU:HD22	1.60	1.19
1:F:351:TYR:CE1	2:M:29:TYR:OH	1.94	1.19
1:L:381:THR:C	1:L:382:SER:N	1.96	1.19
3:N:64:GLU:CB	3:N:93:LEU:CB	2.17	1.19
3:N:68:ALA:H	3:N:87:GLN:NE2	1.33	1.19
3:N:80:ILE:HD13	3:N:116:PHE:CB	1.71	1.19
1:D:187:GLN:NE2	2:M:9:TYR:CD1	2.09	1.19
1:F:185:VAL:HA	2:M:38:ILE:O	1.35	1.19
1:J:384:THR:HG21	2:M:62:ALA:HB2	1.23	1.19
1:B:5:GLN:NE2	1:B:316:THR:HG23	1.40	1.19
1:L:64:ILE:HA	1:L:181:VAL:O	1.42	1.19
3:N:14:VAL:HG22	3:N:16:ASN:H	1.04	1.19
4:P:96:ILE:HG21	4:P:100:LEU:CD1	1.73	1.19
1:E:182:LEU:HD21	1:E:184:ASN:ND2	0.87	1.18
1:F:239:GLN:CB	2:M:45:MET:HE2	1.62	1.18
1:G:247:TYR:CZ	2:M:2:LEU:HD23	1.77	1.18
1:D:388:ASN:OD1	1:I:6:GLN:OE1	1.61	1.18
1:I:281:LEU:CD1	1:I:385:GLU:HB3	1.74	1.18
1:K:282:TYR:HA	1:K:381:THR:OG1	1.34	1.18
1:L:38:VAL:O	1:L:236:TYR:N	1.75	1.18
1:D:391:THR:OG1	1:I:356:GLY:O	1.61	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:111:GLU:OE1	3:N:89:TYR:HB3	1.36	1.18
4:P:103:TYR:O	4:P:107:LEU:HD13	1.01	1.18
1:L:312:ASN:CB	2:M:73:PHE:CZ	2.28	1.17
2:M:24:MET:H	2:M:25:PRO:CD	1.57	1.17
1:L:11:GLN:O	1:L:15:LEU:HD13	1.01	1.17
1:G:105:ASP:N	2:M:7:PHE:CE2	2.13	1.17
1:H:281:LEU:CD1	1:H:385:GLU:OE1	1.92	1.17
1:J:9:PRO:HG3	1:K:34:GLN:HA	1.19	1.17
1:L:312:ASN:HB2	2:M:73:PHE:CZ	1.79	1.17
3:N:62:ASN:CB	3:N:95:PRO:HG2	1.73	1.17
1:D:187:GLN:NE2	2:M:9:TYR:CB	2.08	1.17
1:L:182:LEU:CD1	1:L:184:ASN:ND2	2.08	1.17
3:N:61:ASP:CB	3:N:75:GLU:HB2	1.73	1.17
1:G:239:GLN:CD	1:I:4:VAL:CA	2.12	1.16
1:L:104:PRO:CB	1:L:188:SER:OG	1.91	1.16
1:L:80:HIS:O	1:L:156:ALA:CB	1.92	1.16
1:L:312:ASN:HB2	2:M:73:PHE:HZ	1.09	1.16
3:N:41:TYR:CB	3:N:45:TYR:CG	2.09	1.16
1:G:185:VAL:HG13	1:G:186:PRO:HD3	1.24	1.16
1:L:279:ALA:CA	3:N:43:LEU:HD11	1.74	1.16
1:B:392:ILE:O	1:B:393:SER:OG	1.64	1.16
1:E:189:LYS:HZ2	1:K:61:ASN:CG	1.49	1.16
3:N:39:VAL:CG1	3:N:90:PHE:HB3	1.76	1.15
1:K:102:TYR:O	1:K:190:GLN:HA	1.47	1.15
2:M:45:MET:CB	2:M:48:LEU:CD1	2.23	1.15
2:M:45:MET:HB2	2:M:48:LEU:CD1	1.77	1.15
1:H:7:LEU:HD13	1:H:353:LEU:HD13	1.16	1.15
1:F:239:GLN:CG	2:M:45:MET:HG2	1.75	1.15
1:B:7:LEU:CD2	1:B:353:LEU:HD22	1.77	1.15
1:H:265:GLN:NE2	1:H:393:SER:CB	2.10	1.14
1:C:238:ASP:OD2	1:I:106:ASN:OD1	1.63	1.14
1:L:312:ASN:CB	2:M:73:PHE:HZ	1.60	1.14
1:B:272:VAL:HG11	1:I:264:ALA:CB	1.77	1.14
1:B:395:THR:OG1	1:D:394:THR:C	1.87	1.14
1:E:187:GLN:HA	1:K:185:VAL:HA	1.14	1.14
1:F:383:ARG:HA	2:M:31:VAL:HG21	1.26	1.14
3:N:25:GLN:HB2	3:N:107:SER:OG	0.96	1.14
1:L:7:LEU:HB3	1:L:11:GLN:CB	1.55	1.14
1:D:5:GLN:HE21	1:D:316:THR:HG21	1.11	1.13
1:D:9:PRO:HG3	1:E:34:GLN:CD	1.67	1.13
1:E:8:THR:HB	1:E:11:GLN:HB2	1.30	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:384:THR:O	2:M:33:GLY:HA3	1.42	1.13
1:I:17:ASN:CB	1:I:20:ALA:CB	2.15	1.13
2:M:24:MET:H	2:M:25:PRO:HD3	1.06	1.13
4:P:19:ILE:CG2	4:P:23:PHE:HE1	1.62	1.13
1:C:190:GLN:C	1:C:191:ARG:HG3	1.69	1.13
1:G:245:ASN:O	1:G:246:GLY:N	1.81	1.13
1:H:9:PRO:HB3	1:I:34:GLN:HE22	1.00	1.13
4:P:15:VAL:HG13	4:P:16:LEU:HD12	1.30	1.13
1:D:389:ALA:HB1	1:I:354:GLN:OE1	1.47	1.13
1:E:189:LYS:NZ	1:K:61:ASN:CA	2.11	1.13
1:F:239:GLN:HB3	2:M:45:MET:CE	1.60	1.13
1:J:387:VAL:O	1:J:388:ASN:OD1	1.67	1.13
1:L:78:ASN:O	1:L:156:ALA:CA	1.96	1.13
1:B:5:GLN:CG	1:B:310:THR:HG21	1.79	1.13
1:D:387:VAL:CG2	1:I:6:GLN:NE2	2.10	1.12
1:D:257:LEU:HG	1:D:383:ARG:HG2	1.13	1.12
1:L:353:LEU:HA	2:M:76:PRO:CD	1.79	1.12
3:N:62:ASN:HB2	3:N:95:PRO:O	1.47	1.12
4:P:42:THR:O	4:P:45:GLN:HG3	1.49	1.12
1:B:44:THR:N	1:K:191:ARG:NH2	1.96	1.12
1:G:185:VAL:HG21	2:M:4:ASN:O	1.46	1.12
1:L:353:LEU:HA	2:M:76:PRO:HG3	1.14	1.12
1:A:245:ASN:O	1:A:246:GLY:N	1.81	1.12
1:K:7:LEU:HA	1:K:12:GLN:NE2	1.64	1.12
1:L:108:ARG:HH11	3:N:89:TYR:HB3	1.01	1.12
1:K:182:LEU:HD13	1:K:254:LEU:HD13	1.24	1.11
1:B:269:THR:HG21	1:I:372:ARG:HD3	1.17	1.11
1:D:7:LEU:HD22	1:D:353:LEU:CD2	1.80	1.11
1:E:8:THR:HG22	1:E:11:GLN:H	0.98	1.11
1:E:381:THR:CA	1:E:382:SER:N	2.12	1.11
1:G:239:GLN:CG	1:I:4:VAL:N	2.12	1.11
1:J:8:THR:HG23	1:J:9:PRO:HD2	1.12	1.11
1:D:108:ARG:HH22	1:I:314:SER:CA	1.46	1.11
1:F:312:ASN:HA	2:M:21:THR:OG1	1.49	1.11
1:G:34:GLN:NE2	1:I:9:PRO:CB	1.89	1.11
1:H:7:LEU:CD2	1:H:353:LEU:CD2	2.25	1.11
1:J:16:ARG:NH1	1:J:21:MET:HE1	1.64	1.11
1:B:44:THR:N	1:K:191:ARG:CZ	2.13	1.11
1:F:311:ALA:HB1	2:M:23:THR:HB	1.25	1.11
3:N:45:TYR:C	3:N:46:LEU:HD12	1.71	1.11
1:I:257:LEU:HD12	1:I:386:LEU:HD22	1.32	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:41:TYR:HB3	3:N:45:TYR:HB2	1.27	1.10
3:N:61:ASP:CB	3:N:75:GLU:CB	2.26	1.10
3:N:80:ILE:HG12	3:N:117:LEU:H	1.07	1.10
1:E:106:ASN:ND2	1:K:62:VAL:HG11	1.66	1.10
2:M:68:GLN:O	4:P:41:MET:SD	2.06	1.10
4:P:96:ILE:CD1	4:P:100:LEU:HD21	1.81	1.10
1:A:255:SER:C	1:A:383:ARG:CD	2.17	1.10
1:B:281:LEU:HD11	1:B:385:GLU:HB2	1.20	1.10
1:F:353:LEU:HA	2:M:26:LEU:HA	1.13	1.10
1:G:382:SER:CA	1:G:383:ARG:N	2.13	1.10
1:I:281:LEU:HD11	1:I:385:GLU:HB3	1.24	1.10
2:M:21:THR:HG22	2:M:23:THR:H	1.16	1.10
4:P:18:LEU:O	4:P:22:TRP:HD1	1.35	1.10
1:B:5:GLN:NE2	1:B:316:THR:HG21	1.34	1.10
1:B:389:ALA:HB2	1:D:354:GLN:HE22	1.17	1.10
1:L:104:PRO:HB3	1:L:188:SER:C	1.72	1.10
1:D:11:GLN:OE1	1:D:351:TYR:CD2	2.04	1.09
1:J:313:PHE:HZ	1:K:239:GLN:HG3	1.14	1.09
3:N:62:ASN:HB3	3:N:95:PRO:HG2	1.26	1.09
3:N:68:ALA:HB3	3:N:87:GLN:HG2	1.34	1.09
1:B:272:VAL:CG1	1:I:264:ALA:HB3	1.81	1.09
1:B:313:PHE:CE1	1:I:387:VAL:HG23	1.88	1.09
3:N:60:ILE:HD11	3:N:97:ARG:HH11	1.07	1.09
1:L:56:ASP:OD2	3:N:11:VAL:HG12	1.49	1.09
3:N:60:ILE:HD13	3:N:97:ARG:NH1	1.64	1.09
1:B:356:GLY:O	1:I:391:THR:OG1	1.70	1.09
1:D:5:GLN:NE2	1:D:316:THR:HG21	1.67	1.09
1:D:5:GLN:N	1:E:239:GLN:HE22	1.19	1.09
1:E:381:THR:HG1	1:E:382:SER:N	1.50	1.09
1:J:255:SER:HA	1:J:383:ARG:HD2	1.22	1.09
2:M:45:MET:HB3	2:M:48:LEU:HD11	1.30	1.08
1:B:4:VAL:O	1:B:313:PHE:CD1	2.05	1.08
1:K:101:TYR:OH	1:K:190:GLN:CD	1.73	1.08
1:L:11:GLN:C	1:L:15:LEU:HD13	1.72	1.08
1:L:265:GLN:NE2	3:N:40:LYS:HE3	1.50	1.08
1:L:312:ASN:CG	2:M:73:PHE:CZ	2.17	1.08
1:D:187:GLN:NE2	2:M:9:TYR:HD1	1.45	1.08
1:L:108:ARG:CA	3:N:89:TYR:OH	2.00	1.08
1:C:181:VAL:CG1	1:C:182:LEU:N	2.16	1.08
1:L:353:LEU:CD2	2:M:76:PRO:HG3	1.84	1.08
2:M:6:GLN:O	2:M:8:PRO:HD3	1.52	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:39:VAL:HG13	3:N:90:PHE:HB3	1.09	1.08
1:F:247:TYR:HE2	2:M:43:GLN:NE2	1.44	1.07
1:G:185:VAL:HG22	2:M:7:PHE:O	1.45	1.07
3:N:80:ILE:HG12	3:N:117:LEU:N	1.69	1.07
1:B:281:LEU:HD13	1:B:385:GLU:HB3	1.33	1.07
1:D:372:ARG:NH1	1:I:272:VAL:HG21	1.55	1.07
1:F:255:SER:HB3	2:M:35:ILE:HD11	1.32	1.07
1:F:311:ALA:CB	2:M:23:THR:CB	2.32	1.07
1:B:272:VAL:HG11	1:I:264:ALA:HB3	1.11	1.07
1:L:7:LEU:HB3	1:L:11:GLN:HB3	1.36	1.07
4:P:96:ILE:HD13	4:P:100:LEU:HD21	1.37	1.07
3:N:28:ARG:HH11	3:N:37:GLU:CD	1.56	1.07
1:F:185:VAL:HG21	2:M:37:GLY:HA3	1.09	1.07
1:F:185:VAL:CG1	2:M:38:ILE:N	2.16	1.07
1:A:63:GLY:N	1:A:184:ASN:CG	2.07	1.06
1:D:7:LEU:HD22	1:D:353:LEU:HD22	1.25	1.06
1:G:63:GLY:N	1:G:184:ASN:CG	2.07	1.06
1:D:387:VAL:HG22	1:I:6:GLN:CD	1.74	1.06
1:F:239:GLN:CD	2:M:45:MET:SD	2.34	1.06
1:G:239:GLN:CD	1:I:4:VAL:HA	1.74	1.06
1:J:4:VAL:N	1:K:239:GLN:HG3	1.71	1.06
1:J:184:ASN:ND2	1:J:247:TYR:CE1	2.22	1.06
1:B:11:GLN:OE1	1:B:351:TYR:CD2	2.08	1.06
1:B:11:GLN:OE1	1:B:351:TYR:HD2	1.37	1.06
1:G:185:VAL:HG21	2:M:7:PHE:O	1.54	1.06
1:D:281:LEU:HD21	1:D:385:GLU:CB	1.85	1.06
1:K:103:ASP:HA	1:K:190:GLN:HG2	1.37	1.06
1:D:11:GLN:O	1:D:15:LEU:CD1	2.04	1.06
1:K:63:GLY:O	1:K:183:ALA:HB3	1.54	1.06
1:L:6:GLN:O	1:L:7:LEU:HD13	1.56	1.06
3:N:57:CYS:SG	3:N:101:VAL:HG23	1.93	1.06
1:B:11:GLN:O	1:B:15:LEU:CD1	2.04	1.05
1:E:187:GLN:HA	1:K:184:ASN:O	1.54	1.05
1:E:182:LEU:CD2	1:E:184:ASN:CG	2.16	1.05
1:K:7:LEU:CA	1:K:12:GLN:HE22	1.69	1.05
4:P:96:ILE:HG21	4:P:100:LEU:HD13	1.11	1.05
1:D:5:GLN:NE2	1:E:36:TYR:CD2	2.23	1.05
1:F:311:ALA:HB1	2:M:21:THR:HG21	1.34	1.05
1:G:239:GLN:OE1	1:I:4:VAL:HA	1.57	1.05
1:H:281:LEU:HD13	1:H:385:GLU:CB	1.70	1.05
1:B:7:LEU:HD22	1:B:353:LEU:HD22	1.07	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:282:TYR:HE2	1:D:386:LEU:CG	1.69	1.05
1:F:239:GLN:CG	2:M:45:MET:CG	2.30	1.05
1:I:11:GLN:O	1:I:15:LEU:CD1	2.04	1.05
1:J:311:ALA:O	1:J:312:ASN:OD1	1.72	1.05
1:D:387:VAL:CG2	1:I:6:GLN:CD	2.24	1.04
1:B:5:GLN:CB	1:B:310:THR:HG21	1.87	1.04
1:D:282:TYR:CE2	1:D:386:LEU:CG	2.41	1.04
1:L:38:VAL:HG23	1:L:238:ASP:CB	1.86	1.04
1:C:8:THR:HG23	1:C:9:PRO:HD2	1.08	1.04
1:F:383:ARG:HA	2:M:31:VAL:CG2	1.86	1.04
1:G:34:GLN:HE22	1:I:9:PRO:HB2	0.90	1.04
1:L:111:GLU:OE1	3:N:89:TYR:CG	2.10	1.04
3:N:28:ARG:NH1	3:N:37:GLU:CD	2.08	1.04
1:F:239:GLN:HG2	2:M:45:MET:SD	1.95	1.04
1:L:80:HIS:O	1:L:156:ALA:HB2	1.54	1.04
4:P:106:SER:O	4:P:110:TYR:CD2	2.11	1.04
1:D:9:PRO:CG	1:E:34:GLN:OE1	2.05	1.03
3:N:37:GLU:HB2	3:N:92:LEU:HB3	1.38	1.03
3:N:66:ASP:O	3:N:87:GLN:NE2	1.91	1.03
1:B:281:LEU:HD21	1:B:385:GLU:C	1.78	1.03
1:C:14:ALA:HA	1:C:17:ASN:ND2	1.73	1.03
4:P:106:SER:O	4:P:110:TYR:HD2	1.41	1.03
1:D:7:LEU:CD2	1:D:353:LEU:HD22	1.87	1.03
1:D:108:ARG:HH22	1:I:314:SER:HA	0.91	1.03
1:I:5:GLN:CG	1:I:310:THR:HG21	1.89	1.03
1:J:382:SER:O	2:M:60:TYR:HE1	1.39	1.03
1:K:102:TYR:O	1:K:190:GLN:CA	2.06	1.03
1:D:387:VAL:HG21	1:I:6:GLN:NE2	1.72	1.03
1:K:282:TYR:C	1:K:381:THR:OG1	1.95	1.03
1:L:353:LEU:CA	2:M:76:PRO:HG3	1.88	1.03
1:B:5:GLN:CD	1:B:310:THR:CG2	2.27	1.03
3:N:37:GLU:O	3:N:92:LEU:HB2	1.59	1.03
3:N:50:GLN:HE21	3:N:86:LYS:HE2	1.24	1.03
3:N:67:GLY:CA	3:N:87:GLN:HE22	1.70	1.03
3:N:68:ALA:HB3	3:N:87:GLN:CG	1.89	1.03
1:F:35:SER:HB3	1:F:240:LEU:HD23	1.37	1.02
1:F:185:VAL:HG13	2:M:38:ILE:N	1.74	1.02
1:J:9:PRO:HG2	1:K:34:GLN:OE1	1.58	1.02
3:N:64:GLU:CD	3:N:93:LEU:HB3	1.79	1.02
3:N:67:GLY:N	3:N:87:GLN:NE2	1.96	1.02
1:J:8:THR:HG23	1:J:9:PRO:CD	1.80	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:108:ARG:CZ	3:N:89:TYR:HA	1.88	1.02
1:F:356:GLY:HA3	2:M:23:THR:HG22	1.40	1.02
1:J:313:PHE:HE2	1:K:238:ASP:OD2	1.40	1.02
1:J:384:THR:HG22	2:M:62:ALA:HB2	1.04	1.02
1:L:38:VAL:CG2	1:L:238:ASP:HB2	1.88	1.02
3:N:89:TYR:O	3:N:91:PRO:HD3	1.58	1.02
1:G:382:SER:HB2	1:G:383:ARG:N	1.60	1.02
1:L:108:ARG:HA	3:N:89:TYR:OH	1.58	1.02
1:L:265:GLN:NE2	3:N:40:LYS:CD	2.23	1.02
2:M:41:ALA:O	2:M:42:ARG:CG	2.06	1.02
1:A:63:GLY:N	1:A:184:ASN:ND2	2.07	1.02
1:F:185:VAL:HG22	2:M:37:GLY:C	1.75	1.02
2:M:72:THR:HG21	4:P:44:ASN:HB3	1.42	1.02
1:A:255:SER:CB	1:A:383:ARG:HD2	1.89	1.01
1:B:5:GLN:CD	1:B:310:THR:HG23	1.81	1.01
1:J:16:ARG:CZ	1:J:21:MET:HE3	1.88	1.01
1:B:5:GLN:HB3	1:B:310:THR:HG21	1.40	1.01
1:H:281:LEU:HD11	1:H:385:GLU:HB2	1.02	1.01
1:K:102:TYR:O	1:K:190:GLN:CB	2.07	1.01
1:L:6:GLN:O	1:L:7:LEU:HB2	1.59	1.01
1:B:5:GLN:OE1	1:B:310:THR:CG2	2.09	1.01
1:D:281:LEU:HD21	1:D:386:LEU:N	1.76	1.01
1:F:185:VAL:CG2	2:M:37:GLY:CA	2.35	1.01
1:G:63:GLY:N	1:G:184:ASN:ND2	2.07	1.01
1:L:353:LEU:CA	2:M:76:PRO:CD	2.38	1.01
3:N:81:LYS:CB	3:N:113:PRO:CG	2.27	1.01
4:P:52:THR:O	4:P:53:LEU:HD12	1.58	1.01
1:B:311:ALA:HB3	1:I:390:GLY:O	1.60	1.01
1:G:185:VAL:CG1	1:G:186:PRO:HD3	1.90	1.01
2:M:24:MET:N	2:M:25:PRO:CD	2.16	1.01
4:P:96:ILE:HD12	4:P:100:LEU:HD23	1.41	1.01
1:B:395:THR:CG2	1:I:395:THR:C	2.21	1.01
1:C:104:PRO:CB	1:C:188:SER:O	2.07	1.01
1:F:353:LEU:HD12	2:M:29:TYR:CZ	1.95	1.01
1:G:185:VAL:CG2	2:M:4:ASN:HB2	1.90	1.01
1:H:281:LEU:HD21	1:H:385:GLU:C	1.81	1.01
1:L:104:PRO:HB2	1:L:188:SER:OG	1.58	1.01
1:B:358:VAL:HA	1:B:358:VAL:HG22	1.41	1.00
3:N:5:ASN:CB	3:N:6:PRO:HD3	1.72	1.00
3:N:65:ASN:ND2	3:N:85:GLY:O	1.92	1.00
4:P:96:ILE:CB	4:P:100:LEU:HD22	1.91	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:ARG:NH1	1:I:272:VAL:HG23	1.73	1.00
1:E:188:SER:OG	1:E:189:LYS:O	1.79	1.00
1:H:7:LEU:HD21	1:H:353:LEU:HD22	1.38	1.00
1:I:254:LEU:O	1:I:383:ARG:NH1	1.95	1.00
3:N:112:VAL:HG22	3:N:113:PRO:HD2	1.31	1.00
1:J:382:SER:C	2:M:60:TYR:CE1	2.34	1.00
3:N:47:ALA:O	3:N:48:ASP:OD1	1.76	1.00
3:N:64:GLU:HB3	3:N:93:LEU:HB2	1.39	1.00
1:D:187:GLN:O	1:G:187:GLN:HG2	1.62	1.00
1:D:281:LEU:CD2	1:D:385:GLU:C	2.29	1.00
1:D:389:ALA:HB1	1:I:354:GLN:CD	1.82	1.00
1:F:185:VAL:CG2	2:M:38:ILE:N	2.23	1.00
1:L:282:TYR:CZ	3:N:42:ASP:OD2	2.13	1.00
1:F:16:ARG:O	1:F:17:ASN:N	1.95	1.00
1:L:104:PRO:HB3	1:L:188:SER:O	1.59	1.00
2:M:67:ILE:HG22	4:P:41:MET:HE1	1.44	1.00
3:N:112:VAL:HG22	3:N:113:PRO:CD	1.79	1.00
1:B:108:ARG:CZ	1:D:314:SER:HA	1.84	0.99
1:J:16:ARG:NH1	1:J:21:MET:CE	2.24	0.99
1:B:108:ARG:NE	1:D:314:SER:HB2	1.76	0.99
2:M:2:LEU:O	2:M:9:TYR:CE2	2.15	0.99
3:N:68:ALA:N	3:N:87:GLN:CD	2.00	0.99
1:F:239:GLN:CG	2:M:45:MET:SD	2.49	0.99
1:G:382:SER:HB2	1:G:383:ARG:H	0.84	0.99
1:L:280:ASN:HB3	1:L:352:THR:OG1	1.62	0.99
1:D:281:LEU:HD21	1:D:385:GLU:C	1.83	0.99
1:F:239:GLN:CA	2:M:45:MET:HE2	1.92	0.99
1:D:11:GLN:O	1:D:15:LEU:HD13	1.63	0.99
1:H:7:LEU:CD1	1:H:353:LEU:HD13	1.93	0.99
2:M:78:ILE:O	4:P:53:LEU:HD21	1.61	0.99
3:N:31:PHE:CZ	3:N:100:PHE:CD2	2.36	0.99
1:B:311:ALA:CB	1:I:390:GLY:O	2.11	0.99
1:D:277:GLN:HE21	1:D:394:THR:HG23	1.24	0.99
1:L:279:ALA:HA	3:N:43:LEU:HD11	1.40	0.99
3:N:28:ARG:HH11	3:N:37:GLU:CG	1.65	0.99
1:L:280:ASN:CG	1:L:352:THR:HG21	1.82	0.99
1:F:35:SER:CB	1:F:240:LEU:CD2	2.40	0.99
1:B:392:ILE:O	1:B:393:SER:O	1.80	0.99
1:D:187:GLN:CG	2:M:9:TYR:CE1	2.43	0.99
1:H:281:LEU:HD21	1:H:386:LEU:N	1.77	0.99
1:K:7:LEU:CA	1:K:12:GLN:NE2	2.25	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:19:ILE:HG23	4:P:23:PHE:HE1	1.24	0.98
1:H:7:LEU:HD13	1:H:353:LEU:CD1	1.92	0.98
1:H:9:PRO:HG3	1:I:34:GLN:OE1	1.64	0.98
3:N:80:ILE:HG21	3:N:116:PHE:CG	1.96	0.98
1:B:358:VAL:CA	1:B:358:VAL:HB	1.47	0.98
1:E:189:LYS:HZ2	1:K:61:ASN:HB2	0.83	0.98
1:F:357:ASN:H	2:M:23:THR:CG2	1.75	0.98
1:J:386:LEU:CD1	2:M:62:ALA:HB1	1.93	0.98
1:L:104:PRO:HA	1:L:189:LYS:O	1.64	0.98
3:N:80:ILE:HG23	3:N:116:PHE:CA	1.63	0.98
3:N:13:PRO:HD2	3:N:68:ALA:HB1	1.43	0.98
1:L:279:ALA:C	3:N:43:LEU:HD11	1.83	0.98
1:L:38:VAL:HG23	1:L:238:ASP:HB2	1.00	0.98
1:G:309:ARG:CD	1:G:314:SER:HA	1.94	0.97
1:D:7:LEU:HD13	1:D:353:LEU:HD13	1.44	0.97
1:G:255:SER:OG	1:G:386:LEU:HD21	1.64	0.97
1:H:9:PRO:CB	1:I:34:GLN:HE22	1.77	0.97
3:N:91:PRO:O	3:N:92:LEU:HD12	1.62	0.97
1:D:187:GLN:HG3	2:M:9:TYR:CD1	1.96	0.97
1:E:257:LEU:CG	1:E:383:ARG:HE	1.76	0.97
1:F:239:GLN:OE1	2:M:45:MET:SD	2.22	0.97
1:J:184:ASN:HD21	1:J:240:LEU:HD12	1.26	0.97
3:N:82:CYS:SG	3:N:116:PHE:HE2	1.72	0.97
1:D:281:LEU:CG	1:D:385:GLU:HB3	1.78	0.97
4:P:96:ILE:HG22	4:P:100:LEU:HD13	1.46	0.97
1:B:384:THR:O	1:B:387:VAL:CG1	2.13	0.97
1:D:108:ARG:CZ	1:I:314:SER:N	2.22	0.97
1:D:281:LEU:HD22	1:D:385:GLU:CB	1.79	0.97
1:D:281:LEU:HD22	1:D:385:GLU:HB3	1.01	0.97
1:I:384:THR:O	1:I:387:VAL:CG1	2.13	0.97
1:L:311:ALA:O	1:L:312:ASN:OD1	1.81	0.97
1:L:354:GLN:HA	2:M:75:GLN:HG2	1.43	0.97
3:N:39:VAL:HG13	3:N:90:PHE:CB	1.94	0.97
1:D:389:ALA:HB2	1:I:354:GLN:HE22	0.96	0.97
1:E:8:THR:CG2	1:E:11:GLN:H	1.78	0.97
1:F:185:VAL:CA	2:M:38:ILE:O	2.13	0.97
1:F:356:GLY:CA	2:M:23:THR:HG22	1.94	0.97
3:N:80:ILE:HG12	3:N:117:LEU:O	1.63	0.97
1:E:188:SER:OG	1:E:189:LYS:N	1.95	0.97
1:G:34:GLN:NE2	1:I:9:PRO:HB3	1.79	0.97
1:K:104:PRO:O	1:K:188:SER:OG	1.82	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:353:LEU:CA	2:M:76:PRO:CG	2.42	0.97
1:C:104:PRO:HB3	1:C:188:SER:HB3	1.44	0.97
1:F:353:LEU:HD13	2:M:27:LEU:O	1.65	0.97
3:N:49:THR:CG2	3:N:112:VAL:CG1	2.37	0.97
1:F:384:THR:O	2:M:33:GLY:N	1.98	0.96
1:I:11:GLN:O	1:I:15:LEU:HD13	1.63	0.96
3:N:5:ASN:HB3	3:N:6:PRO:HD3	1.44	0.96
1:B:7:LEU:HD13	1:B:353:LEU:HD13	1.47	0.96
1:B:11:GLN:O	1:B:15:LEU:HD13	1.63	0.96
4:P:96:ILE:HD13	4:P:100:LEU:CD2	1.87	0.96
1:D:384:THR:O	1:D:387:VAL:CG1	2.13	0.96
1:F:311:ALA:HB1	2:M:23:THR:CB	1.92	0.96
4:P:50:SER:O	4:P:51:VAL:HG12	1.65	0.96
1:B:108:ARG:HH21	1:D:314:SER:N	1.54	0.96
1:C:184:ASN:HB2	1:C:247:TYR:CE1	2.00	0.96
1:F:16:ARG:C	1:F:17:ASN:N	2.18	0.96
1:G:247:TYR:OH	2:M:2:LEU:CD2	2.14	0.96
1:B:6:GLN:HB2	1:I:388:ASN:HA	1.45	0.96
1:F:35:SER:CB	1:F:240:LEU:HD23	1.94	0.96
1:H:384:THR:O	1:H:387:VAL:CG1	2.13	0.96
1:L:263:SER:CB	3:N:40:LYS:CE	2.37	0.96
1:B:17:ASN:C	1:B:20:ALA:H	1.65	0.96
1:E:187:GLN:HA	1:K:185:VAL:CA	1.96	0.96
4:P:38:PRO:N	4:P:39:PRO:CD	2.29	0.96
1:D:187:GLN:HA	1:G:187:GLN:HE21	1.30	0.96
1:B:44:THR:H	1:K:191:ARG:NH2	1.58	0.95
1:C:190:GLN:OE1	1:C:191:ARG:N	1.99	0.95
1:F:185:VAL:HG13	2:M:38:ILE:H	1.26	0.95
1:G:239:GLN:NE2	1:I:313:PHE:HZ	1.64	0.95
1:D:21:MET:HA	1:D:252:ILE:HD12	1.47	0.95
1:L:193:LYS:NZ	3:N:67:GLY:O	2.00	0.95
3:N:31:PHE:CZ	3:N:100:PHE:HD2	1.80	0.95
1:B:358:VAL:HA	1:B:358:VAL:CG1	1.80	0.95
1:F:185:VAL:HG11	2:M:38:ILE:H	1.31	0.95
2:M:15:ILE:N	2:M:16:PRO:CD	2.30	0.95
1:B:257:LEU:HG	1:B:383:ARG:HG2	1.45	0.95
1:B:277:GLN:HB2	1:B:394:THR:OG1	0.78	0.95
1:D:108:ARG:NH2	1:I:314:SER:HA	1.46	0.95
1:E:182:LEU:CD2	1:E:184:ASN:HD21	1.53	0.95
3:N:62:ASN:HB3	3:N:95:PRO:CG	1.95	0.95
1:J:384:THR:HG21	2:M:62:ALA:CB	1.88	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:15:TYR:CE2	3:N:88:GLY:HA2	2.01	0.95
1:E:311:ALA:HB3	2:M:47:PHE:CE1	2.01	0.95
1:F:185:VAL:HG13	2:M:38:ILE:CB	1.97	0.95
1:I:281:LEU:CD1	1:I:385:GLU:CB	2.40	0.95
1:L:63:GLY:O	1:L:183:ALA:N	2.00	0.95
3:N:41:TYR:HB3	3:N:45:TYR:CD2	1.90	0.95
4:P:42:THR:O	4:P:45:GLN:CG	2.14	0.95
1:B:384:THR:O	1:B:387:VAL:HG13	1.67	0.94
1:B:392:ILE:HG22	1:B:393:SER:H	1.29	0.94
1:F:353:LEU:HA	2:M:26:LEU:CA	1.97	0.94
1:J:308:GLN:HE22	1:J:345:ASN:HD21	1.03	0.94
3:N:14:VAL:HG22	3:N:16:ASN:N	1.80	0.94
1:A:312:ASN:ND2	1:K:281:LEU:HB3	1.82	0.94
1:B:281:LEU:CD2	1:B:385:GLU:HB3	1.96	0.94
1:F:185:VAL:HG13	2:M:38:ILE:HB	1.48	0.94
1:D:11:GLN:CD	1:D:351:TYR:HD2	1.71	0.94
1:D:372:ARG:HH12	1:I:272:VAL:CG2	1.75	0.94
1:E:187:GLN:CA	1:K:185:VAL:HA	1.96	0.94
1:F:386:LEU:HD13	2:M:33:GLY:O	1.67	0.94
1:H:254:LEU:O	1:H:383:ARG:CZ	2.15	0.94
1:F:15:LEU:C	1:F:17:ASN:OD1	2.05	0.94
1:I:392:ILE:C	1:I:393:SER:CA	2.32	0.94
1:K:34:GLN:C	1:K:35:SER:N	2.20	0.94
3:N:28:ARG:HH12	3:N:37:GLU:CG	1.79	0.94
1:D:187:GLN:NE2	2:M:9:TYR:CG	2.36	0.94
1:G:15:LEU:CD2	1:G:18:GLN:NE2	1.93	0.94
1:J:313:PHE:CE2	1:K:238:ASP:OD2	2.21	0.94
1:F:10:ALA:HB2	2:M:26:LEU:CD2	1.98	0.94
3:N:18:CYS:O	3:N:19:ASP:OD1	1.85	0.94
1:B:281:LEU:CG	1:B:385:GLU:HB3	1.98	0.93
1:F:383:ARG:CA	2:M:31:VAL:HG21	1.98	0.93
3:N:92:LEU:C	3:N:93:LEU:HD12	1.89	0.93
4:P:50:SER:O	4:P:51:VAL:CG1	2.15	0.93
3:N:49:THR:CG2	3:N:82:CYS:C	2.36	0.93
1:G:251:LEU:HD13	1:G:388:ASN:OD1	1.67	0.93
1:L:104:PRO:C	1:L:188:SER:OG	2.06	0.93
1:B:17:ASN:HB3	1:B:20:ALA:HB2	1.47	0.93
1:C:104:PRO:CB	1:C:188:SER:HB3	1.97	0.93
1:D:281:LEU:HD11	1:D:382:SER:OG	1.68	0.93
1:G:309:ARG:NE	1:G:314:SER:HA	1.82	0.93
1:I:384:THR:O	1:I:387:VAL:HG13	1.67	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:16:ARG:CZ	1:J:21:MET:CE	2.47	0.93
1:B:395:THR:OG1	1:D:395:THR:N	1.96	0.93
1:H:384:THR:O	1:H:387:VAL:HG13	1.67	0.93
3:N:13:PRO:N	3:N:69:PHE:CZ	2.37	0.93
1:E:311:ALA:O	2:M:47:PHE:CE1	2.21	0.93
1:C:181:VAL:C	1:C:182:LEU:N	2.23	0.93
1:F:185:VAL:HG22	2:M:38:ILE:O	1.69	0.93
4:P:19:ILE:CG2	4:P:23:PHE:CE1	2.51	0.93
1:F:281:LEU:HG	2:M:29:TYR:CE1	2.04	0.93
3:N:80:ILE:CG1	3:N:117:LEU:H	1.82	0.93
1:B:5:GLN:CG	1:B:310:THR:CG2	2.46	0.93
1:D:17:ASN:C	1:D:21:MET:H	1.73	0.93
1:J:383:ARG:C	2:M:60:TYR:CE1	2.41	0.93
2:M:45:MET:HB2	2:M:48:LEU:HD13	1.50	0.93
1:D:387:VAL:HG21	1:I:6:GLN:HE22	1.32	0.92
1:D:372:ARG:HH11	1:I:272:VAL:HG21	0.77	0.92
3:N:37:GLU:HB2	3:N:92:LEU:CB	1.99	0.92
1:H:7:LEU:HD22	1:H:353:LEU:HD21	1.45	0.92
1:H:281:LEU:HD13	1:H:385:GLU:HB3	0.94	0.92
1:L:80:HIS:O	1:L:156:ALA:HB1	1.66	0.92
1:A:255:SER:HA	1:A:383:ARG:NE	1.83	0.92
1:D:384:THR:O	1:D:387:VAL:HG13	1.67	0.92
1:E:189:LYS:NZ	1:K:61:ASN:CG	2.13	0.92
1:J:182:LEU:CD2	1:J:249:LEU:HD13	1.98	0.92
1:L:6:GLN:O	1:L:7:LEU:CD1	2.16	0.92
1:J:385:GLU:C	1:J:386:LEU:HD12	1.90	0.92
1:B:279:ALA:HB2	1:B:391:THR:O	1.70	0.92
1:D:5:GLN:H	1:E:239:GLN:NE2	1.61	0.92
3:N:41:TYR:CA	3:N:45:TYR:HD2	1.66	0.92
4:P:37:GLY:C	4:P:39:PRO:CD	2.37	0.92
4:P:96:ILE:CG1	4:P:100:LEU:HD22	2.00	0.92
1:D:5:GLN:HE22	1:E:36:TYR:HE2	1.10	0.92
1:D:389:ALA:CB	1:I:354:GLN:CD	2.37	0.92
1:F:354:GLN:HA	2:M:26:LEU:HD21	1.52	0.92
1:J:7:LEU:HD13	1:J:351:TYR:O	1.70	0.92
1:B:392:ILE:HG22	1:B:393:SER:N	1.83	0.92
1:K:7:LEU:HA	1:K:12:GLN:HE22	1.25	0.92
1:I:185:VAL:HG13	1:I:186:PRO:HD3	1.51	0.92
1:A:312:ASN:HD21	1:K:281:LEU:HB3	1.32	0.91
1:F:185:VAL:HG22	2:M:38:ILE:N	1.82	0.91
1:F:185:VAL:HG22	2:M:38:ILE:C	1.90	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:277:GLN:HB2	1:I:394:THR:OG1	1.70	0.91
1:K:17:ASN:O	1:K:20:ALA:N	2.03	0.91
1:L:280:ASN:CB	1:L:352:THR:OG1	2.17	0.91
1:B:282:TYR:CE2	1:B:386:LEU:HG	2.05	0.91
2:M:75:GLN:CB	4:P:51:VAL:H	1.83	0.91
3:N:81:LYS:HD2	3:N:113:PRO:CB	1.99	0.91
1:B:269:THR:HG21	1:I:372:ARG:CD	2.00	0.91
1:E:8:THR:HG22	1:E:11:GLN:N	1.84	0.91
3:N:45:TYR:O	3:N:46:LEU:HD12	1.69	0.91
1:E:187:GLN:O	1:K:185:VAL:O	1.88	0.91
1:E:280:ASN:OD1	1:E:352:THR:HG21	1.71	0.91
1:J:382:SER:C	2:M:60:TYR:HE1	1.71	0.91
1:D:11:GLN:CD	1:D:351:TYR:CD2	2.44	0.91
1:I:257:LEU:CD2	1:I:383:ARG:HG2	2.01	0.91
1:J:313:PHE:CZ	1:K:239:GLN:HG3	2.05	0.91
1:L:38:VAL:HG21	1:L:238:ASP:OD2	1.69	0.91
1:L:182:LEU:HD11	1:L:184:ASN:HD22	1.17	0.91
1:J:255:SER:HA	1:J:383:ARG:CD	2.01	0.91
1:K:245:ASN:O	1:K:245:ASN:C	0.71	0.91
1:B:185:VAL:HG13	1:B:186:PRO:HD3	1.51	0.91
1:D:386:LEU:C	1:I:312:ASN:OD1	2.09	0.91
1:F:311:ALA:HB3	2:M:23:THR:HB	1.52	0.91
1:G:385:GLU:C	1:G:386:LEU:HD12	1.92	0.91
1:A:255:SER:O	1:A:383:ARG:CB	2.19	0.90
1:A:313:PHE:HE1	1:K:383:ARG:HA	1.29	0.90
1:B:395:THR:HG22	1:I:395:THR:C	1.67	0.90
1:F:311:ALA:HB2	2:M:23:THR:HG21	1.50	0.90
1:K:7:LEU:CB	1:K:12:GLN:HE22	1.84	0.90
1:L:6:GLN:O	1:L:7:LEU:CB	2.19	0.90
1:L:265:GLN:HG2	3:N:40:LYS:HZ1	1.36	0.90
1:L:265:GLN:HE22	3:N:40:LYS:CE	1.83	0.90
1:F:357:ASN:H	2:M:23:THR:HG21	1.35	0.90
3:N:25:GLN:CB	3:N:107:SER:HG	1.77	0.90
1:A:63:GLY:N	1:A:184:ASN:OD1	2.05	0.90
1:H:9:PRO:HB3	1:I:34:GLN:NE2	1.85	0.90
1:L:7:LEU:CB	1:L:11:GLN:CB	2.45	0.90
2:M:15:ILE:N	2:M:16:PRO:HD2	1.74	0.90
4:P:42:THR:O	4:P:45:GLN:NE2	2.00	0.90
1:H:265:GLN:HE22	1:H:393:SER:HB2	1.09	0.90
1:L:353:LEU:C	2:M:76:PRO:CD	2.40	0.90
3:N:60:ILE:HD12	3:N:97:ARG:HD3	1.48	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:245:ASN:O	1:C:245:ASN:C	0.70	0.90
1:F:353:LEU:CA	2:M:26:LEU:HA	2.00	0.90
1:D:187:GLN:HE22	2:M:9:TYR:CA	1.84	0.90
1:J:11:GLN:OE1	1:J:353:LEU:HD21	1.71	0.90
1:E:187:GLN:C	1:K:185:VAL:O	2.11	0.90
1:J:184:ASN:ND2	1:J:240:LEU:HD12	1.85	0.90
1:J:386:LEU:HD11	2:M:62:ALA:CB	2.02	0.90
1:L:265:GLN:NE2	3:N:40:LYS:HZ2	1.69	0.90
4:P:37:GLY:O	4:P:39:PRO:HD2	1.70	0.90
1:C:14:ALA:HA	1:C:17:ASN:HD22	1.34	0.90
1:D:257:LEU:CG	1:D:383:ARG:HG2	2.01	0.90
1:D:281:LEU:CD2	1:D:385:GLU:HB2	1.98	0.90
3:N:65:ASN:HD21	3:N:71:ILE:HD12	1.17	0.90
1:A:245:ASN:O	1:A:245:ASN:C	0.69	0.89
1:H:255:SER:O	1:H:383:ARG:HG3	1.71	0.89
1:L:353:LEU:O	2:M:76:PRO:CD	2.18	0.89
1:L:311:ALA:O	1:L:312:ASN:CG	2.10	0.89
1:L:6:GLN:C	1:L:7:LEU:CD1	2.40	0.89
3:N:62:ASN:CB	3:N:95:PRO:O	2.21	0.89
3:N:80:ILE:HG22	3:N:116:PHE:HA	1.50	0.89
1:D:185:VAL:HG13	1:D:186:PRO:HD3	1.50	0.89
1:D:281:LEU:HD21	1:D:386:LEU:HD12	1.52	0.89
1:E:187:GLN:C	1:K:185:VAL:C	2.31	0.89
1:G:245:ASN:O	1:G:245:ASN:C	0.69	0.89
1:H:185:VAL:HG13	1:H:186:PRO:HD3	1.50	0.89
1:I:17:ASN:CA	1:I:20:ALA:H	1.79	0.89
1:L:76:ILE:HB	1:L:154:ILE:CD1	2.03	0.89
1:L:186:PRO:O	1:L:187:GLN:HB2	1.71	0.89
3:N:66:ASP:C	3:N:87:GLN:HE22	1.56	0.89
1:E:182:LEU:HD21	1:E:184:ASN:HD22	1.36	0.89
1:F:185:VAL:CG2	2:M:37:GLY:HA3	2.00	0.89
1:F:239:GLN:HG2	2:M:45:MET:HE2	1.04	0.89
1:F:280:ASN:OD1	1:F:352:THR:HG21	1.71	0.89
1:G:63:GLY:N	1:G:184:ASN:OD1	2.05	0.89
3:N:61:ASP:HB2	3:N:75:GLU:HB2	0.90	0.89
1:B:355:TYR:OH	1:B:393:SER:O	1.88	0.89
1:I:254:LEU:O	1:I:383:ARG:CZ	2.21	0.89
1:C:104:PRO:HB3	1:C:188:SER:CB	2.04	0.88
1:D:389:ALA:HB1	1:I:354:GLN:NE2	1.85	0.88
1:F:383:ARG:HG2	2:M:31:VAL:CG2	2.03	0.88
1:J:308:GLN:HE22	1:J:345:ASN:ND2	1.69	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:64:GLU:OE1	3:N:93:LEU:CB	2.21	0.88
1:E:189:LYS:HZ1	1:K:61:ASN:N	1.67	0.88
1:L:77:THR:HA	1:L:158:ALA:O	1.73	0.88
1:B:389:ALA:HB2	1:D:354:GLN:NE2	1.88	0.88
4:P:38:PRO:N	4:P:39:PRO:HD2	1.84	0.88
1:L:151:PRO:HD2	1:L:162:LEU:HD22	1.56	0.88
3:N:37:GLU:CB	3:N:92:LEU:HB3	2.03	0.88
3:N:49:THR:HG21	3:N:112:VAL:CG1	2.01	0.88
4:P:35:TRP:CD2	4:P:110:TYR:HD1	1.74	0.88
1:D:282:TYR:HE2	1:D:386:LEU:HG	0.80	0.88
1:H:254:LEU:O	1:H:383:ARG:NH2	2.06	0.88
1:L:64:ILE:CA	1:L:181:VAL:O	2.21	0.88
1:L:263:SER:OG	3:N:40:LYS:HE2	0.70	0.88
1:B:106:ASN:OD1	1:E:238:ASP:OD2	1.92	0.88
1:D:187:GLN:O	1:G:187:GLN:CG	2.22	0.88
1:L:353:LEU:C	2:M:76:PRO:HD2	1.94	0.88
1:L:353:LEU:HD23	2:M:76:PRO:HG3	1.53	0.88
1:C:8:THR:HG22	1:C:9:PRO:HD2	0.88	0.87
1:B:395:THR:HG1	1:D:394:THR:C	1.73	0.87
1:F:16:ARG:C	1:F:17:ASN:CG	2.25	0.87
1:H:281:LEU:CD1	1:H:385:GLU:CG	2.52	0.87
1:I:355:TYR:HE2	1:I:394:THR:HG1	0.89	0.87
1:B:5:GLN:HE22	1:B:316:THR:CG2	1.87	0.87
1:G:185:VAL:HG13	2:M:7:PHE:HB2	1.55	0.87
3:N:64:GLU:OE1	3:N:93:LEU:HD23	1.75	0.87
1:L:183:ALA:C	1:L:184:ASN:N	2.27	0.87
1:F:312:ASN:HB3	2:M:20:PRO:HG2	1.56	0.87
1:K:182:LEU:HD13	1:K:254:LEU:CD1	2.04	0.87
1:F:255:SER:CB	2:M:35:ILE:HD11	2.05	0.87
1:G:257:LEU:HD21	1:G:383:ARG:HH21	1.38	0.87
3:N:49:THR:CB	3:N:112:VAL:HG12	2.02	0.87
3:N:60:ILE:CG1	3:N:97:ARG:HD2	2.04	0.87
1:D:187:GLN:HE22	2:M:9:TYR:CB	1.80	0.87
1:I:7:LEU:HD22	1:I:353:LEU:CD2	2.05	0.87
1:J:254:LEU:O	1:J:383:ARG:NE	2.08	0.87
1:E:8:THR:O	1:E:12:GLN:HG3	1.75	0.87
1:E:311:ALA:CB	2:M:47:PHE:HE1	1.87	0.87
4:P:19:ILE:O	4:P:23:PHE:HD1	1.58	0.86
1:I:382:SER:O	1:I:386:LEU:HD13	1.75	0.86
1:L:265:GLN:HE22	3:N:40:LYS:CD	1.84	0.86
1:B:382:SER:O	1:B:386:LEU:HD13	1.75	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:281:LEU:CD2	1:H:385:GLU:C	2.44	0.86
1:B:354:GLN:OE1	1:I:389:ALA:HB1	1.75	0.86
1:H:5:GLN:OE1	1:I:36:TYR:CE1	2.28	0.86
1:D:9:PRO:HG3	1:E:34:GLN:NE2	1.90	0.86
1:E:187:GLN:O	1:K:186:PRO:HD3	1.75	0.86
1:G:239:GLN:CD	1:I:313:PHE:HZ	1.79	0.86
1:L:108:ARG:NH1	3:N:89:TYR:HB3	1.68	0.86
3:N:27:VAL:CB	3:N:27:VAL:N	2.37	0.86
1:L:280:ASN:OD1	1:L:352:THR:CG2	2.21	0.86
3:N:13:PRO:N	3:N:69:PHE:CE1	2.43	0.86
4:P:16:LEU:O	4:P:20:TRP:HD1	1.58	0.86
1:H:382:SER:OG	1:H:385:GLU:HG3	1.76	0.86
1:L:353:LEU:HA	2:M:76:PRO:HD3	1.57	0.86
3:N:112:VAL:O	3:N:114:LEU:HD12	1.76	0.86
3:N:64:GLU:HB2	3:N:93:LEU:HB2	0.86	0.86
1:D:382:SER:OG	1:D:385:GLU:HG3	1.76	0.85
1:K:104:PRO:HB2	1:K:187:GLN:OE1	1.75	0.85
3:N:49:THR:CG2	3:N:83:PRO:CA	2.27	0.85
4:P:24:ARG:O	4:P:28:ALA:HB2	1.76	0.85
1:B:313:PHE:CZ	1:I:387:VAL:HG23	2.10	0.85
1:F:239:GLN:HA	2:M:45:MET:HE2	1.58	0.85
1:H:185:VAL:CG1	1:H:186:PRO:HD3	2.06	0.85
1:H:265:GLN:HE22	1:H:393:SER:CB	1.83	0.85
4:P:18:LEU:O	4:P:22:TRP:CD1	2.27	0.85
1:B:277:GLN:HB2	1:B:394:THR:CB	2.06	0.85
1:D:387:VAL:HG22	1:I:6:GLN:OE1	1.74	0.85
1:D:108:ARG:CZ	1:I:313:PHE:O	2.23	0.85
1:G:353:LEU:H	1:G:353:LEU:HD12	1.41	0.85
1:I:257:LEU:HG	1:I:383:ARG:HG2	1.59	0.85
3:N:55:VAL:HG22	3:N:56:GLN:N	1.91	0.85
3:N:61:ASP:HB2	3:N:75:GLU:HB3	1.54	0.85
3:N:62:ASN:CB	3:N:95:PRO:CG	2.52	0.85
1:G:309:ARG:HG3	1:G:313:PHE:O	1.76	0.85
1:H:355:TYR:CZ	1:H:394:THR:OG1	2.28	0.85
2:M:6:GLN:O	2:M:8:PRO:CD	2.25	0.85
1:F:383:ARG:HG2	2:M:31:VAL:HG21	1.59	0.85
1:I:382:SER:OG	1:I:385:GLU:HG3	1.76	0.85
1:E:187:GLN:CA	1:K:184:ASN:O	2.24	0.85
1:H:382:SER:O	1:H:386:LEU:HD13	1.75	0.85
1:I:185:VAL:CG1	1:I:186:PRO:HD3	2.06	0.85
3:N:80:ILE:HD13	3:N:116:PHE:HB3	0.87	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:80:ILE:HG23	3:N:116:PHE:HA	0.86	0.85
1:B:382:SER:OG	1:B:385:GLU:HG3	1.76	0.85
1:C:181:VAL:C	1:C:182:LEU:CA	2.45	0.85
1:K:102:TYR:O	1:K:190:GLN:HB3	1.76	0.85
1:J:386:LEU:HD11	2:M:62:ALA:HB1	1.59	0.84
1:B:358:VAL:CA	1:B:358:VAL:CB	0.85	0.84
1:E:187:GLN:O	1:K:185:VAL:C	2.14	0.84
1:G:62:VAL:C	1:G:184:ASN:OD1	2.15	0.84
2:M:2:LEU:O	2:M:9:TYR:HE2	1.57	0.84
1:J:382:SER:O	2:M:60:TYR:CE1	2.28	0.84
4:P:103:TYR:C	4:P:107:LEU:HD13	1.97	0.84
1:A:384:THR:O	1:A:385:GLU:HB2	1.75	0.84
1:D:382:SER:O	1:D:386:LEU:HD13	1.75	0.84
3:N:68:ALA:CB	3:N:87:GLN:HG2	2.07	0.84
1:H:355:TYR:CE2	1:H:394:THR:OG1	2.31	0.84
1:B:382:SER:OG	1:B:385:GLU:CG	2.26	0.84
1:J:8:THR:HG22	1:J:9:PRO:HD2	0.85	0.84
1:L:151:PRO:O	1:L:215:TYR:OH	1.94	0.84
4:P:35:TRP:O	4:P:36:GLU:HB2	1.77	0.84
1:C:8:THR:HG23	1:C:9:PRO:CD	1.89	0.84
1:E:187:GLN:HA	1:K:184:ASN:C	1.97	0.84
1:F:247:TYR:CZ	2:M:43:GLN:NE2	2.45	0.84
2:M:67:ILE:CG2	4:P:41:MET:HE1	2.07	0.84
3:N:28:ARG:O	3:N:103:ARG:HB2	1.78	0.84
3:N:65:ASN:ND2	3:N:71:ILE:CD1	2.39	0.84
1:D:17:ASN:CA	1:D:20:ALA:H	1.79	0.83
1:D:382:SER:OG	1:D:385:GLU:CG	2.26	0.83
1:E:189:LYS:HZ3	1:K:61:ASN:CA	1.79	0.83
1:E:191:ARG:HE	1:K:62:VAL:HG23	1.42	0.83
1:G:247:TYR:CZ	2:M:2:LEU:CD2	2.60	0.83
1:K:104:PRO:HB3	1:K:187:GLN:HB2	1.58	0.83
1:B:185:VAL:CG1	1:B:186:PRO:HD3	2.06	0.83
1:H:382:SER:OG	1:H:385:GLU:CG	2.26	0.83
1:J:21:MET:HA	1:J:252:ILE:HD12	1.60	0.83
1:L:265:GLN:NE2	3:N:40:LYS:HD2	1.93	0.83
3:N:81:LYS:CG	3:N:113:PRO:CG	2.56	0.83
1:D:11:GLN:NE2	1:D:351:TYR:HD2	1.76	0.83
1:H:12:GLN:HA	1:H:15:LEU:HD13	1.58	0.83
1:I:382:SER:OG	1:I:385:GLU:CG	2.26	0.83
3:N:60:ILE:HD12	3:N:97:ARG:NE	1.93	0.83
4:P:19:ILE:HG23	4:P:23:PHE:CE1	2.13	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:239:GLN:CA	2:M:45:MET:CE	2.53	0.83
1:G:309:ARG:HG3	1:G:314:SER:C	1.99	0.83
1:L:312:ASN:CG	2:M:73:PHE:HE2	1.78	0.83
1:B:264:ALA:HB3	1:D:272:VAL:HG11	1.60	0.83
1:B:279:ALA:CB	1:B:391:THR:O	2.27	0.83
1:D:187:GLN:HE21	2:M:9:TYR:HB3	1.41	0.83
3:N:81:LYS:HB2	3:N:113:PRO:HB2	1.61	0.83
1:J:5:GLN:HE22	1:K:38:VAL:CG2	1.92	0.83
1:K:282:TYR:HA	1:K:381:THR:HB	1.61	0.83
1:B:282:TYR:HE2	1:B:386:LEU:HG	1.43	0.83
1:G:15:LEU:HD22	1:G:18:GLN:HE22	1.42	0.83
1:H:281:LEU:CD1	1:H:385:GLU:CD	2.47	0.83
1:F:185:VAL:HG13	2:M:38:ILE:CA	2.08	0.82
1:F:251:LEU:HB3	1:F:385:GLU:OE1	1.78	0.82
1:F:312:ASN:HB3	2:M:20:PRO:CG	2.08	0.82
1:F:382:SER:HB3	1:F:383:ARG:CA	2.09	0.82
1:H:355:TYR:OH	1:H:392:ILE:O	1.95	0.82
1:I:16:ARG:O	1:I:18:GLN:N	2.12	0.82
1:L:111:GLU:OE1	3:N:89:TYR:HB2	1.77	0.82
3:N:67:GLY:C	3:N:87:GLN:NE2	2.31	0.82
1:A:62:VAL:C	1:A:184:ASN:OD1	2.16	0.82
1:E:189:LYS:HD3	1:K:61:ASN:HD22	1.42	0.82
1:H:5:GLN:OE1	1:I:36:TYR:CD1	2.31	0.82
1:K:283:ARG:H	1:K:381:THR:HG1	1.24	0.82
1:A:255:SER:C	1:A:383:ARG:CG	2.41	0.82
1:F:251:LEU:O	1:F:385:GLU:OE2	1.98	0.82
1:H:381:THR:CA	1:H:382:SER:N	2.42	0.82
1:L:65:VAL:HG21	1:L:190:GLN:OE1	1.78	0.82
3:N:14:VAL:CG2	3:N:16:ASN:H	1.88	0.82
1:F:383:ARG:CB	2:M:31:VAL:CG2	2.58	0.82
1:H:282:TYR:CE2	1:H:386:LEU:HG	2.13	0.82
4:P:19:ILE:HG22	4:P:23:PHE:CE1	2.14	0.82
1:B:354:GLN:HE22	1:I:389:ALA:HB2	1.45	0.82
3:N:49:THR:OG1	3:N:112:VAL:CG1	2.28	0.82
1:B:17:ASN:C	1:B:20:ALA:N	2.28	0.82
1:E:311:ALA:CB	2:M:47:PHE:CE1	2.60	0.82
3:N:41:TYR:CB	3:N:45:TYR:CB	2.46	0.82
1:B:382:SER:HG	1:B:385:GLU:HG3	1.45	0.81
1:F:384:THR:O	2:M:33:GLY:C	2.17	0.81
1:J:383:ARG:HB2	1:J:384:THR:N	1.95	0.81
1:H:7:LEU:HD22	1:H:353:LEU:HD22	1.30	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:101:TYR:O	3:N:89:TYR:OH	1.98	0.81
1:A:309:ARG:HG2	1:A:310:THR:C	2.00	0.81
1:A:353:LEU:H	1:A:353:LEU:HD12	1.41	0.81
1:B:354:GLN:NE2	1:I:389:ALA:HB2	1.94	0.81
1:D:384:THR:HA	1:D:387:VAL:CG1	2.11	0.81
1:E:28:ARG:HD3	1:E:175:THR:O	1.80	0.81
1:F:239:GLN:HB3	2:M:45:MET:HE1	0.83	0.81
1:L:170:LEU:HD13	1:L:181:VAL:HG21	1.60	0.81
1:L:282:TYR:HE1	3:N:42:ASP:OD2	1.63	0.81
3:N:49:THR:HG23	3:N:83:PRO:HA	0.82	0.81
3:N:81:LYS:CD	3:N:113:PRO:CB	2.57	0.81
3:N:81:LYS:CG	3:N:113:PRO:HG3	2.10	0.81
1:B:17:ASN:CB	1:B:20:ALA:HB2	2.10	0.81
1:D:257:LEU:HG	1:D:383:ARG:CG	2.05	0.81
1:D:281:LEU:HD21	1:D:385:GLU:HB2	1.56	0.81
1:E:7:LEU:O	1:E:8:THR:OG1	1.98	0.81
1:F:255:SER:HB3	2:M:35:ILE:CD1	2.10	0.81
1:G:257:LEU:HD21	1:G:383:ARG:NH2	1.95	0.81
1:J:384:THR:CG2	2:M:62:ALA:CA	2.58	0.81
3:N:103:ARG:HB3	3:N:105:LEU:HD11	1.61	0.81
1:F:311:ALA:CB	2:M:23:THR:CG2	2.57	0.81
1:F:386:LEU:CD1	2:M:33:GLY:O	2.28	0.81
1:I:8:THR:C	1:I:9:PRO:CA	2.49	0.81
1:J:384:THR:OG1	2:M:60:TYR:HB3	1.79	0.81
1:I:277:GLN:CG	1:I:394:THR:HB	2.08	0.81
3:N:80:ILE:CG1	3:N:117:LEU:O	2.28	0.81
4:P:15:VAL:HG13	4:P:16:LEU:CD1	2.09	0.81
1:A:255:SER:C	1:A:383:ARG:HG3	2.00	0.81
1:B:384:THR:HA	1:B:387:VAL:CG1	2.11	0.81
1:F:11:GLN:C	1:F:15:LEU:HD13	2.01	0.81
1:I:384:THR:HA	1:I:387:VAL:CG1	2.11	0.81
1:L:265:GLN:HE22	3:N:40:LYS:HD2	1.43	0.81
1:H:384:THR:HA	1:H:387:VAL:CG1	2.11	0.81
4:P:24:ARG:O	4:P:28:ALA:N	2.14	0.81
1:D:16:ARG:C	1:D:18:GLN:N	2.34	0.81
1:F:312:ASN:OD1	2:M:21:THR:CB	2.20	0.81
1:A:309:ARG:HG3	1:A:313:PHE:O	1.79	0.80
1:F:383:ARG:CA	2:M:31:VAL:CG2	2.57	0.80
1:G:23:ALA:O	1:G:24:ASN:N	2.14	0.80
4:P:24:ARG:O	4:P:28:ALA:CB	2.29	0.80
1:B:44:THR:H	1:K:191:ARG:NE	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:THR:C	1:B:387:VAL:HG12	2.02	0.80
3:N:50:GLN:HE21	3:N:86:LYS:CE	1.93	0.80
1:B:8:THR:C	1:B:9:PRO:CA	2.49	0.80
1:I:7:LEU:HD13	1:I:353:LEU:HD22	1.61	0.80
1:E:182:LEU:HD21	1:E:184:ASN:HD21	1.09	0.80
1:G:251:LEU:HD11	1:G:388:ASN:CG	2.01	0.80
1:B:358:VAL:C	1:B:358:VAL:CB	2.50	0.80
1:E:108:ARG:HD3	1:J:314:SER:HB2	1.60	0.80
1:K:104:PRO:CB	1:K:187:GLN:HB2	2.12	0.80
4:P:7:LEU:H	4:P:7:LEU:HD12	1.46	0.80
1:F:239:GLN:CD	2:M:45:MET:HG2	2.00	0.80
1:G:23:ALA:CA	1:G:24:ASN:N	2.44	0.80
1:G:247:TYR:OH	2:M:2:LEU:HD23	1.76	0.80
1:H:384:THR:C	1:H:387:VAL:HG12	2.02	0.80
1:J:308:GLN:NE2	1:J:345:ASN:HD21	1.78	0.80
4:P:96:ILE:HB	4:P:100:LEU:HD22	1.64	0.80
1:H:5:GLN:NE2	1:I:36:TYR:CG	2.49	0.80
1:I:7:LEU:HD13	1:I:353:LEU:HD13	1.61	0.80
3:N:49:THR:OG1	3:N:112:VAL:HG12	1.81	0.80
1:F:10:ALA:HB2	2:M:26:LEU:HD23	1.61	0.80
1:G:239:GLN:NE2	1:I:313:PHE:CZ	2.50	0.80
1:K:63:GLY:O	1:K:183:ALA:CB	2.30	0.80
3:N:37:GLU:CB	3:N:92:LEU:CB	2.59	0.80
1:B:395:THR:HG21	1:I:395:THR:C	2.00	0.80
1:H:265:GLN:HE21	1:H:393:SER:HB2	1.41	0.80
1:L:78:ASN:CB	1:L:154:ILE:O	2.30	0.80
3:N:55:VAL:HG22	3:N:56:GLN:H	1.45	0.80
1:C:104:PRO:O	1:C:188:SER:OG	1.99	0.79
1:C:186:PRO:O	1:C:187:GLN:HG3	1.82	0.79
1:F:239:GLN:CD	2:M:45:MET:CG	2.50	0.79
1:J:5:GLN:N	1:J:313:PHE:CZ	2.50	0.79
1:J:384:THR:HG21	2:M:61:HIS:C	2.00	0.79
1:L:353:LEU:CD2	2:M:76:PRO:CG	2.60	0.79
1:B:9:PRO:CG	1:C:34:GLN:OE1	2.23	0.79
1:J:28:ARG:HG3	1:J:177:LEU:HD12	1.65	0.79
3:N:27:VAL:CB	3:N:27:VAL:C	2.48	0.79
1:B:281:LEU:CD2	1:B:385:GLU:C	2.51	0.79
2:M:14:PRO:O	2:M:16:PRO:HD2	1.82	0.79
1:A:313:PHE:HE1	1:K:383:ARG:CA	1.81	0.79
1:I:355:TYR:HE2	1:I:394:THR:OG1	1.66	0.79
1:L:77:THR:HG23	1:L:158:ALA:O	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:353:LEU:HD22	2:M:76:PRO:CG	2.12	0.79
3:N:49:THR:HG21	3:N:82:CYS:O	1.80	0.79
1:B:313:PHE:HE1	1:I:387:VAL:HG23	1.41	0.79
1:F:351:TYR:HH	2:M:29:TYR:HE2	1.20	0.79
1:L:7:LEU:O	1:L:11:GLN:HG3	1.82	0.79
1:D:384:THR:C	1:D:387:VAL:HG12	2.02	0.79
1:G:185:VAL:HB	2:M:4:ASN:HB2	0.81	0.79
1:I:80:HIS:CD2	1:I:83:GLU:H	2.01	0.79
3:N:60:ILE:CD1	3:N:97:ARG:CD	2.19	0.79
1:B:357:ASN:C	1:B:358:VAL:CA	2.50	0.79
1:H:282:TYR:HE2	1:H:386:LEU:HG	1.44	0.79
1:J:16:ARG:HD3	1:J:21:MET:CE	2.12	0.79
1:A:80:HIS:CD2	1:A:83:GLU:H	2.01	0.78
1:C:104:PRO:HB3	1:C:188:SER:C	2.02	0.78
3:N:60:ILE:CD1	3:N:97:ARG:CZ	2.60	0.78
3:N:28:ARG:CZ	3:N:37:GLU:HG2	2.12	0.78
1:D:17:ASN:HA	1:D:20:ALA:H	1.48	0.78
1:D:21:MET:HA	1:D:252:ILE:CD1	2.12	0.78
1:I:277:GLN:CB	1:I:394:THR:OG1	2.31	0.78
1:I:384:THR:C	1:I:387:VAL:HG12	2.02	0.78
3:N:27:VAL:CA	3:N:27:VAL:CG1	2.61	0.78
1:G:80:HIS:CD2	1:G:83:GLU:H	2.01	0.78
1:C:102:TYR:O	1:C:190:GLN:HG2	1.84	0.78
1:C:184:ASN:HB2	1:C:247:TYR:HE1	1.47	0.78
1:G:182:LEU:CD2	2:M:4:ASN:HB3	2.13	0.78
1:I:17:ASN:C	1:I:21:MET:H	1.86	0.78
1:J:80:HIS:CD2	1:J:83:GLU:H	2.01	0.78
3:N:67:GLY:C	3:N:87:GLN:HE22	1.87	0.78
1:B:80:HIS:CD2	1:B:83:GLU:H	2.01	0.78
1:D:187:GLN:HE22	2:M:9:TYR:HA	1.48	0.78
1:I:7:LEU:HD22	1:I:353:LEU:HD22	1.63	0.78
1:J:31:VAL:O	1:J:35:SER:N	2.17	0.78
1:L:6:GLN:C	1:L:7:LEU:HD12	2.04	0.78
3:N:49:THR:HB	3:N:112:VAL:HG11	0.78	0.78
1:B:389:ALA:CB	1:D:354:GLN:OE1	2.32	0.78
1:L:180:ALA:HB3	1:L:254:LEU:HD23	1.65	0.78
3:N:80:ILE:HG23	3:N:116:PHE:C	2.03	0.78
1:F:247:TYR:HE2	2:M:43:GLN:HE21	1.23	0.78
3:N:41:TYR:C	3:N:45:TYR:HD2	1.85	0.78
3:N:94:VAL:CG2	3:N:103:ARG:NH1	2.42	0.78
1:B:4:VAL:CB	1:B:4:VAL:N	2.46	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:80:HIS:CD2	1:D:83:GLU:H	2.01	0.77
1:L:283:ARG:NH1	1:L:382:SER:HB3	1.99	0.77
3:N:112:VAL:O	3:N:114:LEU:CD1	2.32	0.77
1:B:108:ARG:NH2	1:D:313:PHE:O	2.17	0.77
1:E:182:LEU:HD23	1:E:184:ASN:OD1	1.83	0.77
1:E:189:LYS:HD3	1:K:61:ASN:ND2	1.98	0.77
1:I:257:LEU:CG	1:I:383:ARG:HG2	2.13	0.77
1:J:239:GLN:O	1:J:241:PRO:HD3	1.84	0.77
3:N:91:PRO:C	3:N:92:LEU:CD1	2.46	0.77
1:I:17:ASN:CB	1:I:20:ALA:HB3	2.05	0.77
4:P:35:TRP:CD2	4:P:110:TYR:CD1	2.38	0.77
4:P:52:THR:C	4:P:53:LEU:CD1	2.45	0.77
1:D:108:ARG:NH2	1:I:313:PHE:O	2.17	0.77
2:M:45:MET:HB3	2:M:48:LEU:CD1	2.01	0.77
1:G:106:ASN:ND2	1:G:191:ARG:HH22	1.83	0.77
1:G:185:VAL:HG23	2:M:4:ASN:H	1.50	0.77
1:I:17:ASN:HA	1:I:20:ALA:H	1.48	0.77
1:I:382:SER:HG	1:I:385:GLU:HG3	1.47	0.77
1:J:391:THR:OG1	2:M:67:ILE:HG23	1.84	0.77
1:L:7:LEU:HB3	1:L:11:GLN:HB2	1.63	0.77
1:L:11:GLN:O	1:L:15:LEU:HD12	1.83	0.77
1:L:265:GLN:NE2	3:N:40:LYS:HZ1	1.79	0.77
1:B:354:GLN:HE22	1:I:389:ALA:CB	1.97	0.77
1:D:4:VAL:O	1:D:313:PHE:CE1	2.37	0.77
1:H:80:HIS:CD2	1:H:83:GLU:H	2.01	0.77
1:I:7:LEU:CD2	1:I:353:LEU:HD22	2.14	0.77
1:L:265:GLN:CG	3:N:40:LYS:HZ1	1.97	0.77
1:D:372:ARG:HH12	1:I:272:VAL:HG23	1.39	0.77
1:L:353:LEU:CB	2:M:76:PRO:HG3	2.15	0.77
3:N:53:THR:O	3:N:79:ARG:NE	2.12	0.77
3:N:116:PHE:C	3:N:117:LEU:HD12	2.05	0.77
1:D:187:GLN:OE1	2:M:9:TYR:CD1	2.37	0.77
1:I:17:ASN:HB3	1:I:20:ALA:HB2	0.79	0.77
3:N:65:ASN:HD22	3:N:71:ILE:HD12	1.47	0.77
4:P:13:GLY:O	4:P:17:ILE:HG13	1.85	0.77
1:B:106:ASN:ND2	1:B:191:ARG:HH22	1.83	0.77
1:B:257:LEU:CG	1:B:383:ARG:HG2	2.14	0.77
1:E:311:ALA:O	2:M:47:PHE:HE1	1.65	0.77
1:I:4:VAL:N	1:I:4:VAL:CB	2.46	0.77
1:I:7:LEU:CD1	1:I:353:LEU:HD22	2.14	0.77
1:F:11:GLN:O	1:F:15:LEU:HD12	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ASN:ND2	1:A:191:ARG:HH22	1.83	0.76
1:B:63:GLY:HA2	1:B:184:ASN:ND2	2.01	0.76
1:B:5:GLN:CD	1:B:310:THR:HG21	1.99	0.76
1:D:106:ASN:ND2	1:D:191:ARG:HH22	1.83	0.76
2:M:75:GLN:HB3	4:P:51:VAL:H	1.51	0.76
4:P:42:THR:O	4:P:45:GLN:CD	2.23	0.76
1:A:63:GLY:H	1:A:184:ASN:HD21	1.32	0.76
1:A:354:GLN:HB2	1:A:357:ASN:ND2	1.99	0.76
1:B:272:VAL:CG1	1:I:264:ALA:CB	2.51	0.76
1:E:106:ASN:ND2	1:K:62:VAL:CG1	2.46	0.76
1:H:63:GLY:HA2	1:H:184:ASN:ND2	2.01	0.76
1:H:106:ASN:ND2	1:H:191:ARG:HH22	1.83	0.76
1:G:63:GLY:H	1:G:184:ASN:HD21	1.32	0.76
1:G:354:GLN:HB2	1:G:357:ASN:ND2	1.99	0.76
1:H:308:GLN:HE22	1:H:345:ASN:HD21	1.34	0.76
1:L:78:ASN:O	1:L:157:GLY:N	2.18	0.76
3:N:25:GLN:HB2	3:N:107:SER:HG	0.95	0.76
4:P:5:LYS:C	4:P:6:LEU:HD12	2.06	0.76
1:B:358:VAL:N	1:B:358:VAL:CB	2.48	0.76
1:I:308:GLN:HE22	1:I:345:ASN:HD21	1.34	0.76
4:P:6:LEU:HB3	4:P:7:LEU:HD12	1.68	0.76
1:B:257:LEU:HD12	1:B:386:LEU:HD22	1.67	0.76
1:C:280:ASN:OD1	1:C:352:THR:HG21	1.86	0.76
1:I:106:ASN:ND2	1:I:191:ARG:HH22	1.83	0.76
1:K:380:PHE:O	1:K:381:THR:OG1	2.01	0.76
1:A:255:SER:HA	1:A:383:ARG:CZ	2.14	0.76
1:F:185:VAL:CG2	2:M:38:ILE:O	2.33	0.76
1:K:280:ASN:OD1	1:K:352:THR:HG21	1.86	0.76
3:N:49:THR:HG21	3:N:112:VAL:HG13	1.67	0.76
1:D:7:LEU:HD13	1:D:353:LEU:HD22	1.68	0.76
1:B:4:VAL:CB	1:B:4:VAL:C	2.55	0.75
1:H:4:VAL:N	1:I:239:GLN:OE1	2.19	0.75
1:I:257:LEU:N	1:I:381:THR:O	2.15	0.75
1:J:106:ASN:ND2	1:J:191:ARG:HH22	1.83	0.75
1:C:14:ALA:CA	1:C:17:ASN:ND2	2.49	0.75
1:F:281:LEU:HA	2:M:29:TYR:CE1	2.21	0.75
1:L:7:LEU:O	1:L:11:GLN:CG	2.35	0.75
1:K:101:TYR:OH	1:K:190:GLN:CG	2.34	0.75
2:M:4:ASN:O	2:M:7:PHE:O	2.03	0.75
1:B:280:ASN:O	1:B:281:LEU:HB3	1.87	0.75
1:B:311:ALA:CB	1:I:390:GLY:C	2.54	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17:ASN:CB	1:D:20:ALA:HB3	2.05	0.75
1:E:257:LEU:HG	1:E:383:ARG:HE	1.49	0.75
1:J:21:MET:HA	1:J:252:ILE:CD1	2.16	0.75
1:H:281:LEU:HD13	1:H:385:GLU:CG	2.14	0.75
4:P:96:ILE:HD12	4:P:100:LEU:HD22	1.32	0.75
1:B:354:GLN:HB2	1:B:357:ASN:ND2	2.01	0.75
1:D:389:ALA:CB	1:I:354:GLN:OE1	2.31	0.75
1:B:108:ARG:NH1	1:D:314:SER:CA	2.37	0.75
1:B:354:GLN:NE2	1:I:389:ALA:CB	2.49	0.75
1:D:354:GLN:HB2	1:D:357:ASN:ND2	2.02	0.75
1:E:8:THR:CB	1:E:11:GLN:HB2	2.13	0.75
1:G:382:SER:C	1:G:383:ARG:CA	2.54	0.75
1:G:35:SER:C	1:G:36:TYR:CA	2.56	0.75
3:N:66:ASP:C	3:N:87:GLN:HE21	1.74	0.75
1:A:255:SER:HA	1:A:383:ARG:HD2	0.79	0.74
1:L:76:ILE:O	1:L:154:ILE:HD13	1.86	0.74
3:N:62:ASN:ND2	3:N:95:PRO:HG2	2.02	0.74
1:A:308:GLN:HE22	1:A:345:ASN:HD21	1.34	0.74
1:F:351:TYR:OH	2:M:29:TYR:HE2	1.60	0.74
1:F:383:ARG:CG	2:M:31:VAL:HG21	2.17	0.74
1:L:257:LEU:CA	1:L:258:TYR:N	2.50	0.74
1:D:63:GLY:HA2	1:D:184:ASN:ND2	2.01	0.74
1:E:312:ASN:OD1	2:M:47:PHE:CE1	2.39	0.74
1:F:357:ASN:N	2:M:23:THR:CG2	2.50	0.74
1:K:104:PRO:CB	1:K:187:GLN:CB	2.65	0.74
1:D:281:LEU:CD2	1:D:386:LEU:HD12	2.17	0.74
1:G:185:VAL:CG1	2:M:7:PHE:HB2	2.18	0.74
1:I:11:GLN:OE1	1:I:351:TYR:CD2	2.40	0.74
1:B:281:LEU:HD21	1:B:386:LEU:N	2.01	0.74
1:J:354:GLN:HB2	1:J:357:ASN:ND2	2.02	0.74
1:L:182:LEU:HD11	1:L:184:ASN:HD21	1.43	0.74
1:L:280:ASN:CG	1:L:352:THR:CG2	2.55	0.74
3:N:50:GLN:NE2	3:N:86:LYS:HE2	2.00	0.74
1:D:17:ASN:HB3	1:D:20:ALA:HB2	0.79	0.74
1:L:64:ILE:CG2	1:L:180:ALA:HB1	2.17	0.74
4:P:26:ARG:HB2	4:P:27:PRO:HD3	1.68	0.74
1:A:384:THR:O	1:A:385:GLU:CB	2.36	0.74
1:B:41:GLN:HG2	1:K:106:ASN:ND2	2.03	0.74
1:D:281:LEU:CD2	1:D:385:GLU:CA	2.65	0.74
1:D:386:LEU:O	1:I:312:ASN:OD1	2.06	0.74
1:C:14:ALA:O	1:C:17:ASN:ND2	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:60:ILE:HD12	3:N:97:ARG:HD2	0.74	0.74
1:D:17:ASN:HB2	1:D:20:ALA:CB	2.18	0.74
1:D:308:GLN:HE22	1:D:345:ASN:HD21	1.34	0.74
1:F:311:ALA:O	1:F:312:ASN:OD1	2.05	0.74
1:K:17:ASN:O	1:K:20:ALA:HB3	1.87	0.74
1:L:312:ASN:ND2	2:M:73:PHE:CE1	2.51	0.74
1:I:63:GLY:HA2	1:I:184:ASN:ND2	2.01	0.74
1:I:281:LEU:HD11	1:I:385:GLU:HB2	1.68	0.74
1:I:354:GLN:HB2	1:I:357:ASN:ND2	2.02	0.74
1:K:191:ARG:C	1:K:192:LEU:CA	2.56	0.74
1:L:353:LEU:CA	2:M:76:PRO:HD3	2.11	0.74
1:H:355:TYR:OH	1:H:394:THR:OG1	1.83	0.73
1:H:355:TYR:CE1	1:H:391:THR:HB	2.23	0.73
1:J:280:ASN:HD22	1:J:355:TYR:N	1.86	0.73
4:P:103:TYR:O	4:P:107:LEU:HD12	1.87	0.73
1:L:104:PRO:CA	1:L:188:SER:OG	2.35	0.73
3:N:15:TYR:CD2	3:N:47:ALA:CB	2.72	0.73
1:B:185:VAL:HG13	1:B:186:PRO:CD	2.18	0.73
1:J:28:ARG:NH2	1:J:253:ASP:OD1	2.19	0.73
1:L:78:ASN:C	1:L:156:ALA:HA	2.08	0.73
3:N:28:ARG:HH12	3:N:37:GLU:CB	2.00	0.73
3:N:103:ARG:HB3	3:N:105:LEU:CD1	2.17	0.73
1:B:43:GLU:C	1:K:191:ARG:NH2	2.34	0.73
1:C:190:GLN:C	1:C:191:ARG:CG	2.55	0.73
1:D:280:ASN:HD22	1:D:355:TYR:N	1.86	0.73
1:H:354:GLN:HB2	1:H:357:ASN:ND2	2.02	0.73
1:L:312:ASN:CB	2:M:73:PHE:CE2	2.63	0.73
1:F:311:ALA:HB2	2:M:23:THR:CG2	2.18	0.73
1:H:392:ILE:CG2	1:H:393:SER:N	2.11	0.73
1:L:263:SER:HB2	3:N:40:LYS:CE	2.16	0.73
1:D:5:GLN:HE21	1:D:316:THR:CG2	1.97	0.73
1:F:382:SER:O	1:F:383:ARG:HG3	1.88	0.73
1:H:384:THR:O	1:H:387:VAL:HG12	1.89	0.73
1:J:384:THR:HG21	2:M:62:ALA:CA	2.16	0.73
1:L:265:GLN:CD	3:N:40:LYS:NZ	2.41	0.73
3:N:80:ILE:CG2	3:N:116:PHE:CB	2.41	0.73
3:N:112:VAL:CB	3:N:113:PRO:HD2	2.13	0.73
1:B:308:GLN:HE22	1:B:345:ASN:HD21	1.34	0.73
1:D:277:GLN:N	1:D:394:THR:OG1	2.19	0.73
1:E:311:ALA:O	1:E:312:ASN:OD1	2.05	0.73
1:G:309:ARG:HG3	1:G:314:SER:O	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:309:ARG:HG3	1:G:314:SER:CA	2.19	0.73
1:H:12:GLN:CA	1:H:15:LEU:HD13	2.17	0.73
1:J:182:LEU:HD22	1:J:249:LEU:HD13	1.71	0.73
1:B:254:LEU:O	1:B:383:ARG:CZ	2.37	0.73
1:I:185:VAL:HG13	1:I:186:PRO:CD	2.18	0.73
3:N:15:TYR:CD2	3:N:47:ALA:HB3	2.23	0.73
1:F:351:TYR:CZ	2:M:29:TYR:CZ	2.75	0.73
1:G:247:TYR:CE1	2:M:2:LEU:HD23	2.24	0.73
1:H:5:GLN:NE2	1:I:36:TYR:CE2	2.38	0.73
1:I:280:ASN:HD22	1:I:355:TYR:N	1.86	0.73
1:L:182:LEU:HD21	1:L:184:ASN:HD21	1.54	0.73
1:A:309:ARG:HG2	1:A:310:THR:O	1.88	0.73
1:H:185:VAL:HG13	1:H:186:PRO:CD	2.18	0.73
1:B:352:THR:HB	1:B:357:ASN:HB2	1.71	0.72
1:F:383:ARG:CB	2:M:31:VAL:HG21	2.18	0.72
1:I:384:THR:O	1:I:387:VAL:HG12	1.89	0.72
1:I:17:ASN:N	1:I:18:GLN:N	2.38	0.72
3:N:59:TYR:HB3	3:N:98:ALA:N	2.02	0.72
1:A:255:SER:HA	1:A:383:ARG:NH1	1.97	0.72
1:G:280:ASN:HD22	1:G:355:TYR:N	1.86	0.72
1:H:7:LEU:O	1:H:8:THR:HB	1.89	0.72
1:I:281:LEU:CD2	1:I:385:GLU:HB3	2.18	0.72
1:F:354:GLN:HA	2:M:26:LEU:CD2	2.19	0.72
1:H:254:LEU:O	1:H:383:ARG:NH1	2.21	0.72
1:H:280:ASN:HD22	1:H:355:TYR:N	1.86	0.72
2:M:47:PHE:C	2:M:48:LEU:HD12	2.08	0.72
1:E:381:THR:HA	1:E:382:SER:N	2.02	0.72
1:F:383:ARG:CG	2:M:31:VAL:CG2	2.67	0.72
1:J:313:PHE:HZ	1:K:239:GLN:CG	1.99	0.72
1:B:358:VAL:HA	1:B:358:VAL:CB	0.99	0.72
1:E:182:LEU:HD23	1:E:184:ASN:CG	2.10	0.72
1:J:9:PRO:HG2	1:K:34:GLN:CD	2.09	0.72
1:J:182:LEU:HD21	1:J:249:LEU:CD1	2.20	0.72
3:N:64:GLU:CB	3:N:93:LEU:HB3	2.19	0.72
1:A:280:ASN:HD22	1:A:355:TYR:N	1.86	0.72
1:B:280:ASN:HD22	1:B:355:TYR:N	1.86	0.72
1:G:310:THR:OG1	1:G:313:PHE:HB2	1.89	0.72
1:K:29:GLN:O	1:K:33:GLN:HG3	1.90	0.72
1:K:348:LYS:CE	1:L:35:SER:O	2.38	0.72
1:L:102:TYR:CE2	3:N:13:PRO:HG3	2.24	0.72
3:N:112:VAL:HG22	3:N:113:PRO:N	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:GLN:O	1:C:33:GLN:HG3	1.90	0.72
1:F:281:LEU:HA	2:M:29:TYR:HE1	1.55	0.72
1:G:308:GLN:HE22	1:G:345:ASN:HD21	1.34	0.72
3:N:80:ILE:HG21	3:N:116:PHE:HA	0.88	0.72
1:B:384:THR:O	1:B:387:VAL:HG12	1.89	0.72
1:B:394:THR:O	1:B:395:THR:O	2.08	0.72
1:E:106:ASN:CG	1:K:62:VAL:CG1	2.58	0.72
1:E:108:ARG:NH1	1:J:314:SER:HA	2.04	0.72
3:N:62:ASN:HD22	3:N:95:PRO:HG2	1.53	0.72
1:B:392:ILE:O	1:B:393:SER:CB	2.24	0.71
1:D:185:VAL:HG13	1:D:186:PRO:CD	2.18	0.71
1:L:102:TYR:CE2	3:N:89:TYR:HE2	2.08	0.71
1:H:281:LEU:CG	1:H:385:GLU:HB3	2.17	0.71
1:I:8:THR:CA	1:I:9:PRO:N	2.47	0.71
1:B:11:GLN:CD	1:B:351:TYR:HD2	1.92	0.71
1:C:104:PRO:CB	1:C:188:SER:CB	2.65	0.71
1:C:311:ALA:O	1:C:312:ASN:OD1	2.09	0.71
1:G:15:LEU:HD23	1:G:18:GLN:HE21	1.44	0.71
1:I:355:TYR:OH	1:I:393:SER:C	2.29	0.71
1:K:311:ALA:O	1:K:312:ASN:OD1	2.09	0.71
1:H:4:VAL:N	1:I:239:GLN:CG	2.53	0.71
1:H:384:THR:HA	1:H:387:VAL:HG12	1.72	0.71
1:I:384:THR:HA	1:I:387:VAL:HG12	1.72	0.71
1:I:384:THR:CA	1:I:387:VAL:HG12	2.21	0.71
1:J:186:PRO:HB3	2:M:66:GLY:HA2	1.72	0.71
1:K:282:TYR:HA	1:K:381:THR:CG2	2.21	0.71
1:B:384:THR:CA	1:B:387:VAL:HG12	2.21	0.71
1:D:254:LEU:O	1:D:383:ARG:NH1	2.24	0.71
1:F:239:GLN:CD	2:M:45:MET:CE	2.58	0.71
1:F:351:TYR:CZ	2:M:29:TYR:CE2	2.77	0.71
1:G:34:GLN:NE2	1:I:9:PRO:HB2	1.76	0.71
1:L:65:VAL:N	1:L:181:VAL:O	2.23	0.71
1:L:265:GLN:CG	3:N:40:LYS:NZ	2.53	0.71
1:D:7:LEU:CD1	1:D:353:LEU:HD22	2.19	0.71
1:D:384:THR:CA	1:D:387:VAL:HG12	2.21	0.71
1:E:187:GLN:HG2	1:K:184:ASN:O	1.89	0.71
1:F:29:GLN:O	1:F:33:GLN:HG3	1.90	0.71
1:F:357:ASN:N	2:M:23:THR:HG21	2.05	0.71
1:H:265:GLN:HE21	1:H:393:SER:CB	2.00	0.71
1:L:38:VAL:CG2	1:L:238:ASP:CB	2.59	0.71
1:B:5:GLN:HG2	1:B:310:THR:CG2	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:8:THR:CG2	1:E:11:GLN:CG	2.42	0.71
1:E:29:GLN:O	1:E:33:GLN:HG3	1.90	0.71
1:J:386:LEU:HD13	2:M:62:ALA:HB1	1.69	0.71
1:L:28:ARG:HD3	1:L:175:THR:O	1.90	0.71
1:D:7:LEU:HD13	1:D:353:LEU:CD1	2.19	0.71
1:D:16:ARG:O	1:D:17:ASN:OD1	2.09	0.71
1:D:17:ASN:N	1:D:18:GLN:N	2.38	0.71
1:F:311:ALA:CB	2:M:21:THR:HG21	2.19	0.71
3:N:15:TYR:CG	3:N:47:ALA:HB3	2.25	0.71
3:N:28:ARG:HH12	3:N:37:GLU:HB3	1.55	0.71
1:F:351:TYR:CZ	2:M:29:TYR:OH	2.23	0.71
1:F:393:SER:OG	1:F:394:THR:N	2.24	0.71
2:M:24:MET:N	2:M:25:PRO:HD2	2.03	0.71
1:D:394:THR:O	1:D:395:THR:O	2.08	0.71
1:G:182:LEU:HD21	2:M:4:ASN:HB3	1.73	0.71
1:I:80:HIS:HD2	1:I:83:GLU:H	1.39	0.71
1:G:35:SER:CA	1:G:36:TYR:N	2.53	0.70
1:L:64:ILE:HD11	1:L:249:LEU:HD22	1.73	0.70
1:L:108:ARG:HH12	3:N:89:TYR:CA	1.99	0.70
1:B:108:ARG:CZ	1:D:313:PHE:O	2.37	0.70
1:F:311:ALA:CB	2:M:23:THR:HG21	2.20	0.70
1:G:280:ASN:O	1:G:281:LEU:HB3	1.91	0.70
1:J:384:THR:HG21	2:M:62:ALA:N	2.06	0.70
1:K:282:TYR:CA	1:K:381:THR:CB	2.51	0.70
1:B:354:GLN:HB2	1:B:357:ASN:HD21	1.54	0.70
1:H:4:VAL:N	1:I:239:GLN:NE2	2.39	0.70
1:L:279:ALA:HA	3:N:43:LEU:CD1	2.19	0.70
3:N:65:ASN:HB2	3:N:69:PHE:O	1.92	0.70
1:H:280:ASN:O	1:H:281:LEU:HB3	1.91	0.70
1:H:384:THR:CA	1:H:387:VAL:HG12	2.21	0.70
1:I:354:GLN:HB2	1:I:357:ASN:HD21	1.56	0.70
1:L:109:HIS:N	3:N:89:TYR:OH	2.24	0.70
3:N:15:TYR:HE2	3:N:88:GLY:HA2	1.51	0.70
3:N:112:VAL:CG2	3:N:113:PRO:N	2.54	0.70
4:P:7:LEU:H	4:P:7:LEU:CD1	2.03	0.70
1:L:104:PRO:HB3	1:L:188:SER:CB	2.21	0.70
1:L:279:ALA:CA	3:N:43:LEU:CD1	2.63	0.70
3:N:7:ASN:HB3	3:N:8:GLN:HA	1.74	0.70
1:B:384:THR:HA	1:B:387:VAL:HG12	1.72	0.70
1:E:98:ARG:NH2	1:E:111:GLU:OE2	2.25	0.70
1:H:16:ARG:O	1:H:17:ASN:OD1	2.09	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:348:LYS:HE3	1:L:35:SER:O	1.92	0.70
3:N:89:TYR:O	3:N:91:PRO:CD	2.36	0.70
1:F:354:GLN:CA	2:M:26:LEU:HD21	2.21	0.70
1:F:382:SER:CA	1:F:383:ARG:N	2.53	0.70
1:F:392:ILE:HG22	1:F:394:THR:O	1.90	0.70
1:J:34:GLN:C	1:J:35:SER:N	2.45	0.70
1:L:104:PRO:HB3	1:L:188:SER:OG	1.88	0.70
1:E:106:ASN:CG	1:K:62:VAL:HG11	2.10	0.70
1:H:392:ILE:HG22	1:H:393:SER:H	0.57	0.70
4:P:12:GLY:O	4:P:15:VAL:CG1	2.40	0.70
1:B:8:THR:CA	1:B:9:PRO:N	2.47	0.70
1:G:185:VAL:CG2	2:M:4:ASN:CB	2.67	0.70
1:K:104:PRO:HB2	1:K:187:GLN:CB	2.21	0.70
1:L:75:ALA:CA	1:L:160:GLY:O	2.31	0.70
1:L:98:ARG:NH2	1:L:111:GLU:OE2	2.25	0.70
1:L:182:LEU:CG	1:L:184:ASN:ND2	2.55	0.70
1:A:280:ASN:O	1:A:281:LEU:HB3	1.91	0.70
1:B:108:ARG:NH1	1:D:314:SER:HB2	1.75	0.70
1:J:80:HIS:HD2	1:J:83:GLU:H	1.39	0.70
1:L:78:ASN:HB2	1:L:154:ILE:O	1.92	0.70
1:D:5:GLN:CD	1:E:36:TYR:CE2	2.65	0.69
1:F:353:LEU:HD22	2:M:26:LEU:C	2.06	0.69
2:M:67:ILE:CG2	4:P:41:MET:CE	2.70	0.69
1:H:7:LEU:CD1	1:H:353:LEU:HD22	2.22	0.69
3:N:15:TYR:HB2	3:N:47:ALA:HB3	1.73	0.69
3:N:41:TYR:CA	3:N:45:TYR:CE2	2.49	0.69
1:B:5:GLN:OE1	1:B:310:THR:HG23	1.83	0.69
1:D:280:ASN:O	1:D:281:LEU:HB3	1.91	0.69
1:H:310:THR:HG22	1:H:358:VAL:HG22	1.75	0.69
1:I:277:GLN:HB2	1:I:394:THR:CB	2.21	0.69
3:N:60:ILE:HG22	3:N:62:ASN:OD1	1.91	0.69
3:N:80:ILE:CG1	3:N:117:LEU:N	2.47	0.69
1:C:181:VAL:C	1:C:182:LEU:HB2	2.13	0.69
1:E:80:HIS:CD2	1:E:83:GLU:H	2.11	0.69
1:E:381:THR:OG1	1:E:382:SER:N	2.24	0.69
1:G:239:GLN:CG	1:I:4:VAL:HA	1.99	0.69
1:L:29:GLN:O	1:L:33:GLN:HG3	1.90	0.69
1:G:382:SER:OG	1:G:383:ARG:N	2.25	0.69
1:L:80:HIS:CD2	1:L:83:GLU:H	2.11	0.69
4:P:19:ILE:O	4:P:23:PHE:CD1	2.45	0.69
1:D:310:THR:HG22	1:D:358:VAL:HG22	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:80:HIS:CD2	1:K:83:GLU:H	2.10	0.69
1:B:4:VAL:O	1:B:313:PHE:CZ	2.44	0.69
1:G:80:HIS:HD2	1:G:83:GLU:H	1.39	0.69
1:H:354:GLN:HB2	1:H:357:ASN:HD21	1.56	0.69
1:I:394:THR:O	1:I:395:THR:O	2.08	0.69
1:L:52:ARG:NH1	3:N:8:GLN:HG2	2.08	0.69
4:P:107:LEU:C	4:P:111:LEU:HD13	2.07	0.69
1:E:188:SER:HA	1:K:185:VAL:O	1.93	0.69
1:G:255:SER:OG	1:G:386:LEU:CD2	2.41	0.69
1:K:98:ARG:NH2	1:K:111:GLU:OE2	2.25	0.69
1:L:35:SER:HB2	1:L:36:TYR:N	2.07	0.69
2:M:67:ILE:HG22	4:P:41:MET:CE	2.20	0.69
3:N:81:LYS:CB	3:N:113:PRO:CB	2.70	0.69
1:B:254:LEU:O	1:B:383:ARG:NH1	2.26	0.69
1:B:372:ARG:HD3	1:D:269:THR:HG21	1.73	0.69
1:C:98:ARG:NH2	1:C:111:GLU:OE2	2.25	0.69
1:D:354:GLN:HB2	1:D:357:ASN:HD21	1.56	0.69
1:F:80:HIS:CD2	1:F:83:GLU:H	2.11	0.69
1:L:76:ILE:CG2	1:L:154:ILE:HD12	2.23	0.69
3:N:28:ARG:HH11	3:N:37:GLU:HG2	1.26	0.69
1:F:98:ARG:NH2	1:F:111:GLU:OE2	2.25	0.69
1:J:4:VAL:O	1:J:4:VAL:HG22	1.93	0.69
1:B:9:PRO:HG3	1:C:34:GLN:CD	2.12	0.68
1:B:395:THR:HG1	1:D:395:THR:N	1.85	0.68
1:H:7:LEU:O	1:H:8:THR:CB	2.40	0.68
1:I:4:VAL:N	1:I:4:VAL:C	2.46	0.68
1:I:280:ASN:O	1:I:281:LEU:HB3	1.91	0.68
1:D:382:SER:HG	1:D:385:GLU:HG3	1.55	0.68
1:F:281:LEU:CB	2:M:29:TYR:HE1	2.06	0.68
1:H:9:PRO:CG	1:I:34:GLN:OE1	2.40	0.68
1:A:80:HIS:HD2	1:A:83:GLU:H	1.39	0.68
1:D:384:THR:O	1:D:387:VAL:HG12	1.89	0.68
1:E:8:THR:HB	1:E:11:GLN:CB	2.18	0.68
1:E:187:GLN:C	1:K:185:VAL:CA	2.61	0.68
1:G:185:VAL:HG21	2:M:4:ASN:C	2.12	0.68
1:I:17:ASN:HB2	1:I:20:ALA:CB	2.18	0.68
1:B:389:ALA:HB1	1:D:354:GLN:OE1	1.92	0.68
1:C:104:PRO:HB2	1:C:188:SER:HB3	1.75	0.68
1:D:80:HIS:HD2	1:D:83:GLU:H	1.39	0.68
1:D:277:GLN:NE2	1:D:394:THR:HG23	2.06	0.68
1:D:281:LEU:HD21	1:D:385:GLU:CA	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:384:THR:HA	1:D:387:VAL:HG12	1.72	0.68
1:E:381:THR:C	1:E:382:SER:CA	2.61	0.68
1:J:354:GLN:HB2	1:J:357:ASN:HD21	1.56	0.68
1:C:80:HIS:CD2	1:C:83:GLU:H	2.11	0.68
3:N:29:GLY:O	3:N:30:TYR:CG	2.46	0.68
3:N:60:ILE:HD13	3:N:97:ARG:CZ	2.23	0.68
1:D:11:GLN:OE1	1:D:351:TYR:CE2	2.46	0.68
1:G:239:GLN:HG2	1:I:4:VAL:N	2.08	0.68
1:J:280:ASN:O	1:J:281:LEU:HB3	1.91	0.68
1:B:108:ARG:CZ	1:D:314:SER:N	2.39	0.68
1:F:10:ALA:CB	2:M:26:LEU:HD23	2.24	0.68
1:H:257:LEU:HG	1:H:383:ARG:HG2	1.75	0.68
1:B:313:PHE:O	1:I:108:ARG:NE	2.24	0.68
1:I:80:HIS:HD2	1:I:82:THR:H	1.42	0.68
1:J:251:LEU:HD22	1:J:385:GLU:HB3	1.75	0.68
3:N:44:THR:O	3:N:44:THR:HG22	1.93	0.68
1:D:106:ASN:OD1	1:G:238:ASP:OD2	2.12	0.68
1:H:106:ASN:HD22	1:H:191:ARG:HH22	1.42	0.68
1:J:28:ARG:HH21	1:J:253:ASP:CG	1.96	0.68
1:D:80:HIS:HD2	1:D:82:THR:H	1.42	0.67
1:F:10:ALA:HB2	2:M:26:LEU:HD22	1.73	0.67
1:I:106:ASN:HD22	1:I:191:ARG:HH22	1.42	0.67
1:L:56:ASP:OD2	3:N:11:VAL:CG1	2.38	0.67
1:L:108:ARG:HH12	3:N:89:TYR:HA	1.47	0.67
1:D:185:VAL:CG1	1:D:186:PRO:HD3	2.06	0.67
1:D:281:LEU:HD22	1:D:385:GLU:C	2.12	0.67
1:H:80:HIS:HD2	1:H:83:GLU:H	1.39	0.67
4:P:12:GLY:C	4:P:16:LEU:HD13	2.11	0.67
1:I:257:LEU:HD12	1:I:386:LEU:CD2	2.19	0.67
3:N:81:LYS:HB3	3:N:113:PRO:HG2	0.76	0.67
1:B:310:THR:HG22	1:B:358:VAL:HG22	1.77	0.67
1:B:358:VAL:N	1:B:358:VAL:C	2.47	0.67
1:F:312:ASN:O	2:M:20:PRO:HB2	1.95	0.67
1:G:309:ARG:CG	1:G:313:PHE:O	2.42	0.67
1:L:353:LEU:C	2:M:76:PRO:HD3	2.14	0.67
4:P:12:GLY:O	4:P:16:LEU:HD12	1.91	0.67
1:D:24:ASN:CG	1:D:252:ILE:HB	2.14	0.67
1:J:184:ASN:HD22	1:J:247:TYR:HE1	1.31	0.67
1:K:104:PRO:HB3	1:K:187:GLN:CB	2.24	0.67
1:L:353:LEU:CB	2:M:76:PRO:CG	2.72	0.67
3:N:27:VAL:O	3:N:28:ARG:HG3	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:SER:HA	1:A:383:ARG:HD3	1.65	0.67
1:C:185:VAL:CG2	1:C:247:TYR:HE1	2.06	0.67
1:D:395:THR:OG1	1:I:394:THR:C	2.31	0.67
1:G:353:LEU:H	1:G:353:LEU:CD1	2.08	0.67
1:I:17:ASN:HB2	1:I:20:ALA:HB2	1.72	0.67
3:N:23:GLY:HA3	3:N:109:LYS:HD2	1.75	0.67
1:A:353:LEU:H	1:A:353:LEU:CD1	2.08	0.67
1:C:61:ASN:H	1:I:189:LYS:HE2	1.58	0.67
1:D:372:ARG:NH1	1:I:272:VAL:HG22	2.02	0.67
1:K:348:LYS:NZ	1:L:32:LEU:O	2.20	0.67
1:A:255:SER:O	1:A:383:ARG:HB2	1.92	0.67
1:D:387:VAL:HG23	1:I:6:GLN:NE2	2.08	0.67
3:N:32:ASP:OD1	3:N:99:LYS:HG2	1.94	0.67
1:F:312:ASN:CB	2:M:20:PRO:HG2	2.24	0.67
1:A:80:HIS:HD2	1:A:82:THR:H	1.42	0.67
1:B:80:HIS:HD2	1:B:82:THR:H	1.42	0.67
1:B:108:ARG:NH1	1:D:314:SER:HA	2.08	0.67
1:D:281:LEU:HD22	1:D:385:GLU:CA	2.26	0.67
1:E:80:HIS:HD2	1:E:83:GLU:H	1.43	0.67
1:F:35:SER:CB	1:F:240:LEU:HD21	2.25	0.67
1:J:16:ARG:NE	1:J:21:MET:HE3	2.09	0.67
4:P:96:ILE:CG2	4:P:100:LEU:CD1	2.45	0.67
1:C:80:HIS:HD2	1:C:83:GLU:H	1.43	0.66
1:F:384:THR:C	2:M:33:GLY:HA3	2.14	0.66
1:I:277:GLN:CG	1:I:394:THR:CB	2.65	0.66
1:J:21:MET:HG2	1:J:252:ILE:HD13	1.77	0.66
1:B:7:LEU:HD13	1:B:353:LEU:CD1	2.23	0.66
1:E:188:SER:CA	1:K:185:VAL:O	2.43	0.66
1:G:106:ASN:HD22	1:G:191:ARG:HH22	1.42	0.66
1:G:185:VAL:HG13	1:G:186:PRO:CD	2.15	0.66
1:D:9:PRO:CB	1:E:34:GLN:HE22	2.07	0.66
1:D:106:ASN:HD22	1:D:191:ARG:HH22	1.42	0.66
1:F:351:TYR:CE1	2:M:29:TYR:CZ	2.83	0.66
1:G:15:LEU:N	1:G:15:LEU:HD12	2.10	0.66
1:B:392:ILE:C	1:B:393:SER:O	2.34	0.66
1:D:281:LEU:HA	1:D:385:GLU:OE1	1.95	0.66
1:I:11:GLN:OE1	1:I:351:TYR:HD2	1.77	0.66
1:L:38:VAL:HG21	1:L:238:ASP:CG	2.16	0.66
1:L:257:LEU:C	1:L:258:TYR:CA	2.63	0.66
1:L:263:SER:HB2	3:N:40:LYS:HE3	1.76	0.66
2:M:75:GLN:HB2	4:P:51:VAL:H	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:61:ASP:CA	3:N:75:GLU:HB2	2.25	0.66
1:C:60:ALA:HA	1:I:189:LYS:NZ	2.11	0.66
1:C:181:VAL:O	1:C:182:LEU:HA	1.95	0.66
1:D:281:LEU:CD1	1:D:382:SER:OG	2.42	0.66
1:H:185:VAL:CG1	1:H:186:PRO:CD	2.74	0.66
1:H:355:TYR:HE1	1:H:391:THR:HB	1.60	0.66
1:K:24:ASN:HB2	1:K:252:ILE:HD12	1.77	0.66
3:N:15:TYR:CB	3:N:47:ALA:HB3	2.25	0.66
3:N:64:GLU:HB2	3:N:93:LEU:CA	2.25	0.66
1:J:80:HIS:HD2	1:J:82:THR:H	1.42	0.66
3:N:68:ALA:CA	3:N:87:GLN:CD	2.63	0.66
4:P:42:THR:C	4:P:45:GLN:HG3	2.11	0.66
1:D:108:ARG:HH21	1:I:314:SER:N	1.88	0.66
1:E:308:GLN:HE22	1:E:345:ASN:HD21	1.44	0.66
1:G:105:ASP:N	2:M:7:PHE:CZ	2.63	0.66
1:C:308:GLN:HE22	1:C:345:ASN:HD21	1.44	0.66
1:H:80:HIS:HD2	1:H:82:THR:H	1.42	0.66
1:H:382:SER:HG	1:H:385:GLU:HG3	1.59	0.66
1:I:311:ALA:O	1:I:312:ASN:HB2	1.95	0.66
2:M:45:MET:CG	2:M:48:LEU:HD11	2.01	0.66
3:N:31:PHE:CE1	3:N:100:PHE:CD2	2.84	0.66
3:N:62:ASN:HD22	3:N:95:PRO:CG	2.08	0.66
3:N:64:GLU:OE1	3:N:93:LEU:CD2	2.43	0.66
3:N:80:ILE:HG22	3:N:115:PHE:O	1.96	0.66
1:D:185:VAL:CG1	1:D:186:PRO:CD	2.74	0.66
1:H:5:GLN:NE2	1:H:316:THR:HG21	2.11	0.66
1:J:106:ASN:HD22	1:J:191:ARG:HH22	1.42	0.66
1:J:383:ARG:O	2:M:60:TYR:HD1	1.77	0.66
1:B:106:ASN:HD22	1:B:191:ARG:HH22	1.42	0.66
1:E:257:LEU:CG	1:E:383:ARG:NE	2.47	0.66
1:G:80:HIS:HD2	1:G:82:THR:H	1.42	0.66
1:I:185:VAL:CG1	1:I:186:PRO:CD	2.74	0.66
1:L:104:PRO:CA	1:L:189:LYS:O	2.40	0.66
1:L:150:ALA:CA	1:L:151:PRO:N	2.58	0.66
1:D:4:VAL:O	1:D:313:PHE:CD1	2.48	0.65
1:K:101:TYR:CZ	1:K:190:GLN:CG	2.77	0.65
3:N:81:LYS:HD2	3:N:113:PRO:HB3	1.77	0.65
1:A:106:ASN:HD22	1:A:191:ARG:HH22	1.42	0.65
1:B:185:VAL:CG1	1:B:186:PRO:CD	2.74	0.65
1:B:277:GLN:CB	1:B:394:THR:CB	2.70	0.65
1:E:80:HIS:HD2	1:E:82:THR:H	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:189:LYS:HG2	1:K:61:ASN:HB2	1.78	0.65
1:F:308:GLN:HE22	1:F:345:ASN:HD21	1.44	0.65
1:J:385:GLU:O	1:J:386:LEU:HD12	1.95	0.65
1:L:61:ASN:HD21	1:L:189:LYS:HA	1.59	0.65
1:L:104:PRO:CB	1:L:188:SER:CB	2.74	0.65
1:L:180:ALA:HB3	1:L:254:LEU:CD2	2.25	0.65
2:M:21:THR:HG22	2:M:23:THR:N	2.01	0.65
1:B:277:GLN:CG	1:B:394:THR:CB	2.68	0.65
1:F:35:SER:HB3	1:F:240:LEU:HD22	1.76	0.65
1:K:7:LEU:HA	1:K:12:GLN:HE21	1.60	0.65
1:L:170:LEU:HD13	1:L:181:VAL:CG2	2.26	0.65
3:N:80:ILE:CG2	3:N:116:PHE:C	2.60	0.65
1:F:80:HIS:HD2	1:F:83:GLU:H	1.43	0.65
3:N:41:TYR:CB	3:N:45:TYR:HB2	2.15	0.65
1:K:80:HIS:HD2	1:K:82:THR:H	1.45	0.65
1:A:311:ALA:HB1	1:K:281:LEU:CD2	2.26	0.65
1:B:80:HIS:HD2	1:B:83:GLU:H	1.39	0.65
1:C:8:THR:HG22	1:C:9:PRO:CG	2.24	0.65
1:C:280:ASN:O	1:C:281:LEU:HB2	1.97	0.65
1:E:187:GLN:O	1:E:188:SER:O	2.14	0.65
1:F:186:PRO:CD	2:M:40:GLN:HG3	2.25	0.65
1:F:281:LEU:CA	2:M:29:TYR:HE1	2.08	0.65
1:K:8:THR:N	1:K:12:GLN:HE21	1.95	0.65
3:N:28:ARG:NH1	3:N:37:GLU:CB	2.55	0.65
1:L:6:GLN:C	1:L:7:LEU:HD13	2.11	0.65
1:L:308:GLN:HE22	1:L:345:ASN:HD21	1.44	0.65
4:P:107:LEU:O	4:P:111:LEU:HD12	1.85	0.65
1:C:80:HIS:HD2	1:C:82:THR:H	1.45	0.65
1:J:182:LEU:HD11	1:J:240:LEU:HD11	1.79	0.65
1:L:37:PRO:HA	1:L:237:LEU:HA	1.78	0.65
1:L:182:LEU:HD21	1:L:184:ASN:ND2	2.12	0.65
1:L:279:ALA:HB1	3:N:43:LEU:CD1	2.27	0.65
3:N:62:ASN:CG	3:N:95:PRO:HG2	2.16	0.65
3:N:80:ILE:HG23	3:N:117:LEU:N	2.12	0.65
1:B:7:LEU:HD13	1:B:353:LEU:HD22	1.78	0.65
1:D:187:GLN:HB2	2:M:9:TYR:HE1	0.52	0.65
1:E:191:ARG:HE	1:K:62:VAL:CG2	2.10	0.65
1:F:15:LEU:O	1:F:18:GLN:HB2	1.96	0.65
1:J:9:PRO:CG	1:K:34:GLN:OE1	2.43	0.65
1:K:308:GLN:HE22	1:K:345:ASN:HD21	1.44	0.65
1:L:77:THR:CA	1:L:158:ALA:O	2.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:80:ILE:HG22	3:N:81:LYS:N	2.12	0.65
1:J:5:GLN:N	1:J:313:PHE:CE1	2.48	0.64
1:J:239:GLN:NE2	2:M:72:THR:HA	2.12	0.64
2:M:2:LEU:N	2:M:2:LEU:HD12	2.12	0.64
1:G:23:ALA:C	1:G:24:ASN:N	2.50	0.64
1:H:148:ILE:HG22	1:I:138:PRO:CG	2.27	0.64
1:J:11:GLN:OE1	1:J:353:LEU:CD2	2.43	0.64
1:K:104:PRO:C	1:K:188:SER:OG	2.36	0.64
3:N:41:TYR:O	3:N:45:TYR:HB2	1.97	0.64
4:P:96:ILE:CG2	4:P:100:LEU:HD22	2.27	0.64
1:L:36:TYR:HB2	1:L:239:GLN:HB2	1.80	0.64
1:E:312:ASN:ND2	2:M:46:PRO:O	2.31	0.64
1:G:385:GLU:O	1:G:386:LEU:HD12	1.97	0.64
1:I:4:VAL:N	1:I:5:GLN:N	2.45	0.64
1:I:16:ARG:C	1:I:18:GLN:N	2.50	0.64
1:J:353:LEU:HB3	2:M:55:VAL:HG21	1.79	0.64
3:N:37:GLU:C	3:N:92:LEU:HB2	2.18	0.64
1:D:277:GLN:HB2	1:D:394:THR:OG1	1.96	0.64
1:I:5:GLN:HG2	1:I:310:THR:OG1	1.97	0.64
1:I:11:GLN:O	1:I:15:LEU:HD12	1.98	0.64
1:J:11:GLN:HB3	1:J:15:LEU:HD11	1.77	0.64
1:J:63:GLY:HA2	1:J:240:LEU:HG	1.79	0.64
1:F:353:LEU:CD2	2:M:27:LEU:N	1.99	0.64
1:I:281:LEU:HD21	1:I:385:GLU:C	2.17	0.64
1:K:191:ARG:CA	1:K:192:LEU:N	2.60	0.64
1:L:80:HIS:HD2	1:L:82:THR:H	1.45	0.64
1:L:80:HIS:HD2	1:L:83:GLU:H	1.43	0.64
1:L:381:THR:CA	1:L:382:SER:N	2.60	0.64
1:D:277:GLN:CB	1:D:394:THR:OG1	2.46	0.64
4:P:24:ARG:C	4:P:27:PRO:HD2	2.18	0.64
1:B:7:LEU:CD1	1:B:353:LEU:HD22	2.28	0.64
1:J:322:LYS:HE2	1:K:145:MET:O	1.98	0.64
1:K:80:HIS:HD2	1:K:83:GLU:H	1.43	0.64
3:N:79:ARG:O	3:N:117:LEU:O	2.16	0.64
2:M:67:ILE:HG22	2:M:68:GLN:N	2.12	0.64
2:M:77:LEU:N	2:M:77:LEU:HD12	2.13	0.64
4:P:12:GLY:O	4:P:15:VAL:HG13	1.98	0.64
1:K:182:LEU:HD11	1:K:249:LEU:HD13	1.80	0.64
3:N:43:LEU:HD12	3:N:43:LEU:N	2.14	0.63
3:N:81:LYS:CB	3:N:113:PRO:HB2	2.27	0.63
4:P:7:LEU:HD12	4:P:7:LEU:N	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:96:ILE:HG21	4:P:100:LEU:CD2	2.28	0.63
1:L:279:ALA:HB1	3:N:42:ASP:HB2	1.80	0.63
3:N:94:VAL:HG22	3:N:103:ARG:HH12	1.60	0.63
4:P:100:LEU:HD12	4:P:100:LEU:N	2.13	0.63
1:D:9:PRO:CG	1:E:34:GLN:HE22	2.12	0.63
1:E:191:ARG:NE	1:K:62:VAL:HG23	2.13	0.63
1:F:80:HIS:HD2	1:F:82:THR:H	1.45	0.63
1:D:322:LYS:HE2	1:E:145:MET:O	1.97	0.63
1:D:386:LEU:C	1:I:312:ASN:CG	2.47	0.63
1:J:21:MET:HG2	1:J:252:ILE:CD1	2.28	0.63
3:N:64:GLU:CG	3:N:93:LEU:HB3	2.28	0.63
1:F:353:LEU:HD21	2:M:27:LEU:HD13	1.81	0.63
1:F:384:THR:O	2:M:33:GLY:O	2.17	0.63
1:F:239:GLN:HA	2:M:45:MET:CE	2.25	0.63
1:F:239:GLN:HG3	2:M:45:MET:HG2	1.76	0.63
1:G:185:VAL:CG2	2:M:4:ASN:O	2.36	0.63
1:J:5:GLN:OE1	1:K:36:TYR:CD2	2.52	0.63
1:K:280:ASN:O	1:K:281:LEU:HB2	1.97	0.63
1:B:272:VAL:CG2	1:I:372:ARG:NH1	2.62	0.63
1:L:150:ALA:C	1:L:151:PRO:CA	2.67	0.63
1:E:187:GLN:HA	1:K:185:VAL:N	2.12	0.63
1:L:75:ALA:HB1	1:L:159:THR:CG2	2.29	0.63
1:E:8:THR:HG21	1:E:11:GLN:CB	2.29	0.62
1:G:239:GLN:HG2	1:I:4:VAL:HB	1.81	0.62
3:N:49:THR:HG23	3:N:83:PRO:N	2.12	0.62
1:A:312:ASN:ND2	1:K:381:THR:HG22	2.14	0.62
1:C:385:GLU:C	1:C:386:LEU:HD12	2.20	0.62
1:E:8:THR:CG2	1:E:11:GLN:CB	2.76	0.62
1:J:7:LEU:HD12	1:J:7:LEU:N	2.14	0.62
1:L:78:ASN:O	1:L:156:ALA:C	2.36	0.62
3:N:57:CYS:SG	3:N:101:VAL:CG2	2.81	0.62
1:B:17:ASN:HB3	1:B:20:ALA:CB	2.25	0.62
1:B:277:GLN:CG	1:B:394:THR:OG1	2.46	0.62
1:E:381:THR:CB	1:E:382:SER:N	2.62	0.62
1:I:308:GLN:HE22	1:I:345:ASN:ND2	1.97	0.62
3:N:69:PHE:H	3:N:87:GLN:HE21	1.47	0.62
1:B:4:VAL:O	1:B:4:VAL:HG22	1.98	0.62
1:D:384:THR:HA	1:D:387:VAL:HG11	1.81	0.62
1:E:14:ALA:O	1:E:18:GLN:HG3	1.99	0.62
1:H:384:THR:HA	1:H:387:VAL:HG11	1.81	0.62
1:F:383:ARG:HG2	2:M:31:VAL:HG23	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:311:ALA:O	1:J:312:ASN:CG	2.38	0.62
1:L:56:ASP:O	3:N:7:ASN:ND2	2.32	0.62
3:N:79:ARG:NH2	3:N:104:HIS:CB	2.29	0.62
3:N:81:LYS:O	3:N:115:PHE:O	2.18	0.62
1:E:51:ASN:O	1:K:45:GLN:HG3	1.99	0.62
1:G:106:ASN:HD22	1:G:191:ARG:NH2	1.98	0.62
1:G:185:VAL:HG23	2:M:4:ASN:N	2.14	0.62
1:H:7:LEU:CG	1:H:353:LEU:HD22	2.28	0.62
1:H:381:THR:C	1:H:382:SER:CA	2.68	0.62
1:L:65:VAL:HB	1:L:181:VAL:HB	1.80	0.62
3:N:62:ASN:CB	3:N:95:PRO:CD	2.78	0.62
3:N:64:GLU:HB3	3:N:93:LEU:HD22	1.81	0.62
1:B:11:GLN:O	1:B:15:LEU:HD12	1.98	0.62
1:B:308:GLN:HE22	1:B:345:ASN:ND2	1.98	0.62
3:N:64:GLU:HB3	3:N:93:LEU:CB	2.10	0.62
1:B:17:ASN:CB	1:B:20:ALA:CB	2.77	0.62
1:B:281:LEU:CD2	1:B:385:GLU:CB	2.75	0.62
3:N:14:VAL:CG2	3:N:16:ASN:HB2	2.29	0.62
3:N:49:THR:HB	3:N:112:VAL:HG12	1.66	0.62
1:G:185:VAL:N	1:G:186:PRO:CD	2.63	0.62
1:H:7:LEU:HD12	1:H:7:LEU:N	2.15	0.62
1:L:177:LEU:O	1:L:178:THR:C	2.34	0.62
1:L:283:ARG:HH11	1:L:382:SER:HB3	1.63	0.62
3:N:44:THR:O	3:N:44:THR:CG2	2.47	0.62
3:N:62:ASN:HB3	3:N:95:PRO:CD	2.28	0.62
1:B:7:LEU:HD12	1:B:7:LEU:N	2.15	0.62
1:F:351:TYR:OH	2:M:29:TYR:CZ	2.25	0.62
1:I:7:LEU:HD13	1:I:353:LEU:CD2	2.30	0.62
1:I:281:LEU:HD21	1:I:385:GLU:HB3	1.82	0.62
1:A:386:LEU:HD12	1:A:386:LEU:N	2.15	0.61
1:B:106:ASN:HD22	1:B:191:ARG:NH2	1.98	0.61
1:B:387:VAL:HG23	1:D:313:PHE:HE1	1.64	0.61
1:C:62:VAL:N	1:C:183:ALA:HB3	2.14	0.61
1:D:7:LEU:N	1:D:7:LEU:HD12	2.15	0.61
1:D:17:ASN:HB2	1:D:20:ALA:HB2	1.72	0.61
1:D:308:GLN:HE22	1:D:345:ASN:ND2	1.98	0.61
1:D:386:LEU:N	1:D:386:LEU:HD12	2.15	0.61
1:H:281:LEU:HD22	1:H:385:GLU:O	2.00	0.61
1:J:255:SER:CA	1:J:383:ARG:HD2	2.13	0.61
4:P:50:SER:C	4:P:51:VAL:HG12	2.19	0.61
1:D:106:ASN:HD22	1:D:191:ARG:NH2	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:104:PRO:C	2:M:7:PHE:CE2	2.73	0.61
1:I:7:LEU:N	1:I:7:LEU:HD12	2.15	0.61
1:J:106:ASN:HD22	1:J:191:ARG:NH2	1.98	0.61
1:L:76:ILE:O	1:L:154:ILE:HG21	1.99	0.61
2:M:1:ALA:C	2:M:2:LEU:HD12	2.20	0.61
1:B:384:THR:HA	1:B:387:VAL:HG11	1.81	0.61
1:D:5:GLN:NE2	1:E:36:TYR:CZ	2.63	0.61
1:E:257:LEU:HG	1:E:383:ARG:NE	2.14	0.61
1:G:309:ARG:CG	1:G:314:SER:HA	2.30	0.61
1:I:257:LEU:HB2	1:I:381:THR:HG22	1.82	0.61
1:C:60:ALA:HA	1:I:189:LYS:HZ3	1.65	0.61
1:F:185:VAL:HG22	2:M:38:ILE:CA	2.29	0.61
1:H:5:GLN:NE2	1:H:316:THR:CG2	2.63	0.61
1:I:384:THR:HA	1:I:387:VAL:HG11	1.81	0.61
1:K:17:ASN:O	1:K:20:ALA:CB	2.48	0.61
1:L:280:ASN:CG	1:L:352:THR:CB	2.69	0.61
1:G:239:GLN:HG3	1:I:4:VAL:HA	1.59	0.61
1:G:239:GLN:CD	1:I:313:PHE:CZ	2.68	0.61
1:K:184:ASN:H	1:K:185:VAL:HG22	1.63	0.61
3:N:50:GLN:OE1	3:N:52:PHE:HZ	1.84	0.61
1:A:106:ASN:HD22	1:A:191:ARG:NH2	1.98	0.61
1:A:308:GLN:HE22	1:A:345:ASN:ND2	1.98	0.61
1:F:281:LEU:CG	2:M:29:TYR:CE1	2.83	0.61
1:H:5:GLN:CD	1:I:36:TYR:CG	2.74	0.61
1:I:277:GLN:CD	1:I:394:THR:OG1	2.31	0.61
1:L:104:PRO:O	1:L:188:SER:OG	2.19	0.61
1:B:386:LEU:N	1:B:386:LEU:HD12	2.16	0.61
1:D:282:TYR:CD2	1:D:381:THR:HB	2.36	0.61
1:D:387:VAL:CG2	1:I:6:GLN:OE1	2.43	0.61
1:G:308:GLN:HE22	1:G:345:ASN:ND2	1.98	0.61
1:G:309:ARG:HD3	1:G:314:SER:HA	1.83	0.61
1:I:106:ASN:HD22	1:I:191:ARG:NH2	1.98	0.61
1:I:311:ALA:O	1:I:312:ASN:CB	2.43	0.61
1:L:76:ILE:CB	1:L:154:ILE:CD1	2.78	0.61
1:A:255:SER:O	1:A:383:ARG:CD	2.31	0.61
1:B:311:ALA:HB3	1:I:390:GLY:C	2.16	0.61
1:G:255:SER:CB	1:G:386:LEU:HG	2.30	0.61
1:H:25:LEU:O	1:H:29:GLN:HG3	2.01	0.61
1:H:308:GLN:HE22	1:H:345:ASN:ND2	1.98	0.61
1:J:184:ASN:CG	1:J:240:LEU:HD12	2.21	0.61
1:K:7:LEU:HB3	1:K:12:GLN:HE22	1.60	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:38:VAL:HB	1:L:236:TYR:CG	2.35	0.61
3:N:37:GLU:CB	3:N:92:LEU:HB2	2.31	0.61
3:N:60:ILE:HD12	3:N:97:ARG:CZ	2.28	0.61
1:F:185:VAL:CG2	2:M:37:GLY:O	2.48	0.61
1:F:311:ALA:HB1	2:M:21:THR:CG2	2.22	0.61
1:H:106:ASN:HD22	1:H:191:ARG:NH2	1.98	0.61
1:I:25:LEU:O	1:I:29:GLN:HG3	2.01	0.61
1:J:9:PRO:CG	1:K:34:GLN:HA	2.13	0.61
1:J:15:LEU:HD12	1:J:15:LEU:N	2.16	0.61
1:A:255:SER:CA	1:A:383:ARG:NH1	2.60	0.60
1:F:15:LEU:HD12	1:F:15:LEU:N	2.16	0.60
1:B:25:LEU:O	1:B:29:GLN:HG3	2.01	0.60
1:J:251:LEU:HD22	1:J:385:GLU:CG	2.30	0.60
4:P:14:LEU:HD12	4:P:14:LEU:N	2.16	0.60
1:D:108:ARG:NH2	1:I:313:PHE:C	2.37	0.60
1:E:108:ARG:CD	1:J:314:SER:HB2	2.29	0.60
1:E:187:GLN:CG	1:K:184:ASN:O	2.49	0.60
1:H:382:SER:O	1:H:386:LEU:CD1	2.49	0.60
1:L:38:VAL:CG2	1:L:238:ASP:OD2	2.48	0.60
1:L:65:VAL:HG21	1:L:190:GLN:NE2	2.16	0.60
4:P:107:LEU:HD12	4:P:107:LEU:N	2.17	0.60
1:A:15:LEU:N	1:A:15:LEU:HD12	2.17	0.60
1:A:309:ARG:CG	1:A:310:THR:O	2.48	0.60
1:C:190:GLN:CA	1:C:191:ARG:HG3	2.30	0.60
1:D:281:LEU:CA	1:D:385:GLU:OE1	2.44	0.60
1:D:353:LEU:HD12	1:D:353:LEU:N	2.17	0.60
1:F:383:ARG:HB3	2:M:31:VAL:HG22	1.83	0.60
1:H:311:ALA:O	1:H:312:ASN:CB	2.49	0.60
1:H:386:LEU:N	1:H:386:LEU:HD12	2.16	0.60
3:N:29:GLY:O	3:N:30:TYR:CD2	2.54	0.60
1:B:353:LEU:HD12	1:B:353:LEU:N	2.17	0.60
1:H:281:LEU:CD2	1:H:385:GLU:O	2.49	0.60
4:P:50:SER:O	4:P:51:VAL:HG13	2.00	0.60
1:B:5:GLN:HG2	1:B:310:THR:OG1	2.01	0.60
1:C:185:VAL:N	1:C:186:PRO:CD	2.62	0.60
1:H:353:LEU:HD12	1:H:353:LEU:N	2.17	0.60
1:J:25:LEU:O	1:J:29:GLN:HG3	2.01	0.60
1:L:108:ARG:C	3:N:89:TYR:OH	2.40	0.60
1:L:279:ALA:CB	3:N:43:LEU:HD11	2.30	0.60
1:D:5:GLN:HG2	1:D:310:THR:HG21	1.84	0.60
1:D:17:ASN:C	1:D:21:MET:N	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:5:GLN:HG2	1:I:310:THR:CB	2.32	0.60
1:J:182:LEU:HB2	1:J:254:LEU:HD13	1.82	0.60
1:L:104:PRO:CB	1:L:188:SER:O	2.42	0.60
1:B:264:ALA:HB3	1:D:272:VAL:CG1	2.30	0.60
1:D:11:GLN:O	1:D:15:LEU:HD12	1.98	0.60
1:F:353:LEU:CA	2:M:26:LEU:CB	2.77	0.60
1:F:382:SER:C	1:F:383:ARG:N	2.55	0.60
1:H:381:THR:HA	1:H:382:SER:N	2.17	0.60
1:I:386:LEU:HD12	1:I:386:LEU:N	2.16	0.60
4:P:6:LEU:HD12	4:P:6:LEU:N	2.16	0.60
1:B:257:LEU:CD2	1:B:383:ARG:HG2	2.31	0.60
1:B:395:THR:HG21	1:I:395:THR:O	2.01	0.60
1:F:16:ARG:C	1:F:18:GLN:H	2.05	0.60
1:H:7:LEU:HD21	1:H:353:LEU:CD2	2.15	0.60
1:H:281:LEU:HD21	1:H:386:LEU:CA	2.32	0.60
1:I:7:LEU:HD13	1:I:353:LEU:CD1	2.32	0.60
1:I:384:THR:CA	1:I:387:VAL:CG1	2.80	0.60
1:J:184:ASN:ND2	1:J:247:TYR:CD1	2.70	0.60
1:L:15:LEU:HD12	1:L:15:LEU:N	2.16	0.60
3:N:49:THR:CG2	3:N:83:PRO:N	2.63	0.60
4:P:52:THR:O	4:P:53:LEU:CD1	2.42	0.60
1:A:25:LEU:O	1:A:29:GLN:HG3	2.01	0.60
1:E:186:PRO:O	1:E:187:GLN:HG3	2.02	0.60
1:G:309:ARG:HG2	1:G:310:THR:O	2.01	0.60
1:E:15:LEU:HD12	1:E:15:LEU:N	2.17	0.59
1:G:25:LEU:O	1:G:29:GLN:HG3	2.01	0.59
1:I:382:SER:O	1:I:386:LEU:CD1	2.49	0.59
1:I:384:THR:C	1:I:387:VAL:CG1	2.67	0.59
1:J:31:VAL:HG22	1:J:241:PRO:HG2	1.84	0.59
3:N:39:VAL:HG12	3:N:92:LEU:CD1	2.32	0.59
4:P:18:LEU:HD12	4:P:18:LEU:N	2.16	0.59
1:B:354:GLN:CD	1:I:389:ALA:HB1	2.21	0.59
1:J:353:LEU:HD12	1:J:353:LEU:N	2.17	0.59
3:N:14:VAL:HG21	3:N:16:ASN:HB2	1.84	0.59
3:N:94:VAL:HG22	3:N:103:ARG:HH11	1.56	0.59
4:P:35:TRP:O	4:P:36:GLU:CB	2.47	0.59
1:D:15:LEU:HD12	1:D:15:LEU:N	2.17	0.59
1:F:185:VAL:CB	2:M:38:ILE:N	2.65	0.59
1:H:255:SER:O	1:H:383:ARG:CG	2.49	0.59
1:L:182:LEU:CG	1:L:184:ASN:CG	2.70	0.59
3:N:41:TYR:CG	3:N:45:TYR:CD2	2.61	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:102:TYR:CE2	3:N:89:TYR:CE2	2.90	0.59
3:N:37:GLU:HB3	3:N:92:LEU:CD2	2.33	0.59
4:P:38:PRO:N	4:P:39:PRO:HD3	2.15	0.59
1:D:20:ALA:C	1:D:252:ILE:HD11	2.23	0.59
1:F:382:SER:C	1:F:383:ARG:HG3	2.22	0.59
1:J:239:GLN:HE22	2:M:72:THR:CA	2.16	0.59
3:N:27:VAL:CA	3:N:27:VAL:CG2	2.77	0.59
3:N:62:ASN:HD22	3:N:95:PRO:CB	2.15	0.59
3:N:62:ASN:HD22	3:N:95:PRO:HB2	1.66	0.59
3:N:65:ASN:CB	3:N:69:PHE:O	2.50	0.59
1:D:255:SER:HA	1:D:383:ARG:NH1	2.16	0.59
1:D:382:SER:O	1:D:386:LEU:CD1	2.49	0.59
1:I:15:LEU:HD12	1:I:15:LEU:N	2.17	0.59
1:L:7:LEU:CB	1:L:11:GLN:HB2	2.24	0.59
4:P:111:LEU:HD12	4:P:111:LEU:N	2.18	0.59
1:B:15:LEU:HD12	1:B:15:LEU:N	2.17	0.59
1:D:388:ASN:OD1	1:I:6:GLN:CB	2.51	0.59
1:H:15:LEU:HD12	1:H:15:LEU:N	2.17	0.59
1:E:257:LEU:CD1	1:E:383:ARG:HE	2.16	0.59
1:E:281:LEU:HD21	1:J:354:GLN:HE22	1.68	0.59
1:I:80:HIS:CD2	1:I:82:THR:H	2.21	0.59
3:N:60:ILE:HD11	3:N:97:ARG:NH1	1.92	0.59
1:B:7:LEU:CG	1:B:353:LEU:HD22	2.31	0.59
1:H:279:ALA:CB	1:H:391:THR:O	2.51	0.59
1:L:279:ALA:CB	3:N:43:LEU:CD1	2.81	0.59
1:L:280:ASN:CG	1:L:352:THR:OG1	2.40	0.59
2:M:68:GLN:N	4:P:41:MET:CE	2.66	0.59
1:C:104:PRO:C	1:C:188:SER:OG	2.40	0.58
1:F:247:TYR:CD1	1:F:249:LEU:HD21	2.38	0.58
1:F:281:LEU:HG	2:M:29:TYR:HE1	1.64	0.58
1:G:23:ALA:O	1:G:26:GLN:N	2.36	0.58
1:J:186:PRO:CB	2:M:66:GLY:HA2	2.33	0.58
1:A:80:HIS:CD2	1:A:82:THR:H	2.21	0.58
1:B:4:VAL:N	1:B:5:GLN:N	2.45	0.58
1:B:382:SER:OG	1:B:385:GLU:CD	2.42	0.58
1:I:353:LEU:N	1:I:353:LEU:HD12	2.17	0.58
3:N:58:ILE:HG22	3:N:58:ILE:O	2.03	0.58
1:B:322:LYS:HE2	1:C:145:MET:O	2.03	0.58
1:B:389:ALA:CA	1:D:354:GLN:OE1	2.51	0.58
1:H:9:PRO:HG3	1:I:34:GLN:CD	2.23	0.58
3:N:59:TYR:CB	3:N:98:ALA:N	2.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:ARG:CD	1:D:314:SER:HB2	2.33	0.58
1:C:181:VAL:C	1:C:182:LEU:CB	2.71	0.58
1:C:386:LEU:HD12	1:C:386:LEU:N	2.18	0.58
1:E:187:GLN:CA	1:K:184:ASN:C	2.70	0.58
1:E:310:THR:OG1	2:M:46:PRO:HB3	2.03	0.58
1:G:63:GLY:N	1:G:184:ASN:HD21	1.95	0.58
1:L:78:ASN:HB3	1:L:154:ILE:O	2.03	0.58
3:N:92:LEU:HD12	3:N:92:LEU:N	2.18	0.58
1:B:80:HIS:CD2	1:B:82:THR:H	2.21	0.58
1:D:4:VAL:HG11	1:D:313:PHE:HB3	1.85	0.58
1:J:309:ARG:CG	1:J:310:THR:N	2.65	0.58
1:K:7:LEU:HD12	1:K:7:LEU:N	2.18	0.58
1:K:17:ASN:O	1:K:20:ALA:CA	2.51	0.58
1:L:78:ASN:HB3	1:L:155:ALA:C	2.23	0.58
2:M:27:LEU:N	2:M:27:LEU:HD12	2.19	0.58
1:B:389:ALA:HA	1:D:354:GLN:OE1	2.04	0.58
1:D:9:PRO:HG3	1:E:34:GLN:HE22	1.67	0.58
1:G:80:HIS:CD2	1:G:82:THR:H	2.22	0.58
1:H:382:SER:OG	1:H:385:GLU:CD	2.42	0.58
1:J:80:HIS:CD2	1:J:82:THR:H	2.21	0.58
1:L:182:LEU:HG	1:L:184:ASN:CG	2.23	0.58
3:N:114:LEU:HD12	3:N:114:LEU:N	2.19	0.58
1:H:80:HIS:CD2	1:H:82:THR:H	2.21	0.58
1:I:382:SER:OG	1:I:385:GLU:CD	2.42	0.58
1:J:280:ASN:HD22	1:J:355:TYR:H	1.52	0.58
1:K:104:PRO:CB	1:K:187:GLN:HB3	2.33	0.58
3:N:21:GLY:H	3:N:46:LEU:HD21	1.67	0.58
4:P:21:LEU:N	4:P:21:LEU:HD12	2.17	0.58
1:B:281:LEU:HD21	1:B:385:GLU:CB	2.34	0.58
1:B:311:ALA:O	1:B:312:ASN:CB	2.49	0.58
1:C:15:LEU:HD12	1:C:15:LEU:N	2.19	0.58
1:C:43:GLU:HG3	1:I:52:ARG:CZ	2.34	0.58
1:C:187:GLN:NE2	1:I:187:GLN:CG	2.47	0.58
1:F:16:ARG:C	1:F:17:ASN:CB	2.72	0.58
1:G:354:GLN:HB2	1:G:357:ASN:CG	2.24	0.58
1:H:280:ASN:HD22	1:H:355:TYR:H	1.52	0.58
1:L:109:HIS:CE1	1:L:257:LEU:HD22	2.39	0.58
2:M:6:GLN:C	2:M:8:PRO:HD3	2.15	0.58
3:N:93:LEU:HD12	3:N:93:LEU:N	2.19	0.58
1:F:103:ASP:HB2	1:F:104:PRO:CD	2.34	0.58
1:F:353:LEU:CD2	2:M:27:LEU:HD13	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:34:GLN:CB	1:L:241:PRO:HB3	2.34	0.58
1:L:183:ALA:CA	1:L:184:ASN:N	2.67	0.58
3:N:31:PHE:CD2	3:N:100:PHE:CD1	2.67	0.58
1:C:7:LEU:HD12	1:C:7:LEU:N	2.18	0.58
1:G:107:GLN:HG2	1:G:383:ARG:HH21	1.69	0.58
3:N:68:ALA:HB3	3:N:87:GLN:CD	2.22	0.58
1:B:384:THR:CA	1:B:387:VAL:CG1	2.80	0.57
1:L:265:GLN:CD	3:N:40:LYS:HZ2	2.04	0.57
3:N:46:LEU:HD12	3:N:46:LEU:N	2.17	0.57
4:P:36:GLU:C	4:P:38:PRO:HD3	2.25	0.57
1:D:382:SER:OG	1:D:385:GLU:CD	2.42	0.57
1:F:386:LEU:N	1:F:386:LEU:HD12	2.19	0.57
1:K:103:ASP:HB2	1:K:104:PRO:CD	2.34	0.57
1:L:111:GLU:CD	3:N:89:TYR:HB3	2.21	0.57
1:C:103:ASP:HB2	1:C:104:PRO:CD	2.34	0.57
1:E:189:LYS:CE	1:K:61:ASN:HB2	2.32	0.57
1:J:386:LEU:HD12	1:J:386:LEU:N	2.19	0.57
3:N:68:ALA:CB	3:N:87:GLN:CG	2.71	0.57
1:B:382:SER:O	1:B:386:LEU:CD1	2.49	0.57
1:G:354:GLN:CD	1:G:357:ASN:HD21	2.08	0.57
1:I:277:GLN:CB	1:I:394:THR:CB	2.82	0.57
1:I:280:ASN:HD22	1:I:355:TYR:H	1.51	0.57
3:N:62:ASN:CG	3:N:95:PRO:O	2.42	0.57
4:P:37:GLY:N	4:P:38:PRO:CD	2.68	0.57
1:B:17:ASN:O	1:B:21:MET:N	2.34	0.57
1:B:280:ASN:HD22	1:B:355:TYR:H	1.52	0.57
1:L:103:ASP:HB2	1:L:104:PRO:CD	2.34	0.57
1:A:269:THR:HG22	1:K:263:SER:HB2	1.86	0.57
1:B:5:GLN:OE1	1:B:310:THR:HG21	1.95	0.57
1:E:8:THR:HG21	1:E:11:GLN:HG3	0.69	0.57
1:F:247:TYR:HD1	1:F:249:LEU:HD21	1.69	0.57
1:K:308:GLN:HE22	1:K:345:ASN:ND2	2.03	0.57
2:M:3:ILE:HA	2:M:9:TYR:CD2	2.39	0.57
1:D:384:THR:CA	1:D:387:VAL:CG1	2.80	0.57
1:F:35:SER:HB2	1:F:240:LEU:CD2	2.30	0.57
1:J:313:PHE:HE2	1:K:238:ASP:CG	2.08	0.57
1:L:65:VAL:HG21	1:L:190:GLN:HE22	1.70	0.57
3:N:52:PHE:HB2	3:N:75:GLU:OE2	2.04	0.57
1:B:387:VAL:HG23	1:D:313:PHE:CE1	2.40	0.57
1:D:258:TYR:HB2	1:D:380:PHE:HE2	1.70	0.57
1:G:185:VAL:N	1:G:186:PRO:HD2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:4:VAL:N	1:J:313:PHE:HZ	2.01	0.57
1:L:312:ASN:HB2	2:M:73:PHE:CE2	2.31	0.57
1:E:103:ASP:HB2	1:E:104:PRO:CD	2.34	0.57
1:E:187:GLN:NE2	1:K:247:TYR:OH	2.37	0.57
1:F:239:GLN:NE2	2:M:45:MET:HG2	2.18	0.57
1:J:184:ASN:OD1	1:J:240:LEU:CD1	2.52	0.57
1:J:384:THR:HB	2:M:62:ALA:HA	1.86	0.57
1:L:182:LEU:CD2	1:L:184:ASN:HD21	2.18	0.57
3:N:57:CYS:CB	3:N:101:VAL:HG23	2.34	0.57
4:P:12:GLY:O	4:P:15:VAL:HG12	2.03	0.57
1:G:182:LEU:HD23	2:M:4:ASN:HB3	1.84	0.57
1:A:354:GLN:CD	1:A:357:ASN:HD21	2.08	0.56
1:B:17:ASN:N	1:B:18:GLN:N	2.53	0.56
1:D:187:GLN:CB	2:M:9:TYR:CD1	2.63	0.56
1:E:7:LEU:HD12	1:E:7:LEU:N	2.20	0.56
1:E:280:ASN:O	1:E:281:LEU:HB2	2.04	0.56
1:F:7:LEU:N	1:F:7:LEU:HD12	2.21	0.56
1:F:383:ARG:HB3	2:M:31:VAL:CG2	2.35	0.56
1:K:8:THR:O	1:K:12:GLN:HG3	2.05	0.56
1:L:38:VAL:CG2	1:L:238:ASP:CG	2.73	0.56
1:B:17:ASN:C	1:B:18:GLN:N	2.59	0.56
1:D:311:ALA:O	1:D:312:ASN:CB	2.49	0.56
1:D:391:THR:HG22	1:D:392:ILE:N	2.20	0.56
1:F:281:LEU:CG	2:M:29:TYR:HE1	2.17	0.56
1:J:9:PRO:CG	1:K:34:GLN:CD	2.73	0.56
1:J:310:THR:HG22	1:J:358:VAL:HG22	1.87	0.56
1:K:7:LEU:C	1:K:12:GLN:NE2	2.58	0.56
4:P:10:VAL:HG22	4:P:14:LEU:HD11	1.87	0.56
4:P:53:LEU:HD12	4:P:53:LEU:N	2.19	0.56
1:C:181:VAL:C	1:C:182:LEU:HA	2.25	0.56
1:D:277:GLN:HG3	1:D:394:THR:CG2	2.35	0.56
1:D:277:GLN:H	1:D:394:THR:HG1	1.50	0.56
1:E:308:GLN:HE22	1:E:345:ASN:ND2	2.03	0.56
1:G:382:SER:C	1:G:383:ARG:HG3	2.25	0.56
1:K:15:LEU:HD12	1:K:15:LEU:N	2.20	0.56
1:L:308:GLN:HE22	1:L:345:ASN:ND2	2.03	0.56
3:N:68:ALA:CB	3:N:87:GLN:CD	2.73	0.56
3:N:105:LEU:HD12	3:N:105:LEU:N	2.20	0.56
4:P:16:LEU:HD12	4:P:16:LEU:N	2.20	0.56
4:P:39:PRO:HG2	4:P:42:THR:OG1	2.06	0.56
1:A:354:GLN:HB2	1:A:357:ASN:CG	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:63:GLY:CA	1:D:184:ASN:ND2	2.68	0.56
1:F:308:GLN:HE22	1:F:345:ASN:ND2	2.03	0.56
1:H:391:THR:HG22	1:H:392:ILE:N	2.20	0.56
3:N:64:GLU:CG	3:N:93:LEU:CB	2.84	0.56
4:P:16:LEU:O	4:P:20:TRP:CD1	2.49	0.56
4:P:96:ILE:HG21	4:P:100:LEU:HD22	1.87	0.56
1:F:383:ARG:CA	2:M:31:VAL:HG22	2.36	0.56
1:I:391:THR:HG22	1:I:392:ILE:N	2.20	0.56
1:J:281:LEU:HD13	2:M:58:GLN:HG2	1.87	0.56
1:F:185:VAL:HG22	2:M:37:GLY:O	2.05	0.56
1:F:280:ASN:O	1:F:281:LEU:HB2	2.04	0.56
1:H:17:ASN:HB3	1:H:20:ALA:CB	2.36	0.56
1:K:348:LYS:NZ	1:L:35:SER:O	2.38	0.56
3:N:40:LYS:O	3:N:45:TYR:CE2	2.59	0.56
1:D:187:GLN:NE2	2:M:9:TYR:HA	2.20	0.56
1:I:6:GLN:C	1:I:7:LEU:N	2.59	0.56
1:B:392:ILE:CG2	1:B:393:SER:N	2.63	0.56
1:E:311:ALA:O	1:E:312:ASN:CG	2.44	0.56
1:F:353:LEU:HD22	2:M:27:LEU:CA	2.24	0.56
3:N:48:ASP:O	3:N:86:LYS:HE3	2.06	0.56
3:N:81:LYS:HD3	3:N:113:PRO:HG3	0.61	0.56
4:P:37:GLY:N	4:P:38:PRO:HD3	2.20	0.56
1:B:5:GLN:HG2	1:B:310:THR:HG21	1.75	0.56
1:F:311:ALA:O	1:F:312:ASN:CG	2.44	0.56
3:N:25:GLN:CG	3:N:107:SER:OG	2.51	0.56
1:G:185:VAL:CG2	2:M:4:ASN:CA	2.84	0.56
1:C:352:THR:O	1:C:353:LEU:CB	2.54	0.55
1:D:7:LEU:HD13	1:D:353:LEU:CD2	2.35	0.55
1:F:247:TYR:OH	2:M:43:GLN:NE2	2.37	0.55
1:L:151:PRO:HD2	1:L:162:LEU:CD2	2.34	0.55
3:N:57:CYS:SG	3:N:101:VAL:HA	2.46	0.55
1:B:358:VAL:HA	1:B:358:VAL:HG13	1.83	0.55
1:E:189:LYS:HZ1	1:K:61:ASN:CG	2.07	0.55
1:J:4:VAL:N	1:J:313:PHE:CZ	2.74	0.55
1:L:6:GLN:O	1:L:7:LEU:CG	2.55	0.55
1:L:282:TYR:OH	3:N:42:ASP:OD2	2.23	0.55
1:B:264:ALA:CB	1:D:272:VAL:HG11	2.33	0.55
1:C:15:LEU:HD12	1:C:15:LEU:H	1.72	0.55
1:D:9:PRO:CG	1:E:34:GLN:NE2	2.63	0.55
1:D:395:THR:HA	1:I:395:THR:C	2.26	0.55
1:L:77:THR:CG2	1:L:158:ALA:O	2.51	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:104:PRO:HB3	1:L:188:SER:CA	2.36	0.55
1:L:182:LEU:HD21	1:L:184:ASN:OD1	2.06	0.55
1:B:391:THR:HG22	1:B:392:ILE:N	2.20	0.55
1:E:352:THR:O	1:E:353:LEU:HB2	2.07	0.55
1:L:59:PRO:HD2	1:L:190:GLN:O	2.06	0.55
2:M:48:LEU:HD12	2:M:48:LEU:N	2.21	0.55
3:N:21:GLY:O	3:N:46:LEU:HD22	2.06	0.55
4:P:14:LEU:HD12	4:P:14:LEU:H	1.72	0.55
4:P:24:ARG:HA	4:P:27:PRO:HG2	1.88	0.55
1:D:311:ALA:O	1:D:312:ASN:HB2	2.07	0.55
1:F:352:THR:O	1:F:353:LEU:HB2	2.07	0.55
1:H:281:LEU:CD2	1:H:385:GLU:HB3	2.35	0.55
1:I:257:LEU:HD21	1:I:383:ARG:HG2	1.88	0.55
1:K:80:HIS:CD2	1:K:82:THR:H	2.25	0.55
1:B:41:GLN:HG2	1:K:106:ASN:HD21	1.72	0.55
1:D:280:ASN:HD22	1:D:355:TYR:H	1.51	0.55
1:F:352:THR:O	1:F:353:LEU:CB	2.55	0.55
1:K:8:THR:N	1:K:12:GLN:NE2	2.54	0.55
1:L:34:GLN:HB3	1:L:241:PRO:HB3	1.89	0.55
3:N:37:GLU:HB3	3:N:92:LEU:CB	2.36	0.55
1:B:6:GLN:C	1:B:7:LEU:N	2.59	0.55
1:D:80:HIS:CD2	1:D:82:THR:H	2.22	0.55
1:E:280:ASN:CB	1:E:352:THR:OG1	2.54	0.55
1:E:352:THR:O	1:E:353:LEU:CB	2.54	0.55
1:G:35:SER:O	1:I:348:LYS:HE3	2.07	0.55
3:N:50:GLN:OE1	3:N:52:PHE:CZ	2.60	0.55
1:B:311:ALA:O	1:B:312:ASN:HB2	2.07	0.55
1:C:308:GLN:HE22	1:C:345:ASN:ND2	2.03	0.55
1:E:312:ASN:OD1	2:M:47:PHE:CZ	2.60	0.55
1:F:383:ARG:CB	2:M:31:VAL:HG22	2.32	0.55
1:G:23:ALA:O	1:G:24:ASN:C	2.45	0.55
1:L:352:THR:O	1:L:353:LEU:HB2	2.06	0.55
3:N:49:THR:CB	3:N:83:PRO:HA	2.32	0.55
1:A:255:SER:CA	1:A:383:ARG:NE	2.54	0.55
1:B:272:VAL:HG23	1:I:372:ARG:NH1	2.22	0.55
1:C:181:VAL:O	1:C:182:LEU:CA	2.54	0.55
1:F:10:ALA:CB	2:M:26:LEU:CD2	2.78	0.55
1:K:283:ARG:HD3	1:K:381:THR:HA	1.89	0.55
1:L:352:THR:O	1:L:353:LEU:CB	2.54	0.55
3:N:117:LEU:N	3:N:117:LEU:HD12	2.22	0.55
1:A:387:VAL:HG22	1:A:388:ASN:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:352:THR:O	1:C:353:LEU:HB2	2.07	0.55
1:E:106:ASN:CG	1:K:62:VAL:HG13	2.27	0.55
1:F:280:ASN:CB	1:F:352:THR:OG1	2.54	0.55
1:F:356:GLY:CA	2:M:23:THR:CG2	2.78	0.55
1:I:5:GLN:CG	1:I:310:THR:CG2	2.72	0.55
1:J:241:PRO:HB2	1:J:248:ILE:HB	1.89	0.55
1:L:102:TYR:CZ	3:N:13:PRO:HG3	2.42	0.55
1:L:278:TYR:O	1:L:280:ASN:OD1	2.24	0.55
1:D:281:LEU:HG	1:D:381:THR:OG1	2.07	0.54
1:L:182:LEU:CD2	1:L:184:ASN:ND2	2.70	0.54
1:L:85:VAL:O	1:L:153:THR:HG22	2.07	0.54
4:P:52:THR:HG22	4:P:53:LEU:N	2.23	0.54
1:B:15:LEU:O	1:B:16:ARG:HB2	2.08	0.54
1:B:272:VAL:HG21	1:I:372:ARG:HH11	1.72	0.54
1:K:352:THR:O	1:K:353:LEU:CB	2.55	0.54
3:N:80:ILE:HG21	3:N:116:PHE:CD2	2.40	0.54
1:A:24:ASN:N	1:A:25:LEU:N	2.53	0.54
1:C:186:PRO:C	1:C:187:GLN:HG3	2.22	0.54
1:G:239:GLN:CG	1:I:4:VAL:CB	2.85	0.54
1:G:386:LEU:HD12	1:G:386:LEU:N	2.23	0.54
1:H:384:THR:CA	1:H:387:VAL:CG1	2.80	0.54
1:B:17:ASN:CA	1:B:20:ALA:H	2.21	0.54
1:E:264:ALA:CB	1:J:272:VAL:CG1	2.86	0.54
1:F:35:SER:HB2	1:F:240:LEU:HD23	1.84	0.54
1:F:185:VAL:CB	2:M:38:ILE:O	2.55	0.54
1:H:311:ALA:O	1:H:312:ASN:HB2	2.07	0.54
1:J:184:ASN:OD1	1:J:240:LEU:HD12	2.08	0.54
1:L:353:LEU:O	2:M:75:GLN:HB3	2.07	0.54
4:P:96:ILE:HG21	4:P:100:LEU:CG	2.36	0.54
1:B:17:ASN:CA	1:B:18:GLN:N	2.69	0.54
1:B:189:LYS:NZ	1:E:60:ALA:HA	2.22	0.54
1:B:272:VAL:HG21	1:I:372:ARG:NH1	2.22	0.54
1:F:16:ARG:C	1:F:17:ASN:CA	2.75	0.54
1:J:281:LEU:CD1	2:M:58:GLN:HG2	2.38	0.54
1:J:383:ARG:N	2:M:60:TYR:CE1	2.75	0.54
1:K:352:THR:O	1:K:353:LEU:HB2	2.06	0.54
4:P:106:SER:OG	4:P:107:LEU:HD12	2.07	0.54
1:A:309:ARG:CG	1:A:313:PHE:O	2.55	0.54
1:C:15:LEU:H	1:C:15:LEU:CD1	2.21	0.54
1:K:104:PRO:HB2	1:K:187:GLN:HB3	1.88	0.54
1:L:7:LEU:CB	1:L:11:GLN:HB3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:265:GLN:HG2	3:N:40:LYS:NZ	2.14	0.54
3:N:39:VAL:HG12	3:N:92:LEU:HD13	1.88	0.54
1:I:282:TYR:CE2	1:I:386:LEU:HG	2.43	0.54
1:J:251:LEU:HD22	1:J:385:GLU:CB	2.37	0.54
4:P:12:GLY:HA2	4:P:15:VAL:CG1	2.37	0.54
1:D:282:TYR:CD2	1:D:381:THR:CB	2.91	0.54
1:F:80:HIS:CD2	1:F:82:THR:H	2.25	0.54
1:H:384:THR:C	1:H:387:VAL:CG1	2.67	0.54
1:K:32:LEU:HD11	1:K:175:THR:O	2.08	0.54
1:K:102:TYR:O	1:K:190:GLN:CG	2.56	0.54
3:N:13:PRO:CD	3:N:68:ALA:HB1	2.27	0.54
3:N:82:CYS:SG	3:N:116:PHE:CZ	2.92	0.54
1:D:7:LEU:CG	1:D:353:LEU:HD22	2.36	0.54
1:F:25:LEU:O	1:F:29:GLN:HG3	2.08	0.54
1:J:16:ARG:CD	1:J:21:MET:CE	2.79	0.54
1:L:35:SER:C	1:L:36:TYR:N	2.61	0.54
1:E:186:PRO:O	1:K:184:ASN:O	2.25	0.53
1:H:17:ASN:HB3	1:H:20:ALA:HB2	1.89	0.53
1:I:281:LEU:CG	1:I:385:GLU:HB3	2.35	0.53
1:J:8:THR:HG23	1:J:9:PRO:HD3	1.79	0.53
1:K:101:TYR:CZ	1:K:190:GLN:HG2	2.41	0.53
1:L:15:LEU:HD12	1:L:15:LEU:H	1.72	0.53
1:A:312:ASN:HD22	1:K:381:THR:HG22	1.73	0.53
1:D:282:TYR:CZ	1:D:386:LEU:HG	2.31	0.53
1:F:281:LEU:HG	2:M:29:TYR:CD1	2.42	0.53
1:I:5:GLN:OE1	1:I:310:THR:HG22	1.99	0.53
1:A:255:SER:CA	1:A:383:ARG:CZ	2.86	0.53
1:A:354:GLN:NE2	1:K:386:LEU:O	2.41	0.53
1:F:353:LEU:CD2	2:M:26:LEU:HA	2.39	0.53
1:I:15:LEU:O	1:I:16:ARG:HB2	2.08	0.53
1:K:8:THR:H	1:K:12:GLN:HE21	1.55	0.53
1:L:77:THR:CB	1:L:158:ALA:O	2.56	0.53
4:P:12:GLY:HA2	4:P:15:VAL:HG12	1.89	0.53
1:D:187:GLN:HA	1:G:187:GLN:NE2	2.13	0.53
1:G:309:ARG:HE	1:G:314:SER:HA	1.69	0.53
1:L:7:LEU:HD12	1:L:7:LEU:N	2.21	0.53
1:D:384:THR:C	1:D:387:VAL:CG1	2.67	0.53
1:E:189:LYS:HZ3	1:K:61:ASN:HB2	1.57	0.53
1:H:279:ALA:HB2	1:H:391:THR:O	2.08	0.53
1:B:41:GLN:CG	1:K:106:ASN:ND2	2.71	0.53
1:C:80:HIS:CD2	1:C:82:THR:H	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:ARG:HH12	1:J:318:LYS:NZ	2.06	0.53
1:E:187:GLN:O	1:K:186:PRO:CD	2.54	0.53
1:B:108:ARG:NE	1:D:313:PHE:O	2.42	0.53
1:D:258:TYR:HB2	1:D:380:PHE:CE2	2.43	0.53
1:H:15:LEU:O	1:H:16:ARG:HB2	2.08	0.53
1:H:392:ILE:HG22	1:H:393:SER:CA	2.32	0.53
1:J:5:GLN:HE22	1:K:38:VAL:HG22	1.73	0.53
1:K:25:LEU:O	1:K:29:GLN:HG3	2.08	0.53
1:L:78:ASN:HB3	1:L:155:ALA:O	2.08	0.53
3:N:80:ILE:HG22	3:N:81:LYS:H	1.71	0.53
1:A:280:ASN:HD22	1:A:355:TYR:H	1.57	0.53
1:G:185:VAL:CG1	1:G:186:PRO:CD	2.77	0.53
1:L:311:ALA:O	1:L:312:ASN:CB	2.54	0.53
1:B:6:GLN:HB2	1:I:387:VAL:O	2.09	0.53
1:B:6:GLN:CB	1:I:388:ASN:HA	2.31	0.53
1:B:355:TYR:OH	1:B:392:ILE:C	2.47	0.53
1:E:25:LEU:O	1:E:29:GLN:HG3	2.08	0.53
1:H:355:TYR:HE2	1:H:394:THR:CB	2.21	0.53
1:I:355:TYR:CE2	1:I:394:THR:OG1	2.48	0.53
1:L:15:LEU:CD1	1:L:15:LEU:H	2.22	0.53
1:L:75:ALA:HB1	1:L:159:THR:HG23	1.90	0.53
2:M:67:ILE:CG2	2:M:68:GLN:N	2.72	0.53
3:N:49:THR:HG21	3:N:83:PRO:CA	2.30	0.53
1:F:354:GLN:CA	2:M:26:LEU:CD2	2.85	0.53
1:K:282:TYR:CA	1:K:381:THR:CG2	2.86	0.53
2:M:68:GLN:O	4:P:41:MET:CE	2.57	0.53
4:P:14:LEU:H	4:P:14:LEU:CD1	2.22	0.53
1:B:358:VAL:CA	1:B:358:VAL:HG23	2.26	0.52
1:C:104:PRO:CG	1:C:188:SER:O	2.57	0.52
1:J:386:LEU:HD11	2:M:62:ALA:HB3	1.88	0.52
1:L:8:THR:O	1:L:12:GLN:HG3	2.08	0.52
3:N:41:TYR:CG	3:N:45:TYR:CE2	2.90	0.52
1:B:277:GLN:CA	1:B:394:THR:OG1	2.50	0.52
1:D:15:LEU:O	1:D:16:ARG:HB2	2.07	0.52
1:E:8:THR:CG2	1:E:11:GLN:N	2.58	0.52
1:E:108:ARG:NH1	1:J:314:SER:CA	2.71	0.52
1:F:15:LEU:O	1:F:17:ASN:OD1	2.26	0.52
1:B:6:GLN:HB3	1:I:388:ASN:CG	2.28	0.52
1:C:14:ALA:O	1:C:17:ASN:CG	2.48	0.52
1:C:184:ASN:OD1	1:C:185:VAL:HB	2.08	0.52
1:C:279:ALA:O	1:C:280:ASN:O	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:80:HIS:CD2	1:E:82:THR:H	2.25	0.52
1:F:239:GLN:OE1	2:M:45:MET:CE	2.57	0.52
1:I:17:ASN:C	1:I:21:MET:N	2.47	0.52
1:J:307:SER:HB2	1:J:318:LYS:HA	1.90	0.52
1:L:25:LEU:O	1:L:29:GLN:HG3	2.08	0.52
3:N:60:ILE:CB	3:N:97:ARG:HD2	2.39	0.52
1:C:25:LEU:O	1:C:29:GLN:HG3	2.08	0.52
1:L:80:HIS:CD2	1:L:82:THR:H	2.25	0.52
1:L:102:TYR:OH	3:N:13:PRO:HG3	2.10	0.52
3:N:62:ASN:HB2	3:N:95:PRO:CG	2.38	0.52
3:N:80:ILE:CG2	3:N:115:PHE:O	2.54	0.52
1:A:310:THR:OG1	1:A:313:PHE:HB2	2.09	0.52
1:E:312:ASN:HB2	2:M:46:PRO:HA	1.90	0.52
1:D:307:SER:OG	1:D:315:ASP:HB3	2.10	0.52
1:E:182:LEU:HG	1:E:184:ASN:N	2.25	0.52
1:H:316:THR:HB	1:I:36:TYR:HE2	1.75	0.52
1:I:305:TYR:CZ	1:I:318:LYS:HE3	2.45	0.52
3:N:71:ILE:HD11	3:N:85:GLY:HA3	1.92	0.52
1:B:305:TYR:CZ	1:B:318:LYS:HE3	2.45	0.52
1:D:281:LEU:CD2	1:D:386:LEU:N	2.55	0.52
1:H:319:LEU:HD21	1:I:39:ILE:HG23	1.92	0.52
1:I:307:SER:OG	1:I:315:ASP:HB3	2.10	0.52
3:N:80:ILE:CG2	3:N:116:PHE:CG	2.82	0.52
3:N:80:ILE:HD13	3:N:116:PHE:CA	2.38	0.52
1:E:187:GLN:CA	1:K:185:VAL:CA	2.69	0.52
1:H:148:ILE:HG22	1:I:138:PRO:CD	2.40	0.52
1:H:307:SER:OG	1:H:315:ASP:HB3	2.10	0.52
2:M:26:LEU:HD12	2:M:26:LEU:N	2.24	0.52
1:D:187:GLN:O	1:G:187:GLN:HG3	2.07	0.52
1:D:305:TYR:CZ	1:D:318:LYS:HE3	2.45	0.52
1:F:280:ASN:HB3	1:F:352:THR:OG1	2.10	0.52
1:G:305:TYR:CZ	1:G:318:LYS:HE3	2.45	0.52
1:H:106:ASN:ND2	1:H:191:ARG:NH2	2.56	0.52
1:K:101:TYR:OH	1:K:190:GLN:HG2	2.07	0.52
1:L:65:VAL:HG21	1:L:190:GLN:CD	2.30	0.52
1:B:255:SER:O	1:B:383:ARG:HG3	2.10	0.52
1:B:313:PHE:HE1	1:I:387:VAL:CG2	2.20	0.52
1:H:305:TYR:CZ	1:H:318:LYS:HE3	2.45	0.52
1:K:279:ALA:O	1:K:280:ASN:O	2.27	0.52
1:K:283:ARG:N	1:K:381:THR:HG1	1.89	0.52
3:N:64:GLU:OE1	3:N:93:LEU:CG	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:TYR:CZ	1:A:318:LYS:HE3	2.45	0.51
1:F:392:ILE:CD1	2:M:40:GLN:HA	2.40	0.51
4:P:12:GLY:CA	4:P:15:VAL:HG12	2.41	0.51
1:B:281:LEU:CD2	1:B:385:GLU:O	2.58	0.51
1:C:14:ALA:C	1:C:17:ASN:ND2	2.63	0.51
1:E:7:LEU:O	1:E:8:THR:CB	2.57	0.51
1:H:352:THR:HB	1:H:357:ASN:HB2	1.92	0.51
1:L:312:ASN:OD1	2:M:73:PHE:CE2	2.56	0.51
1:L:353:LEU:O	2:M:75:GLN:CB	2.58	0.51
1:D:264:ALA:HB3	1:I:272:VAL:CG1	2.39	0.51
1:E:279:ALA:O	1:E:280:ASN:O	2.28	0.51
1:E:280:ASN:HB3	1:E:352:THR:OG1	2.10	0.51
1:J:352:THR:HB	1:J:357:ASN:HB2	1.92	0.51
1:L:38:VAL:HB	1:L:236:TYR:CD1	2.45	0.51
4:P:106:SER:HB2	4:P:110:TYR:HE2	1.73	0.51
1:C:184:ASN:OD1	1:C:185:VAL:CG2	2.58	0.51
1:E:264:ALA:HB3	1:J:272:VAL:CG1	2.41	0.51
1:E:311:ALA:C	2:M:47:PHE:HE1	2.13	0.51
1:L:102:TYR:OH	3:N:68:ALA:HB2	2.10	0.51
3:N:13:PRO:CD	3:N:69:PHE:CE1	2.93	0.51
3:N:62:ASN:CB	3:N:95:PRO:HD2	2.40	0.51
3:N:79:ARG:C	3:N:80:ILE:HG13	2.30	0.51
4:P:52:THR:HG22	4:P:53:LEU:H	1.76	0.51
1:G:255:SER:HB3	1:G:386:LEU:HG	1.93	0.51
1:J:239:GLN:HE22	2:M:72:THR:HA	1.74	0.51
1:J:305:TYR:CZ	1:J:318:LYS:HE3	2.45	0.51
3:N:13:PRO:N	3:N:69:PHE:HZ	2.04	0.51
4:P:11:GLY:O	4:P:15:VAL:HG12	2.10	0.51
1:A:307:SER:OG	1:A:315:ASP:HB3	2.10	0.51
1:D:389:ALA:HB1	1:I:354:GLN:HE22	1.51	0.51
1:G:309:ARG:HG3	1:G:314:SER:HA	1.92	0.51
1:J:5:GLN:NE2	1:K:38:VAL:CG2	2.69	0.51
3:N:41:TYR:C	3:N:45:TYR:CD2	2.65	0.51
1:A:312:ASN:HD21	1:K:281:LEU:CB	2.14	0.51
1:F:11:GLN:HB3	1:F:15:LEU:HD11	1.93	0.51
1:K:312:ASN:O	1:K:313:PHE:HB2	2.11	0.51
1:A:62:VAL:HA	1:A:184:ASN:CG	2.16	0.51
1:B:307:SER:OG	1:B:315:ASP:HB3	2.10	0.51
1:F:353:LEU:CD2	2:M:27:LEU:CD1	2.88	0.51
3:N:62:ASN:HB3	3:N:95:PRO:HD2	1.91	0.51
3:N:65:ASN:ND2	3:N:85:GLY:C	2.63	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:61:ASN:HB3	1:C:183:ALA:HB1	1.93	0.51
1:I:308:GLN:NE2	1:I:345:ASN:HD21	2.07	0.51
1:J:186:PRO:HB3	2:M:66:GLY:CA	2.41	0.51
3:N:49:THR:HG21	3:N:82:CYS:C	2.27	0.51
3:N:62:ASN:HB2	3:N:95:PRO:CD	2.40	0.51
3:N:64:GLU:HB3	3:N:93:LEU:CD2	2.40	0.51
3:N:80:ILE:CB	3:N:117:LEU:H	2.24	0.51
1:A:49:PRO:HG3	1:A:228:ILE:HD12	1.93	0.51
1:A:281:LEU:HD11	1:A:382:SER:OG	2.10	0.51
1:A:387:VAL:CG2	1:A:388:ASN:N	2.74	0.51
1:B:106:ASN:ND2	1:B:191:ARG:NH2	2.56	0.51
1:E:108:ARG:HH11	1:J:314:SER:HB2	1.76	0.51
1:F:11:GLN:HA	1:F:14:ALA:HB3	1.92	0.51
1:F:279:ALA:O	1:F:280:ASN:O	2.28	0.51
1:J:49:PRO:HG3	1:J:228:ILE:HD12	1.93	0.51
1:L:74:ALA:O	1:L:161:GLU:HA	2.10	0.51
1:L:177:LEU:O	1:L:179:GLY:N	2.44	0.51
1:L:353:LEU:HB3	2:M:76:PRO:CG	2.41	0.51
1:H:392:ILE:O	1:H:393:SER:C	2.49	0.50
1:L:108:ARG:NH1	3:N:89:TYR:C	2.59	0.50
1:C:64:ILE:HG12	1:C:182:LEU:CD1	2.40	0.50
1:C:186:PRO:C	1:C:187:GLN:CG	2.76	0.50
1:C:312:ASN:O	1:C:313:PHE:HB2	2.11	0.50
1:G:15:LEU:N	1:G:15:LEU:CD1	2.73	0.50
1:G:49:PRO:HG3	1:G:228:ILE:HD12	1.93	0.50
2:M:18:PRO:O	2:M:20:PRO:HD3	2.11	0.50
2:M:67:ILE:HG23	4:P:41:MET:CE	2.40	0.50
1:C:185:VAL:CG2	1:C:247:TYR:CE1	2.92	0.50
1:F:311:ALA:HB3	2:M:23:THR:CG2	2.41	0.50
1:I:352:THR:HB	1:I:357:ASN:HB2	1.92	0.50
4:P:21:LEU:HD12	4:P:21:LEU:H	1.75	0.50
1:C:14:ALA:HA	1:C:17:ASN:HD21	1.70	0.50
1:G:307:SER:OG	1:G:315:ASP:HB3	2.10	0.50
1:H:280:ASN:ND2	1:H:355:TYR:HB2	2.27	0.50
1:I:13:ALA:O	1:I:16:ARG:HG2	2.12	0.50
1:K:108:ARG:HD2	1:K:111:GLU:OE1	2.12	0.50
1:D:49:PRO:HG3	1:D:228:ILE:HD12	1.93	0.50
1:D:52:ARG:CZ	1:G:43:GLU:HG3	2.41	0.50
1:D:280:ASN:ND2	1:D:355:TYR:HB2	2.27	0.50
1:D:352:THR:HB	1:D:357:ASN:HB2	1.92	0.50
1:F:392:ILE:O	1:F:393:SER:C	2.48	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:16:ARG:HH11	1:J:21:MET:HE1	1.65	0.50
1:J:387:VAL:C	1:J:388:ASN:OD1	2.45	0.50
3:N:30:TYR:O	3:N:101:VAL:HG12	2.11	0.50
3:N:79:ARG:NH2	3:N:104:HIS:O	2.45	0.50
1:A:280:ASN:ND2	1:A:355:TYR:HB2	2.27	0.50
1:B:189:LYS:HE2	1:E:61:ASN:H	1.77	0.50
1:F:353:LEU:CD1	2:M:27:LEU:O	2.50	0.50
1:H:319:LEU:HD21	1:I:39:ILE:CG2	2.42	0.50
1:B:49:PRO:HG3	1:B:228:ILE:HD12	1.94	0.50
1:B:311:ALA:HB2	1:I:391:THR:HA	1.93	0.50
1:C:7:LEU:HD12	1:C:7:LEU:H	1.77	0.50
1:H:63:GLY:CA	1:H:184:ASN:ND2	2.67	0.50
3:N:14:VAL:CG2	3:N:16:ASN:CB	2.89	0.50
1:B:13:ALA:O	1:B:16:ARG:HG2	2.12	0.50
1:F:239:GLN:HG2	2:M:45:MET:HG3	1.81	0.50
1:F:353:LEU:HB3	2:M:26:LEU:HB3	1.94	0.50
1:F:356:GLY:HA2	2:M:23:THR:HG22	1.89	0.50
1:G:145:MET:O	1:I:322:LYS:HE2	2.12	0.50
1:G:280:ASN:HD22	1:G:355:TYR:H	1.57	0.50
1:J:9:PRO:HG3	1:K:34:GLN:CA	2.13	0.50
1:J:180:ALA:O	1:J:254:LEU:HD23	2.12	0.50
1:J:351:TYR:OH	2:M:58:GLN:NE2	2.42	0.50
1:C:185:VAL:HG23	1:C:247:TYR:HE1	1.75	0.50
1:G:280:ASN:ND2	1:G:355:TYR:HB2	2.27	0.50
1:H:281:LEU:HD22	1:H:385:GLU:C	2.28	0.50
1:J:7:LEU:HD11	1:J:352:THR:O	2.12	0.50
4:P:37:GLY:CA	4:P:39:PRO:HD2	2.37	0.50
1:B:280:ASN:ND2	1:B:355:TYR:HB2	2.27	0.49
1:B:389:ALA:CB	1:D:354:GLN:NE2	2.69	0.49
1:I:257:LEU:HG	1:I:383:ARG:CG	2.37	0.49
1:I:280:ASN:ND2	1:I:355:TYR:HB2	2.27	0.49
4:P:21:LEU:H	4:P:21:LEU:CD1	2.25	0.49
1:D:13:ALA:O	1:D:16:ARG:HG2	2.12	0.49
1:D:106:ASN:ND2	1:D:191:ARG:NH2	2.56	0.49
1:D:386:LEU:O	1:I:312:ASN:CG	2.48	0.49
1:H:355:TYR:HE2	1:H:394:THR:OG1	1.93	0.49
1:J:280:ASN:ND2	1:J:355:TYR:HB2	2.27	0.49
1:G:185:VAL:CB	2:M:4:ASN:CB	2.43	0.49
1:H:14:ALA:O	1:H:16:ARG:HG3	2.13	0.49
1:F:108:ARG:HD2	1:F:111:GLU:OE1	2.12	0.49
1:G:185:VAL:H	1:G:186:PRO:HD2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:307:SER:OG	1:J:315:ASP:HB3	2.12	0.49
3:N:80:ILE:CG2	3:N:116:PHE:CD2	2.96	0.49
1:B:372:ARG:HH11	1:D:272:VAL:HG21	1.78	0.49
1:D:14:ALA:O	1:D:16:ARG:HG3	2.13	0.49
1:F:353:LEU:HD12	2:M:29:TYR:OH	2.11	0.49
1:G:103:ASP:HB2	1:G:104:PRO:CD	2.43	0.49
1:L:353:LEU:CG	2:M:76:PRO:HG3	2.42	0.49
4:P:10:VAL:CG2	4:P:14:LEU:HD11	2.42	0.49
4:P:18:LEU:HD12	4:P:18:LEU:H	1.78	0.49
1:B:187:GLN:CB	1:E:186:PRO:HA	2.38	0.49
1:C:64:ILE:HG12	1:C:182:LEU:HD13	1.95	0.49
1:E:98:ARG:NH1	1:J:318:LYS:NZ	2.61	0.49
1:E:106:ASN:CB	1:K:62:VAL:HG13	2.42	0.49
1:I:277:GLN:HG3	1:I:394:THR:HB	1.90	0.49
1:L:109:HIS:O	3:N:89:TYR:HE1	1.95	0.49
1:B:103:ASP:HB2	1:B:104:PRO:CD	2.43	0.49
1:B:354:GLN:CD	1:I:389:ALA:CB	2.79	0.49
1:E:108:ARG:HD2	1:E:111:GLU:OE1	2.12	0.49
1:G:308:GLN:NE2	1:G:345:ASN:HD21	2.07	0.49
1:I:49:PRO:HG3	1:I:228:ILE:HD12	1.93	0.49
3:N:13:PRO:CA	3:N:69:PHE:CZ	2.91	0.49
4:P:1:MET:SD	4:P:3:LYS:HE3	2.52	0.49
1:B:14:ALA:O	1:B:16:ARG:HG3	2.13	0.49
1:B:391:THR:HG22	1:B:392:ILE:H	1.77	0.49
1:C:108:ARG:HD2	1:C:111:GLU:OE1	2.12	0.49
1:E:189:LYS:CG	1:K:61:ASN:HB2	2.41	0.49
1:E:312:ASN:ND2	2:M:46:PRO:HA	2.27	0.49
1:H:49:PRO:HG3	1:H:228:ILE:HD12	1.93	0.49
1:H:391:THR:HG22	1:H:392:ILE:H	1.77	0.49
2:M:2:LEU:N	2:M:2:LEU:CD1	2.75	0.49
1:A:103:ASP:HB2	1:A:104:PRO:CD	2.43	0.49
1:E:8:THR:CB	1:E:11:GLN:CB	2.86	0.49
1:F:392:ILE:O	1:F:393:SER:O	2.29	0.49
1:H:103:ASP:HB2	1:H:104:PRO:CD	2.43	0.49
1:K:104:PRO:HA	1:K:188:SER:OG	2.12	0.49
1:L:35:SER:C	1:L:36:TYR:HA	2.33	0.49
3:N:68:ALA:CA	3:N:87:GLN:NE2	2.61	0.49
1:B:354:GLN:NE2	1:I:389:ALA:HB1	2.24	0.49
1:F:353:LEU:HD12	2:M:29:TYR:CE2	2.46	0.49
1:H:257:LEU:HD12	1:H:386:LEU:HD22	1.95	0.49
1:K:308:GLN:NE2	1:K:345:ASN:HD21	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:76:ILE:HB	1:L:154:ILE:HD11	1.93	0.49
1:L:182:LEU:CD2	1:L:184:ASN:OD1	2.60	0.49
1:D:103:ASP:HB2	1:D:104:PRO:CD	2.43	0.48
1:D:281:LEU:HD11	1:D:385:GLU:HB2	1.14	0.48
1:D:388:ASN:OD1	1:I:6:GLN:HB3	2.12	0.48
1:H:308:GLN:NE2	1:H:345:ASN:HD21	2.07	0.48
1:J:183:ALA:O	1:J:184:ASN:C	2.50	0.48
4:P:111:LEU:HD12	4:P:111:LEU:H	1.77	0.48
1:B:372:ARG:NH1	1:D:272:VAL:HG21	2.28	0.48
1:E:311:ALA:HB1	2:M:47:PHE:CE1	2.45	0.48
1:I:277:GLN:CB	1:I:394:THR:HB	2.43	0.48
1:K:103:ASP:HA	1:K:190:GLN:CG	2.26	0.48
1:A:308:GLN:NE2	1:A:345:ASN:HD21	2.07	0.48
1:B:357:ASN:O	1:B:358:VAL:CA	2.61	0.48
1:D:391:THR:HG22	1:D:392:ILE:H	1.77	0.48
3:N:71:ILE:CD1	3:N:85:GLY:HA3	2.43	0.48
4:P:18:LEU:H	4:P:18:LEU:CD1	2.26	0.48
1:D:11:GLN:CD	1:D:351:TYR:CE2	2.87	0.48
1:G:251:LEU:CD1	1:G:388:ASN:CG	2.70	0.48
1:I:386:LEU:HD12	1:I:386:LEU:H	1.79	0.48
1:L:52:ARG:CZ	3:N:8:GLN:HG2	2.42	0.48
3:N:80:ILE:CG2	3:N:81:LYS:N	2.76	0.48
1:D:187:GLN:HB3	1:G:187:GLN:HG3	1.95	0.48
1:E:107:GLN:HG2	1:E:383:ARG:CZ	2.44	0.48
1:I:391:THR:HG22	1:I:392:ILE:H	1.77	0.48
3:N:21:GLY:N	3:N:46:LEU:HD21	2.27	0.48
3:N:23:GLY:HA3	3:N:109:LYS:CD	2.40	0.48
1:A:312:ASN:ND2	1:K:381:THR:CG2	2.76	0.48
1:B:272:VAL:HG23	1:I:372:ARG:HH12	1.77	0.48
1:E:15:LEU:HD12	1:E:15:LEU:H	1.77	0.48
1:I:103:ASP:HB2	1:I:104:PRO:CD	2.42	0.48
2:M:15:ILE:N	2:M:16:PRO:HD3	2.25	0.48
3:N:92:LEU:O	3:N:93:LEU:HD12	2.14	0.48
4:P:12:GLY:C	4:P:15:VAL:HG12	2.34	0.48
1:H:392:ILE:HG22	1:H:393:SER:CB	2.44	0.48
1:I:120:VAL:HG21	1:I:260:LEU:HD13	1.96	0.48
1:L:182:LEU:CD1	1:L:184:ASN:HD21	2.09	0.48
1:C:104:PRO:HB3	1:C:188:SER:CA	2.44	0.48
1:C:186:PRO:O	1:C:187:GLN:CG	2.26	0.48
1:E:8:THR:O	1:E:12:GLN:CG	2.56	0.48
1:I:14:ALA:O	1:I:16:ARG:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:76:ILE:HG22	1:L:154:ILE:HD12	1.96	0.48
1:L:280:ASN:O	1:L:281:LEU:HD13	2.14	0.48
3:N:112:VAL:HG23	3:N:113:PRO:HD2	0.48	0.48
1:B:102:TYR:CE2	1:B:108:ARG:HG3	2.49	0.48
1:F:15:LEU:CA	1:F:17:ASN:OD1	2.61	0.48
1:F:353:LEU:HD21	2:M:27:LEU:HB2	1.95	0.48
1:G:120:VAL:HG21	1:G:260:LEU:HD13	1.96	0.48
1:L:52:ARG:HH12	3:N:8:GLN:HG2	1.79	0.48
1:L:102:TYR:HE2	3:N:13:PRO:HG3	1.77	0.48
2:M:77:LEU:HD12	2:M:77:LEU:H	1.79	0.48
3:N:39:VAL:CG1	3:N:92:LEU:HD11	2.44	0.48
4:P:100:LEU:CD1	4:P:100:LEU:N	2.76	0.48
1:A:314:SER:OG	1:A:315:ASP:CA	2.35	0.47
1:C:184:ASN:N	1:C:185:VAL:O	2.47	0.47
1:D:102:TYR:CE2	1:D:108:ARG:HG3	2.49	0.47
1:E:186:PRO:O	1:E:187:GLN:CG	2.62	0.47
1:E:281:LEU:N	1:E:281:LEU:HD12	2.29	0.47
3:N:21:GLY:O	3:N:46:LEU:CD2	2.63	0.47
4:P:26:ARG:N	4:P:27:PRO:HD2	2.30	0.47
1:B:7:LEU:CD1	1:B:7:LEU:N	2.77	0.47
1:C:7:LEU:H	1:C:7:LEU:CD1	2.26	0.47
1:D:5:GLN:OE1	1:E:36:TYR:CZ	2.67	0.47
1:D:387:VAL:HG22	1:D:388:ASN:OD1	2.15	0.47
1:G:239:GLN:CG	1:I:4:VAL:HB	2.44	0.47
1:J:102:TYR:CE2	1:J:108:ARG:HG3	2.49	0.47
1:J:120:VAL:HG21	1:J:260:LEU:HD13	1.96	0.47
1:A:309:ARG:HG2	1:A:310:THR:N	2.29	0.47
1:F:239:GLN:OE1	2:M:45:MET:HE1	2.15	0.47
1:J:16:ARG:HH11	1:J:21:MET:CE	2.21	0.47
1:J:28:ARG:NE	1:J:253:ASP:OD2	2.41	0.47
1:L:102:TYR:CZ	3:N:89:TYR:CE2	3.02	0.47
4:P:52:THR:CA	4:P:53:LEU:HD12	2.38	0.47
1:A:120:VAL:HG21	1:A:260:LEU:HD13	1.96	0.47
1:B:386:LEU:HD12	1:B:386:LEU:H	1.79	0.47
1:C:281:LEU:HD12	1:C:281:LEU:N	2.29	0.47
1:D:120:VAL:HG21	1:D:260:LEU:HD13	1.96	0.47
3:N:112:VAL:CG2	3:N:113:PRO:CG	2.82	0.47
1:E:308:GLN:NE2	1:E:345:ASN:HD21	2.11	0.47
1:F:281:LEU:HD12	1:F:281:LEU:N	2.29	0.47
1:G:239:GLN:CG	1:I:313:PHE:CZ	2.96	0.47
1:I:102:TYR:CE2	1:I:108:ARG:HG3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:103:ASP:HB2	1:J:104:PRO:CD	2.43	0.47
1:L:59:PRO:HB2	1:L:190:GLN:HB2	1.95	0.47
3:N:39:VAL:CG1	3:N:92:LEU:CD1	2.92	0.47
4:P:107:LEU:CD1	4:P:107:LEU:H	2.27	0.47
1:B:120:VAL:HG21	1:B:260:LEU:HD13	1.96	0.47
1:C:61:ASN:C	1:C:183:ALA:CB	2.83	0.47
1:D:24:ASN:HB2	1:D:252:ILE:HG13	1.97	0.47
1:F:255:SER:CA	2:M:35:ILE:HD11	2.45	0.47
1:G:23:ALA:O	1:G:25:LEU:N	2.48	0.47
1:H:7:LEU:CD1	1:H:7:LEU:N	2.77	0.47
1:H:102:TYR:CE2	1:H:108:ARG:HG3	2.49	0.47
1:I:255:SER:O	1:I:383:ARG:HG3	2.15	0.47
1:I:386:LEU:CD1	1:I:386:LEU:H	2.28	0.47
1:J:182:LEU:HD21	1:J:249:LEU:HD11	1.93	0.47
1:K:281:LEU:HD12	1:K:281:LEU:N	2.29	0.47
1:L:36:TYR:CB	1:L:239:GLN:HB2	2.44	0.47
4:P:111:LEU:CD1	4:P:111:LEU:H	2.28	0.47
1:A:314:SER:OG	1:A:315:ASP:CB	2.62	0.47
1:D:386:LEU:CD1	1:D:386:LEU:H	2.28	0.47
1:D:391:THR:OG1	1:I:356:GLY:C	2.45	0.47
1:E:187:GLN:HG2	1:K:184:ASN:C	2.35	0.47
1:G:102:TYR:CE2	1:G:108:ARG:HG3	2.49	0.47
1:G:107:GLN:HG2	1:G:383:ARG:NH2	2.30	0.47
1:G:316:THR:HG21	1:H:36:TYR:CE2	2.50	0.47
1:I:7:LEU:CD1	1:I:7:LEU:N	2.77	0.47
1:I:279:ALA:CB	1:I:391:THR:O	2.63	0.47
1:J:240:LEU:HD22	1:J:240:LEU:HA	1.80	0.47
1:L:102:TYR:CZ	3:N:89:TYR:HE2	2.32	0.47
2:M:77:LEU:N	2:M:77:LEU:CD1	2.77	0.47
3:N:59:TYR:CE1	3:N:98:ALA:HA	2.11	0.47
3:N:60:ILE:CG2	3:N:62:ASN:OD1	2.61	0.47
3:N:79:ARG:O	3:N:80:ILE:HG13	2.15	0.47
4:P:6:LEU:N	4:P:6:LEU:CD1	2.78	0.47
1:A:102:TYR:CE2	1:A:108:ARG:HG3	2.49	0.47
1:B:311:ALA:HB2	1:I:390:GLY:O	2.06	0.47
1:B:389:ALA:CB	1:D:354:GLN:CD	2.83	0.47
1:E:8:THR:CB	1:E:11:GLN:CG	2.92	0.47
1:E:15:LEU:H	1:E:15:LEU:CD1	2.26	0.47
1:E:182:LEU:HG	1:E:183:ALA:C	2.35	0.47
1:H:17:ASN:O	1:H:20:ALA:N	2.47	0.47
1:H:120:VAL:HG21	1:H:260:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:38:VAL:O	1:L:236:TYR:CA	2.59	0.47
1:L:193:LYS:HZ3	3:N:68:ALA:HA	1.80	0.47
3:N:30:TYR:O	3:N:101:VAL:CG1	2.63	0.47
1:H:386:LEU:CD1	1:H:386:LEU:H	2.28	0.47
1:J:182:LEU:CD2	1:J:249:LEU:CD1	2.75	0.47
1:L:281:LEU:HD12	1:L:281:LEU:N	2.29	0.47
2:M:3:ILE:HA	2:M:9:TYR:CE2	2.49	0.47
1:B:63:GLY:CA	1:B:184:ASN:ND2	2.67	0.47
1:D:275:VAL:O	1:D:394:THR:HG21	2.14	0.47
1:D:282:TYR:CD2	1:D:381:THR:OG1	2.68	0.47
1:F:15:LEU:CD1	1:F:15:LEU:N	2.78	0.47
1:L:15:LEU:CD1	1:L:15:LEU:N	2.78	0.47
1:L:76:ILE:HB	1:L:154:ILE:HD12	1.91	0.47
1:L:279:ALA:C	3:N:43:LEU:CD1	2.71	0.47
4:P:107:LEU:HD12	4:P:107:LEU:H	1.78	0.47
1:A:316:THR:HG21	1:B:36:TYR:CE2	2.50	0.46
1:E:322:LYS:HE2	1:F:145:MET:O	2.15	0.46
1:F:392:ILE:HD12	2:M:40:GLN:HA	1.97	0.46
1:I:7:LEU:HD22	1:I:353:LEU:HD21	1.93	0.46
1:L:37:PRO:HA	1:L:237:LEU:CA	2.44	0.46
3:N:112:VAL:O	3:N:114:LEU:HD11	2.13	0.46
1:A:63:GLY:N	1:A:184:ASN:HD21	1.95	0.46
1:A:386:LEU:N	1:A:386:LEU:CD1	2.78	0.46
3:N:79:ARG:CZ	3:N:104:HIS:O	2.63	0.46
3:N:80:ILE:CG2	3:N:117:LEU:N	2.77	0.46
3:N:80:ILE:HG12	3:N:117:LEU:C	2.32	0.46
3:N:94:VAL:HG22	3:N:103:ARG:CZ	2.37	0.46
1:C:190:GLN:CB	1:C:191:ARG:HG3	2.46	0.46
1:D:187:GLN:CA	1:G:187:GLN:HE21	2.14	0.46
1:I:15:LEU:HD12	1:I:15:LEU:H	1.80	0.46
1:A:255:SER:HB2	1:A:383:ARG:HB2	1.97	0.46
1:A:310:THR:O	1:A:311:ALA:C	2.54	0.46
1:F:386:LEU:HD12	2:M:33:GLY:O	2.13	0.46
1:H:387:VAL:HG22	1:H:388:ASN:OD1	2.14	0.46
1:I:281:LEU:HD13	1:I:385:GLU:HB3	1.81	0.46
1:L:79:ASN:HA	1:L:157:GLY:H	1.80	0.46
3:N:19:ASP:OD2	3:N:110:LYS:HA	2.15	0.46
4:P:6:LEU:HB3	4:P:7:LEU:CD1	2.41	0.46
1:B:386:LEU:CD1	1:B:386:LEU:H	2.28	0.46
1:D:59:PRO:HD2	1:D:190:GLN:HB2	1.98	0.46
1:I:277:GLN:HB2	1:I:394:THR:HB	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:43:LEU:CD1	3:N:43:LEU:N	2.77	0.46
1:G:59:PRO:HD2	1:G:190:GLN:HB2	1.98	0.46
1:H:185:VAL:O	1:H:185:VAL:HG22	2.16	0.46
1:J:184:ASN:HD21	1:J:240:LEU:CD1	2.12	0.46
1:K:316:THR:HG21	1:L:36:TYR:CE2	2.51	0.46
1:L:39:ILE:HG23	1:L:39:ILE:O	2.15	0.46
1:E:257:LEU:HD11	1:E:383:ARG:HE	1.81	0.46
1:G:255:SER:HB2	2:M:6:GLN:NE2	2.31	0.46
1:H:386:LEU:HD12	1:H:386:LEU:H	1.79	0.46
2:M:23:THR:HA	2:M:25:PRO:HD2	1.97	0.46
4:P:96:ILE:HB	4:P:100:LEU:HB2	1.98	0.46
1:D:21:MET:CA	1:D:252:ILE:CD1	2.89	0.46
1:F:184:ASN:O	1:F:186:PRO:HD3	2.16	0.46
1:F:281:LEU:HA	2:M:29:TYR:CZ	2.51	0.46
1:H:59:PRO:HD2	1:H:190:GLN:HB2	1.98	0.46
1:I:59:PRO:HD2	1:I:190:GLN:HB2	1.98	0.46
1:I:185:VAL:H	1:I:186:PRO:HD2	1.49	0.46
1:K:15:LEU:HD12	1:K:15:LEU:H	1.80	0.46
1:K:322:LYS:HE2	1:L:145:MET:O	2.16	0.46
1:L:308:GLN:NE2	1:L:345:ASN:HD21	2.11	0.46
4:P:22:TRP:O	4:P:26:ARG:HG3	2.16	0.46
1:B:353:LEU:CD1	1:B:353:LEU:N	2.79	0.46
1:E:12:GLN:O	1:E:16:ARG:HG3	2.16	0.46
1:E:106:ASN:HB2	1:K:62:VAL:HG13	1.98	0.46
1:E:108:ARG:HH11	1:J:314:SER:CB	2.29	0.46
1:F:240:LEU:N	2:M:43:GLN:OE1	2.49	0.46
1:F:312:ASN:CG	2:M:20:PRO:HG2	2.36	0.46
1:G:239:GLN:HG2	1:I:4:VAL:CB	2.46	0.46
1:K:282:TYR:CA	1:K:381:THR:HG21	2.38	0.46
1:L:182:LEU:HD21	1:L:184:ASN:CG	2.36	0.46
3:N:14:VAL:HG22	3:N:16:ASN:HB2	1.97	0.46
3:N:15:TYR:CD2	3:N:47:ALA:HB2	2.50	0.46
3:N:27:VAL:C	3:N:27:VAL:CG2	2.84	0.46
3:N:65:ASN:HD21	3:N:71:ILE:CD1	2.07	0.46
3:N:71:ILE:HD12	3:N:85:GLY:N	2.31	0.46
4:P:18:LEU:N	4:P:18:LEU:CD1	2.79	0.46
1:A:24:ASN:O	1:A:26:GLN:N	2.45	0.46
1:B:59:PRO:HD2	1:B:190:GLN:HB2	1.98	0.46
1:D:7:LEU:CD1	1:D:7:LEU:N	2.77	0.46
1:G:35:SER:C	1:G:36:TYR:HA	2.35	0.46
1:H:353:LEU:CD1	1:H:353:LEU:N	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:386:LEU:N	1:H:386:LEU:CD1	2.78	0.46
1:A:14:ALA:O	1:A:18:GLN:HG3	2.15	0.45
1:A:59:PRO:HD2	1:A:190:GLN:HB2	1.98	0.45
1:B:7:LEU:HD13	1:B:353:LEU:CD2	2.44	0.45
1:B:108:ARG:HH21	1:D:313:PHE:C	2.03	0.45
1:D:7:LEU:CD1	1:D:353:LEU:HD13	2.30	0.45
1:D:15:LEU:HD12	1:D:15:LEU:H	1.80	0.45
1:D:187:GLN:HG3	2:M:9:TYR:CE1	2.33	0.45
1:G:23:ALA:C	1:G:26:GLN:HB3	2.36	0.45
1:J:7:LEU:N	1:J:7:LEU:CD1	2.77	0.45
1:J:391:THR:HB	4:P:41:MET:HE2	1.97	0.45
1:L:12:GLN:O	1:L:16:ARG:HG3	2.16	0.45
2:M:77:LEU:H	2:M:77:LEU:CD1	2.29	0.45
1:B:372:ARG:NH1	1:D:272:VAL:CG2	2.79	0.45
1:D:5:GLN:CD	1:E:36:TYR:CD2	2.87	0.45
1:E:15:LEU:O	1:E:19:GLN:HG3	2.16	0.45
1:I:257:LEU:HB2	1:I:381:THR:CG2	2.47	0.45
1:I:353:LEU:CD1	1:I:353:LEU:N	2.79	0.45
1:I:386:LEU:N	1:I:386:LEU:CD1	2.78	0.45
1:J:31:VAL:O	1:J:35:SER:CB	2.63	0.45
1:K:34:GLN:O	1:K:35:SER:N	2.48	0.45
1:B:386:LEU:N	1:B:386:LEU:CD1	2.78	0.45
1:E:311:ALA:O	2:M:47:PHE:CD1	2.69	0.45
1:I:255:SER:HA	1:I:383:ARG:HD2	1.97	0.45
1:J:15:LEU:N	1:J:15:LEU:CD1	2.78	0.45
1:A:310:THR:HA	1:A:357:ASN:O	2.17	0.45
1:B:185:VAL:O	1:B:185:VAL:HG22	2.16	0.45
1:C:8:THR:HG22	1:C:9:PRO:N	2.25	0.45
1:C:8:THR:O	1:C:12:GLN:HG3	2.17	0.45
1:D:386:LEU:HD12	1:D:386:LEU:H	1.79	0.45
1:J:5:GLN:OE1	1:K:36:TYR:HD2	1.97	0.45
1:J:353:LEU:N	1:J:353:LEU:CD1	2.79	0.45
3:N:14:VAL:HG22	3:N:16:ASN:CB	2.46	0.45
3:N:80:ILE:CG2	3:N:81:LYS:H	2.30	0.45
3:N:101:VAL:CG2	3:N:102:ALA:N	2.80	0.45
1:B:63:GLY:HA2	1:B:184:ASN:HD21	1.81	0.45
1:D:353:LEU:CD1	1:D:353:LEU:N	2.79	0.45
1:D:386:LEU:N	1:D:386:LEU:CD1	2.78	0.45
1:E:106:ASN:OD1	1:K:62:VAL:HG21	2.16	0.45
1:L:186:PRO:O	1:L:187:GLN:CB	2.54	0.45
1:L:312:ASN:ND2	2:M:73:PHE:CD2	2.76	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:308:GLN:NE2	1:C:345:ASN:HD21	2.11	0.45
1:D:83:GLU:HB3	1:D:218:ALA:HB3	1.99	0.45
1:D:264:ALA:HB3	1:I:272:VAL:HG13	1.98	0.45
1:D:388:ASN:OD1	1:I:6:GLN:CD	2.47	0.45
1:E:15:LEU:N	1:E:15:LEU:CD1	2.80	0.45
1:I:13:ALA:O	1:I:16:ARG:CG	2.65	0.45
1:I:106:ASN:ND2	1:I:191:ARG:NH2	2.56	0.45
1:J:5:GLN:N	1:J:313:PHE:HZ	1.99	0.45
1:K:310:THR:HG22	1:K:358:VAL:HG22	1.99	0.45
1:L:38:VAL:HG11	1:L:236:TYR:CZ	2.52	0.45
2:M:62:ALA:C	2:M:63:ILE:HG13	2.37	0.45
3:N:37:GLU:HB2	3:N:92:LEU:HB2	1.90	0.45
1:A:106:ASN:ND2	1:A:191:ARG:NH2	2.56	0.45
1:B:15:LEU:CD1	1:B:15:LEU:H	2.30	0.45
1:B:15:LEU:CD1	1:B:15:LEU:N	2.80	0.45
1:B:15:LEU:HD12	1:B:15:LEU:H	1.80	0.45
1:E:182:LEU:CD2	1:E:184:ASN:OD1	2.41	0.45
1:H:15:LEU:CD1	1:H:15:LEU:H	2.30	0.45
1:J:384:THR:CG2	2:M:62:ALA:HA	2.46	0.45
3:N:41:TYR:O	3:N:45:TYR:HD2	2.00	0.45
3:N:46:LEU:N	3:N:46:LEU:CD1	2.79	0.45
1:D:21:MET:N	1:D:252:ILE:HD11	2.31	0.45
1:E:187:GLN:HB3	1:E:188:SER:H	1.13	0.45
1:F:351:TYR:HE1	2:M:29:TYR:OH	1.84	0.45
1:G:211:LEU:HD21	1:G:374:LEU:HD13	1.99	0.45
1:J:5:GLN:HE22	1:K:38:VAL:HG21	1.77	0.45
1:L:61:ASN:ND2	1:L:189:LYS:HA	2.28	0.45
1:L:76:ILE:CG2	1:L:154:ILE:CD1	2.94	0.45
3:N:69:PHE:HB2	3:N:85:GLY:O	2.16	0.45
1:B:4:VAL:N	1:B:5:GLN:H	2.13	0.45
1:B:13:ALA:O	1:B:16:ARG:CG	2.65	0.45
1:D:185:VAL:O	1:D:185:VAL:HG22	2.16	0.45
1:G:83:GLU:HB3	1:G:218:ALA:HB3	1.99	0.45
1:I:11:GLN:CD	1:I:351:TYR:HD2	2.21	0.45
4:P:21:LEU:N	4:P:21:LEU:CD1	2.80	0.45
4:P:107:LEU:CD1	4:P:107:LEU:N	2.79	0.45
1:B:52:ARG:NH2	1:E:43:GLU:HG3	2.31	0.45
1:D:15:LEU:CD1	1:D:15:LEU:H	2.30	0.45
1:H:211:LEU:HD21	1:H:374:LEU:HD13	1.99	0.45
1:I:185:VAL:O	1:I:185:VAL:HG22	2.16	0.45
1:I:257:LEU:HD23	1:I:383:ARG:HG2	1.92	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LEU:HD21	1:A:374:LEU:HD13	1.99	0.44
1:D:211:LEU:HD21	1:D:374:LEU:HD13	1.99	0.44
1:F:310:THR:HG22	1:F:358:VAL:HG22	1.99	0.44
1:H:15:LEU:N	1:H:15:LEU:CD1	2.80	0.44
1:H:281:LEU:HD21	1:H:386:LEU:HD12	1.99	0.44
1:L:35:SER:CB	1:L:36:TYR:N	2.78	0.44
1:L:310:THR:HG22	1:L:358:VAL:HG22	1.99	0.44
4:P:14:LEU:N	4:P:14:LEU:CD1	2.79	0.44
4:P:16:LEU:CD1	4:P:16:LEU:H	2.30	0.44
1:A:255:SER:C	1:A:383:ARG:NE	2.69	0.44
1:G:314:SER:C	1:G:315:ASP:CG	2.76	0.44
1:H:15:LEU:HD12	1:H:15:LEU:H	1.80	0.44
1:I:15:LEU:CD1	1:I:15:LEU:N	2.80	0.44
1:I:83:GLU:HB3	1:I:218:ALA:HB3	1.99	0.44
1:J:31:VAL:O	1:J:35:SER:HB3	2.17	0.44
1:J:83:GLU:HB3	1:J:218:ALA:HB3	1.99	0.44
1:D:255:SER:O	1:D:383:ARG:HD2	2.17	0.44
1:E:310:THR:HG22	1:E:358:VAL:HG22	1.99	0.44
1:F:239:GLN:CG	2:M:45:MET:HE1	1.97	0.44
1:J:59:PRO:HD2	1:J:190:GLN:HB2	1.98	0.44
1:K:102:TYR:O	1:K:190:GLN:HG2	2.18	0.44
4:P:16:LEU:HD12	4:P:16:LEU:H	1.81	0.44
1:B:7:LEU:HD13	1:B:353:LEU:CG	2.47	0.44
1:B:52:ARG:CZ	1:E:43:GLU:HG3	2.47	0.44
1:B:211:LEU:HD21	1:B:374:LEU:HD13	1.99	0.44
1:B:308:GLN:NE2	1:B:345:ASN:HD21	2.07	0.44
1:B:384:THR:C	1:B:387:VAL:CG1	2.67	0.44
1:C:187:GLN:HG3	1:I:187:GLN:HB2	1.44	0.44
1:D:4:VAL:CG1	1:D:313:PHE:CB	2.87	0.44
1:D:277:GLN:HG3	1:D:394:THR:HG23	1.99	0.44
1:G:239:GLN:NE2	1:I:4:VAL:HG23	2.33	0.44
1:G:255:SER:CB	2:M:6:GLN:NE2	2.80	0.44
1:H:5:GLN:OE1	1:I:36:TYR:CZ	2.70	0.44
1:K:280:ASN:CG	1:K:352:THR:OG1	2.56	0.44
1:L:65:VAL:CG2	1:L:190:GLN:HE22	2.30	0.44
2:M:3:ILE:HA	2:M:9:TYR:HD2	1.81	0.44
1:D:13:ALA:O	1:D:16:ARG:CG	2.65	0.44
1:H:255:SER:HA	1:H:383:ARG:CZ	2.48	0.44
1:I:15:LEU:CD1	1:I:15:LEU:H	2.30	0.44
1:J:383:ARG:CB	1:J:384:THR:N	2.75	0.44
1:K:15:LEU:H	1:K:15:LEU:CD1	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:104:PRO:C	1:L:188:SER:HG	2.19	0.44
4:P:4:LYS:HB3	4:P:6:LEU:HD13	1.99	0.44
1:A:15:LEU:N	1:A:15:LEU:CD1	2.79	0.44
4:P:26:ARG:N	4:P:27:PRO:CD	2.80	0.44
1:B:83:GLU:HB3	1:B:218:ALA:HB3	1.99	0.44
1:D:15:LEU:CD1	1:D:15:LEU:N	2.80	0.44
1:D:254:LEU:O	1:D:383:ARG:CZ	2.65	0.44
1:G:61:ASN:HB3	1:G:183:ALA:O	2.18	0.44
1:H:83:GLU:HB3	1:H:218:ALA:HB3	1.99	0.44
1:H:355:TYR:CE2	1:H:394:THR:CB	3.00	0.44
3:N:37:GLU:HB3	3:N:92:LEU:HD23	2.00	0.44
3:N:50:GLN:HB2	3:N:52:PHE:HE1	1.83	0.44
3:N:63:ALA:HB2	3:N:73:VAL:HG21	1.79	0.44
3:N:65:ASN:ND2	3:N:71:ILE:HB	2.32	0.44
3:N:71:ILE:CD1	3:N:85:GLY:CA	2.96	0.44
4:P:26:ARG:HB2	4:P:27:PRO:CD	2.42	0.44
1:A:61:ASN:HB3	1:A:183:ALA:O	2.18	0.44
1:C:103:ASP:HB2	1:C:104:PRO:HD2	2.00	0.44
1:E:187:GLN:CB	1:K:184:ASN:O	2.66	0.44
1:G:106:ASN:ND2	1:G:191:ARG:NH2	2.56	0.44
4:P:15:VAL:O	4:P:19:ILE:HG13	2.18	0.44
1:A:83:GLU:HB3	1:A:218:ALA:HB3	1.99	0.44
1:B:185:VAL:O	1:B:185:VAL:CG2	2.65	0.44
1:B:307:SER:HB2	1:B:318:LYS:HA	2.00	0.44
1:E:151:PRO:HD2	1:E:162:LEU:HD22	2.00	0.44
2:M:67:ILE:HG23	4:P:41:MET:HE3	1.98	0.44
3:N:61:ASP:H	3:N:75:GLU:HB2	1.83	0.44
1:A:270:PRO:HD2	1:K:264:ALA:O	2.18	0.43
1:B:277:GLN:HG3	1:B:394:THR:HG21	1.12	0.43
1:D:61:ASN:HB3	1:D:183:ALA:O	2.18	0.43
1:D:185:VAL:O	1:D:185:VAL:CG2	2.65	0.43
1:E:316:THR:HG21	1:F:36:TYR:CE2	2.52	0.43
1:F:308:GLN:NE2	1:F:345:ASN:HD21	2.11	0.43
1:H:148:ILE:HG22	1:I:138:PRO:HD2	2.00	0.43
1:K:12:GLN:HA	1:K:15:LEU:HD13	1.99	0.43
2:M:4:ASN:O	2:M:7:PHE:C	2.54	0.43
3:N:92:LEU:CD1	3:N:92:LEU:N	2.80	0.43
3:N:114:LEU:CD1	3:N:114:LEU:N	2.81	0.43
1:A:381:THR:HG23	1:A:382:SER:N	2.31	0.43
1:D:189:LYS:HE2	1:G:61:ASN:H	1.83	0.43
1:I:211:LEU:HD21	1:I:374:LEU:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:15:ILE:O	2:M:15:ILE:CG2	2.66	0.43
1:C:280:ASN:CG	1:C:352:THR:OG1	2.56	0.43
1:G:247:TYR:OH	2:M:2:LEU:HD22	2.11	0.43
1:H:185:VAL:O	1:H:185:VAL:CG2	2.65	0.43
1:I:279:ALA:HB2	1:I:391:THR:O	2.17	0.43
1:K:7:LEU:N	1:K:7:LEU:CD1	2.80	0.43
1:K:188:SER:OG	1:K:189:LYS:N	2.44	0.43
3:N:81:LYS:HB2	3:N:113:PRO:CB	2.32	0.43
1:B:61:ASN:HB3	1:B:183:ALA:O	2.18	0.43
1:C:15:LEU:N	1:C:15:LEU:CD1	2.81	0.43
1:C:310:THR:HG22	1:C:358:VAL:HG22	1.99	0.43
1:I:260:LEU:HA	1:I:377:TYR:O	2.19	0.43
1:K:282:TYR:CA	1:K:381:THR:HG1	2.19	0.43
2:M:27:LEU:N	2:M:27:LEU:CD1	2.81	0.43
3:N:105:LEU:CD1	3:N:105:LEU:N	2.81	0.43
1:A:307:SER:HB2	1:A:318:LYS:HA	2.00	0.43
1:C:7:LEU:N	1:C:7:LEU:CD1	2.80	0.43
1:C:43:GLU:HG3	1:I:52:ARG:NH1	2.32	0.43
1:D:187:GLN:HE22	2:M:9:TYR:HB3	1.47	0.43
1:E:189:LYS:CD	1:K:61:ASN:HB2	2.49	0.43
1:F:182:LEU:HD11	1:F:184:ASN:ND2	2.34	0.43
1:G:185:VAL:HG23	2:M:4:ASN:HB2	1.91	0.43
1:H:5:GLN:NE2	1:H:316:THR:HG22	2.34	0.43
1:H:36:TYR:HA	1:H:37:PRO:HD3	1.83	0.43
1:I:61:ASN:HB3	1:I:183:ALA:O	2.18	0.43
1:I:63:GLY:HA2	1:I:184:ASN:HD21	1.81	0.43
1:I:63:GLY:CA	1:I:184:ASN:ND2	2.68	0.43
1:J:211:LEU:HD21	1:J:374:LEU:HD13	1.99	0.43
1:D:307:SER:HB2	1:D:318:LYS:HA	2.00	0.43
1:E:103:ASP:HB2	1:E:104:PRO:HD2	1.99	0.43
1:E:184:ASN:O	1:E:186:PRO:HD2	2.18	0.43
1:G:239:GLN:NE2	1:I:4:VAL:HB	2.34	0.43
1:I:102:TYR:HB2	1:I:191:ARG:HB2	2.01	0.43
1:I:355:TYR:OH	1:I:393:SER:N	2.52	0.43
1:J:61:ASN:HB3	1:J:183:ALA:O	2.18	0.43
1:K:184:ASN:HD22	1:K:249:LEU:HD11	1.84	0.43
1:B:41:GLN:CG	1:K:106:ASN:HD21	2.29	0.43
1:B:108:ARG:HH12	1:D:314:SER:HA	1.84	0.43
1:B:260:LEU:HA	1:B:377:TYR:O	2.19	0.43
1:D:102:TYR:HB2	1:D:191:ARG:HB2	2.01	0.43
1:D:308:GLN:NE2	1:D:345:ASN:HD21	2.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:307:SER:HB2	1:G:318:LYS:HA	2.00	0.43
1:J:260:LEU:HA	1:J:377:TYR:O	2.19	0.43
1:K:15:LEU:N	1:K:15:LEU:CD1	2.82	0.43
1:K:24:ASN:OD1	1:K:252:ILE:HB	2.18	0.43
1:K:103:ASP:HB2	1:K:104:PRO:HD2	1.99	0.43
1:K:151:PRO:HD2	1:K:162:LEU:HD22	2.00	0.43
1:L:6:GLN:CB	1:L:7:LEU:HD12	2.48	0.43
1:L:103:ASP:HB2	1:L:104:PRO:HD2	2.00	0.43
3:N:58:ILE:O	3:N:58:ILE:CG2	2.66	0.43
3:N:93:LEU:N	3:N:93:LEU:CD1	2.81	0.43
4:P:16:LEU:CD1	4:P:16:LEU:N	2.82	0.43
1:L:150:ALA:HA	1:L:151:PRO:N	2.32	0.43
1:A:102:TYR:HB2	1:A:191:ARG:HB2	2.01	0.43
1:F:353:LEU:HD23	2:M:26:LEU:HA	2.01	0.43
1:H:5:GLN:CD	1:I:36:TYR:CD1	2.91	0.43
3:N:61:ASP:N	3:N:75:GLU:HB2	2.34	0.43
3:N:112:VAL:HG22	3:N:113:PRO:CG	2.42	0.43
4:P:24:ARG:O	4:P:28:ALA:CA	2.65	0.43
1:D:260:LEU:HA	1:D:377:TYR:O	2.19	0.43
1:J:386:LEU:CD1	1:J:386:LEU:N	2.82	0.43
1:L:265:GLN:HE22	3:N:40:LYS:HE3	1.55	0.43
3:N:71:ILE:HD12	3:N:85:GLY:CA	2.49	0.43
1:D:11:GLN:NE2	1:D:351:TYR:CD2	2.69	0.42
1:I:185:VAL:O	1:I:185:VAL:CG2	2.65	0.42
1:J:102:TYR:HB2	1:J:191:ARG:HB2	2.01	0.42
2:M:75:GLN:HB3	2:M:76:PRO:HD2	2.00	0.42
3:N:101:VAL:HG22	3:N:102:ALA:N	2.34	0.42
1:A:260:LEU:HA	1:A:377:TYR:O	2.19	0.42
1:C:151:PRO:HD2	1:C:162:LEU:HD22	2.00	0.42
1:C:386:LEU:N	1:C:386:LEU:CD1	2.80	0.42
1:F:281:LEU:HA	2:M:29:TYR:OH	2.19	0.42
1:F:386:LEU:CD1	1:F:386:LEU:N	2.81	0.42
1:G:102:TYR:HB2	1:G:191:ARG:HB2	2.01	0.42
1:G:260:LEU:HA	1:G:377:TYR:O	2.19	0.42
1:H:61:ASN:HB3	1:H:183:ALA:O	2.18	0.42
1:H:102:TYR:HB2	1:H:191:ARG:HB2	2.01	0.42
1:I:307:SER:HB2	1:I:318:LYS:HA	2.00	0.42
1:J:32:LEU:HD23	1:J:237:LEU:HD13	2.01	0.42
1:G:185:VAL:HG21	2:M:4:ASN:CA	2.48	0.42
1:B:277:GLN:HG3	1:B:394:THR:CB	2.33	0.42
1:E:7:LEU:N	1:E:7:LEU:CD1	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:188:SER:OG	1:E:189:LYS:C	2.55	0.42
1:F:151:PRO:HD2	1:F:162:LEU:HD22	2.00	0.42
1:J:247:TYR:OH	2:M:68:GLN:HA	2.19	0.42
2:M:48:LEU:CD1	2:M:48:LEU:N	2.82	0.42
2:M:59:THR:O	2:M:60:TYR:CG	2.72	0.42
3:N:23:GLY:CA	3:N:109:LYS:HD2	2.45	0.42
1:A:242:VAL:HG22	1:A:247:TYR:CD2	2.55	0.42
1:B:102:TYR:HB2	1:B:191:ARG:HB2	2.01	0.42
1:C:185:VAL:H	1:C:186:PRO:CD	2.31	0.42
1:C:185:VAL:H	1:C:186:PRO:HD3	1.84	0.42
1:C:284:TYR:HB2	1:C:350:ILE:HB	2.01	0.42
1:E:189:LYS:HZ2	1:K:61:ASN:ND2	2.10	0.42
1:H:16:ARG:C	1:H:17:ASN:OD1	2.58	0.42
1:H:320:ASP:OD2	1:I:233:TYR:OH	2.27	0.42
1:J:5:GLN:NE2	1:K:38:VAL:HG21	2.34	0.42
1:K:8:THR:HG21	1:K:11:GLN:NE2	2.35	0.42
1:L:193:LYS:NZ	3:N:68:ALA:HA	2.34	0.42
2:M:4:ASN:HA	2:M:5:PRO:HD2	1.86	0.42
3:N:28:ARG:NH1	3:N:37:GLU:OE1	2.51	0.42
3:N:68:ALA:CA	3:N:87:GLN:HG2	2.49	0.42
1:G:36:TYR:HA	1:G:37:PRO:HD3	1.83	0.42
1:G:255:SER:HB2	2:M:6:GLN:HE22	1.85	0.42
1:H:307:SER:HB2	1:H:318:LYS:HA	2.00	0.42
1:L:284:TYR:HB2	1:L:350:ILE:HB	2.01	0.42
3:N:65:ASN:HD21	3:N:85:GLY:N	2.17	0.42
3:N:71:ILE:CD1	3:N:85:GLY:N	2.83	0.42
1:C:187:GLN:HG2	1:I:187:GLN:HB3	1.09	0.42
1:D:7:LEU:HD13	1:D:353:LEU:CG	2.49	0.42
1:E:182:LEU:HG	1:E:183:ALA:N	2.35	0.42
1:E:182:LEU:CG	1:E:183:ALA:N	2.83	0.42
1:G:255:SER:HG	1:G:386:LEU:HD21	1.77	0.42
1:H:9:PRO:CB	1:I:34:GLN:NE2	2.61	0.42
1:K:284:TYR:HB2	1:K:350:ILE:HB	2.02	0.42
3:N:45:TYR:C	3:N:46:LEU:CD1	2.63	0.42
1:A:15:LEU:HD12	1:A:15:LEU:H	1.84	0.42
1:C:181:VAL:O	1:C:182:LEU:N	2.53	0.42
1:F:242:VAL:HG22	1:F:247:TYR:CD2	2.55	0.42
1:G:242:VAL:HG22	1:G:247:TYR:CD2	2.55	0.42
1:H:242:VAL:HG22	1:H:247:TYR:CD2	2.55	0.42
1:H:260:LEU:HA	1:H:377:TYR:O	2.19	0.42
1:K:311:ALA:O	1:K:312:ASN:CG	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:66:ASP:CA	3:N:87:GLN:NE2	2.72	0.42
4:P:100:LEU:O	4:P:101:ASN:C	2.56	0.42
1:B:108:ARG:HH12	1:D:314:SER:CA	2.28	0.42
1:E:275:VAL:HG22	1:E:361:VAL:HG22	2.02	0.42
1:F:98:ARG:HE	1:F:98:ARG:HB3	1.69	0.42
1:F:353:LEU:CB	2:M:26:LEU:HA	2.50	0.42
1:I:4:VAL:N	1:I:5:GLN:H	2.13	0.42
1:J:182:LEU:CD1	1:J:240:LEU:HD11	2.49	0.42
1:L:35:SER:CA	1:L:36:TYR:N	2.82	0.42
1:L:280:ASN:O	1:L:281:LEU:HB2	2.20	0.42
1:L:353:LEU:HB3	2:M:76:PRO:HG2	2.01	0.42
1:F:185:VAL:HG11	2:M:38:ILE:N	2.06	0.42
1:G:105:ASP:OD1	2:M:7:PHE:CE1	2.67	0.42
1:K:17:ASN:O	1:K:21:MET:N	2.48	0.42
1:K:182:LEU:HD11	1:K:184:ASN:ND2	2.35	0.42
1:K:184:ASN:N	1:K:185:VAL:HG22	2.33	0.42
1:K:369:GLN:O	1:K:370:ASN:HB2	2.20	0.42
1:L:242:VAL:HG22	1:L:247:TYR:CD2	2.55	0.42
3:N:12:THR:HG23	3:N:68:ALA:O	2.20	0.42
1:C:242:VAL:HG22	1:C:247:TYR:CD2	2.55	0.41
1:C:275:VAL:HG22	1:C:361:VAL:HG22	2.02	0.41
1:D:242:VAL:HG22	1:D:247:TYR:CD2	2.55	0.41
1:E:107:GLN:HG2	1:E:383:ARG:NH2	2.35	0.41
1:E:108:ARG:HD3	1:J:313:PHE:O	2.19	0.41
1:H:355:TYR:OH	1:H:392:ILE:C	2.58	0.41
1:I:391:THR:CG2	1:I:392:ILE:N	2.83	0.41
3:N:66:ASP:HB2	3:N:87:GLN:CD	2.40	0.41
1:B:242:VAL:HG22	1:B:247:TYR:CD2	2.55	0.41
1:D:16:ARG:C	1:D:17:ASN:OD1	2.58	0.41
1:D:52:ARG:NH2	1:G:43:GLU:HG3	2.35	0.41
1:E:98:ARG:NH1	1:J:318:LYS:HZ1	2.18	0.41
1:H:391:THR:CG2	1:H:392:ILE:N	2.83	0.41
1:I:242:VAL:HG22	1:I:247:TYR:CD2	2.55	0.41
1:J:36:TYR:HA	1:J:37:PRO:HD3	1.83	0.41
1:K:275:VAL:HG22	1:K:361:VAL:HG22	2.02	0.41
2:M:68:GLN:O	4:P:41:MET:HE1	2.21	0.41
1:B:24:ASN:CG	1:B:252:ILE:HB	2.41	0.41
1:F:284:TYR:HB2	1:F:350:ILE:HB	2.01	0.41
1:F:369:GLN:O	1:F:370:ASN:HB2	2.20	0.41
1:J:182:LEU:HB2	1:J:254:LEU:CD1	2.49	0.41
2:M:72:THR:CG2	4:P:44:ASN:HB3	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:LEU:CD1	1:A:15:LEU:H	2.32	0.41
1:B:11:GLN:CD	1:B:351:TYR:CD2	2.79	0.41
1:B:260:LEU:HD22	1:B:378:GLU:HG2	2.03	0.41
1:C:369:GLN:O	1:C:370:ASN:HB2	2.20	0.41
1:D:391:THR:CG2	1:D:392:ILE:N	2.83	0.41
1:L:35:SER:OG	1:L:237:LEU:HD13	2.21	0.41
1:L:369:GLN:O	1:L:370:ASN:HB2	2.20	0.41
4:P:45:GLN:N	4:P:46:PRO:HD3	2.35	0.41
4:P:111:LEU:CD1	4:P:111:LEU:N	2.80	0.41
1:C:182:LEU:HD11	1:C:184:ASN:ND2	2.35	0.41
1:D:4:VAL:O	1:D:4:VAL:HG22	2.13	0.41
1:E:264:ALA:CB	1:J:272:VAL:HG11	2.50	0.41
1:F:103:ASP:HB2	1:F:104:PRO:HD2	2.00	0.41
1:F:386:LEU:N	2:M:33:GLY:O	2.53	0.41
1:G:260:LEU:HD22	1:G:378:GLU:HG2	2.02	0.41
1:H:89:ASP:HA	1:I:140:LYS:HD2	2.02	0.41
1:L:7:LEU:CD1	1:L:7:LEU:N	2.83	0.41
1:L:11:GLN:C	1:L:15:LEU:CD1	2.53	0.41
1:L:111:GLU:HB2	3:N:89:TYR:CD1	2.56	0.41
1:L:275:VAL:HG22	1:L:361:VAL:HG22	2.02	0.41
3:N:66:ASP:CB	3:N:87:GLN:CD	2.89	0.41
1:A:309:ARG:CG	1:A:310:THR:N	2.84	0.41
1:B:257:LEU:HG	1:B:383:ARG:CG	2.31	0.41
1:F:386:LEU:HD22	2:M:34:ARG:HG2	2.02	0.41
3:N:91:PRO:O	3:N:92:LEU:CD1	2.50	0.41
1:C:102:TYR:O	1:C:190:GLN:CG	2.61	0.41
1:C:311:ALA:O	1:C:312:ASN:CG	2.58	0.41
1:E:242:VAL:HG22	1:E:247:TYR:CD2	2.55	0.41
1:E:285:LEU:HD23	1:E:349:PRO:HG3	2.03	0.41
1:I:17:ASN:HB2	1:I:20:ALA:HB3	1.95	0.41
1:I:260:LEU:HD22	1:I:378:GLU:HG2	2.03	0.41
1:I:392:ILE:O	1:I:393:SER:O	2.39	0.41
1:K:12:GLN:CA	1:K:15:LEU:HD13	2.51	0.41
1:L:7:LEU:C	1:L:11:GLN:HB2	2.41	0.41
3:N:117:LEU:N	3:N:117:LEU:CD1	2.83	0.41
1:A:311:ALA:C	1:A:313:PHE:H	2.24	0.41
1:A:352:THR:OG1	1:A:354:GLN:O	2.36	0.41
1:C:162:LEU:HD23	1:C:162:LEU:N	2.36	0.41
1:E:106:ASN:OD1	1:K:62:VAL:CG2	2.69	0.41
1:F:16:ARG:C	1:F:18:GLN:N	2.73	0.41
1:F:278:TYR:O	1:F:280:ASN:OD1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:6:GLN:HB3	1:J:7:LEU:HA	2.02	0.41
1:K:8:THR:HG21	1:K:11:GLN:HG3	2.02	0.41
1:L:14:ALA:O	1:L:18:GLN:HG3	2.20	0.41
1:L:61:ASN:HD21	1:L:189:LYS:CA	2.29	0.41
1:L:162:LEU:N	1:L:162:LEU:HD23	2.36	0.41
1:B:24:ASN:OD1	1:B:252:ILE:HB	2.21	0.41
1:B:52:ARG:NH1	1:E:43:GLU:HG3	2.36	0.41
1:C:14:ALA:HB3	1:C:15:LEU:HD12	2.03	0.41
1:D:387:VAL:O	1:I:6:GLN:HB2	2.21	0.41
1:E:278:TYR:O	1:E:280:ASN:OD1	2.39	0.41
1:E:284:TYR:HB2	1:E:350:ILE:HB	2.01	0.41
1:F:7:LEU:N	1:F:7:LEU:CD1	2.83	0.41
1:F:83:GLU:HB3	1:F:218:ALA:HB3	2.03	0.41
1:G:309:ARG:CG	1:G:314:SER:C	2.82	0.41
1:G:386:LEU:N	1:G:386:LEU:CD1	2.84	0.41
1:I:281:LEU:HD21	1:I:385:GLU:CB	2.49	0.41
1:I:355:TYR:OH	1:I:392:ILE:C	2.59	0.41
1:K:17:ASN:C	1:K:20:ALA:H	2.17	0.41
1:K:242:VAL:HG22	1:K:247:TYR:CD2	2.55	0.41
1:L:280:ASN:ND2	1:L:352:THR:HG21	2.35	0.41
1:L:310:THR:O	1:L:312:ASN:N	2.54	0.41
2:M:41:ALA:O	2:M:42:ARG:CB	2.51	0.41
3:N:60:ILE:HB	3:N:97:ARG:HD2	2.01	0.41
1:B:79:ASN:O	1:B:79:ASN:CG	2.60	0.41
1:C:182:LEU:HD22	1:C:254:LEU:HD13	2.03	0.41
1:C:352:THR:O	1:C:353:LEU:HG	2.21	0.41
1:D:63:GLY:HA2	1:D:184:ASN:HD21	1.81	0.41
1:F:275:VAL:HG22	1:F:361:VAL:HG22	2.02	0.41
1:F:311:ALA:HB1	2:M:23:THR:OG1	2.20	0.41
1:H:9:PRO:CD	1:I:34:GLN:OE1	2.69	0.41
1:H:382:SER:HG	1:H:385:GLU:CG	2.26	0.41
1:H:394:THR:HG22	1:H:395:THR:O	2.20	0.41
3:N:49:THR:HG23	3:N:82:CYS:C	2.22	0.41
3:N:60:ILE:CD1	3:N:97:ARG:NE	2.64	0.41
1:C:83:GLU:HB3	1:C:218:ALA:HB3	2.03	0.40
1:C:280:ASN:CB	1:C:352:THR:OG1	2.69	0.40
1:D:264:ALA:CB	1:I:272:VAL:CG1	2.98	0.40
1:F:162:LEU:N	1:F:162:LEU:HD23	2.36	0.40
1:K:83:GLU:HB3	1:K:218:ALA:HB3	2.03	0.40
1:B:269:THR:CG2	1:I:372:ARG:HD3	2.12	0.40
1:D:260:LEU:HD22	1:D:378:GLU:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:187:GLN:CA	1:K:185:VAL:N	2.81	0.40
1:F:285:LEU:HD23	1:F:349:PRO:HG3	2.03	0.40
1:H:9:PRO:HD3	1:I:34:GLN:OE1	2.21	0.40
1:H:260:LEU:HD22	1:H:378:GLU:HG2	2.03	0.40
1:J:354:GLN:HG2	2:M:54:ALA:O	2.21	0.40
1:K:280:ASN:CB	1:K:352:THR:OG1	2.69	0.40
4:P:56:ALA:HB3	4:P:100:LEU:HD23	2.03	0.40
1:D:79:ASN:O	1:D:79:ASN:CG	2.60	0.40
1:F:39:ILE:O	1:F:39:ILE:HG23	2.22	0.40
1:H:79:ASN:O	1:H:79:ASN:CG	2.60	0.40
1:J:16:ARG:NE	1:J:21:MET:CE	2.77	0.40
1:J:384:THR:HG22	2:M:62:ALA:HB1	1.82	0.40
1:K:352:THR:O	1:K:353:LEU:HG	2.22	0.40
1:L:35:SER:C	1:L:36:TYR:CA	2.89	0.40
3:N:47:ALA:C	3:N:48:ASP:OD1	2.56	0.40
1:C:285:LEU:HD23	1:C:349:PRO:HG3	2.03	0.40
1:E:83:GLU:HB3	1:E:218:ALA:HB3	2.03	0.40
1:E:264:ALA:CB	1:J:272:VAL:HG13	2.51	0.40
1:F:16:ARG:HB2	1:F:17:ASN:HD22	1.47	0.40
1:F:312:ASN:O	1:F:313:PHE:HB2	2.21	0.40
1:F:353:LEU:HD22	2:M:26:LEU:CA	2.52	0.40
1:G:23:ALA:N	1:G:24:ASN:N	2.69	0.40
1:G:79:ASN:O	1:G:79:ASN:CG	2.60	0.40
1:J:79:ASN:O	1:J:79:ASN:CG	2.60	0.40
1:J:106:ASN:ND2	1:J:191:ARG:NH2	2.56	0.40
1:K:285:LEU:HD23	1:K:349:PRO:HG3	2.03	0.40
1:L:183:ALA:C	1:L:184:ASN:CA	2.90	0.40
1:F:281:LEU:N	1:F:281:LEU:CD1	2.85	0.40
1:F:352:THR:O	1:F:353:LEU:HG	2.21	0.40
1:J:353:LEU:O	2:M:55:VAL:HG23	2.21	0.40
2:M:15:ILE:O	2:M:15:ILE:HG22	2.22	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 X-ray entries followed by that with respect to entries of similar resolution.

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	378/395 (96%)	358 (95%)	14 (4%)	6 (2%)	9 45
1	B	386/395 (98%)	366 (95%)	11 (3%)	9 (2%)	6 37
1	C	379/395 (96%)	356 (94%)	18 (5%)	5 (1%)	12 48
1	D	388/395 (98%)	368 (95%)	13 (3%)	7 (2%)	8 42
1	E	376/395 (95%)	354 (94%)	17 (4%)	5 (1%)	12 48
1	F	382/395 (97%)	359 (94%)	18 (5%)	5 (1%)	12 48
1	G	371/395 (94%)	354 (95%)	12 (3%)	5 (1%)	12 48
1	H	390/395 (99%)	368 (94%)	15 (4%)	7 (2%)	8 42
1	I	386/395 (98%)	367 (95%)	11 (3%)	8 (2%)	7 39
1	J	384/395 (97%)	364 (95%)	13 (3%)	7 (2%)	8 42
1	K	380/395 (96%)	350 (92%)	25 (7%)	5 (1%)	12 48
1	L	373/395 (94%)	348 (93%)	17 (5%)	8 (2%)	7 39
2	M	81/83 (98%)	65 (80%)	8 (10%)	8 (10%)	0 10
3	N	112/126 (89%)	94 (84%)	6 (5%)	12 (11%)	0 8
4	P	76/117 (65%)	57 (75%)	11 (14%)	8 (10%)	0 8
All	All	4842/5066 (96%)	4528 (94%)	209 (4%)	105 (2%)	6 38

All (105) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	PRO
1	A	244	GLN
1	A	353	LEU
1	B	8	THR
1	B	186	PRO
1	B	312	ASN
1	B	353	LEU
1	B	393	SER
1	C	185	VAL
1	C	187	GLN
1	C	244	GLN
1	D	8	THR
1	D	186	PRO
1	D	312	ASN
1	D	353	LEU

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Mol	Chain	Res	Type
1	D	393	SER
1	E	8	THR
1	E	187	GLN
1	E	188	SER
1	E	280	ASN
1	F	247	TYR
1	F	248	ILE
1	F	280	ASN
1	G	186	PRO
1	G	244	GLN
1	G	353	LEU
1	H	8	THR
1	H	186	PRO
1	H	312	ASN
1	H	353	LEU
1	I	8	THR
1	I	186	PRO
1	I	312	ASN
1	I	353	LEU
1	J	186	PRO
1	J	314	SER
1	J	353	LEU
1	K	188	SER
1	K	244	GLN
1	L	187	GLN
1	L	312	ASN
1	L	313	PHE
2	M	12	PRO
2	M	51	PRO
3	N	6	PRO
3	N	13	PRO
3	N	28	ARG
3	N	91	PRO
3	N	95	PRO
3	N	111	SER
4	P	46	PRO
4	P	50	SER
4	P	54	PRO
1	A	385	GLU
1	B	16	ARG
1	B	314	SER
1	C	311	ALA

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Mol	Chain	Res	Type
1	D	314	SER
1	E	311	ALA
1	F	311	ALA
1	F	393	SER
1	G	314	SER
1	H	314	SER
1	I	16	ARG
1	J	312	ASN
1	K	311	ALA
1	L	7	LEU
1	L	8	THR
3	N	24	PRO
3	N	27	VAL
3	N	55	VAL
4	P	31	VAL
4	P	36	GLU
1	A	311	ALA
1	C	281	LEU
1	G	382	SER
1	I	314	SER
1	J	239	GLN
1	K	281	LEU
1	L	281	LEU
2	M	81	GLN
3	N	83	PRO
3	N	100	PHE
1	A	312	ASN
1	J	185	VAL
1	J	187	GLN
2	M	15	ILE
4	P	39	PRO
1	I	393	SER
1	L	311	ALA
2	M	24	MET
2	M	41	ALA
4	P	51	VAL
1	B	392	ILE
1	L	237	LEU
4	P	45	GLN
1	B	185	VAL
1	D	185	VAL
1	H	185	VAL

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Mol	Chain	Res	Type
1	H	392	ILE
1	I	185	VAL
2	M	25	PRO
2	M	46	PRO
1	K	185	VAL
3	N	80	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	312/326 (96%)	310 (99%)	2 (1%)	86	92
1	B	324/326 (99%)	322 (99%)	2 (1%)	86	92
1	C	318/326 (98%)	315 (99%)	3 (1%)	78	87
1	D	324/326 (99%)	323 (100%)	1 (0%)	92	95
1	E	312/326 (96%)	308 (99%)	4 (1%)	69	82
1	F	319/326 (98%)	317 (99%)	2 (1%)	86	92
1	G	311/326 (95%)	310 (100%)	1 (0%)	92	95
1	H	324/326 (99%)	323 (100%)	1 (0%)	92	95
1	I	324/326 (99%)	322 (99%)	2 (1%)	86	92
1	J	321/326 (98%)	318 (99%)	3 (1%)	78	87
1	K	317/326 (97%)	312 (98%)	5 (2%)	62	79
1	L	313/326 (96%)	309 (99%)	4 (1%)	69	82
2	M	66/66 (100%)	66 (100%)	0	100	100
3	N	92/102 (90%)	92 (100%)	0	100	100
4	P	65/94 (69%)	65 (100%)	0	100	100
All	All	4042/4174 (97%)	4012 (99%)	30 (1%)	84	90

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	310	THR
1	A	315	ASP
1	B	4	VAL
1	B	315	ASP
1	C	162	LEU
1	C	186	PRO
1	C	355	TYR
1	D	315	ASP
1	E	162	LEU
1	E	186	PRO
1	E	188	SER
1	E	355	TYR
1	F	162	LEU
1	F	355	TYR
1	G	315	ASP
1	H	315	ASP
1	I	4	VAL
1	I	315	ASP
1	J	240	LEU
1	J	241	PRO
1	J	315	ASP
1	K	162	LEU
1	K	185	VAL
1	K	186	PRO
1	K	188	SER
1	K	355	TYR
1	L	37	PRO
1	L	162	LEU
1	L	237	LEU
1	L	355	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	61	ASN
1	A	79	ASN
1	A	80	HIS
1	A	106	ASN
1	A	190	GLN
1	A	200	ASN
1	A	280	ASN
1	A	312	ASN

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Mol	Chain	Res	Type
1	A	345	ASN
1	A	357	ASN
1	B	17	ASN
1	B	41	GLN
1	B	61	ASN
1	B	79	ASN
1	B	80	HIS
1	B	106	ASN
1	B	190	GLN
1	B	200	ASN
1	B	265	GLN
1	B	280	ASN
1	B	345	ASN
1	B	357	ASN
1	C	17	ASN
1	C	41	GLN
1	C	80	HIS
1	C	187	GLN
1	C	190	GLN
1	C	271	ASN
1	C	345	ASN
1	C	354	GLN
1	D	5	GLN
1	D	41	GLN
1	D	61	ASN
1	D	79	ASN
1	D	80	HIS
1	D	106	ASN
1	D	187	GLN
1	D	190	GLN
1	D	200	ASN
1	D	277	GLN
1	D	280	ASN
1	D	345	ASN
1	D	357	ASN
1	E	41	GLN
1	E	80	HIS
1	E	187	GLN
1	E	271	ASN
1	E	345	ASN
1	E	354	GLN
1	F	41	GLN

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Mol	Chain	Res	Type
1	F	80	HIS
1	F	271	ASN
1	F	345	ASN
1	F	354	GLN
1	G	18	GLN
1	G	41	GLN
1	G	61	ASN
1	G	79	ASN
1	G	80	HIS
1	G	106	ASN
1	G	187	GLN
1	G	190	GLN
1	G	200	ASN
1	G	239	GLN
1	G	280	ASN
1	G	345	ASN
1	G	357	ASN
1	H	5	GLN
1	H	41	GLN
1	H	61	ASN
1	H	79	ASN
1	H	80	HIS
1	H	106	ASN
1	H	190	GLN
1	H	200	ASN
1	H	265	GLN
1	H	280	ASN
1	H	345	ASN
1	I	17	ASN
1	I	33	GLN
1	I	41	GLN
1	I	61	ASN
1	I	80	HIS
1	I	106	ASN
1	I	190	GLN
1	I	200	ASN
1	I	280	ASN
1	I	345	ASN
1	I	354	GLN
1	I	357	ASN
1	J	5	GLN
1	J	41	GLN

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Mol	Chain	Res	Type
1	J	61	ASN
1	J	79	ASN
1	J	80	HIS
1	J	106	ASN
1	J	190	GLN
1	J	200	ASN
1	J	280	ASN
1	J	345	ASN
1	J	357	ASN
1	K	12	GLN
1	K	41	GLN
1	K	61	ASN
1	K	80	HIS
1	K	106	ASN
1	K	271	ASN
1	K	345	ASN
1	K	354	GLN
1	L	41	GLN
1	L	80	HIS
1	L	190	GLN
1	L	271	ASN
1	L	345	ASN
1	L	354	GLN
2	M	6	GLN
2	M	43	GLN
2	M	58	GLN
3	N	50	GLN
3	N	62	ASN
3	N	65	ASN
3	N	87	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	I	15
1	D	14
1	B	14
1	J	11
1	F	9
1	H	9
3	N	9
1	L	8
1	G	7
1	K	7
1	C	6
1	A	6
2	M	5
4	P	4
1	E	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	383:ARG	C	384:THR	N	3.74
1	C	190:GLN	C	191:ARG	N	3.53
1	D	17:ASN	C	18:GLN	N	3.14
1	I	17:ASN	C	18:GLN	N	3.14
1	L	35:SER	C	36:TYR	N	2.61
1	B	6:GLN	C	7:LEU	N	2.59

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	17:ASN	C	18:GLN	N	2.59
1	I	6:GLN	C	7:LEU	N	2.59
1	F	382:SER	C	383:ARG	N	2.55
1	G	23:ALA	C	24:ASN	N	2.50
1	J	34:GLN	C	35:SER	N	2.45
1	L	183:ALA	C	184:ASN	N	2.27
1	C	181:VAL	C	182:LEU	N	2.23
1	K	34:GLN	C	35:SER	N	2.20
1	F	16:ARG	C	17:ASN	N	2.18
1	A	24:ASN	C	25:LEU	N	1.98
1	L	381:THR	C	382:SER	N	1.96
1	L	150:ALA	C	151:PRO	N	1.94
1	H	381:THR	C	382:SER	N	1.83
1	K	191:ARG	C	192:LEU	N	1.78
1	G	35:SER	C	36:TYR	N	1.76
1	E	381:THR	C	382:SER	N	1.72
1	I	392:ILE	C	393:SER	N	1.71
1	L	257:LEU	C	258:TYR	N	1.71
1	G	382:SER	C	383:ARG	N	1.70
1	B	8:THR	C	9:PRO	N	1.69
1	I	8:THR	C	9:PRO	N	1.69
1	J	384:THR	C	385:GLU	N	1.69
1	N	55:VAL	C	56:GLN	N	1.66
1	J	187:GLN	C	188:SER	N	1.61
1	B	392:ILE	C	393:SER	N	1.60
1	N	16:ASN	C	17:GLY	N	1.60
1	K	279:ALA	C	280:ASN	N	1.20
1	M	67:ILE	C	68:GLN	N	1.20
1	N	18:CYS	C	19:ASP	N	1.20
1	N	54:GLY	C	55:VAL	N	1.20
1	C	279:ALA	C	280:ASN	N	1.19
1	D	26:GLN	C	27:ALA	N	1.19
1	F	393:SER	C	394:THR	N	1.19
1	M	11:GLY	C	12:PRO	N	1.19
1	P	4:LYS	C	5:LYS	N	1.18
1	P	33:SER	C	34:ASN	N	1.18
1	D	357:ASN	C	358:VAL	N	1.17
1	D	380:PHE	C	381:THR	N	1.17
1	H	357:ASN	C	358:VAL	N	1.17
1	I	357:ASN	C	358:VAL	N	1.17
1	J	184:ASN	C	185:VAL	N	1.17
1	J	357:ASN	C	358:VAL	N	1.17

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	391:THR	C	392:ILE	N	1.16
1	M	41:ALA	C	42:ARG	N	1.16
1	P	32:ALA	C	33:SER	N	1.15
1	B	389:ALA	C	390:GLY	N	1.14
1	D	389:ALA	C	390:GLY	N	1.14
1	H	389:ALA	C	390:GLY	N	1.14
1	I	389:ALA	C	390:GLY	N	1.14
1	D	356:GLY	C	357:ASN	N	1.13
1	H	356:GLY	C	357:ASN	N	1.13
1	I	356:GLY	C	357:ASN	N	1.13
1	J	356:GLY	C	357:ASN	N	1.13
1	L	161:GLU	C	162:LEU	N	1.13
1	C	311:ALA	C	312:ASN	N	1.12
1	K	311:ALA	C	312:ASN	N	1.12
1	L	311:ALA	C	312:ASN	N	1.12
1	N	27:VAL	C	28:ARG	N	1.12
1	P	31:VAL	C	32:ALA	N	1.12
1	B	245:ASN	C	246:GLY	N	1.11
1	D	245:ASN	C	246:GLY	N	1.11
1	H	245:ASN	C	246:GLY	N	1.11
1	I	245:ASN	C	246:GLY	N	1.11
1	M	46:PRO	C	47:PHE	N	1.11
1	N	65:ASN	C	66:ASP	N	1.10
1	A	356:GLY	C	357:ASN	N	1.09
1	E	279:ALA	C	280:ASN	N	1.09
1	F	279:ALA	C	280:ASN	N	1.09
1	G	356:GLY	C	357:ASN	N	1.09
1	M	64:GLY	C	65:THR	N	1.09
1	N	17:GLY	C	18:CYS	N	1.09
1	D	392:ILE	C	393:SER	N	1.08
1	B	357:ASN	C	358:VAL	N	1.07
1	J	250:PRO	C	251:LEU	N	1.07
1	J	313:PHE	C	314:SER	N	1.07
1	B	185:VAL	C	186:PRO	N	1.04
1	D	185:VAL	C	186:PRO	N	1.04
1	H	185:VAL	C	186:PRO	N	1.04
1	I	185:VAL	C	186:PRO	N	1.04
1	A	183:ALA	C	184:ASN	N	1.03
1	F	247:TYR	C	248:ILE	N	1.03
1	G	183:ALA	C	184:ASN	N	1.03
1	N	57:CYS	C	58:ILE	N	1.03
1	B	394:THR	C	395:THR	N	1.00

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	394:THR	C	395:THR	N	1.00
1	I	394:THR	C	395:THR	N	1.00
1	N	111:SER	C	112:VAL	N	1.00
1	B	352:THR	C	353:LEU	N	0.99
1	D	352:THR	C	353:LEU	N	0.99
1	H	352:THR	C	353:LEU	N	0.99
1	I	352:THR	C	353:LEU	N	0.99
1	J	352:THR	C	353:LEU	N	0.99
1	E	311:ALA	C	312:ASN	N	0.98
1	F	311:ALA	C	312:ASN	N	0.98
1	I	313:PHE	C	314:SER	N	0.98
1	B	16:ARG	C	17:ASN	N	0.95
1	I	16:ARG	C	17:ASN	N	0.95
1	J	256:THR	C	257:LEU	N	0.95
1	L	312:ASN	C	313:PHE	N	0.94
1	A	381:THR	C	382:SER	N	0.93
1	K	380:PHE	C	381:THR	N	0.92
1	A	243:GLY	C	244:GLN	N	0.91
1	B	311:ALA	C	312:ASN	N	0.91
1	D	311:ALA	C	312:ASN	N	0.91
1	D	313:PHE	C	314:SER	N	0.91
1	G	243:GLY	C	244:GLN	N	0.91
1	H	311:ALA	C	312:ASN	N	0.91
1	H	313:PHE	C	314:SER	N	0.91
1	B	313:PHE	C	314:SER	N	0.90
1	I	311:ALA	C	312:ASN	N	0.90
1	C	243:GLY	C	244:GLN	N	0.88
1	K	243:GLY	C	244:GLN	N	0.88
1	I	7:LEU	C	8:THR	N	0.86
1	B	7:LEU	C	8:THR	N	0.85
1	D	7:LEU	C	8:THR	N	0.85
1	F	239:GLN	C	240:LEU	N	0.76
1	C	186:PRO	C	187:GLN	N	0.71
1	G	313:PHE	C	314:SER	N	0.71
1	F	186:PRO	C	187:GLN	N	0.67
1	K	186:PRO	C	187:GLN	N	0.63
1	A	313:PHE	C	314:SER	N	0.51

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.