



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 05:12 PM UTC

PDB ID : 1JNB / pdb_00001jnb
Title : CONNECTOR PROTEIN FROM BACTERIOPHAGE PHI29
Authors : Simpson, A.A.; Leiman, P.G.; Tao, Y.; He, Y.; Badasso, M.O.; Jardine, P.J.;
Anderson, D.L.; Rossmann, M.G.
Deposited on : 2001-07-23
Resolution : 3.20 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

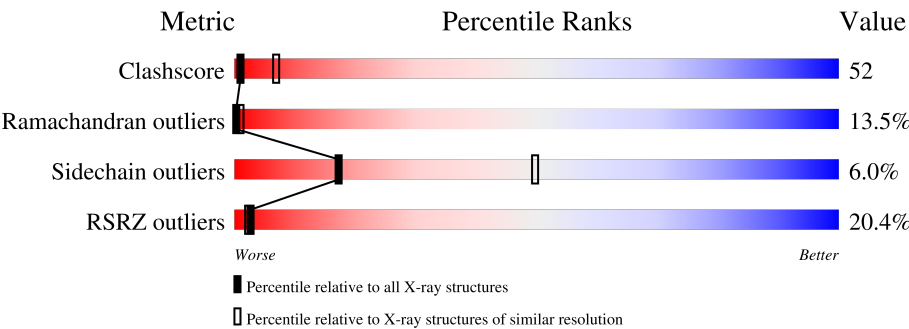
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	309	14% 33%34%14%•17%
1	B	309	17% 34%33%14%•17%
1	C	309	20% 34%34%14%•17%
1	D	309	17% 32%35%14%•17%
1	E	309	22% 35%32%14%•17%
1	F	309	21% 34%33%15%•17%
1	G	309	16% 33%33%14%•17%

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Mol	Chain	Length	Quality of chain
1	H	309	18%32%35%15%•17%
1	I	309	17%35%32%15%•17%
1	J	309	12%33%34%14%•17%
1	K	309	17%33%34%14%•17%
1	L	309	14%34%32%15%•17%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25236 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.

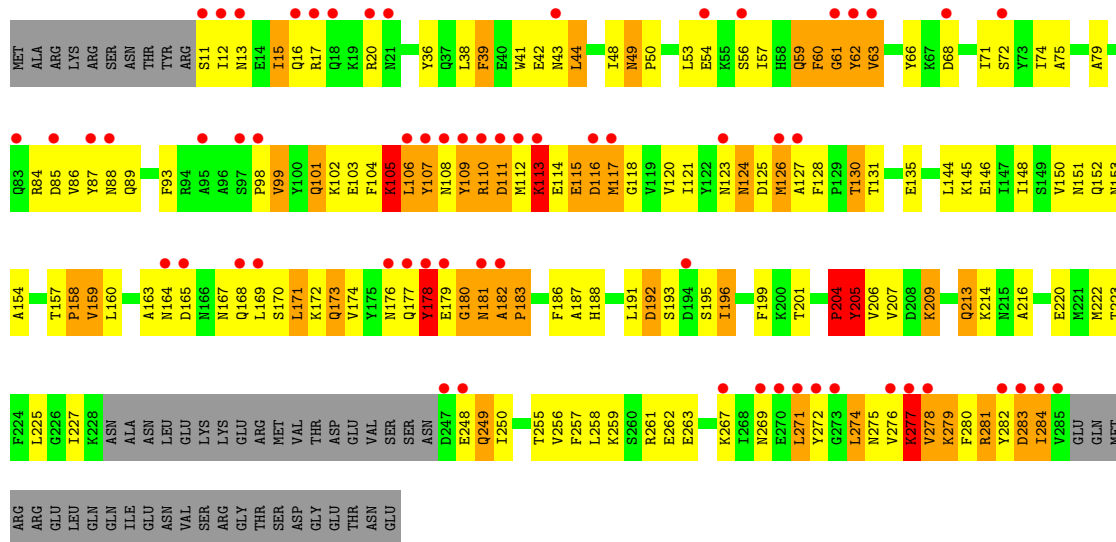
- Molecule 1 is a protein called UPPER COLLAR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	B	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	C	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	D	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	E	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	F	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	G	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	H	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	I	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	J	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	K	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	L	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			

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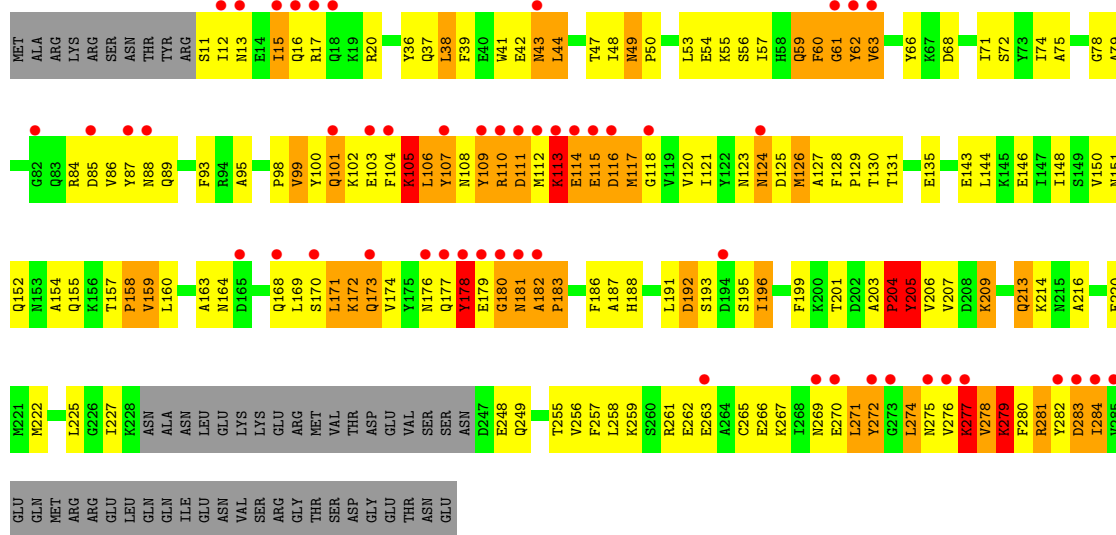
• Molecule 1: UPPER COLLAR PROTEIN

Chain C: 20% 34% 34% 14% 17%



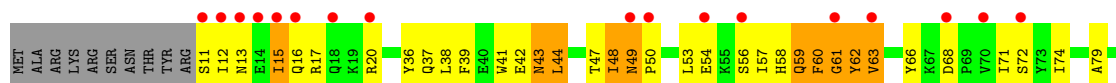
• Molecule 1: UPPER COLLAR PROTEIN

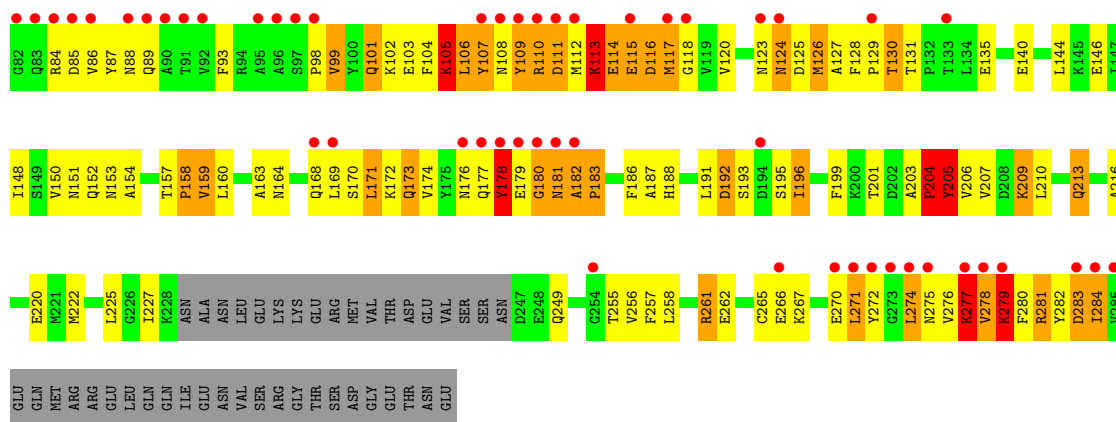
Chain D: 17% 32% 35% 14% 17%



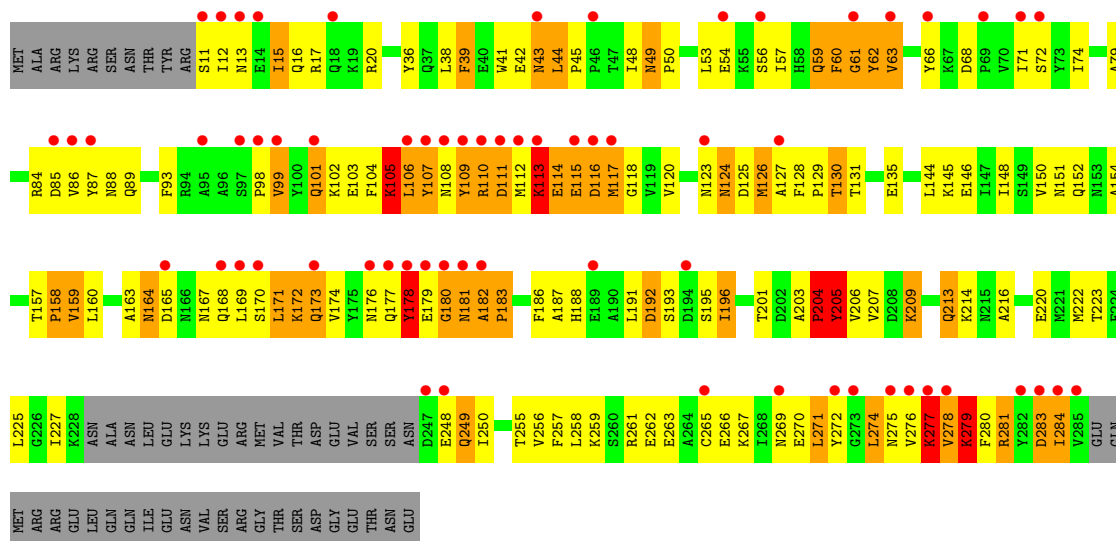
• Molecule 1: UPPER COLLAR PROTEIN

Chain E: 22% 35% 32% 14% 17%

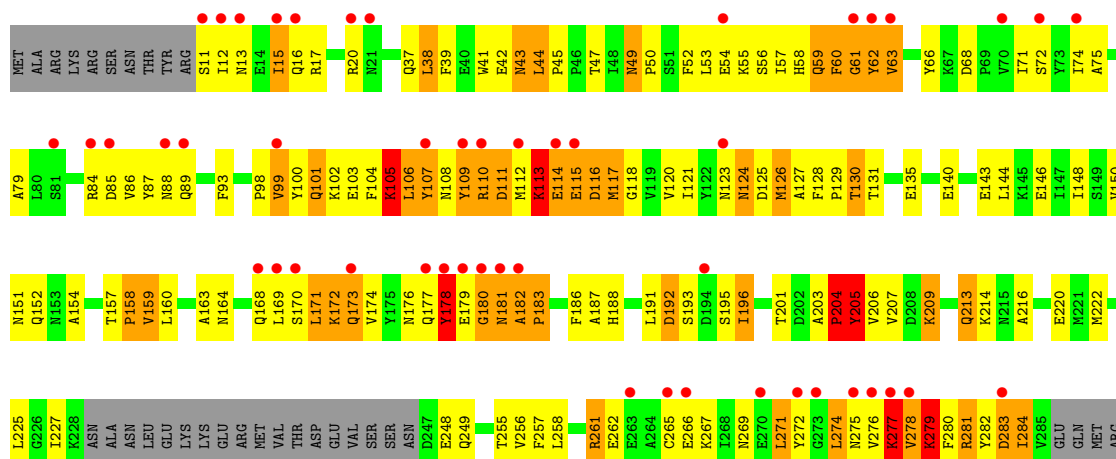




● Molecule 1: UPPER COLLAR PROTEIN



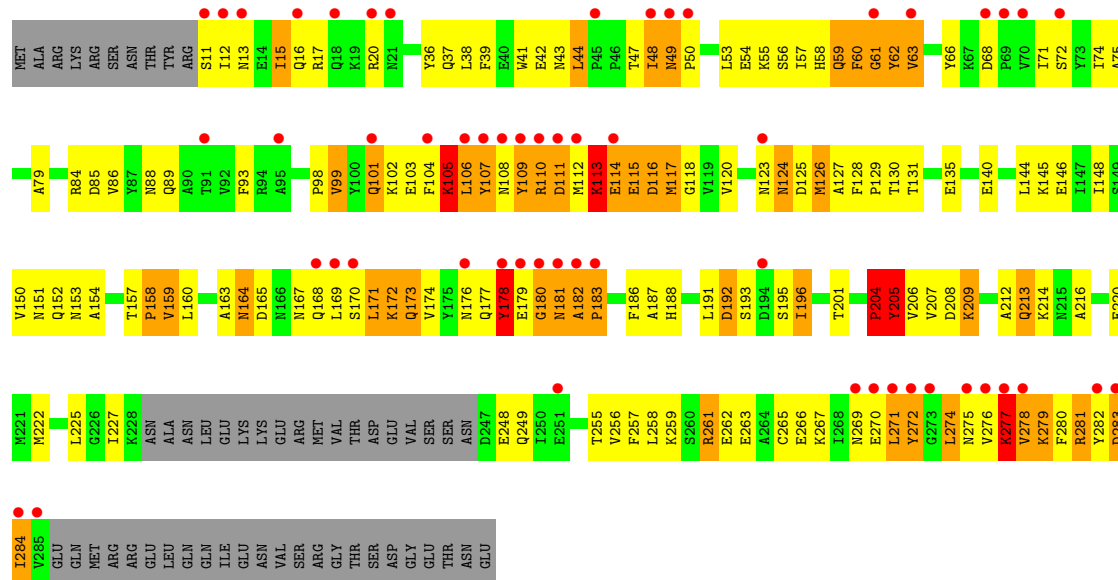
● Molecule 1: UPPER COLLAR PROTEIN



ARG
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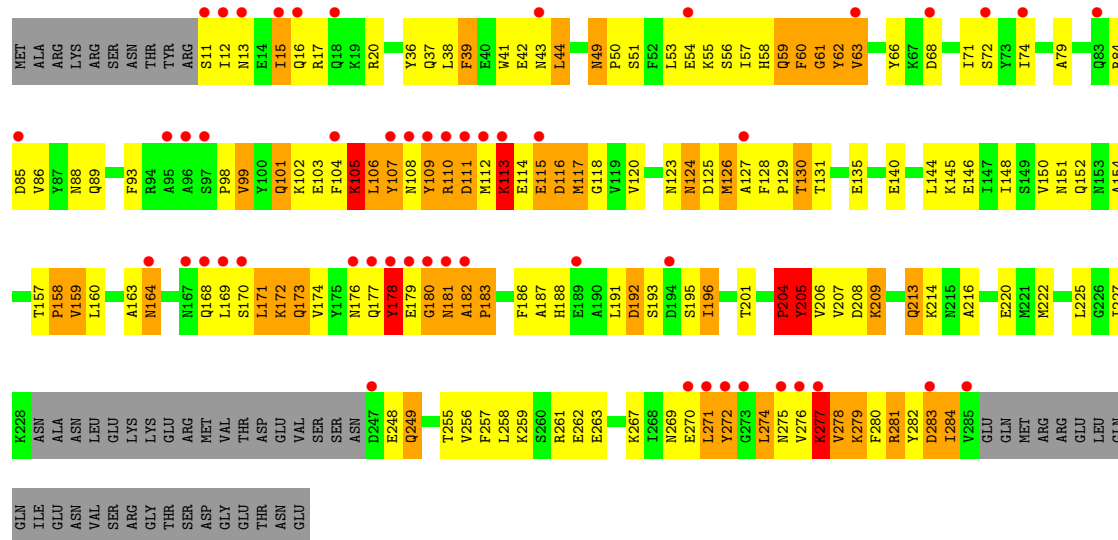
● Molecule 1: UPPER COLLAR PROTEIN

Chain H: 18% 32% 35% 15% 17%



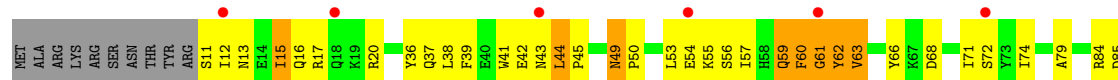
● Molecule 1: UPPER COLLAR PROTEIN

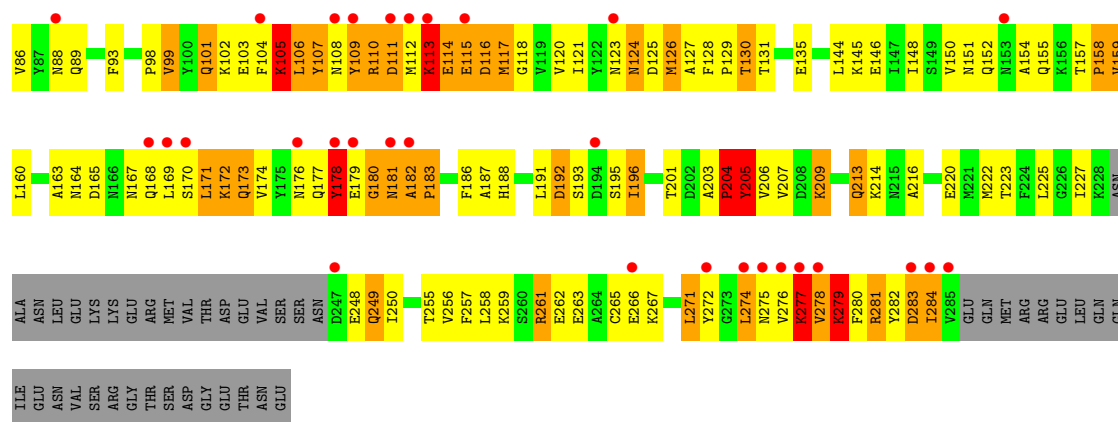
Chain I: 17% 35% 32% 15% 17%



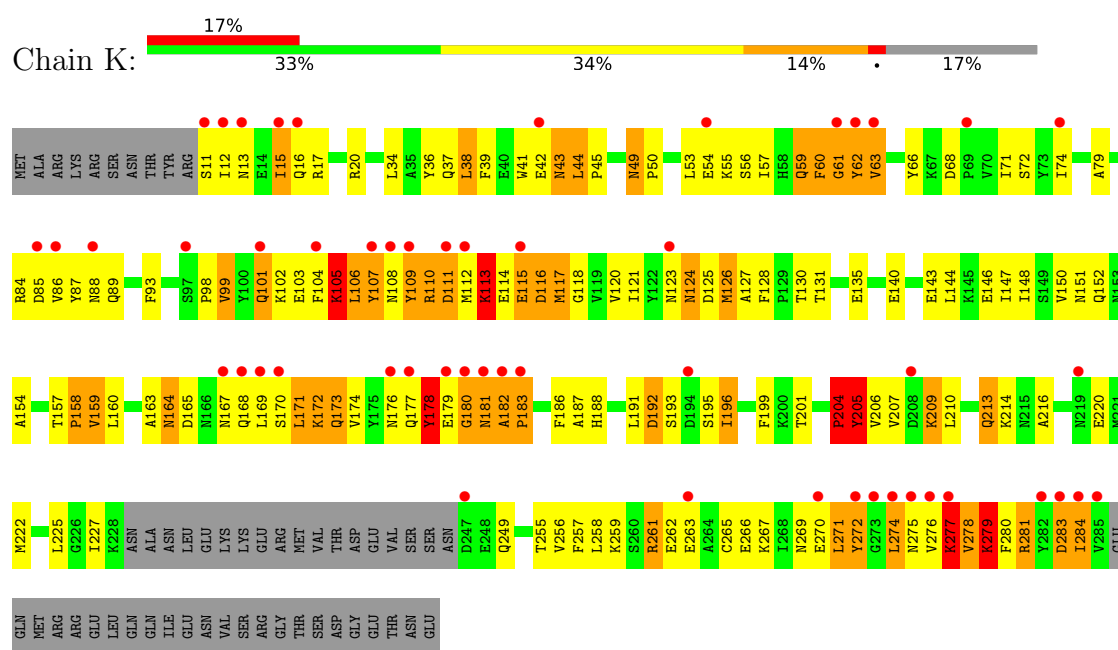
● Molecule 1: UPPER COLLAR PROTEIN

Chain J: 12% 33% 34% 14% 17%

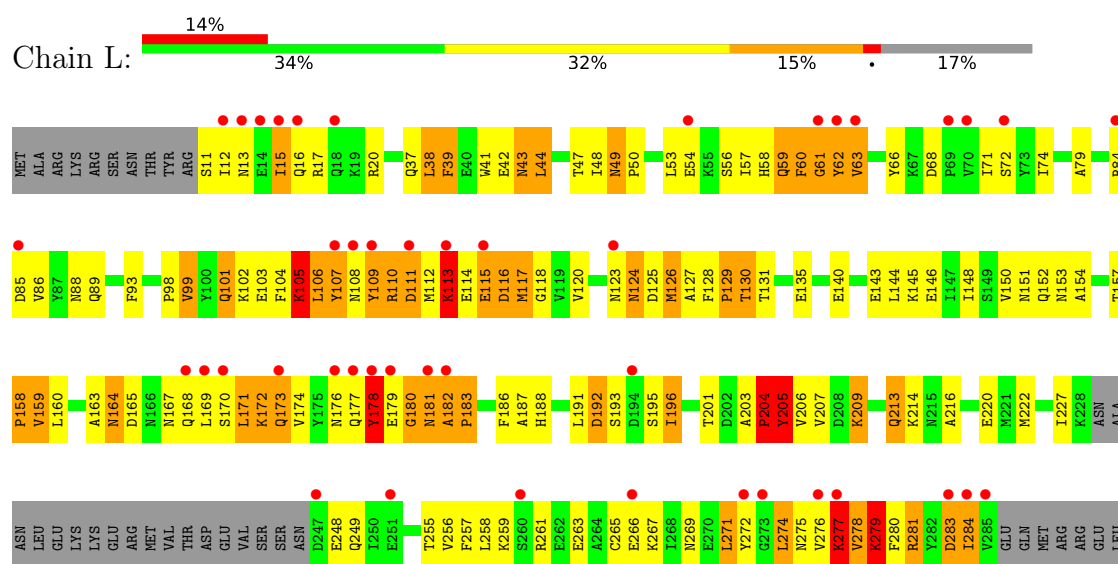




● Molecule 1: UPPER COLLAR PROTEIN



● Molecule 1: UPPER COLLAR PROTEIN



GLN
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ARG
GLY
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ASP
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GLU
THR
ASN
GLU

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.16Å 169.24Å 185.44Å 90.00° 114.10° 90.00°	Depositor
Resolution (Å)	9.00 – 3.20 9.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.5 (9.00-3.20) 94.9 (9.00-3.20)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.81 (at 3.19Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.284 , 0.301 0.282 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	56.0	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 84.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	25236	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.56	0/2150	1.06	16/2913 (0.5%)
1	B	0.55	0/2150	1.05	16/2913 (0.5%)
1	C	0.54	0/2150	1.05	14/2913 (0.5%)
1	D	0.52	0/2150	1.05	17/2913 (0.6%)
1	E	0.49	0/2150	1.04	16/2913 (0.5%)
1	F	0.53	0/2150	1.04	18/2913 (0.6%)
1	G	0.52	0/2150	1.05	18/2913 (0.6%)
1	H	0.51	0/2150	1.04	13/2913 (0.4%)
1	I	0.55	0/2150	1.05	13/2913 (0.4%)
1	J	0.55	0/2150	1.07	16/2913 (0.5%)
1	K	0.53	0/2150	1.05	18/2913 (0.6%)
1	L	0.55	0/2150	1.05	17/2913 (0.6%)
All	All	0.53	0/25800	1.05	192/34956 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
All	All	0	12

There are no bond length outliers.

All (192) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	157	THR	N-CA-C	9.35	124.65	108.75
1	A	116	ASP	N-CA-C	-9.11	98.54	111.56
1	K	116	ASP	N-CA-C	-8.94	98.78	111.56
1	G	116	ASP	N-CA-C	-8.92	98.81	111.56
1	F	116	ASP	N-CA-C	-8.88	98.86	111.56
1	L	116	ASP	N-CA-C	-8.83	98.93	111.56
1	C	116	ASP	N-CA-C	-8.82	98.95	111.56
1	E	116	ASP	N-CA-C	-8.80	98.98	111.56
1	B	116	ASP	N-CA-C	-8.72	99.09	111.56
1	D	116	ASP	N-CA-C	-8.71	99.11	111.56
1	I	116	ASP	N-CA-C	-8.67	99.16	111.56
1	H	116	ASP	N-CA-C	-8.59	99.28	111.56
1	J	116	ASP	N-CA-C	-8.34	99.63	111.56
1	G	157	THR	N-CA-C	7.81	124.49	108.71
1	A	157	THR	N-CA-C	7.81	124.49	108.71
1	D	157	THR	N-CA-C	7.81	124.48	108.71
1	I	157	THR	N-CA-C	7.71	124.28	108.71
1	K	157	THR	N-CA-C	7.69	124.25	108.71
1	E	157	THR	N-CA-C	7.61	124.09	108.71
1	L	157	THR	N-CA-C	7.59	124.05	108.71
1	F	157	THR	N-CA-C	7.52	123.90	108.71
1	B	157	THR	N-CA-C	7.52	123.90	108.71
1	I	106	LEU	N-CA-C	7.46	121.56	109.40
1	J	106	LEU	N-CA-C	7.40	121.46	109.40
1	J	105	LYS	N-CA-C	-7.38	95.08	110.80
1	A	105	LYS	N-CA-C	-7.34	95.16	110.80
1	L	106	LEU	N-CA-C	7.33	121.34	109.40
1	E	105	LYS	N-CA-C	-7.31	95.22	110.80
1	H	157	THR	N-CA-C	7.30	123.46	108.71
1	A	106	LEU	N-CA-C	7.29	121.28	109.40
1	K	105	LYS	N-CA-C	-7.28	95.29	110.80
1	C	105	LYS	N-CA-C	-7.27	95.31	110.80
1	F	105	LYS	N-CA-C	-7.27	95.31	110.80
1	L	158	PRO	N-CA-C	-7.27	97.49	112.47
1	C	157	THR	N-CA-C	7.27	123.39	108.71
1	G	105	LYS	N-CA-C	-7.27	95.32	110.80
1	C	158	PRO	N-CA-C	-7.26	97.52	112.47
1	B	105	LYS	N-CA-C	-7.25	95.36	110.80
1	D	105	LYS	N-CA-C	-7.25	95.36	110.80
1	K	106	LEU	N-CA-C	7.24	121.20	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	105	LYS	N-CA-C	-7.24	95.38	110.80
1	I	105	LYS	N-CA-C	-7.24	95.39	110.80
1	H	105	LYS	N-CA-C	-7.20	95.47	110.80
1	H	158	PRO	N-CA-C	-7.20	97.64	112.47
1	F	106	LEU	N-CA-C	7.20	121.13	109.40
1	H	106	LEU	N-CA-C	7.18	121.11	109.40
1	E	106	LEU	N-CA-C	7.16	121.07	109.40
1	E	158	PRO	N-CA-C	-7.14	97.76	112.47
1	G	106	LEU	N-CA-C	7.12	121.01	109.40
1	C	106	LEU	N-CA-C	7.12	121.01	109.40
1	F	158	PRO	N-CA-C	-7.06	97.93	112.47
1	K	158	PRO	N-CA-C	-7.00	98.05	112.47
1	D	158	PRO	N-CA-C	-6.99	98.06	112.47
1	B	158	PRO	N-CA-C	-6.98	98.09	112.47
1	D	106	LEU	N-CA-C	6.97	120.82	109.59
1	B	38	LEU	N-CA-C	-6.97	99.97	110.28
1	G	158	PRO	N-CA-C	-6.96	98.13	112.47
1	B	106	LEU	N-CA-C	6.90	120.64	109.40
1	A	158	PRO	N-CA-C	-6.89	98.28	112.47
1	I	158	PRO	N-CA-C	-6.86	98.34	112.47
1	J	158	PRO	N-CA-C	-6.80	98.46	112.47
1	K	111	ASP	N-CA-C	-6.49	105.23	113.01
1	B	111	ASP	N-CA-C	-6.47	105.25	113.01
1	A	111	ASP	N-CA-C	-6.46	105.26	113.01
1	E	111	ASP	N-CA-C	-6.44	105.28	113.01
1	D	111	ASP	N-CA-C	-6.42	105.30	113.01
1	D	59	GLN	N-CA-C	-6.41	99.19	109.96
1	H	111	ASP	N-CA-C	-6.41	105.32	113.01
1	J	59	GLN	N-CA-C	-6.41	99.19	109.96
1	L	111	ASP	N-CA-C	-6.39	105.34	113.01
1	C	15	ILE	N-CA-C	6.39	117.14	110.62
1	F	111	ASP	N-CA-C	-6.38	105.36	113.01
1	I	111	ASP	N-CA-C	-6.35	105.39	113.01
1	C	111	ASP	N-CA-C	-6.35	105.39	113.01
1	G	111	ASP	N-CA-C	-6.32	105.43	113.01
1	K	15	ILE	N-CA-C	6.25	116.99	110.62
1	K	59	GLN	N-CA-C	-6.25	99.47	109.96
1	D	15	ILE	N-CA-C	6.24	116.99	110.62
1	L	15	ILE	N-CA-C	6.22	116.97	110.62
1	H	59	GLN	N-CA-C	-6.22	99.51	109.96
1	B	59	GLN	N-CA-C	-6.22	99.51	109.96
1	A	15	ILE	N-CA-C	6.22	116.96	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	ILE	N-CA-C	6.20	116.94	110.62
1	G	15	ILE	N-CA-C	6.20	116.94	110.62
1	D	220	GLU	N-CA-C	-6.18	104.46	111.07
1	F	59	GLN	N-CA-C	-6.18	99.58	109.96
1	G	59	GLN	N-CA-C	-6.18	99.58	109.96
1	F	15	ILE	N-CA-C	6.17	116.91	110.62
1	A	59	GLN	N-CA-C	-6.16	99.61	109.96
1	I	15	ILE	N-CA-C	6.14	116.88	110.62
1	L	59	GLN	N-CA-C	-6.13	99.66	109.96
1	E	59	GLN	N-CA-C	-6.12	99.68	109.96
1	J	111	ASP	N-CA-C	-6.10	105.69	113.01
1	H	15	ILE	N-CA-C	6.10	116.84	110.62
1	J	15	ILE	N-CA-C	6.05	116.79	110.62
1	E	15	ILE	N-CA-C	6.02	116.76	110.62
1	I	59	GLN	N-CA-C	-6.01	99.87	109.96
1	C	59	GLN	N-CA-C	-5.99	99.90	109.96
1	L	220	GLU	N-CA-C	-5.96	104.69	111.07
1	D	173	GLN	N-CA-C	-5.88	106.15	113.55
1	B	274	LEU	N-CA-C	5.81	117.08	107.20
1	J	173	GLN	N-CA-C	-5.81	106.23	113.55
1	G	220	GLU	N-CA-C	-5.80	104.86	111.07
1	L	274	LEU	N-CA-C	5.80	117.06	107.20
1	A	173	GLN	N-CA-C	-5.79	106.25	113.55
1	A	274	LEU	N-CA-C	5.77	117.01	107.20
1	K	274	LEU	N-CA-C	5.75	116.97	107.20
1	E	173	GLN	N-CA-C	-5.74	106.31	113.55
1	G	274	LEU	N-CA-C	5.72	116.92	107.20
1	J	220	GLU	N-CA-C	-5.70	104.97	111.07
1	J	274	LEU	N-CA-C	5.67	116.84	107.20
1	H	48	ILE	N-CA-C	5.67	116.02	107.80
1	G	249	GLN	N-CA-C	-5.65	105.20	111.36
1	C	173	GLN	N-CA-C	-5.64	106.44	113.55
1	C	249	GLN	N-CA-C	-5.64	105.21	111.36
1	L	249	GLN	N-CA-C	-5.63	105.22	111.36
1	J	249	GLN	N-CA-C	-5.63	105.22	111.36
1	C	220	GLU	N-CA-C	-5.61	105.06	111.07
1	D	274	LEU	N-CA-C	5.61	116.74	107.20
1	I	173	GLN	N-CA-C	-5.61	106.49	113.55
1	L	130	THR	N-CA-C	-5.60	106.45	113.28
1	F	173	GLN	N-CA-C	-5.60	106.49	113.55
1	E	274	LEU	N-CA-C	5.60	116.72	107.20
1	B	130	THR	N-CA-C	-5.59	106.46	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	130	THR	N-CA-C	-5.58	106.47	113.28
1	I	274	LEU	N-CA-C	5.52	116.59	107.20
1	H	274	LEU	N-CA-C	5.52	116.59	107.20
1	C	274	LEU	N-CA-C	5.51	116.57	107.20
1	H	173	GLN	N-CA-C	-5.51	106.61	113.55
1	K	173	GLN	N-CA-C	-5.49	106.63	113.55
1	H	220	GLU	N-CA-C	-5.49	105.19	111.07
1	E	48	ILE	N-CA-C	5.48	115.75	107.80
1	I	220	GLU	N-CA-C	-5.47	105.22	111.07
1	A	220	GLU	N-CA-C	-5.46	105.22	111.07
1	B	220	GLU	N-CA-C	-5.46	105.22	111.07
1	D	249	GLN	N-CA-C	-5.46	105.41	111.36
1	G	173	GLN	N-CA-C	-5.44	106.69	113.55
1	J	130	THR	N-CA-C	-5.44	106.65	113.28
1	G	130	THR	N-CA-C	-5.43	106.66	113.28
1	L	173	GLN	N-CA-C	-5.42	106.72	113.55
1	E	220	GLU	N-CA-C	-5.41	105.28	111.07
1	C	130	THR	N-CA-C	-5.39	106.55	113.23
1	D	130	THR	N-CA-C	-5.37	106.73	113.28
1	A	45	PRO	CA-C-N	5.35	125.06	119.82
1	A	45	PRO	C-N-CA	5.35	125.06	119.82
1	K	38	LEU	N-CA-C	-5.34	102.37	110.28
1	B	173	GLN	N-CA-C	-5.33	106.83	113.55
1	D	43	ASN	CB-CA-C	-5.33	110.45	116.63
1	K	43	ASN	CB-CA-C	-5.32	110.46	116.63
1	K	249	GLN	N-CA-C	-5.32	105.56	111.36
1	H	249	GLN	N-CA-C	-5.32	105.57	111.36
1	A	249	GLN	N-CA-C	-5.28	105.61	111.36
1	J	45	PRO	CA-C-N	5.26	124.98	119.82
1	J	45	PRO	C-N-CA	5.26	124.98	119.82
1	L	38	LEU	N-CA-C	-5.26	103.08	110.50
1	L	129	PRO	N-CA-C	-5.24	103.05	111.38
1	E	249	GLN	N-CA-C	-5.23	105.66	111.36
1	F	249	GLN	N-CA-C	-5.22	105.67	111.36
1	B	249	GLN	N-CA-C	-5.22	105.67	111.36
1	K	45	PRO	CA-C-N	5.21	124.93	119.82
1	K	45	PRO	C-N-CA	5.21	124.93	119.82
1	A	279	LYS	N-CA-C	5.21	121.90	110.80
1	K	130	THR	N-CA-C	-5.21	106.93	113.28
1	D	38	LEU	N-CA-C	-5.19	102.71	110.23
1	C	48	ILE	N-CA-C	5.18	115.31	107.80
1	F	220	GLU	N-CA-C	-5.16	105.55	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	220	GLU	N-CA-C	-5.16	105.55	111.07
1	B	43	ASN	CB-CA-C	-5.15	110.66	116.63
1	F	274	LEU	N-CA-C	5.13	116.42	107.49
1	E	130	THR	N-CA-C	-5.13	106.87	113.23
1	B	279	LYS	N-CA-C	5.12	121.71	110.80
1	K	279	LYS	N-CA-C	5.12	121.70	110.80
1	I	130	THR	N-CA-C	-5.11	107.04	113.28
1	G	279	LYS	N-CA-C	5.11	121.68	110.80
1	E	43	ASN	CB-CA-C	-5.10	110.71	116.63
1	L	43	ASN	CB-CA-C	-5.10	110.72	116.63
1	F	279	LYS	N-CA-C	5.09	121.64	110.80
1	F	43	ASN	CB-CA-C	-5.08	110.73	116.63
1	L	279	LYS	N-CA-C	5.08	121.63	110.80
1	G	45	PRO	CA-C-N	5.08	124.79	119.82
1	G	45	PRO	C-N-CA	5.08	124.79	119.82
1	F	45	PRO	CA-C-N	5.07	124.79	119.82
1	F	45	PRO	C-N-CA	5.07	124.79	119.82
1	G	38	LEU	N-CA-C	-5.06	102.89	110.23
1	G	43	ASN	CB-CA-C	-5.06	110.76	116.63
1	D	279	LYS	N-CA-C	5.04	121.53	110.80
1	E	279	LYS	N-CA-C	5.03	121.52	110.80
1	F	48	ILE	N-CA-C	5.03	115.09	107.80
1	F	130	THR	N-CA-C	-5.02	107.15	113.28
1	J	279	LYS	N-CA-C	5.02	121.49	110.80
1	I	249	GLN	N-CA-C	-5.01	105.90	111.36
1	D	48	ILE	N-CA-C	5.01	115.06	107.80

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	205	TYR	Sidechain
1	B	205	TYR	Sidechain
1	C	205	TYR	Sidechain
1	D	205	TYR	Sidechain
1	E	205	TYR	Sidechain
1	F	205	TYR	Sidechain
1	G	205	TYR	Sidechain
1	H	205	TYR	Sidechain
1	I	205	TYR	Sidechain
1	J	205	TYR	Sidechain
1	K	205	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	L	205	TYR	Sidechain

5.2 Too-close contacts ⓘ

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	2103	0	2052	242	0
1	B	2103	0	2052	241	0
1	C	2103	0	2052	271	0
1	D	2103	0	2052	269	1
1	E	2103	0	2052	226	0
1	F	2103	0	2052	241	0
1	G	2103	0	2052	258	0
1	H	2103	0	2052	241	0
1	I	2103	0	2052	235	1
1	J	2103	0	2052	239	0
1	K	2103	0	2052	237	0
1	L	2103	0	2052	231	0
All	All	25236	0	24624	2577	1

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 52.

All (2577) 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:A:159:VAL:HG11	1:L:201:THR:HG23	1.25	1.18
1:G:87:TYR:OH	1:H:48:ILE:HA	1.43	1.18
1:H:201:THR:HG23	1:I:159:VAL:HG11	1.29	1.12
1:D:87:TYR:OH	1:E:48:ILE:HA	1.50	1.10
1:C:110:ARG:HH22	1:D:72:SER:HB2	1.12	1.09
1:I:201:THR:HG23	1:J:159:VAL:HG11	1.29	1.09
1:C:201:THR:HG23	1:D:159:VAL:HG11	1.31	1.08
1:F:201:THR:HG23	1:G:159:VAL:HG11	1.37	1.07
1:K:201:THR:HG23	1:L:159:VAL:HG11	1.35	1.05
1:F:163:ALA:HB3	1:G:187:ALA:HB2	1.41	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:ASN:HD21	1:B:257:PHE:HD2	1.06	1.02
1:K:11:SER:HB3	1:L:176:ASN:HD22	1.20	1.02
1:G:123:ASN:HD21	1:G:257:PHE:HD2	1.08	1.02
1:A:11:SER:HB3	1:B:176:ASN:HD22	1.20	1.01
1:E:201:THR:HG23	1:F:159:VAL:HG11	1.38	1.00
1:L:123:ASN:HD21	1:L:257:PHE:HD2	1.05	0.99
1:L:169:LEU:HD22	1:L:173:GLN:HE22	1.29	0.98
1:F:110:ARG:HH22	1:G:72:SER:HB2	1.25	0.98
1:D:123:ASN:HD21	1:D:257:PHE:HD2	1.07	0.98
1:K:87:TYR:OH	1:L:48:ILE:HA	1.63	0.98
1:G:169:LEU:HD22	1:G:173:GLN:HE22	1.28	0.97
1:J:123:ASN:HD21	1:J:257:PHE:HD2	1.08	0.97
1:K:11:SER:HB3	1:L:176:ASN:ND2	1.78	0.97
1:C:163:ALA:HB3	1:D:187:ALA:HB2	1.47	0.97
1:K:123:ASN:HD21	1:K:257:PHE:HD2	1.06	0.97
1:B:169:LEU:HD22	1:B:173:GLN:HE22	1.29	0.96
1:D:169:LEU:HD22	1:D:173:GLN:HE22	1.30	0.96
1:I:123:ASN:HD21	1:I:257:PHE:HD2	1.08	0.96
1:I:163:ALA:HB3	1:J:187:ALA:HB2	1.47	0.96
1:H:169:LEU:HD22	1:H:173:GLN:HE22	1.31	0.96
1:C:169:LEU:HD22	1:C:173:GLN:HE22	1.30	0.96
1:E:169:LEU:HD22	1:E:173:GLN:HE22	1.28	0.95
1:H:163:ALA:HB3	1:I:187:ALA:HB2	1.45	0.95
1:A:201:THR:HG23	1:B:159:VAL:HG11	1.46	0.95
1:J:201:THR:HG23	1:K:159:VAL:HG11	1.48	0.95
1:A:123:ASN:HD21	1:A:257:PHE:HD2	1.07	0.95
1:B:201:THR:HG23	1:C:159:VAL:HG11	1.48	0.95
1:D:201:THR:HG23	1:E:159:VAL:HG11	1.46	0.95
1:J:163:ALA:HB3	1:K:187:ALA:HB2	1.44	0.95
1:C:110:ARG:NH2	1:D:72:SER:HB2	1.82	0.95
1:E:123:ASN:HD21	1:E:257:PHE:HD2	1.07	0.94
1:G:163:ALA:HB3	1:H:187:ALA:HB2	1.49	0.94
1:A:187:ALA:HB2	1:L:163:ALA:HB3	1.49	0.94
1:D:163:ALA:HB3	1:E:187:ALA:HB2	1.49	0.93
1:G:201:THR:HG23	1:H:159:VAL:HG11	1.51	0.93
1:C:123:ASN:HD21	1:C:257:PHE:HD2	1.08	0.93
1:K:169:LEU:HD22	1:K:173:GLN:HE22	1.30	0.93
1:J:169:LEU:HD22	1:J:173:GLN:HE22	1.30	0.93
1:H:71:ILE:HB	1:H:74:ILE:HD11	1.50	0.93
1:H:123:ASN:HD21	1:H:257:PHE:HD2	1.07	0.93
1:B:163:ALA:HB3	1:C:187:ALA:HB2	1.47	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:169:LEU:HD22	1:I:173:GLN:HE22	1.33	0.92
1:A:169:LEU:HD22	1:A:173:GLN:HE22	1.31	0.92
1:E:71:ILE:HB	1:E:74:ILE:HD11	1.51	0.92
1:B:71:ILE:HB	1:B:74:ILE:HD11	1.52	0.92
1:F:71:ILE:HB	1:F:74:ILE:HD11	1.52	0.92
1:A:163:ALA:HB3	1:B:187:ALA:HB2	1.52	0.91
1:E:163:ALA:HB3	1:F:187:ALA:HB2	1.49	0.91
1:F:169:LEU:HD22	1:F:173:GLN:HE22	1.34	0.91
1:K:163:ALA:HB3	1:L:187:ALA:HB2	1.49	0.91
1:F:123:ASN:HD21	1:F:257:PHE:HD2	1.07	0.91
1:J:11:SER:HB3	1:K:176:ASN:HD22	1.33	0.91
1:G:71:ILE:HB	1:G:74:ILE:HD11	1.51	0.91
1:C:71:ILE:HB	1:C:74:ILE:HD11	1.50	0.91
1:K:71:ILE:HB	1:K:74:ILE:HD11	1.53	0.91
1:L:71:ILE:HB	1:L:74:ILE:HD11	1.51	0.91
1:A:71:ILE:HB	1:A:74:ILE:HD11	1.50	0.91
1:D:71:ILE:HB	1:D:74:ILE:HD11	1.51	0.89
1:A:11:SER:HB3	1:B:176:ASN:ND2	1.87	0.89
1:B:11:SER:HB3	1:C:176:ASN:ND2	1.88	0.88
1:C:248:GLU:OE2	1:D:227:ILE:HA	1.73	0.88
1:J:71:ILE:HB	1:J:74:ILE:HD11	1.53	0.88
1:I:71:ILE:HB	1:I:74:ILE:HD11	1.54	0.87
1:E:192:ASP:O	1:E:195:SER:HB3	1.75	0.86
1:C:171:LEU:C	1:C:173:GLN:H	1.84	0.85
1:K:192:ASP:O	1:K:195:SER:HB3	1.76	0.85
1:D:171:LEU:C	1:D:173:GLN:H	1.85	0.85
1:L:169:LEU:HD22	1:L:173:GLN:NE2	1.92	0.85
1:L:192:ASP:O	1:L:195:SER:HB3	1.77	0.85
1:C:248:GLU:HG3	1:D:227:ILE:CG2	2.06	0.84
1:D:154:ALA:HA	1:F:182:ALA:HB2	1.59	0.84
1:B:11:SER:HB3	1:C:176:ASN:HD22	1.42	0.84
1:G:169:LEU:HD22	1:G:173:GLN:NE2	1.91	0.84
1:A:192:ASP:O	1:A:195:SER:HB3	1.78	0.84
1:B:171:LEU:C	1:B:173:GLN:H	1.85	0.84
1:C:248:GLU:CD	1:D:227:ILE:HG23	2.02	0.84
1:J:171:LEU:C	1:J:173:GLN:H	1.85	0.84
1:B:248:GLU:HB3	1:C:282:TYR:CZ	2.11	0.84
1:E:169:LEU:HD22	1:E:173:GLN:NE2	1.91	0.84
1:G:171:LEU:C	1:G:173:GLN:H	1.84	0.84
1:B:154:ALA:HA	1:D:182:ALA:HB2	1.58	0.84
1:B:169:LEU:HD22	1:B:173:GLN:NE2	1.92	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:201:THR:HG22	1:F:201:THR:O	1.78	0.84
1:E:201:THR:O	1:E:201:THR:HG22	1.77	0.84
1:G:192:ASP:O	1:G:195:SER:HB3	1.77	0.84
1:B:192:ASP:O	1:B:195:SER:HB3	1.78	0.83
1:E:171:LEU:C	1:E:173:GLN:H	1.86	0.83
1:C:248:GLU:HG3	1:D:227:ILE:HG23	1.58	0.83
1:J:169:LEU:HD22	1:J:173:GLN:NE2	1.92	0.83
1:C:169:LEU:HD22	1:C:173:GLN:NE2	1.93	0.83
1:H:192:ASP:O	1:H:195:SER:HB3	1.78	0.83
1:H:171:LEU:C	1:H:173:GLN:H	1.84	0.83
1:F:171:LEU:C	1:F:173:GLN:H	1.84	0.83
1:H:169:LEU:HD22	1:H:173:GLN:NE2	1.93	0.83
1:I:171:LEU:C	1:I:173:GLN:H	1.86	0.83
1:A:171:LEU:C	1:A:173:GLN:H	1.86	0.83
1:A:169:LEU:HD22	1:A:173:GLN:NE2	1.94	0.82
1:D:192:ASP:O	1:D:195:SER:HB3	1.77	0.82
1:I:148:ILE:O	1:I:152:GLN:HG3	1.77	0.82
1:J:192:ASP:O	1:J:195:SER:HB3	1.79	0.82
1:K:169:LEU:HD22	1:K:173:GLN:NE2	1.93	0.82
1:C:66:TYR:HB2	1:C:104:PHE:CE2	2.15	0.82
1:H:201:THR:HG22	1:H:201:THR:O	1.77	0.82
1:D:169:LEU:HD22	1:D:173:GLN:NE2	1.93	0.82
1:F:66:TYR:HB2	1:F:104:PHE:CE2	2.15	0.82
1:H:66:TYR:HB2	1:H:104:PHE:CE2	2.14	0.82
1:J:66:TYR:HB2	1:J:104:PHE:CE2	2.15	0.82
1:K:171:LEU:C	1:K:173:GLN:H	1.86	0.82
1:C:192:ASP:O	1:C:195:SER:HB3	1.78	0.82
1:L:66:TYR:HB2	1:L:104:PHE:CE2	2.14	0.82
1:G:201:THR:O	1:G:201:THR:HG22	1.79	0.81
1:D:117:MET:HG3	1:D:118:GLY:H	1.45	0.81
1:A:176:ASN:HD22	1:L:11:SER:HB3	1.43	0.81
1:D:148:ILE:O	1:D:152:GLN:HG3	1.80	0.81
1:A:66:TYR:HB2	1:A:104:PHE:CE2	2.15	0.81
1:F:192:ASP:O	1:F:195:SER:HB3	1.79	0.81
1:D:87:TYR:OH	1:E:47:THR:O	1.97	0.81
1:F:148:ILE:O	1:F:152:GLN:HG3	1.79	0.81
1:J:117:MET:HG3	1:J:118:GLY:H	1.45	0.81
1:K:66:TYR:HB2	1:K:104:PHE:CE2	2.15	0.81
1:E:66:TYR:HB2	1:E:104:PHE:CE2	2.15	0.81
1:J:275:ASN:O	1:J:277:LYS:HG3	1.81	0.81
1:A:117:MET:HG3	1:A:118:GLY:H	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:66:TYR:HB2	1:D:104:PHE:CE2	2.16	0.81
1:L:275:ASN:O	1:L:277:LYS:HG3	1.81	0.81
1:I:192:ASP:O	1:I:195:SER:HB3	1.81	0.80
1:K:201:THR:HG22	1:K:201:THR:O	1.82	0.80
1:B:66:TYR:HB2	1:B:104:PHE:CE2	2.15	0.80
1:I:66:TYR:HB2	1:I:104:PHE:CE2	2.16	0.80
1:I:169:LEU:HD22	1:I:173:GLN:NE2	1.96	0.80
1:A:126:MET:O	1:A:128:PHE:N	2.15	0.80
1:C:201:THR:HG22	1:C:201:THR:O	1.79	0.80
1:F:169:LEU:HD22	1:F:173:GLN:NE2	1.96	0.80
1:G:117:MET:HG3	1:G:118:GLY:H	1.46	0.80
1:I:275:ASN:O	1:I:277:LYS:HG3	1.82	0.80
1:L:201:THR:O	1:L:201:THR:HG22	1.81	0.80
1:G:66:TYR:HB2	1:G:104:PHE:CE2	2.17	0.79
1:K:117:MET:HG3	1:K:118:GLY:H	1.47	0.79
1:C:126:MET:O	1:C:128:PHE:N	2.15	0.79
1:B:148:ILE:O	1:B:152:GLN:HG3	1.82	0.79
1:B:201:THR:O	1:B:201:THR:HG22	1.81	0.79
1:H:148:ILE:O	1:H:152:GLN:HG3	1.83	0.79
1:C:248:GLU:CG	1:D:227:ILE:HG23	2.12	0.79
1:L:117:MET:HG3	1:L:118:GLY:H	1.47	0.79
1:D:222:MET:HE3	1:D:227:ILE:HG21	1.62	0.79
1:B:117:MET:HG3	1:B:118:GLY:H	1.47	0.79
1:B:275:ASN:O	1:B:277:LYS:HG3	1.83	0.79
1:K:148:ILE:O	1:K:152:GLN:HG3	1.83	0.79
1:J:148:ILE:O	1:J:152:GLN:HG3	1.81	0.79
1:K:277:LYS:HD2	1:K:278:VAL:N	1.98	0.79
1:A:182:ALA:HB2	1:K:154:ALA:HA	1.65	0.78
1:F:248:GLU:HG3	1:G:227:ILE:HG23	1.65	0.78
1:L:148:ILE:O	1:L:152:GLN:HG3	1.82	0.78
1:F:277:LYS:HD2	1:F:278:VAL:N	1.98	0.78
1:G:277:LYS:HD2	1:G:278:VAL:N	1.98	0.78
1:L:171:LEU:C	1:L:173:GLN:H	1.86	0.78
1:L:277:LYS:HD2	1:L:278:VAL:N	1.98	0.78
1:D:277:LYS:HD2	1:D:278:VAL:N	1.98	0.78
1:I:277:LYS:HD2	1:I:278:VAL:N	1.98	0.78
1:C:117:MET:HG3	1:C:118:GLY:H	1.49	0.78
1:C:86:VAL:HA	1:D:99:VAL:HG11	1.64	0.78
1:D:11:SER:HB3	1:E:176:ASN:HD22	1.49	0.78
1:D:148:ILE:HG23	1:D:207:VAL:HG13	1.66	0.78
1:F:126:MET:O	1:F:128:PHE:N	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:148:ILE:O	1:G:152:GLN:HG3	1.82	0.78
1:E:117:MET:HG3	1:E:118:GLY:H	1.47	0.78
1:H:117:MET:HG3	1:H:118:GLY:H	1.49	0.78
1:A:148:ILE:O	1:A:152:GLN:HG3	1.84	0.78
1:C:87:TYR:HE1	1:D:75:ALA:O	1.66	0.78
1:F:163:ALA:HB3	1:G:187:ALA:CB	2.14	0.77
1:B:126:MET:HE1	1:C:36:TYR:CE1	2.19	0.77
1:E:275:ASN:O	1:E:277:LYS:HG3	1.85	0.77
1:C:277:LYS:HD2	1:C:278:VAL:N	1.99	0.77
1:E:277:LYS:HD2	1:E:278:VAL:N	1.98	0.77
1:G:87:TYR:CD2	1:H:49:ASN:HB2	2.20	0.77
1:A:275:ASN:O	1:A:277:LYS:HG3	1.84	0.77
1:F:275:ASN:O	1:F:277:LYS:HG3	1.84	0.77
1:G:11:SER:HB3	1:H:176:ASN:HD22	1.50	0.77
1:C:148:ILE:O	1:C:152:GLN:HG3	1.85	0.77
1:C:275:ASN:O	1:C:277:LYS:HG3	1.84	0.77
1:J:11:SER:HB3	1:K:176:ASN:ND2	1.99	0.77
1:C:154:ALA:HA	1:E:182:ALA:HB2	1.66	0.76
1:I:201:THR:O	1:I:201:THR:HG22	1.84	0.76
1:D:11:SER:HB3	1:E:176:ASN:ND2	2.01	0.76
1:H:275:ASN:O	1:H:277:LYS:HG3	1.85	0.76
1:J:201:THR:O	1:J:201:THR:HG22	1.85	0.76
1:B:277:LYS:HD2	1:B:278:VAL:N	2.00	0.76
1:E:148:ILE:O	1:E:152:GLN:HG3	1.84	0.76
1:F:248:GLU:HG3	1:G:227:ILE:CG2	2.15	0.76
1:F:117:MET:HG3	1:F:118:GLY:H	1.48	0.76
1:H:277:LYS:HD2	1:H:278:VAL:N	2.01	0.76
1:G:222:MET:HE3	1:G:227:ILE:HG21	1.68	0.76
1:K:275:ASN:O	1:K:277:LYS:HG3	1.85	0.75
1:A:277:LYS:HD2	1:A:278:VAL:N	2.01	0.75
1:J:37:GLN:O	1:J:281:ARG:HD2	1.87	0.75
1:K:222:MET:HE3	1:K:227:ILE:HG21	1.69	0.75
1:A:201:THR:O	1:A:201:THR:HG22	1.85	0.75
1:D:275:ASN:O	1:D:277:LYS:HG3	1.87	0.75
1:C:163:ALA:HB3	1:D:187:ALA:CB	2.17	0.75
1:D:201:THR:O	1:D:201:THR:HG22	1.85	0.75
1:H:148:ILE:HG23	1:H:207:VAL:HG13	1.69	0.75
1:I:150:VAL:HG13	1:K:180:GLY:HA2	1.69	0.75
1:A:154:ALA:HA	1:C:182:ALA:HB2	1.69	0.74
1:I:117:MET:HG3	1:I:118:GLY:H	1.51	0.74
1:F:110:ARG:NH2	1:G:72:SER:HB2	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:148:ILE:HG23	1:G:207:VAL:HG13	1.68	0.74
1:G:11:SER:HB3	1:H:176:ASN:ND2	2.03	0.74
1:I:148:ILE:HG23	1:I:207:VAL:HG13	1.68	0.74
1:F:124:ASN:HD21	1:F:128:PHE:HB2	1.52	0.74
1:H:163:ALA:HB3	1:I:187:ALA:CB	2.18	0.74
1:G:275:ASN:O	1:G:277:LYS:HG3	1.87	0.74
1:G:154:ALA:HA	1:I:182:ALA:HB2	1.70	0.73
1:B:37:GLN:O	1:B:281:ARG:HD2	1.87	0.73
1:C:150:VAL:HG13	1:E:180:GLY:HA2	1.70	0.73
1:J:277:LYS:HD2	1:J:278:VAL:N	2.04	0.73
1:B:148:ILE:HG23	1:B:207:VAL:HG13	1.69	0.73
1:A:148:ILE:HG23	1:A:207:VAL:HG13	1.71	0.73
1:E:163:ALA:HB3	1:F:187:ALA:CB	2.19	0.73
1:L:126:MET:O	1:L:128:PHE:N	2.21	0.73
1:H:171:LEU:O	1:H:173:GLN:N	2.22	0.73
1:F:248:GLU:OE2	1:G:227:ILE:HA	1.89	0.72
1:J:150:VAL:HG13	1:L:180:GLY:HA2	1.70	0.72
1:D:87:TYR:CD2	1:E:49:ASN:HB2	2.24	0.72
1:D:213:GLN:HG3	1:E:207:VAL:HG11	1.70	0.72
1:L:148:ILE:HG23	1:L:207:VAL:HG13	1.70	0.72
1:L:276:VAL:O	1:L:278:VAL:HG23	1.88	0.72
1:A:159:VAL:CG1	1:L:201:THR:HG23	2.14	0.72
1:B:182:ALA:HB2	1:L:154:ALA:HA	1.71	0.72
1:C:171:LEU:O	1:C:173:GLN:N	2.22	0.72
1:D:171:LEU:O	1:D:173:GLN:N	2.23	0.72
1:F:248:GLU:CD	1:G:227:ILE:HG23	2.15	0.72
1:A:276:VAL:O	1:A:278:VAL:HG23	1.90	0.72
1:C:124:ASN:HD21	1:C:128:PHE:HB2	1.53	0.72
1:F:87:TYR:HE1	1:G:75:ALA:O	1.73	0.72
1:J:222:MET:HE3	1:J:227:ILE:HG21	1.69	0.71
1:C:222:MET:HE3	1:C:227:ILE:HG21	1.71	0.71
1:K:276:VAL:O	1:K:278:VAL:HG23	1.91	0.71
1:F:171:LEU:O	1:F:173:GLN:N	2.22	0.71
1:J:148:ILE:HG23	1:J:207:VAL:HG13	1.72	0.71
1:A:222:MET:HE3	1:A:227:ILE:HG21	1.71	0.71
1:D:163:ALA:HB3	1:E:187:ALA:CB	2.19	0.71
1:B:180:GLY:HA2	1:L:150:VAL:HG13	1.71	0.71
1:J:163:ALA:HB3	1:K:187:ALA:CB	2.21	0.71
1:J:276:VAL:O	1:J:278:VAL:HG23	1.90	0.71
1:B:49:ASN:HD22	1:B:49:ASN:C	1.97	0.71
1:C:144:LEU:HD21	1:D:152:GLN:NE2	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:276:VAL:O	1:I:278:VAL:HG23	1.90	0.71
1:K:148:ILE:HG23	1:K:207:VAL:HG13	1.70	0.71
1:G:276:VAL:O	1:G:278:VAL:HG23	1.91	0.71
1:A:159:VAL:HG11	1:L:201:THR:CG2	2.15	0.70
1:A:213:GLN:HG3	1:B:207:VAL:HG11	1.73	0.70
1:D:276:VAL:O	1:D:278:VAL:HG23	1.91	0.70
1:E:148:ILE:HG23	1:E:207:VAL:HG13	1.71	0.70
1:G:171:LEU:O	1:G:173:GLN:N	2.23	0.70
1:J:49:ASN:HD22	1:J:49:ASN:C	2.00	0.70
1:C:125:ASP:O	1:C:126:MET:HB2	1.91	0.70
1:D:125:ASP:O	1:D:126:MET:HB2	1.91	0.70
1:H:222:MET:HE3	1:H:227:ILE:HG21	1.73	0.70
1:I:49:ASN:C	1:I:49:ASN:HD22	2.00	0.70
1:I:222:MET:HE3	1:I:227:ILE:HG21	1.73	0.70
1:F:222:MET:HE3	1:F:227:ILE:HG21	1.72	0.70
1:K:87:TYR:OH	1:L:47:THR:O	2.07	0.70
1:C:263:GLU:OE1	1:D:50:PRO:HG2	1.92	0.70
1:F:57:ILE:CG2	1:F:123:ASN:HB2	2.22	0.70
1:A:124:ASN:HD21	1:A:128:PHE:HB2	1.56	0.70
1:B:222:MET:HE3	1:B:227:ILE:HG21	1.71	0.70
1:F:86:VAL:HA	1:G:99:VAL:HG11	1.73	0.70
1:A:57:ILE:CG2	1:A:123:ASN:HB2	2.22	0.70
1:C:276:VAL:O	1:C:278:VAL:HG23	1.91	0.70
1:F:276:VAL:O	1:F:278:VAL:HG23	1.92	0.70
1:G:213:GLN:HG3	1:H:207:VAL:HG11	1.73	0.69
1:A:49:ASN:C	1:A:49:ASN:HD22	1.99	0.69
1:A:71:ILE:CB	1:A:74:ILE:HD11	2.23	0.69
1:D:154:ALA:CA	1:F:182:ALA:HB2	2.23	0.69
1:G:37:GLN:O	1:G:281:ARG:HD2	1.91	0.69
1:L:171:LEU:O	1:L:173:GLN:N	2.26	0.69
1:A:125:ASP:O	1:A:126:MET:HB2	1.91	0.69
1:B:276:VAL:O	1:B:278:VAL:HG23	1.93	0.69
1:E:222:MET:HE3	1:E:227:ILE:HG21	1.73	0.69
1:H:276:VAL:O	1:H:278:VAL:HG23	1.91	0.69
1:B:171:LEU:O	1:B:173:GLN:N	2.25	0.69
1:F:148:ILE:HG23	1:F:207:VAL:HG13	1.73	0.69
1:H:201:THR:CG2	1:I:159:VAL:HG11	2.17	0.69
1:J:213:GLN:HG3	1:K:207:VAL:HG11	1.75	0.69
1:I:171:LEU:O	1:I:173:GLN:N	2.25	0.69
1:D:71:ILE:CB	1:D:74:ILE:HD11	2.23	0.69
1:E:276:VAL:O	1:E:278:VAL:HG23	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:163:ALA:HB3	1:H:187:ALA:CB	2.22	0.69
1:C:66:TYR:HB2	1:C:104:PHE:CZ	2.28	0.69
1:E:171:LEU:O	1:E:173:GLN:N	2.25	0.69
1:G:125:ASP:O	1:G:126:MET:HB2	1.93	0.69
1:I:163:ALA:HB3	1:J:187:ALA:CB	2.23	0.69
1:J:71:ILE:CB	1:J:74:ILE:HD11	2.23	0.69
1:C:57:ILE:CG2	1:C:123:ASN:HB2	2.22	0.69
1:H:150:VAL:HG13	1:J:180:GLY:HA2	1.74	0.69
1:L:222:MET:HE3	1:L:227:ILE:HG21	1.73	0.69
1:C:179:GLU:C	1:C:181:ASN:H	2.01	0.68
1:C:248:GLU:CD	1:D:227:ILE:HA	2.18	0.68
1:K:66:TYR:HB2	1:K:104:PHE:CZ	2.29	0.68
1:C:71:ILE:CB	1:C:74:ILE:HD11	2.23	0.68
1:E:66:TYR:HB2	1:E:104:PHE:CZ	2.29	0.68
1:I:125:ASP:O	1:I:126:MET:HB2	1.91	0.68
1:F:179:GLU:C	1:F:181:ASN:H	2.02	0.68
1:G:49:ASN:HD22	1:G:49:ASN:C	2.01	0.68
1:D:179:GLU:C	1:D:181:ASN:H	2.02	0.68
1:A:171:LEU:O	1:A:173:GLN:N	2.27	0.68
1:B:125:ASP:O	1:B:126:MET:HB2	1.92	0.68
1:D:49:ASN:C	1:D:49:ASN:HD22	2.00	0.68
1:F:125:ASP:O	1:F:126:MET:HB2	1.91	0.68
1:F:248:GLU:CG	1:G:227:ILE:HG23	2.23	0.68
1:G:71:ILE:CB	1:G:74:ILE:HD11	2.23	0.68
1:L:71:ILE:CB	1:L:74:ILE:HD11	2.23	0.68
1:B:107:TYR:HB3	1:B:267:LYS:HD3	1.76	0.68
1:C:107:TYR:HB3	1:C:267:LYS:HD3	1.75	0.68
1:H:57:ILE:CG2	1:H:123:ASN:HB2	2.23	0.68
1:H:125:ASP:O	1:H:126:MET:HB2	1.94	0.68
1:K:201:THR:HG23	1:L:159:VAL:CG1	2.19	0.68
1:G:16:GLN:O	1:G:20:ARG:HG3	1.94	0.68
1:G:107:TYR:HB3	1:G:267:LYS:HD3	1.76	0.68
1:H:66:TYR:HB2	1:H:104:PHE:CZ	2.28	0.68
1:J:126:MET:O	1:J:128:PHE:N	2.24	0.68
1:J:274:LEU:O	1:J:274:LEU:HD13	1.94	0.68
1:K:171:LEU:O	1:K:173:GLN:N	2.27	0.68
1:B:126:MET:HE1	1:C:36:TYR:CD1	2.29	0.68
1:C:56:SER:HB3	1:C:63:VAL:HG22	1.76	0.68
1:E:125:ASP:O	1:E:126:MET:HB2	1.93	0.68
1:J:57:ILE:CG2	1:J:123:ASN:HB2	2.24	0.68
1:J:66:TYR:HB2	1:J:104:PHE:CZ	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:57:ILE:CG2	1:L:123:ASN:HB2	2.23	0.68
1:C:148:ILE:HG23	1:C:207:VAL:HG13	1.76	0.68
1:D:154:ALA:CB	1:F:182:ALA:HB2	2.24	0.68
1:F:66:TYR:HB2	1:F:104:PHE:CZ	2.29	0.68
1:H:49:ASN:C	1:H:49:ASN:HD22	2.01	0.68
1:H:71:ILE:CB	1:H:74:ILE:HD11	2.24	0.68
1:H:179:GLU:C	1:H:181:ASN:H	2.02	0.67
1:H:201:THR:HG23	1:I:159:VAL:CG1	2.16	0.67
1:I:57:ILE:CG2	1:I:123:ASN:HB2	2.25	0.67
1:K:57:ILE:CG2	1:K:123:ASN:HB2	2.24	0.67
1:L:49:ASN:C	1:L:49:ASN:HD22	2.00	0.67
1:A:179:GLU:C	1:A:181:ASN:H	2.02	0.67
1:E:57:ILE:CG2	1:E:123:ASN:HB2	2.24	0.67
1:E:71:ILE:CB	1:E:74:ILE:HD11	2.23	0.67
1:F:56:SER:HB3	1:F:63:VAL:HG22	1.76	0.67
1:F:107:TYR:HB3	1:F:267:LYS:HD3	1.75	0.67
1:J:171:LEU:O	1:J:173:GLN:N	2.26	0.67
1:A:176:ASN:ND2	1:L:11:SER:HB3	2.08	0.67
1:H:171:LEU:C	1:H:173:GLN:N	2.53	0.67
1:I:107:TYR:HB3	1:I:267:LYS:HD3	1.76	0.67
1:J:179:GLU:C	1:J:181:ASN:H	2.02	0.67
1:D:38:LEU:O	1:D:39:PHE:HB2	1.91	0.67
1:K:179:GLU:C	1:K:181:ASN:H	2.03	0.67
1:L:179:GLU:C	1:L:181:ASN:H	2.01	0.67
1:A:207:VAL:HG11	1:L:213:GLN:HG3	1.77	0.67
1:D:66:TYR:HB2	1:D:104:PHE:CZ	2.30	0.67
1:G:57:ILE:CG2	1:G:123:ASN:HB2	2.24	0.67
1:G:66:TYR:HB2	1:G:104:PHE:CZ	2.29	0.67
1:G:179:GLU:C	1:G:181:ASN:H	2.03	0.67
1:L:179:GLU:O	1:L:181:ASN:OD1	2.13	0.67
1:B:16:GLN:O	1:B:20:ARG:HG3	1.94	0.67
1:D:107:TYR:HB3	1:D:267:LYS:HD3	1.75	0.67
1:K:125:ASP:O	1:K:126:MET:HB2	1.93	0.67
1:K:201:THR:CG2	1:L:159:VAL:HG11	2.20	0.67
1:B:163:ALA:HB3	1:C:187:ALA:CB	2.21	0.67
1:B:179:GLU:C	1:B:181:ASN:H	2.02	0.67
1:D:57:ILE:CG2	1:D:123:ASN:HB2	2.24	0.67
1:E:107:TYR:HB3	1:E:267:LYS:HD3	1.77	0.67
1:L:125:ASP:O	1:L:126:MET:HB2	1.92	0.67
1:A:163:ALA:HB3	1:B:187:ALA:CB	2.24	0.67
1:D:222:MET:HE3	1:D:227:ILE:CG2	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:144:LEU:HD21	1:J:152:GLN:NE2	2.10	0.67
1:B:57:ILE:CG2	1:B:123:ASN:HB2	2.25	0.67
1:C:179:GLU:O	1:C:181:ASN:N	2.28	0.67
1:E:179:GLU:C	1:E:181:ASN:H	2.02	0.67
1:J:125:ASP:O	1:J:126:MET:HB2	1.93	0.67
1:F:144:LEU:HD21	1:G:152:GLN:NE2	2.09	0.66
1:I:66:TYR:HB2	1:I:104:PHE:CZ	2.29	0.66
1:J:107:TYR:HB3	1:J:267:LYS:HD3	1.77	0.66
1:J:117:MET:HG3	1:J:118:GLY:N	2.10	0.66
1:A:187:ALA:CB	1:L:163:ALA:HB3	2.25	0.66
1:D:62:TYR:HE2	1:D:79:ALA:HA	1.61	0.66
1:D:179:GLU:O	1:D:181:ASN:OD1	2.13	0.66
1:B:66:TYR:HB2	1:B:104:PHE:CZ	2.29	0.66
1:F:16:GLN:O	1:F:20:ARG:HG3	1.95	0.66
1:G:117:MET:HG3	1:G:118:GLY:N	2.10	0.66
1:A:152:GLN:NE2	1:L:144:LEU:HD21	2.11	0.66
1:C:11:SER:HB3	1:D:176:ASN:HD22	1.61	0.66
1:K:49:ASN:C	1:K:49:ASN:HD22	2.01	0.66
1:A:56:SER:HB3	1:A:63:VAL:HG22	1.77	0.66
1:B:62:TYR:HE2	1:B:79:ALA:HA	1.61	0.66
1:E:179:GLU:O	1:E:181:ASN:OD1	2.13	0.66
1:I:126:MET:O	1:I:128:PHE:N	2.28	0.66
1:K:107:TYR:HB3	1:K:267:LYS:HD3	1.76	0.66
1:A:66:TYR:HB2	1:A:104:PHE:CZ	2.30	0.66
1:B:154:ALA:CA	1:D:182:ALA:HB2	2.25	0.66
1:F:49:ASN:C	1:F:49:ASN:HD22	2.03	0.66
1:H:16:GLN:O	1:H:20:ARG:HG3	1.95	0.66
1:I:179:GLU:O	1:I:181:ASN:OD1	2.14	0.66
1:A:179:GLU:O	1:A:181:ASN:N	2.29	0.66
1:L:107:TYR:HB3	1:L:267:LYS:HD3	1.76	0.66
1:A:117:MET:HG3	1:A:118:GLY:N	2.11	0.66
1:F:71:ILE:CB	1:F:74:ILE:HD11	2.25	0.66
1:C:16:GLN:O	1:C:20:ARG:HG3	1.96	0.66
1:C:49:ASN:C	1:C:49:ASN:HD22	2.02	0.66
1:E:201:THR:HG23	1:F:159:VAL:CG1	2.22	0.66
1:H:179:GLU:O	1:H:181:ASN:N	2.29	0.66
1:K:16:GLN:O	1:K:20:ARG:HG3	1.95	0.66
1:K:151:ASN:HD22	1:K:207:VAL:HG23	1.61	0.66
1:L:66:TYR:HB2	1:L:104:PHE:CZ	2.30	0.66
1:C:179:GLU:O	1:C:181:ASN:OD1	2.14	0.66
1:I:179:GLU:C	1:I:181:ASN:H	2.03	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:16:GLN:O	1:D:20:ARG:HG3	1.96	0.65
1:J:154:ALA:HA	1:L:182:ALA:HB2	1.78	0.65
1:A:16:GLN:O	1:A:20:ARG:HG3	1.95	0.65
1:E:49:ASN:HD22	1:E:49:ASN:C	2.03	0.65
1:E:213:GLN:HG3	1:F:207:VAL:HG11	1.79	0.65
1:I:16:GLN:O	1:I:20:ARG:HG3	1.97	0.65
1:I:71:ILE:CB	1:I:74:ILE:HD11	2.25	0.65
1:I:277:LYS:CD	1:I:278:VAL:H	2.10	0.65
1:J:56:SER:HB3	1:J:63:VAL:HG22	1.78	0.65
1:B:151:ASN:HD22	1:B:207:VAL:HG23	1.62	0.65
1:A:107:TYR:HB3	1:A:267:LYS:HD3	1.77	0.65
1:G:56:SER:HB3	1:G:63:VAL:HG22	1.79	0.65
1:G:179:GLU:O	1:G:181:ASN:OD1	2.14	0.65
1:I:158:PRO:O	1:I:159:VAL:HB	1.96	0.65
1:I:171:LEU:C	1:I:173:GLN:N	2.54	0.65
1:E:16:GLN:O	1:E:20:ARG:HG3	1.96	0.65
1:E:117:MET:HG3	1:E:118:GLY:N	2.11	0.65
1:B:71:ILE:CB	1:B:74:ILE:HD11	2.24	0.65
1:B:274:LEU:O	1:B:274:LEU:HD13	1.96	0.65
1:E:179:GLU:O	1:E:181:ASN:N	2.30	0.65
1:H:107:TYR:HB3	1:H:267:LYS:HD3	1.76	0.65
1:H:126:MET:O	1:H:128:PHE:N	2.29	0.65
1:K:163:ALA:HB3	1:L:187:ALA:CB	2.24	0.65
1:B:171:LEU:C	1:B:173:GLN:N	2.53	0.65
1:B:179:GLU:O	1:B:181:ASN:OD1	2.15	0.65
1:D:179:GLU:O	1:D:181:ASN:N	2.28	0.65
1:J:179:GLU:O	1:J:181:ASN:OD1	2.15	0.65
1:B:56:SER:HB3	1:B:63:VAL:HG22	1.77	0.65
1:E:151:ASN:HD22	1:E:207:VAL:HG23	1.61	0.65
1:J:16:GLN:O	1:J:20:ARG:HG3	1.97	0.65
1:K:56:SER:HB3	1:K:63:VAL:HG22	1.79	0.65
1:D:182:ALA:H	1:D:183:PRO:CD	2.10	0.65
1:K:71:ILE:CB	1:K:74:ILE:HD11	2.25	0.65
1:K:277:LYS:CD	1:K:278:VAL:H	2.10	0.65
1:C:182:ALA:H	1:C:183:PRO:CD	2.10	0.64
1:D:117:MET:HG3	1:D:118:GLY:N	2.11	0.64
1:D:277:LYS:CD	1:D:278:VAL:H	2.10	0.64
1:E:171:LEU:C	1:E:173:GLN:N	2.54	0.64
1:H:179:GLU:O	1:H:181:ASN:OD1	2.15	0.64
1:E:182:ALA:H	1:E:183:PRO:CD	2.10	0.64
1:E:277:LYS:CD	1:E:278:VAL:H	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:62:TYR:HE2	1:H:79:ALA:HA	1.61	0.64
1:I:182:ALA:H	1:I:183:PRO:CD	2.10	0.64
1:J:151:ASN:HD22	1:J:207:VAL:HG23	1.62	0.64
1:J:171:LEU:C	1:J:173:GLN:N	2.54	0.64
1:C:39:PHE:HA	1:C:280:PHE:O	1.98	0.64
1:L:16:GLN:O	1:L:20:ARG:HG3	1.97	0.64
1:L:277:LYS:CD	1:L:278:VAL:H	2.10	0.64
1:B:179:GLU:O	1:B:181:ASN:N	2.30	0.64
1:D:151:ASN:HD22	1:D:207:VAL:HG23	1.63	0.64
1:E:62:TYR:HE2	1:E:79:ALA:HA	1.62	0.64
1:F:151:ASN:HD22	1:F:207:VAL:HG23	1.62	0.64
1:F:179:GLU:O	1:F:181:ASN:N	2.31	0.64
1:G:179:GLU:O	1:G:181:ASN:N	2.31	0.64
1:I:56:SER:HB3	1:I:63:VAL:HG22	1.78	0.64
1:A:151:ASN:HD22	1:A:207:VAL:HG23	1.62	0.64
1:A:179:GLU:O	1:A:181:ASN:OD1	2.15	0.64
1:D:171:LEU:C	1:D:173:GLN:N	2.53	0.64
1:F:123:ASN:O	1:F:124:ASN:CG	2.41	0.64
1:G:62:TYR:HE2	1:G:79:ALA:HA	1.63	0.64
1:F:150:VAL:HG13	1:H:180:GLY:HA2	1.79	0.64
1:G:123:ASN:O	1:G:124:ASN:CG	2.41	0.64
1:H:144:LEU:HD21	1:I:152:GLN:NE2	2.12	0.64
1:K:62:TYR:HE2	1:K:79:ALA:HA	1.62	0.64
1:K:158:PRO:O	1:K:159:VAL:HB	1.97	0.64
1:B:158:PRO:O	1:B:159:VAL:HB	1.98	0.64
1:B:277:LYS:CD	1:B:278:VAL:H	2.11	0.64
1:C:154:ALA:CA	1:E:182:ALA:HB2	2.27	0.64
1:H:56:SER:HB3	1:H:63:VAL:HG22	1.79	0.64
1:I:123:ASN:O	1:I:124:ASN:CG	2.40	0.64
1:L:179:GLU:O	1:L:181:ASN:N	2.29	0.64
1:F:117:MET:HG3	1:F:118:GLY:N	2.13	0.64
1:F:179:GLU:O	1:F:181:ASN:OD1	2.15	0.64
1:I:11:SER:HB3	1:J:176:ASN:HD22	1.63	0.64
1:I:277:LYS:CD	1:I:278:VAL:N	2.62	0.63
1:K:117:MET:HG3	1:K:118:GLY:N	2.11	0.63
1:L:123:ASN:O	1:L:124:ASN:CG	2.40	0.63
1:F:62:TYR:HE2	1:F:79:ALA:HA	1.63	0.63
1:G:38:LEU:O	1:G:39:PHE:HB2	1.98	0.63
1:G:277:LYS:CD	1:G:278:VAL:H	2.11	0.63
1:I:179:GLU:O	1:I:181:ASN:N	2.31	0.63
1:J:62:TYR:HE2	1:J:79:ALA:HA	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:62:TYR:HE2	1:L:79:ALA:HA	1.63	0.63
1:C:117:MET:HG3	1:C:118:GLY:N	2.14	0.63
1:H:182:ALA:H	1:H:183:PRO:CD	2.10	0.63
1:K:213:GLN:HG3	1:L:207:VAL:HG11	1.79	0.63
1:A:62:TYR:HE2	1:A:79:ALA:HA	1.62	0.63
1:G:222:MET:HE3	1:G:227:ILE:CG2	2.28	0.63
1:K:144:LEU:HD21	1:L:152:GLN:NE2	2.12	0.63
1:E:126:MET:O	1:E:128:PHE:N	2.31	0.63
1:E:154:ALA:HA	1:G:182:ALA:HB2	1.79	0.63
1:F:182:ALA:H	1:F:183:PRO:CD	2.11	0.63
1:J:179:GLU:O	1:J:181:ASN:N	2.31	0.63
1:D:248:GLU:HB3	1:E:282:TYR:CZ	2.34	0.63
1:F:277:LYS:CD	1:F:278:VAL:H	2.11	0.63
1:I:62:TYR:HE2	1:I:79:ALA:HA	1.63	0.63
1:C:123:ASN:O	1:C:124:ASN:CG	2.42	0.63
1:F:277:LYS:CD	1:F:278:VAL:N	2.62	0.63
1:F:171:LEU:C	1:F:173:GLN:N	2.53	0.63
1:L:182:ALA:H	1:L:183:PRO:CD	2.11	0.63
1:A:158:PRO:O	1:A:159:VAL:HB	1.97	0.63
1:E:56:SER:HB3	1:E:63:VAL:HG22	1.79	0.63
1:H:57:ILE:HG22	1:H:123:ASN:HB2	1.81	0.63
1:I:213:GLN:HG3	1:J:207:VAL:HG11	1.81	0.63
1:I:274:LEU:HD13	1:I:274:LEU:O	1.98	0.63
1:A:274:LEU:HD13	1:A:274:LEU:O	1.98	0.62
1:D:213:GLN:HG3	1:E:207:VAL:CG1	2.29	0.62
1:I:126:MET:HE1	1:J:36:TYR:HE1	1.63	0.62
1:E:274:LEU:O	1:E:274:LEU:HD13	1.99	0.62
1:G:277:LYS:CD	1:G:278:VAL:N	2.62	0.62
1:C:277:LYS:CD	1:C:278:VAL:H	2.11	0.62
1:G:274:LEU:O	1:G:274:LEU:HD13	1.99	0.62
1:H:277:LYS:CD	1:H:278:VAL:H	2.12	0.62
1:C:57:ILE:HG22	1:C:123:ASN:HB2	1.80	0.62
1:D:123:ASN:O	1:D:124:ASN:CG	2.43	0.62
1:F:93:PHE:HB3	1:F:104:PHE:CG	2.35	0.62
1:F:213:GLN:HG3	1:G:207:VAL:HG11	1.80	0.62
1:H:117:MET:HG3	1:H:118:GLY:N	2.13	0.62
1:L:277:LYS:CD	1:L:278:VAL:N	2.62	0.62
1:D:274:LEU:O	1:D:274:LEU:HD13	2.00	0.62
1:E:123:ASN:O	1:E:124:ASN:CG	2.43	0.62
1:K:87:TYR:CD2	1:L:49:ASN:HB2	2.34	0.62
1:K:123:ASN:ND2	1:K:261:ARG:NH2	2.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:179:GLU:O	1:K:181:ASN:N	2.31	0.62
1:K:277:LYS:CD	1:K:278:VAL:N	2.62	0.62
1:G:151:ASN:HD22	1:G:207:VAL:HG23	1.64	0.62
1:K:123:ASN:O	1:K:124:ASN:CG	2.41	0.62
1:K:171:LEU:C	1:K:173:GLN:N	2.54	0.62
1:L:151:ASN:HD22	1:L:207:VAL:HG23	1.64	0.62
1:A:171:LEU:C	1:A:173:GLN:N	2.55	0.62
1:C:151:ASN:HD22	1:C:207:VAL:HG23	1.64	0.62
1:C:277:LYS:CD	1:C:278:VAL:N	2.62	0.62
1:H:274:LEU:O	1:H:274:LEU:HD13	1.99	0.62
1:L:117:MET:HG3	1:L:118:GLY:N	2.13	0.62
1:A:123:ASN:O	1:A:124:ASN:CG	2.42	0.62
1:A:182:ALA:H	1:A:183:PRO:CD	2.12	0.62
1:C:125:ASP:O	1:C:126:MET:HE3	2.00	0.62
1:B:182:ALA:H	1:B:183:PRO:CD	2.12	0.62
1:I:57:ILE:HG22	1:I:123:ASN:HB2	1.82	0.62
1:K:179:GLU:O	1:K:181:ASN:OD1	2.18	0.62
1:K:182:ALA:H	1:K:183:PRO:CD	2.12	0.62
1:D:56:SER:HB3	1:D:63:VAL:HG22	1.81	0.62
1:D:277:LYS:CD	1:D:278:VAL:N	2.62	0.62
1:H:37:GLN:O	1:H:281:ARG:HD2	1.99	0.62
1:I:37:GLN:O	1:I:281:ARG:HD2	2.00	0.62
1:E:93:PHE:HB3	1:E:104:PHE:CG	2.35	0.61
1:F:158:PRO:O	1:F:159:VAL:HB	2.00	0.61
1:B:125:ASP:O	1:B:126:MET:HE3	2.00	0.61
1:C:213:GLN:HG3	1:D:207:VAL:HG11	1.82	0.61
1:D:123:ASN:ND2	1:D:261:ARG:NH2	2.48	0.61
1:F:39:PHE:HA	1:F:280:PHE:O	2.00	0.61
1:G:158:PRO:O	1:G:159:VAL:HB	2.00	0.61
1:J:182:ALA:H	1:J:183:PRO:CD	2.12	0.61
1:J:277:LYS:CD	1:J:278:VAL:H	2.13	0.61
1:B:117:MET:HG3	1:B:118:GLY:N	2.12	0.61
1:C:62:TYR:HE2	1:C:79:ALA:HA	1.65	0.61
1:D:158:PRO:O	1:D:159:VAL:HB	1.99	0.61
1:C:274:LEU:O	1:C:274:LEU:HD13	2.00	0.61
1:H:277:LYS:CD	1:H:278:VAL:N	2.64	0.61
1:J:115:GLU:O	1:J:116:ASP:HB3	2.00	0.61
1:A:277:LYS:CD	1:A:278:VAL:H	2.13	0.61
1:E:123:ASN:ND2	1:E:261:ARG:NH2	2.48	0.61
1:G:93:PHE:HB3	1:G:104:PHE:CG	2.36	0.61
1:H:123:ASN:O	1:H:124:ASN:CG	2.43	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:201:THR:HG23	1:J:159:VAL:CG1	2.20	0.61
1:K:274:LEU:O	1:K:274:LEU:HD13	2.00	0.61
1:A:93:PHE:HB3	1:A:104:PHE:CG	2.35	0.61
1:C:106:LEU:HD22	1:C:120:VAL:HG23	1.83	0.61
1:F:57:ILE:HG22	1:F:123:ASN:HB2	1.80	0.61
1:E:144:LEU:HD21	1:F:152:GLN:NE2	2.15	0.61
1:E:277:LYS:CD	1:E:278:VAL:N	2.62	0.61
1:H:93:PHE:HB3	1:H:104:PHE:CG	2.36	0.61
1:H:168:GLN:NE2	1:H:169:LEU:HG	2.15	0.61
1:H:213:GLN:HG3	1:I:207:VAL:HG11	1.81	0.61
1:J:123:ASN:ND2	1:J:261:ARG:NH2	2.48	0.61
1:K:168:GLN:NE2	1:K:169:LEU:HG	2.16	0.61
1:L:56:SER:HB3	1:L:63:VAL:HG22	1.81	0.61
1:A:277:LYS:CD	1:A:278:VAL:N	2.64	0.61
1:E:12:ILE:HG21	1:E:15:ILE:HB	1.83	0.61
1:D:125:ASP:O	1:D:126:MET:HE3	2.01	0.61
1:H:115:GLU:O	1:H:116:ASP:HB3	2.01	0.61
1:H:158:PRO:O	1:H:159:VAL:HB	2.00	0.61
1:I:93:PHE:HB3	1:I:104:PHE:CG	2.36	0.61
1:J:168:GLN:NE2	1:J:169:LEU:HG	2.16	0.61
1:K:222:MET:HE3	1:K:227:ILE:CG2	2.30	0.61
1:B:123:ASN:O	1:B:124:ASN:CG	2.44	0.61
1:B:277:LYS:CD	1:B:278:VAL:N	2.63	0.61
1:C:158:PRO:O	1:C:159:VAL:HB	2.01	0.61
1:B:12:ILE:HG21	1:B:15:ILE:HB	1.83	0.60
1:H:12:ILE:HG21	1:H:15:ILE:HB	1.83	0.60
1:H:154:ALA:HA	1:J:182:ALA:HB2	1.83	0.60
1:J:222:MET:HE3	1:J:227:ILE:CG2	2.31	0.60
1:B:213:GLN:HG3	1:C:207:VAL:HG11	1.82	0.60
1:D:12:ILE:HG21	1:D:15:ILE:HB	1.84	0.60
1:E:125:ASP:O	1:E:126:MET:HE3	2.01	0.60
1:G:123:ASN:ND2	1:G:261:ARG:NH2	2.48	0.60
1:G:126:MET:HE1	1:H:36:TYR:CE1	2.36	0.60
1:I:117:MET:HG3	1:I:118:GLY:N	2.16	0.60
1:I:151:ASN:HD21	1:I:206:VAL:H	1.49	0.60
1:K:12:ILE:HG21	1:K:15:ILE:HB	1.83	0.60
1:C:125:ASP:O	1:C:126:MET:CB	2.49	0.60
1:G:182:ALA:H	1:G:183:PRO:CD	2.14	0.60
1:J:123:ASN:O	1:J:124:ASN:CG	2.44	0.60
1:A:37:GLN:O	1:A:281:ARG:HD2	2.00	0.60
1:D:125:ASP:O	1:D:126:MET:CB	2.50	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:168:GLN:NE2	1:D:169:LEU:HG	2.16	0.60
1:F:125:ASP:O	1:F:126:MET:HE3	2.01	0.60
1:F:168:GLN:NE2	1:F:169:LEU:HG	2.16	0.60
1:F:12:ILE:HG21	1:F:15:ILE:HB	1.84	0.60
1:H:151:ASN:HD22	1:H:207:VAL:HG23	1.66	0.60
1:J:144:LEU:HD21	1:K:152:GLN:NE2	2.17	0.60
1:L:124:ASN:HD21	1:L:128:PHE:HB2	1.65	0.60
1:A:115:GLU:O	1:A:116:ASP:HB3	2.01	0.60
1:A:144:LEU:HD21	1:B:152:GLN:NE2	2.16	0.60
1:B:123:ASN:ND2	1:B:261:ARG:NH2	2.50	0.60
1:C:168:GLN:NE2	1:C:169:LEU:HG	2.16	0.60
1:E:150:VAL:HG13	1:G:180:GLY:HA2	1.83	0.60
1:H:123:ASN:ND2	1:H:261:ARG:NH2	2.49	0.60
1:K:123:ASN:ND2	1:K:257:PHE:HD2	1.89	0.60
1:L:57:ILE:HG22	1:L:123:ASN:HB2	1.82	0.60
1:B:178:TYR:C	1:B:180:GLY:H	2.10	0.60
1:C:151:ASN:HD21	1:C:206:VAL:H	1.50	0.60
1:C:154:ALA:CB	1:E:182:ALA:HB2	2.32	0.60
1:L:168:GLN:NE2	1:L:169:LEU:HG	2.17	0.60
1:D:93:PHE:HB3	1:D:104:PHE:CG	2.37	0.60
1:G:12:ILE:HG21	1:G:15:ILE:HB	1.84	0.60
1:G:154:ALA:CA	1:I:182:ALA:HB2	2.32	0.60
1:J:277:LYS:CD	1:J:278:VAL:N	2.65	0.60
1:L:60:PHE:HA	1:L:129:PRO:HG3	1.83	0.60
1:A:36:TYR:HE1	1:L:126:MET:HE1	1.66	0.60
1:A:57:ILE:HG22	1:A:123:ASN:HB2	1.84	0.60
1:G:106:LEU:HD22	1:G:120:VAL:HG23	1.84	0.60
1:G:115:GLU:O	1:G:116:ASP:HB3	2.02	0.60
1:J:178:TYR:C	1:J:180:GLY:H	2.10	0.60
1:E:57:ILE:HG22	1:E:123:ASN:HB2	1.84	0.60
1:H:126:MET:HE1	1:I:36:TYR:HE1	1.66	0.60
1:I:123:ASN:ND2	1:I:261:ARG:NH2	2.48	0.60
1:I:125:ASP:O	1:I:126:MET:CB	2.49	0.60
1:K:125:ASP:O	1:K:126:MET:HE3	2.02	0.60
1:L:37:GLN:O	1:L:281:ARG:HD2	2.01	0.60
1:D:57:ILE:HG22	1:D:123:ASN:HB2	1.82	0.59
1:F:249:GLN:HB3	1:G:222:MET:HE2	1.84	0.59
1:L:274:LEU:O	1:L:274:LEU:HD13	2.01	0.59
1:B:115:GLU:O	1:B:116:ASP:HB3	2.02	0.59
1:C:201:THR:HG23	1:D:159:VAL:CG1	2.20	0.59
1:H:39:PHE:HA	1:H:280:PHE:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:178:TYR:C	1:H:180:GLY:H	2.09	0.59
1:J:60:PHE:HD1	1:J:60:PHE:O	1.85	0.59
1:A:12:ILE:HG21	1:A:15:ILE:HB	1.84	0.59
1:C:209:LYS:HD3	1:D:205:TYR:CE2	2.36	0.59
1:H:125:ASP:O	1:H:126:MET:HE3	2.00	0.59
1:L:12:ILE:HG21	1:L:15:ILE:HB	1.84	0.59
1:A:125:ASP:O	1:A:126:MET:HE3	2.03	0.59
1:B:106:LEU:HD22	1:B:120:VAL:HG23	1.84	0.59
1:F:151:ASN:HD21	1:F:206:VAL:H	1.49	0.59
1:J:158:PRO:O	1:J:159:VAL:HB	2.01	0.59
1:K:126:MET:O	1:K:128:PHE:N	2.31	0.59
1:A:182:ALA:HB2	1:K:154:ALA:CA	2.32	0.59
1:A:213:GLN:HG3	1:B:207:VAL:CG1	2.32	0.59
1:C:93:PHE:HB3	1:C:104:PHE:CG	2.37	0.59
1:G:154:ALA:CB	1:I:182:ALA:HB2	2.32	0.59
1:I:168:GLN:NE2	1:I:169:LEU:HG	2.17	0.59
1:C:12:ILE:HG21	1:C:15:ILE:HB	1.84	0.59
1:C:115:GLU:O	1:C:116:ASP:HB3	2.02	0.59
1:D:201:THR:HG23	1:E:159:VAL:CG1	2.28	0.59
1:E:201:THR:O	1:E:201:THR:CG2	2.49	0.59
1:F:248:GLU:CD	1:G:227:ILE:HA	2.27	0.59
1:I:151:ASN:HD22	1:I:207:VAL:HG23	1.66	0.59
1:J:117:MET:HB2	1:J:271:LEU:CD1	2.33	0.59
1:K:115:GLU:O	1:K:116:ASP:HB3	2.01	0.59
1:L:125:ASP:O	1:L:126:MET:CB	2.50	0.59
1:F:125:ASP:O	1:F:126:MET:CB	2.49	0.59
1:J:57:ILE:CG1	1:J:63:VAL:HG21	2.33	0.59
1:L:125:ASP:O	1:L:126:MET:HE3	2.02	0.59
1:A:106:LEU:HD22	1:A:120:VAL:HG23	1.83	0.59
1:B:93:PHE:HB3	1:B:104:PHE:CG	2.37	0.59
1:D:178:TYR:C	1:D:180:GLY:H	2.09	0.59
1:E:115:GLU:O	1:E:116:ASP:HB3	2.00	0.59
1:E:158:PRO:O	1:E:159:VAL:HB	2.02	0.59
1:I:115:GLU:O	1:I:116:ASP:HB3	2.03	0.59
1:L:178:TYR:C	1:L:180:GLY:H	2.11	0.59
1:B:151:ASN:HD21	1:B:206:VAL:H	1.49	0.59
1:B:168:GLN:NE2	1:B:169:LEU:HG	2.18	0.59
1:C:248:GLU:CG	1:D:227:ILE:CG2	2.76	0.59
1:E:168:GLN:NE2	1:E:169:LEU:HG	2.18	0.59
1:E:201:THR:CG2	1:F:159:VAL:HG11	2.24	0.59
1:F:117:MET:CG	1:F:118:GLY:H	2.13	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:274:LEU:HD13	1:F:274:LEU:O	2.02	0.59
1:G:168:GLN:NE2	1:G:169:LEU:HG	2.18	0.59
1:J:43:ASN:O	1:J:44:LEU:HB3	2.03	0.59
1:L:93:PHE:HB3	1:L:104:PHE:CG	2.37	0.59
1:A:168:GLN:NE2	1:A:169:LEU:HG	2.17	0.59
1:C:110:ARG:HB3	1:D:47:THR:HG22	1.84	0.59
1:F:106:LEU:HD22	1:F:120:VAL:HG23	1.84	0.59
1:G:57:ILE:HG22	1:G:123:ASN:HB2	1.83	0.59
1:K:93:PHE:HB3	1:K:104:PHE:CG	2.38	0.59
1:A:43:ASN:O	1:A:44:LEU:HB3	2.01	0.58
1:C:182:ALA:N	1:C:183:PRO:HD3	2.18	0.58
1:D:117:MET:HB2	1:D:271:LEU:CD1	2.33	0.58
1:B:117:MET:HB2	1:B:271:LEU:CD1	2.33	0.58
1:F:115:GLU:O	1:F:116:ASP:HB3	2.02	0.58
1:L:39:PHE:HA	1:L:280:PHE:O	2.03	0.58
1:A:125:ASP:O	1:A:126:MET:CB	2.50	0.58
1:A:222:MET:HE3	1:A:227:ILE:CG2	2.32	0.58
1:E:37:GLN:O	1:E:281:ARG:HD2	2.03	0.58
1:E:178:TYR:C	1:E:180:GLY:H	2.10	0.58
1:G:87:TYR:OH	1:H:47:THR:O	2.07	0.58
1:G:125:ASP:O	1:G:126:MET:HE3	2.03	0.58
1:H:106:LEU:HD22	1:H:120:VAL:HG23	1.85	0.58
1:J:125:ASP:O	1:J:126:MET:CB	2.50	0.58
1:K:117:MET:HB2	1:K:271:LEU:CD1	2.33	0.58
1:K:182:ALA:N	1:K:183:PRO:HD3	2.19	0.58
1:L:115:GLU:O	1:L:116:ASP:HB3	2.02	0.58
1:L:158:PRO:O	1:L:159:VAL:HB	2.02	0.58
1:C:85:ASP:OD1	1:C:86:VAL:N	2.37	0.58
1:D:115:GLU:O	1:D:116:ASP:HB3	2.02	0.58
1:D:248:GLU:HB3	1:E:282:TYR:CE2	2.39	0.58
1:G:178:TYR:C	1:G:180:GLY:H	2.11	0.58
1:J:12:ILE:HG21	1:J:15:ILE:HB	1.83	0.58
1:L:123:ASN:ND2	1:L:257:PHE:HD2	1.90	0.58
1:B:57:ILE:HG22	1:B:123:ASN:HB2	1.86	0.58
1:D:106:LEU:HD22	1:D:120:VAL:HG23	1.85	0.58
1:E:117:MET:HB2	1:E:271:LEU:CD1	2.34	0.58
1:H:126:MET:HE1	1:I:36:TYR:CE1	2.38	0.58
1:I:39:PHE:HA	1:I:280:PHE:O	2.03	0.58
1:I:178:TYR:C	1:I:180:GLY:H	2.11	0.58
1:J:154:ALA:CB	1:L:182:ALA:HB2	2.34	0.58
1:C:201:THR:O	1:C:201:THR:CG2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:ILE:CG1	1:D:63:VAL:HG21	2.33	0.58
1:G:126:MET:O	1:G:128:PHE:N	2.36	0.58
1:H:60:PHE:HA	1:H:129:PRO:HG3	1.86	0.58
1:H:201:THR:O	1:H:201:THR:CG2	2.50	0.58
1:J:93:PHE:HB3	1:J:104:PHE:CG	2.38	0.58
1:K:178:TYR:C	1:K:180:GLY:H	2.11	0.58
1:L:151:ASN:HD21	1:L:206:VAL:H	1.51	0.58
1:L:222:MET:HE3	1:L:227:ILE:CG2	2.34	0.58
1:C:222:MET:HE3	1:C:227:ILE:CG2	2.33	0.58
1:K:151:ASN:HD21	1:K:206:VAL:H	1.52	0.58
1:B:126:MET:HE1	1:C:36:TYR:HE1	1.66	0.58
1:F:154:ALA:HA	1:H:182:ALA:HB2	1.85	0.58
1:C:278:VAL:HG12	1:C:279:LYS:N	2.19	0.58
1:F:60:PHE:O	1:F:61:GLY:C	2.47	0.58
1:F:213:GLN:HG3	1:G:207:VAL:CG1	2.33	0.58
1:G:213:GLN:HG3	1:H:207:VAL:CG1	2.32	0.58
1:I:182:ALA:N	1:I:183:PRO:HD3	2.19	0.58
1:L:117:MET:CG	1:L:118:GLY:H	2.13	0.58
1:A:178:TYR:C	1:A:180:GLY:H	2.12	0.58
1:B:154:ALA:CB	1:D:182:ALA:HB2	2.33	0.58
1:F:123:ASN:ND2	1:F:257:PHE:HD2	1.91	0.58
1:I:12:ILE:HG21	1:I:15:ILE:HB	1.84	0.58
1:A:49:ASN:C	1:A:49:ASN:ND2	2.62	0.57
1:B:126:MET:O	1:B:128:PHE:N	2.35	0.57
1:D:107:TYR:CB	1:D:267:LYS:HD3	2.34	0.57
1:I:117:MET:HB2	1:I:271:LEU:CD1	2.33	0.57
1:L:117:MET:HB2	1:L:271:LEU:CD1	2.34	0.57
1:A:123:ASN:ND2	1:A:261:ARG:NH2	2.52	0.57
1:B:222:MET:HE3	1:B:227:ILE:CG2	2.33	0.57
1:G:43:ASN:O	1:G:44:LEU:HB3	2.04	0.57
1:L:182:ALA:N	1:L:183:PRO:HD3	2.20	0.57
1:C:86:VAL:HA	1:D:99:VAL:CG1	2.34	0.57
1:C:178:TYR:C	1:C:180:GLY:H	2.11	0.57
1:D:222:MET:CE	1:D:227:ILE:HG21	2.34	0.57
1:E:213:GLN:HG3	1:F:207:VAL:CG1	2.34	0.57
1:G:107:TYR:CB	1:G:267:LYS:HD3	2.34	0.57
1:J:124:ASN:HD21	1:J:128:PHE:HB2	1.70	0.57
1:K:107:TYR:CB	1:K:267:LYS:HD3	2.34	0.57
1:B:125:ASP:O	1:B:126:MET:CB	2.52	0.57
1:B:182:ALA:N	1:B:183:PRO:HD3	2.20	0.57
1:C:57:ILE:CG1	1:C:63:VAL:HG21	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:85:ASP:OD1	1:F:86:VAL:N	2.37	0.57
1:F:123:ASN:ND2	1:F:261:ARG:NH2	2.53	0.57
1:F:182:ALA:N	1:F:183:PRO:HD3	2.19	0.57
1:F:222:MET:HE3	1:F:227:ILE:CG2	2.34	0.57
1:H:117:MET:HB2	1:H:271:LEU:CD1	2.34	0.57
1:I:177:GLN:O	1:I:178:TYR:C	2.46	0.57
1:B:43:ASN:O	1:B:44:LEU:HB3	2.03	0.57
1:C:277:LYS:O	1:C:278:VAL:HB	2.05	0.57
1:E:39:PHE:HA	1:E:280:PHE:O	2.03	0.57
1:E:60:PHE:O	1:E:60:PHE:HD1	1.87	0.57
1:H:11:SER:HB3	1:I:176:ASN:HD22	1.69	0.57
1:J:57:ILE:HG22	1:J:123:ASN:HB2	1.84	0.57
1:K:125:ASP:O	1:K:126:MET:CB	2.52	0.57
1:A:117:MET:HB2	1:A:271:LEU:CD1	2.34	0.57
1:C:107:TYR:CB	1:C:267:LYS:HD3	2.34	0.57
1:E:177:GLN:O	1:E:178:TYR:C	2.48	0.57
1:F:107:TYR:CB	1:F:267:LYS:HD3	2.34	0.57
1:G:151:ASN:HD21	1:G:206:VAL:H	1.53	0.57
1:H:125:ASP:O	1:H:126:MET:CB	2.52	0.57
1:J:213:GLN:HG3	1:K:207:VAL:CG1	2.34	0.57
1:K:177:GLN:O	1:K:178:TYR:C	2.47	0.57
1:A:151:ASN:HD21	1:A:206:VAL:H	1.52	0.57
1:B:277:LYS:O	1:B:278:VAL:HB	2.05	0.57
1:C:117:MET:CG	1:C:118:GLY:H	2.13	0.57
1:C:117:MET:HB2	1:C:271:LEU:CD1	2.35	0.57
1:D:115:GLU:CD	1:D:116:ASP:H	2.11	0.57
1:E:106:LEU:HD22	1:E:120:VAL:HG23	1.85	0.57
1:F:112:MET:O	1:F:113:LYS:HB2	2.05	0.57
1:F:117:MET:HB2	1:F:271:LEU:CD1	2.34	0.57
1:G:150:VAL:HG13	1:I:180:GLY:HA2	1.86	0.57
1:I:125:ASP:O	1:I:126:MET:HE3	2.05	0.57
1:K:278:VAL:HG12	1:K:279:LYS:N	2.19	0.57
1:L:171:LEU:C	1:L:173:GLN:N	2.55	0.57
1:A:154:ALA:CB	1:C:182:ALA:HB2	2.35	0.57
1:B:182:ALA:HB2	1:L:154:ALA:CA	2.34	0.57
1:C:177:GLN:O	1:C:178:TYR:C	2.47	0.57
1:C:201:THR:CG2	1:D:159:VAL:HG11	2.21	0.57
1:D:37:GLN:O	1:D:281:ARG:HD2	2.04	0.57
1:E:125:ASP:O	1:E:126:MET:CB	2.52	0.57
1:E:182:ALA:N	1:E:183:PRO:HD3	2.19	0.57
1:G:117:MET:HB2	1:G:271:LEU:CD1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:177:GLN:O	1:G:178:TYR:C	2.48	0.57
1:L:177:GLN:O	1:L:178:TYR:C	2.48	0.57
1:C:249:GLN:NE2	1:D:222:MET:HG3	2.20	0.57
1:D:182:ALA:N	1:D:183:PRO:HD3	2.19	0.57
1:F:278:VAL:HG12	1:F:279:LYS:N	2.20	0.57
1:B:85:ASP:OD1	1:B:86:VAL:N	2.38	0.57
1:H:182:ALA:N	1:H:183:PRO:HD3	2.19	0.57
1:H:278:VAL:HG12	1:H:279:LYS:N	2.20	0.57
1:I:277:LYS:O	1:I:278:VAL:HB	2.05	0.57
1:L:106:LEU:HD22	1:L:120:VAL:HG23	1.87	0.57
1:C:126:MET:HE2	1:D:55:LYS:NZ	2.20	0.56
1:E:42:GLU:HG3	1:E:279:LYS:HE2	1.87	0.56
1:I:123:ASN:ND2	1:I:257:PHE:HD2	1.92	0.56
1:D:49:ASN:C	1:D:49:ASN:ND2	2.63	0.56
1:F:209:LYS:HD3	1:G:205:TYR:CE2	2.41	0.56
1:H:42:GLU:HG3	1:H:279:LYS:HE2	1.87	0.56
1:J:123:ASN:ND2	1:J:261:ARG:HH21	2.03	0.56
1:J:125:ASP:O	1:J:126:MET:HE3	2.05	0.56
1:K:57:ILE:HG22	1:K:123:ASN:HB2	1.87	0.56
1:L:112:MET:O	1:L:113:LYS:HB2	2.05	0.56
1:A:60:PHE:O	1:A:60:PHE:HD1	1.88	0.56
1:A:207:VAL:CG1	1:L:213:GLN:HG3	2.35	0.56
1:B:60:PHE:HD1	1:B:60:PHE:O	1.88	0.56
1:E:107:TYR:CB	1:E:267:LYS:HD3	2.35	0.56
1:E:151:ASN:HD22	1:E:207:VAL:CG2	2.18	0.56
1:G:125:ASP:O	1:G:126:MET:CB	2.52	0.56
1:H:57:ILE:CG1	1:H:63:VAL:HG21	2.35	0.56
1:I:49:ASN:C	1:I:49:ASN:ND2	2.63	0.56
1:I:106:LEU:HD22	1:I:120:VAL:HG23	1.87	0.56
1:I:278:VAL:HG12	1:I:279:LYS:N	2.19	0.56
1:K:60:PHE:O	1:K:61:GLY:C	2.49	0.56
1:L:43:ASN:O	1:L:44:LEU:HB3	2.06	0.56
1:L:85:ASP:OD1	1:L:86:VAL:N	2.38	0.56
1:L:278:VAL:HG12	1:L:279:LYS:N	2.20	0.56
1:B:182:ALA:HB2	1:L:154:ALA:CB	2.36	0.56
1:E:57:ILE:CG1	1:E:63:VAL:HG21	2.35	0.56
1:H:49:ASN:C	1:H:49:ASN:ND2	2.63	0.56
1:J:49:ASN:C	1:J:49:ASN:ND2	2.63	0.56
1:J:107:TYR:CB	1:J:267:LYS:HD3	2.35	0.56
1:K:201:THR:O	1:K:201:THR:CG2	2.53	0.56
1:L:107:TYR:CB	1:L:267:LYS:HD3	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LYS:O	1:A:278:VAL:HB	2.05	0.56
1:I:151:ASN:ND2	1:I:206:VAL:H	2.03	0.56
1:J:106:LEU:HD22	1:J:120:VAL:HG23	1.87	0.56
1:K:39:PHE:HA	1:K:280:PHE:O	2.05	0.56
1:K:43:ASN:O	1:K:44:LEU:HB3	2.06	0.56
1:L:60:PHE:O	1:L:60:PHE:HD1	1.89	0.56
1:B:107:TYR:CB	1:B:267:LYS:HD3	2.35	0.56
1:B:172:LYS:HG3	1:C:179:GLU:OE1	2.06	0.56
1:C:60:PHE:O	1:C:60:PHE:HD1	1.88	0.56
1:F:57:ILE:CG1	1:F:63:VAL:HG21	2.36	0.56
1:F:151:ASN:ND2	1:F:206:VAL:H	2.03	0.56
1:G:201:THR:O	1:G:201:THR:CG2	2.52	0.56
1:H:60:PHE:O	1:H:60:PHE:HD1	1.87	0.56
1:I:107:TYR:CB	1:I:267:LYS:HD3	2.35	0.56
1:L:49:ASN:C	1:L:49:ASN:ND2	2.63	0.56
1:C:123:ASN:ND2	1:C:261:ARG:NH2	2.53	0.56
1:C:283:ASP:CG	1:C:284:ILE:H	2.14	0.56
1:D:151:ASN:HD21	1:D:206:VAL:H	1.53	0.56
1:E:43:ASN:O	1:E:44:LEU:HB3	2.05	0.56
1:H:85:ASP:OD1	1:H:86:VAL:N	2.39	0.56
1:H:151:ASN:HD21	1:H:206:VAL:H	1.54	0.56
1:L:283:ASP:CG	1:L:284:ILE:H	2.14	0.56
1:A:180:GLY:HA2	1:K:150:VAL:HG13	1.88	0.56
1:D:38:LEU:O	1:D:39:PHE:CB	2.53	0.56
1:F:277:LYS:O	1:F:278:VAL:HB	2.06	0.56
1:G:57:ILE:CG1	1:G:63:VAL:HG21	2.36	0.56
1:H:123:ASN:ND2	1:H:257:PHE:HD2	1.91	0.56
1:H:222:MET:HE3	1:H:227:ILE:CG2	2.35	0.56
1:L:277:LYS:O	1:L:278:VAL:HB	2.06	0.56
1:A:107:TYR:CB	1:A:267:LYS:HD3	2.36	0.56
1:B:115:GLU:CD	1:B:116:ASP:H	2.14	0.56
1:B:117:MET:HB2	1:B:271:LEU:HD13	1.88	0.56
1:C:50:PRO:O	1:C:54:GLU:HG3	2.06	0.56
1:E:278:VAL:HG12	1:E:279:LYS:N	2.21	0.56
1:F:123:ASN:O	1:F:124:ASN:OD1	2.24	0.56
1:G:38:LEU:HD21	1:G:227:ILE:HD11	1.88	0.56
1:G:60:PHE:HD1	1:G:60:PHE:O	1.88	0.56
1:H:277:LYS:O	1:H:278:VAL:HB	2.06	0.56
1:I:222:MET:HE3	1:I:227:ILE:CG2	2.35	0.56
1:K:106:LEU:HD22	1:K:120:VAL:HG23	1.86	0.56
1:A:177:GLN:O	1:A:178:TYR:C	2.47	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ASN:ND2	1:B:206:VAL:H	2.04	0.56
1:B:201:THR:O	1:B:201:THR:CG2	2.53	0.56
1:C:112:MET:O	1:C:113:LYS:HB2	2.05	0.56
1:D:43:ASN:O	1:D:44:LEU:HB3	2.06	0.56
1:F:178:TYR:C	1:F:180:GLY:H	2.12	0.56
1:G:151:ASN:HD22	1:G:207:VAL:CG2	2.19	0.56
1:H:43:ASN:O	1:H:44:LEU:HB3	2.06	0.56
1:I:43:ASN:O	1:I:44:LEU:HB3	2.06	0.56
1:A:182:ALA:N	1:A:183:PRO:HD3	2.20	0.55
1:C:151:ASN:ND2	1:C:206:VAL:H	2.03	0.55
1:D:144:LEU:HD21	1:E:152:GLN:NE2	2.21	0.55
1:E:277:LYS:O	1:E:278:VAL:HB	2.06	0.55
1:J:182:ALA:N	1:J:183:PRO:HD3	2.20	0.55
1:A:39:PHE:HA	1:A:280:PHE:O	2.06	0.55
1:B:42:GLU:HG3	1:B:279:LYS:HE2	1.89	0.55
1:C:186:PHE:CD2	1:C:196:ILE:HD11	2.41	0.55
1:F:43:ASN:O	1:F:44:LEU:HB3	2.05	0.55
1:F:111:ASP:OD1	1:G:71:ILE:HG23	2.07	0.55
1:F:177:GLN:O	1:F:178:TYR:C	2.48	0.55
1:G:111:ASP:O	1:G:112:MET:HE2	2.07	0.55
1:J:117:MET:HB2	1:J:271:LEU:HD13	1.88	0.55
1:K:57:ILE:CG1	1:K:63:VAL:HG21	2.36	0.55
1:A:151:ASN:HD22	1:A:207:VAL:CG2	2.20	0.55
1:A:154:ALA:CA	1:C:182:ALA:HB2	2.34	0.55
1:A:278:VAL:HG12	1:A:279:LYS:N	2.22	0.55
1:G:117:MET:CG	1:G:118:GLY:H	2.11	0.55
1:J:111:ASP:O	1:J:112:MET:HE2	2.07	0.55
1:J:151:ASN:HD22	1:J:207:VAL:CG2	2.19	0.55
1:K:115:GLU:CD	1:K:116:ASP:H	2.14	0.55
1:B:57:ILE:CG1	1:B:63:VAL:HG21	2.36	0.55
1:D:60:PHE:O	1:D:60:PHE:HD1	1.89	0.55
1:D:112:MET:O	1:D:113:LYS:HB2	2.07	0.55
1:E:49:ASN:C	1:E:49:ASN:ND2	2.65	0.55
1:F:42:GLU:HG3	1:F:279:LYS:HE2	1.89	0.55
1:G:115:GLU:CD	1:G:116:ASP:H	2.14	0.55
1:H:107:TYR:CB	1:H:267:LYS:HD3	2.35	0.55
1:B:123:ASN:ND2	1:B:257:PHE:HD2	1.90	0.55
1:C:209:LYS:HB3	1:C:209:LYS:NZ	2.22	0.55
1:J:126:MET:HE1	1:K:36:TYR:HE1	1.72	0.55
1:J:283:ASP:CG	1:J:284:ILE:N	2.65	0.55
1:J:283:ASP:CG	1:J:284:ILE:H	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:ASN:O	1:B:44:LEU:CB	2.55	0.55
1:E:85:ASP:OD1	1:E:86:VAL:N	2.40	0.55
1:E:222:MET:HE3	1:E:227:ILE:CG2	2.35	0.55
1:G:283:ASP:CG	1:G:284:ILE:H	2.14	0.55
1:K:277:LYS:O	1:K:278:VAL:HB	2.06	0.55
1:A:205:TYR:CE2	1:L:209:LYS:HD3	2.42	0.55
1:C:43:ASN:O	1:C:44:LEU:HB3	2.06	0.55
1:D:123:ASN:ND2	1:D:257:PHE:HD2	1.90	0.55
1:E:38:LEU:HD21	1:E:227:ILE:HD11	1.89	0.55
1:E:117:MET:HB2	1:E:271:LEU:HD13	1.89	0.55
1:J:42:GLU:HG3	1:J:279:LYS:HE2	1.88	0.55
1:A:117:MET:HB2	1:A:271:LEU:HD13	1.88	0.55
1:B:39:PHE:HA	1:B:280:PHE:O	2.07	0.55
1:B:60:PHE:HA	1:B:129:PRO:HG3	1.87	0.55
1:J:56:SER:O	1:J:59:GLN:O	2.25	0.55
1:K:151:ASN:ND2	1:K:206:VAL:H	2.05	0.55
1:K:213:GLN:HG3	1:L:207:VAL:CG1	2.37	0.55
1:D:177:GLN:O	1:D:178:TYR:C	2.50	0.55
1:H:177:GLN:O	1:H:178:TYR:C	2.50	0.55
1:L:151:ASN:ND2	1:L:206:VAL:H	2.05	0.55
1:F:60:PHE:O	1:F:60:PHE:HD1	1.90	0.55
1:G:123:ASN:ND2	1:G:257:PHE:HD2	1.91	0.55
1:K:49:ASN:C	1:K:49:ASN:ND2	2.64	0.55
1:L:117:MET:HB2	1:L:271:LEU:HD13	1.89	0.55
1:B:56:SER:O	1:B:59:GLN:O	2.26	0.54
1:B:177:GLN:O	1:B:178:TYR:C	2.49	0.54
1:C:110:ARG:CB	1:D:47:THR:HG22	2.37	0.54
1:E:111:ASP:O	1:E:112:MET:HE2	2.07	0.54
1:E:123:ASN:ND2	1:E:261:ARG:HH21	2.05	0.54
1:F:283:ASP:CG	1:F:284:ILE:H	2.15	0.54
1:H:283:ASP:CG	1:H:284:ILE:H	2.15	0.54
1:I:50:PRO:O	1:I:54:GLU:HG3	2.07	0.54
1:I:112:MET:O	1:I:113:LYS:HB2	2.07	0.54
1:I:154:ALA:HA	1:K:182:ALA:HB2	1.89	0.54
1:J:43:ASN:O	1:J:44:LEU:CB	2.55	0.54
1:J:249:GLN:HB3	1:K:222:MET:HE2	1.90	0.54
1:J:277:LYS:O	1:J:278:VAL:HB	2.06	0.54
1:K:50:PRO:O	1:K:54:GLU:HG3	2.06	0.54
1:K:117:MET:HB2	1:K:271:LEU:HD13	1.89	0.54
1:K:123:ASN:ND2	1:K:261:ARG:HH21	2.05	0.54
1:L:123:ASN:O	1:L:124:ASN:OD1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:209:LYS:NZ	1:L:209:LYS:HB3	2.22	0.54
1:B:278:VAL:HG12	1:B:279:LYS:N	2.22	0.54
1:B:283:ASP:CG	1:B:284:ILE:H	2.15	0.54
1:D:150:VAL:HG13	1:F:180:GLY:HA2	1.88	0.54
1:D:278:VAL:HG12	1:D:279:LYS:N	2.22	0.54
1:G:144:LEU:HD21	1:H:152:GLN:NE2	2.21	0.54
1:G:182:ALA:N	1:G:183:PRO:HD3	2.22	0.54
1:K:37:GLN:O	1:K:281:ARG:HD2	2.07	0.54
1:L:283:ASP:CG	1:L:284:ILE:N	2.66	0.54
1:B:38:LEU:O	1:B:39:PHE:HB2	2.06	0.54
1:C:42:GLU:HG3	1:C:279:LYS:HE2	1.88	0.54
1:C:111:ASP:OD1	1:D:71:ILE:HA	2.08	0.54
1:C:283:ASP:CG	1:C:284:ILE:N	2.65	0.54
1:I:57:ILE:CG1	1:I:63:VAL:HG21	2.37	0.54
1:I:117:MET:HB2	1:I:271:LEU:HD13	1.89	0.54
1:K:112:MET:O	1:K:113:LYS:HB2	2.07	0.54
1:L:186:PHE:CD2	1:L:196:ILE:HD11	2.43	0.54
1:A:151:ASN:ND2	1:A:206:VAL:H	2.06	0.54
1:D:42:GLU:HG3	1:D:279:LYS:HE2	1.87	0.54
1:E:115:GLU:CD	1:E:116:ASP:H	2.15	0.54
1:F:111:ASP:O	1:F:112:MET:HE2	2.07	0.54
1:F:263:GLU:OE1	1:G:50:PRO:HG2	2.08	0.54
1:G:278:VAL:HG12	1:G:279:LYS:N	2.21	0.54
1:H:115:GLU:CD	1:H:116:ASP:H	2.16	0.54
1:J:57:ILE:HG13	1:J:63:VAL:HG21	1.89	0.54
1:K:60:PHE:O	1:K:60:PHE:HD1	1.90	0.54
1:B:140:GLU:CD	1:C:145:LYS:HE2	2.32	0.54
1:C:111:ASP:OD1	1:D:71:ILE:HG23	2.07	0.54
1:C:213:GLN:HG3	1:D:207:VAL:CG1	2.37	0.54
1:F:117:MET:HB2	1:F:271:LEU:HD13	1.89	0.54
1:G:201:THR:CG2	1:H:159:VAL:HG11	2.33	0.54
1:I:42:GLU:HG3	1:I:279:LYS:HE2	1.89	0.54
1:I:213:GLN:HG3	1:J:207:VAL:CG1	2.37	0.54
1:J:50:PRO:O	1:J:54:GLU:HG3	2.07	0.54
1:A:36:TYR:CE1	1:L:126:MET:HE1	2.42	0.54
1:A:115:GLU:CD	1:A:116:ASP:H	2.16	0.54
1:A:283:ASP:CG	1:A:284:ILE:H	2.15	0.54
1:C:248:GLU:HG3	1:D:227:ILE:HG22	1.85	0.54
1:D:39:PHE:HA	1:D:280:PHE:O	2.08	0.54
1:D:169:LEU:HD13	1:D:173:GLN:OE1	2.07	0.54
1:E:112:MET:O	1:E:113:LYS:HB2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:178:TYR:C	1:E:180:GLY:N	2.66	0.54
1:G:277:LYS:O	1:G:278:VAL:HB	2.07	0.54
1:H:151:ASN:HD22	1:H:207:VAL:CG2	2.21	0.54
1:I:60:PHE:O	1:I:61:GLY:C	2.51	0.54
1:L:42:GLU:HG3	1:L:279:LYS:HE2	1.89	0.54
1:L:123:ASN:ND2	1:L:261:ARG:NH2	2.55	0.54
1:C:182:ALA:N	1:C:183:PRO:CD	2.71	0.54
1:G:17:ARG:HG2	1:G:20:ARG:NH2	2.23	0.54
1:G:112:MET:O	1:G:113:LYS:HB2	2.07	0.54
1:K:85:ASP:OD1	1:K:86:VAL:N	2.41	0.54
1:L:17:ARG:HG2	1:L:20:ARG:NH2	2.23	0.54
1:A:50:PRO:O	1:A:54:GLU:HG3	2.08	0.54
1:B:213:GLN:HG3	1:C:207:VAL:CG1	2.38	0.54
1:C:17:ARG:HG2	1:C:20:ARG:NH2	2.23	0.54
1:D:117:MET:HB2	1:D:271:LEU:HD13	1.89	0.54
1:D:277:LYS:O	1:D:278:VAL:HB	2.07	0.54
1:E:123:ASN:ND2	1:E:257:PHE:HD2	1.90	0.54
1:E:283:ASP:CG	1:E:284:ILE:H	2.15	0.54
1:G:50:PRO:O	1:G:54:GLU:HG3	2.08	0.54
1:J:174:VAL:O	1:J:177:GLN:HG3	2.07	0.54
1:C:248:GLU:OE1	1:D:227:ILE:HG23	2.08	0.54
1:G:42:GLU:HG3	1:G:279:LYS:HE2	1.89	0.54
1:G:283:ASP:CG	1:G:284:ILE:N	2.65	0.54
1:H:56:SER:O	1:H:59:GLN:O	2.26	0.54
1:I:123:ASN:O	1:I:124:ASN:OD1	2.25	0.54
1:I:209:LYS:HD3	1:J:205:TYR:CE2	2.43	0.54
1:J:151:ASN:HD21	1:J:206:VAL:H	1.54	0.54
1:L:115:GLU:CD	1:L:116:ASP:H	2.16	0.54
1:B:17:ARG:HG2	1:B:20:ARG:NH2	2.23	0.54
1:B:98:PRO:O	1:B:99:VAL:HB	2.08	0.54
1:C:115:GLU:CD	1:C:116:ASP:H	2.16	0.54
1:D:111:ASP:O	1:D:112:MET:HE2	2.08	0.54
1:D:117:MET:CG	1:D:118:GLY:H	2.11	0.54
1:F:151:ASN:HD22	1:F:207:VAL:CG2	2.20	0.54
1:G:43:ASN:O	1:G:44:LEU:CB	2.56	0.54
1:H:178:TYR:C	1:H:180:GLY:N	2.65	0.54
1:I:283:ASP:CG	1:I:284:ILE:H	2.15	0.54
1:J:177:GLN:O	1:J:178:TYR:C	2.50	0.54
1:K:111:ASP:O	1:K:112:MET:HE2	2.08	0.54
1:K:283:ASP:CG	1:K:284:ILE:H	2.16	0.54
1:A:43:ASN:O	1:A:44:LEU:CB	2.54	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:SER:O	1:A:59:GLN:O	2.25	0.53
1:B:38:LEU:HD21	1:B:227:ILE:HD11	1.90	0.53
1:C:209:LYS:HB2	1:D:205:TYR:OH	2.08	0.53
1:D:60:PHE:O	1:D:61:GLY:C	2.52	0.53
1:G:151:ASN:ND2	1:G:206:VAL:H	2.06	0.53
1:H:117:MET:CG	1:H:118:GLY:H	2.14	0.53
1:H:209:LYS:HB3	1:H:209:LYS:NZ	2.22	0.53
1:I:126:MET:HE1	1:J:36:TYR:CE1	2.43	0.53
1:J:38:LEU:HD21	1:J:227:ILE:HD11	1.90	0.53
1:J:115:GLU:CD	1:J:116:ASP:H	2.15	0.53
1:K:283:ASP:CG	1:K:284:ILE:N	2.67	0.53
1:D:71:ILE:HG22	1:D:71:ILE:O	2.08	0.53
1:D:151:ASN:HD22	1:D:207:VAL:CG2	2.21	0.53
1:E:182:ALA:N	1:E:183:PRO:CD	2.72	0.53
1:E:186:PHE:CD2	1:E:196:ILE:HD11	2.42	0.53
1:G:186:PHE:CD2	1:G:196:ILE:HD11	2.43	0.53
1:J:39:PHE:HA	1:J:280:PHE:O	2.07	0.53
1:K:151:ASN:HD22	1:K:207:VAL:CG2	2.20	0.53
1:A:17:ARG:HG2	1:A:20:ARG:NH2	2.24	0.53
1:A:283:ASP:CG	1:A:284:ILE:N	2.66	0.53
1:B:283:ASP:CG	1:B:284:ILE:N	2.66	0.53
1:D:283:ASP:CG	1:D:284:ILE:H	2.16	0.53
1:F:71:ILE:O	1:F:71:ILE:HG22	2.08	0.53
1:H:117:MET:HB2	1:H:271:LEU:HD13	1.89	0.53
1:H:283:ASP:CG	1:H:284:ILE:N	2.67	0.53
1:J:117:MET:CG	1:J:118:GLY:H	2.10	0.53
1:J:172:LYS:HG3	1:K:179:GLU:OE1	2.08	0.53
1:K:169:LEU:HD13	1:K:173:GLN:OE1	2.08	0.53
1:A:42:GLU:HG3	1:A:279:LYS:HE2	1.90	0.53
1:A:123:ASN:ND2	1:A:261:ARG:HH21	2.07	0.53
1:D:123:ASN:ND2	1:D:261:ARG:HH21	2.06	0.53
1:F:56:SER:O	1:F:59:GLN:O	2.26	0.53
1:G:117:MET:HB2	1:G:271:LEU:HD13	1.90	0.53
1:H:123:ASN:ND2	1:H:261:ARG:HH21	2.07	0.53
1:H:154:ALA:CB	1:J:182:ALA:HB2	2.38	0.53
1:I:60:PHE:O	1:I:60:PHE:HD1	1.90	0.53
1:K:42:GLU:HG3	1:K:279:LYS:HE2	1.90	0.53
1:L:182:ALA:N	1:L:183:PRO:CD	2.72	0.53
1:A:11:SER:CB	1:B:176:ASN:HD22	2.08	0.53
1:B:151:ASN:HD22	1:B:207:VAL:CG2	2.20	0.53
1:E:151:ASN:HD21	1:E:206:VAL:H	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:60:PHE:O	1:H:61:GLY:C	2.51	0.53
1:H:112:MET:O	1:H:113:LYS:HB2	2.09	0.53
1:H:182:ALA:N	1:H:183:PRO:CD	2.72	0.53
1:A:182:ALA:HB2	1:K:154:ALA:CB	2.38	0.53
1:B:71:ILE:HG22	1:B:71:ILE:O	2.08	0.53
1:B:112:MET:O	1:B:113:LYS:HB2	2.08	0.53
1:C:49:ASN:C	1:C:49:ASN:ND2	2.65	0.53
1:F:115:GLU:CD	1:F:116:ASP:H	2.16	0.53
1:F:201:THR:O	1:F:201:THR:CG2	2.51	0.53
1:I:85:ASP:OD1	1:I:86:VAL:N	2.41	0.53
1:I:98:PRO:O	1:I:99:VAL:HB	2.09	0.53
1:I:115:GLU:CD	1:I:116:ASP:H	2.15	0.53
1:J:86:VAL:HA	1:K:99:VAL:HG11	1.89	0.53
1:K:117:MET:CG	1:K:118:GLY:H	2.12	0.53
1:L:174:VAL:O	1:L:177:GLN:HG3	2.08	0.53
1:A:169:LEU:HD13	1:A:173:GLN:OE1	2.09	0.53
1:C:171:LEU:C	1:C:173:GLN:N	2.53	0.53
1:G:85:ASP:OD1	1:G:86:VAL:N	2.41	0.53
1:H:59:GLN:O	1:H:60:PHE:CD1	2.62	0.53
1:I:123:ASN:ND2	1:I:261:ARG:HH21	2.05	0.53
1:J:85:ASP:OD1	1:J:86:VAL:N	2.41	0.53
1:B:144:LEU:HD21	1:C:152:GLN:NE2	2.23	0.53
1:C:249:GLN:HB3	1:D:222:MET:HE2	1.89	0.53
1:D:151:ASN:ND2	1:D:206:VAL:H	2.07	0.53
1:E:56:SER:O	1:E:59:GLN:O	2.26	0.53
1:E:60:PHE:O	1:E:61:GLY:C	2.51	0.53
1:I:111:ASP:O	1:I:112:MET:HE2	2.09	0.53
1:K:102:LYS:HG3	1:K:103:GLU:N	2.24	0.53
1:K:178:TYR:C	1:K:180:GLY:N	2.66	0.53
1:B:111:ASP:O	1:B:112:MET:HE2	2.08	0.53
1:F:209:LYS:NZ	1:F:209:LYS:HB3	2.23	0.53
1:F:283:ASP:CG	1:F:284:ILE:N	2.66	0.53
1:J:41:TRP:HA	1:J:277:LYS:HD3	1.91	0.53
1:J:186:PHE:CD2	1:J:196:ILE:HD11	2.44	0.53
1:K:209:LYS:HB3	1:K:209:LYS:NZ	2.24	0.53
1:B:123:ASN:ND2	1:B:261:ARG:HH21	2.07	0.53
1:C:111:ASP:O	1:C:112:MET:HE2	2.08	0.53
1:D:98:PRO:O	1:D:99:VAL:HB	2.09	0.53
1:D:283:ASP:CG	1:D:284:ILE:N	2.67	0.53
1:E:123:ASN:O	1:E:124:ASN:OD1	2.27	0.53
1:I:283:ASP:CG	1:I:284:ILE:N	2.66	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:38:LEU:HD21	1:L:227:ILE:HD11	1.91	0.53
1:L:179:GLU:C	1:L:181:ASN:N	2.67	0.53
1:A:178:TYR:C	1:A:180:GLY:N	2.66	0.52
1:A:179:GLU:OE1	1:L:172:LYS:HG3	2.09	0.52
1:A:186:PHE:CD2	1:A:196:ILE:HD11	2.45	0.52
1:C:102:LYS:HG3	1:C:103:GLU:N	2.24	0.52
1:D:38:LEU:HD21	1:D:227:ILE:HD11	1.91	0.52
1:D:182:ALA:N	1:D:183:PRO:CD	2.72	0.52
1:F:169:LEU:HD13	1:F:173:GLN:OE1	2.08	0.52
1:F:182:ALA:N	1:F:183:PRO:CD	2.72	0.52
1:I:182:ALA:N	1:I:183:PRO:CD	2.72	0.52
1:J:278:VAL:HG12	1:J:279:LYS:N	2.23	0.52
1:K:17:ARG:HG2	1:K:20:ARG:NH2	2.23	0.52
1:K:182:ALA:N	1:K:183:PRO:CD	2.72	0.52
1:L:60:PHE:O	1:L:61:GLY:C	2.52	0.52
1:L:111:ASP:O	1:L:112:MET:HE2	2.09	0.52
1:B:182:ALA:N	1:B:183:PRO:CD	2.72	0.52
1:C:178:TYR:C	1:C:180:GLY:N	2.66	0.52
1:I:178:TYR:C	1:I:180:GLY:N	2.66	0.52
1:J:71:ILE:O	1:J:72:SER:HB3	2.08	0.52
1:K:71:ILE:O	1:K:72:SER:HB3	2.09	0.52
1:L:151:ASN:HD22	1:L:207:VAL:CG2	2.22	0.52
1:A:112:MET:O	1:A:113:LYS:HB2	2.08	0.52
1:C:123:ASN:O	1:C:124:ASN:OD1	2.28	0.52
1:D:85:ASP:OD1	1:D:86:VAL:N	2.42	0.52
1:D:186:PHE:CD2	1:D:196:ILE:HD11	2.44	0.52
1:D:201:THR:CG2	1:E:159:VAL:HG11	2.28	0.52
1:H:50:PRO:O	1:H:54:GLU:HG3	2.09	0.52
1:L:50:PRO:O	1:L:53:LEU:HB3	2.09	0.52
1:A:41:TRP:HA	1:A:277:LYS:HD3	1.92	0.52
1:B:150:VAL:HG13	1:D:180:GLY:HA2	1.92	0.52
1:C:98:PRO:O	1:C:99:VAL:HB	2.09	0.52
1:E:98:PRO:O	1:E:99:VAL:HB	2.09	0.52
1:E:169:LEU:HD13	1:E:173:GLN:OE1	2.09	0.52
1:I:209:LYS:NZ	1:I:209:LYS:HB3	2.23	0.52
1:J:151:ASN:ND2	1:J:206:VAL:H	2.07	0.52
1:J:178:TYR:C	1:J:180:GLY:N	2.66	0.52
1:L:56:SER:O	1:L:59:GLN:O	2.26	0.52
1:L:178:TYR:C	1:L:180:GLY:N	2.66	0.52
1:A:182:ALA:N	1:A:183:PRO:CD	2.73	0.52
1:C:117:MET:HB2	1:C:271:LEU:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:123:ASN:ND2	1:C:257:PHE:HD2	1.92	0.52
1:D:174:VAL:O	1:D:177:GLN:HG3	2.09	0.52
1:E:17:ARG:HG2	1:E:20:ARG:NH2	2.24	0.52
1:E:283:ASP:CG	1:E:284:ILE:N	2.67	0.52
1:K:71:ILE:O	1:K:71:ILE:HG22	2.09	0.52
1:A:57:ILE:CG1	1:A:63:VAL:HG21	2.39	0.52
1:F:41:TRP:HA	1:F:277:LYS:HD3	1.92	0.52
1:F:102:LYS:HG3	1:F:103:GLU:N	2.25	0.52
1:I:17:ARG:HG2	1:I:20:ARG:NH2	2.24	0.52
1:J:98:PRO:O	1:J:99:VAL:HB	2.09	0.52
1:J:182:ALA:N	1:J:183:PRO:CD	2.72	0.52
1:K:43:ASN:O	1:K:44:LEU:CB	2.58	0.52
1:A:282:TYR:CE2	1:L:248:GLU:HB3	2.44	0.52
1:B:169:LEU:HD13	1:B:173:GLN:OE1	2.09	0.52
1:C:93:PHE:HB2	1:C:106:LEU:HD21	1.92	0.52
1:F:154:ALA:CB	1:H:182:ALA:HB2	2.40	0.52
1:G:123:ASN:ND2	1:G:261:ARG:HH21	2.06	0.52
1:L:57:ILE:CG1	1:L:63:VAL:HG21	2.39	0.52
1:L:98:PRO:O	1:L:99:VAL:HB	2.09	0.52
1:A:98:PRO:O	1:A:99:VAL:HB	2.10	0.52
1:B:60:PHE:O	1:B:61:GLY:C	2.52	0.52
1:B:117:MET:CG	1:B:118:GLY:H	2.13	0.52
1:E:71:ILE:O	1:E:71:ILE:HG22	2.10	0.52
1:F:49:ASN:C	1:F:49:ASN:ND2	2.65	0.52
1:G:102:LYS:HG3	1:G:103:GLU:N	2.24	0.52
1:I:186:PHE:CD2	1:I:196:ILE:HD11	2.45	0.52
1:J:17:ARG:HG2	1:J:20:ARG:NH2	2.24	0.52
1:L:93:PHE:HB2	1:L:106:LEU:HD21	1.92	0.52
1:C:60:PHE:O	1:C:61:GLY:C	2.52	0.52
1:D:17:ARG:HG2	1:D:20:ARG:NH2	2.24	0.52
1:D:179:GLU:C	1:D:181:ASN:N	2.68	0.52
1:F:179:GLU:C	1:F:181:ASN:N	2.68	0.52
1:G:71:ILE:HG22	1:G:71:ILE:O	2.08	0.52
1:G:98:PRO:O	1:G:99:VAL:HB	2.10	0.52
1:G:123:ASN:O	1:G:124:ASN:OD1	2.28	0.52
1:H:17:ARG:HG2	1:H:20:ARG:NH2	2.25	0.52
1:I:169:LEU:HD13	1:I:173:GLN:OE1	2.10	0.52
1:K:38:LEU:O	1:K:39:PHE:HB2	2.10	0.52
1:K:38:LEU:HD21	1:K:227:ILE:HD11	1.92	0.52
1:A:85:ASP:OD1	1:A:86:VAL:N	2.43	0.52
1:A:209:LYS:NZ	1:A:209:LYS:HB3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:PRO:O	1:B:54:GLU:HG3	2.10	0.52
1:D:123:ASN:O	1:D:124:ASN:OD1	2.27	0.52
1:D:178:TYR:C	1:D:180:GLY:N	2.65	0.52
1:G:49:ASN:C	1:G:49:ASN:ND2	2.64	0.52
1:G:178:TYR:C	1:G:180:GLY:N	2.67	0.52
1:G:209:LYS:NZ	1:G:209:LYS:HB3	2.25	0.52
1:A:93:PHE:HB2	1:A:106:LEU:HD21	1.92	0.51
1:A:117:MET:CG	1:A:118:GLY:H	2.10	0.51
1:A:123:ASN:O	1:A:124:ASN:OD1	2.28	0.51
1:F:50:PRO:O	1:F:54:GLU:HG3	2.10	0.51
1:I:56:SER:O	1:I:59:GLN:O	2.27	0.51
1:I:93:PHE:HB2	1:I:106:LEU:HD21	1.92	0.51
1:I:201:THR:CG2	1:J:159:VAL:HG11	2.20	0.51
1:G:39:PHE:HA	1:G:280:PHE:O	2.10	0.51
1:H:71:ILE:O	1:H:72:SER:HB3	2.09	0.51
1:I:60:PHE:HA	1:I:129:PRO:HG3	1.91	0.51
1:I:151:ASN:HD22	1:I:207:VAL:CG2	2.23	0.51
1:J:179:GLU:C	1:J:181:ASN:N	2.68	0.51
1:J:274:LEU:HD13	1:J:274:LEU:C	2.35	0.51
1:D:209:LYS:NZ	1:D:209:LYS:HB3	2.25	0.51
1:E:11:SER:HB3	1:F:176:ASN:HD22	1.75	0.51
1:H:93:PHE:HB2	1:H:106:LEU:HD21	1.92	0.51
1:H:151:ASN:ND2	1:H:206:VAL:H	2.07	0.51
1:K:98:PRO:O	1:K:99:VAL:HB	2.10	0.51
1:L:201:THR:O	1:L:201:THR:CG2	2.53	0.51
1:C:86:VAL:HG13	1:D:100:TYR:HB2	1.93	0.51
1:H:111:ASP:O	1:H:112:MET:HE2	2.09	0.51
1:I:41:TRP:CE3	1:I:277:LYS:HE2	2.46	0.51
1:I:71:ILE:O	1:I:71:ILE:HG22	2.10	0.51
1:J:102:LYS:HG3	1:J:103:GLU:N	2.25	0.51
1:J:154:ALA:CA	1:L:182:ALA:HB2	2.39	0.51
1:A:111:ASP:O	1:A:112:MET:HE2	2.11	0.51
1:B:93:PHE:HB2	1:B:106:LEU:HD21	1.92	0.51
1:E:126:MET:HE1	1:F:36:TYR:CE1	2.46	0.51
1:F:38:LEU:HD21	1:F:227:ILE:HD11	1.92	0.51
1:F:178:TYR:C	1:F:180:GLY:N	2.67	0.51
1:K:174:VAL:O	1:K:177:GLN:HG3	2.11	0.51
1:L:41:TRP:CE3	1:L:277:LYS:HE2	2.45	0.51
1:B:143:GLU:OE2	1:C:153:ASN:ND2	2.40	0.51
1:B:248:GLU:HB3	1:C:282:TYR:CE2	2.44	0.51
1:E:174:VAL:O	1:E:177:GLN:HG3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:186:PHE:CD2	1:F:196:ILE:HD11	2.45	0.51
1:G:38:LEU:O	1:G:39:PHE:CB	2.58	0.51
1:G:169:LEU:HD13	1:G:173:GLN:OE1	2.10	0.51
1:G:182:ALA:N	1:G:183:PRO:CD	2.74	0.51
1:H:41:TRP:HA	1:H:277:LYS:HD3	1.92	0.51
1:I:86:VAL:HA	1:J:99:VAL:HG11	1.92	0.51
1:I:277:LYS:CE	1:I:278:VAL:H	2.24	0.51
1:J:112:MET:O	1:J:113:LYS:HB2	2.09	0.51
1:K:50:PRO:O	1:K:53:LEU:HB3	2.11	0.51
1:A:102:LYS:HG3	1:A:103:GLU:N	2.25	0.51
1:B:41:TRP:HA	1:B:277:LYS:HD3	1.93	0.51
1:F:41:TRP:CE3	1:F:277:LYS:HE2	2.45	0.51
1:G:93:PHE:HB2	1:G:106:LEU:HD21	1.93	0.51
1:J:222:MET:CE	1:J:227:ILE:HG21	2.40	0.51
1:L:12:ILE:HG22	1:L:13:ASN:N	2.26	0.51
1:A:201:THR:HG23	1:B:159:VAL:CG1	2.32	0.51
1:C:41:TRP:HA	1:C:277:LYS:HD3	1.92	0.51
1:G:60:PHE:O	1:G:61:GLY:C	2.52	0.51
1:K:277:LYS:CE	1:K:278:VAL:H	2.24	0.51
1:A:60:PHE:O	1:A:61:GLY:C	2.53	0.51
1:C:56:SER:O	1:C:59:GLN:O	2.29	0.51
1:F:110:ARG:HB3	1:G:47:THR:HG22	1.92	0.51
1:F:168:GLN:HE22	1:F:169:LEU:HG	1.76	0.51
1:G:12:ILE:HG22	1:G:13:ASN:N	2.26	0.51
1:H:168:GLN:HE22	1:H:169:LEU:HG	1.75	0.51
1:J:38:LEU:O	1:J:39:PHE:HB2	2.11	0.51
1:J:169:LEU:HD13	1:J:173:GLN:OE1	2.11	0.51
1:K:186:PHE:CD2	1:K:196:ILE:HD11	2.45	0.51
1:C:11:SER:HB3	1:D:176:ASN:ND2	2.24	0.51
1:D:12:ILE:HG22	1:D:13:ASN:N	2.26	0.51
1:D:277:LYS:CE	1:D:278:VAL:H	2.24	0.51
1:E:43:ASN:O	1:E:44:LEU:CB	2.59	0.51
1:F:17:ARG:HG2	1:F:20:ARG:NH2	2.26	0.51
1:G:60:PHE:HA	1:G:129:PRO:HG3	1.93	0.51
1:G:126:MET:HE1	1:H:36:TYR:HE1	1.74	0.51
1:H:71:ILE:O	1:H:71:ILE:HG22	2.11	0.51
1:I:201:THR:O	1:I:201:THR:CG2	2.55	0.51
1:J:71:ILE:O	1:J:71:ILE:HG22	2.10	0.51
1:K:158:PRO:O	1:K:159:VAL:CB	2.59	0.51
1:A:71:ILE:O	1:A:71:ILE:HG22	2.11	0.50
1:C:151:ASN:HD22	1:C:207:VAL:CG2	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:ASN:O	1:D:44:LEU:CB	2.59	0.50
1:D:176:ASN:OD1	1:D:176:ASN:N	2.44	0.50
1:E:50:PRO:O	1:E:54:GLU:HG3	2.10	0.50
1:H:123:ASN:O	1:H:124:ASN:OD1	2.29	0.50
1:L:20:ARG:HG2	1:L:146:GLU:OE1	2.11	0.50
1:A:59:GLN:O	1:A:60:PHE:CD1	2.63	0.50
1:B:174:VAL:O	1:B:177:GLN:HG3	2.11	0.50
1:C:182:ALA:H	1:C:183:PRO:HD3	1.76	0.50
1:G:41:TRP:HA	1:G:277:LYS:HD3	1.93	0.50
1:H:38:LEU:HD21	1:H:227:ILE:HD11	1.91	0.50
1:I:124:ASN:HD21	1:I:128:PHE:HB2	1.75	0.50
1:I:178:TYR:H	1:I:178:TYR:HD2	1.59	0.50
1:K:87:TYR:HH	1:L:48:ILE:HA	1.74	0.50
1:A:158:PRO:O	1:A:159:VAL:CB	2.60	0.50
1:C:71:ILE:O	1:C:71:ILE:HG22	2.10	0.50
1:H:170:SER:C	1:H:171:LEU:O	2.54	0.50
1:H:213:GLN:HG3	1:I:207:VAL:CG1	2.40	0.50
1:I:50:PRO:O	1:I:53:LEU:HB3	2.11	0.50
1:B:41:TRP:CE3	1:B:277:LYS:HE2	2.47	0.50
1:C:41:TRP:CE3	1:C:277:LYS:HE2	2.47	0.50
1:C:169:LEU:HD13	1:C:173:GLN:OE1	2.12	0.50
1:C:277:LYS:CE	1:C:278:VAL:H	2.23	0.50
1:D:126:MET:O	1:D:128:PHE:N	2.39	0.50
1:G:126:MET:HG3	1:H:55:LYS:NZ	2.26	0.50
1:G:201:THR:HG23	1:H:159:VAL:CG1	2.32	0.50
1:L:71:ILE:HG22	1:L:71:ILE:O	2.11	0.50
1:A:123:ASN:ND2	1:A:257:PHE:HD2	1.91	0.50
1:C:168:GLN:HE22	1:C:169:LEU:HG	1.76	0.50
1:D:102:LYS:HG3	1:D:103:GLU:N	2.26	0.50
1:D:168:GLN:HE22	1:D:169:LEU:HG	1.76	0.50
1:E:41:TRP:CE3	1:E:277:LYS:HE2	2.47	0.50
1:F:93:PHE:HB2	1:F:106:LEU:HD21	1.92	0.50
1:H:41:TRP:CE3	1:H:277:LYS:HE2	2.47	0.50
1:I:158:PRO:O	1:I:159:VAL:CB	2.57	0.50
1:I:174:VAL:O	1:I:177:GLN:HG3	2.11	0.50
1:J:12:ILE:HG22	1:J:13:ASN:N	2.26	0.50
1:J:93:PHE:HB2	1:J:106:LEU:HD21	1.93	0.50
1:J:168:GLN:HE22	1:J:169:LEU:HG	1.77	0.50
1:L:43:ASN:O	1:L:44:LEU:CB	2.59	0.50
1:L:84:ARG:HD2	1:L:88:ASN:O	2.12	0.50
1:L:169:LEU:HD13	1:L:173:GLN:OE1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:ILE:O	1:C:72:SER:HB3	2.11	0.50
1:D:71:ILE:O	1:D:72:SER:HB3	2.12	0.50
1:E:41:TRP:HA	1:E:277:LYS:HD3	1.94	0.50
1:E:154:ALA:CA	1:G:182:ALA:HB2	2.42	0.50
1:H:174:VAL:O	1:H:177:GLN:HG3	2.12	0.50
1:I:179:GLU:C	1:I:181:ASN:N	2.70	0.50
1:J:123:ASN:O	1:J:124:ASN:OD1	2.30	0.50
1:J:209:LYS:NZ	1:J:209:LYS:HB3	2.27	0.50
1:K:168:GLN:HE22	1:K:169:LEU:HG	1.77	0.50
1:L:71:ILE:O	1:L:72:SER:HB3	2.11	0.50
1:E:93:PHE:HB2	1:E:106:LEU:HD21	1.94	0.50
1:F:98:PRO:O	1:F:99:VAL:HB	2.11	0.50
1:L:178:TYR:H	1:L:178:TYR:HD2	1.59	0.50
1:B:49:ASN:C	1:B:49:ASN:ND2	2.61	0.50
1:D:60:PHE:HA	1:D:129:PRO:HG3	1.93	0.50
1:E:102:LYS:HG3	1:E:103:GLU:N	2.26	0.50
1:F:123:ASN:ND2	1:F:261:ARG:HH21	2.10	0.50
1:F:201:THR:HG23	1:G:159:VAL:CG1	2.27	0.50
1:H:248:GLU:HB3	1:I:282:TYR:CZ	2.47	0.50
1:I:43:ASN:O	1:I:44:LEU:CB	2.60	0.50
1:J:60:PHE:O	1:J:61:GLY:C	2.55	0.50
1:J:201:THR:O	1:J:201:THR:CG2	2.57	0.50
1:A:71:ILE:O	1:A:72:SER:HB3	2.11	0.50
1:B:104:PHE:O	1:B:105:LYS:HB2	2.12	0.50
1:B:248:GLU:CB	1:C:282:TYR:CZ	2.91	0.50
1:C:104:PHE:O	1:C:105:LYS:HB2	2.12	0.50
1:C:213:GLN:O	1:C:216:ALA:HB3	2.12	0.50
1:D:41:TRP:HA	1:D:277:LYS:HD3	1.94	0.50
1:E:151:ASN:ND2	1:E:206:VAL:H	2.10	0.50
1:H:248:GLU:HB3	1:I:282:TYR:CE2	2.47	0.50
1:I:104:PHE:O	1:I:105:LYS:HB2	2.12	0.50
1:I:170:SER:C	1:I:171:LEU:O	2.55	0.50
1:B:248:GLU:CB	1:C:282:TYR:CE1	2.95	0.49
1:C:170:SER:C	1:C:171:LEU:O	2.55	0.49
1:E:57:ILE:HG13	1:E:63:VAL:HG21	1.94	0.49
1:G:50:PRO:O	1:G:53:LEU:HB3	2.12	0.49
1:G:56:SER:O	1:G:59:GLN:O	2.30	0.49
1:H:186:PHE:CD2	1:H:196:ILE:HD11	2.46	0.49
1:I:182:ALA:H	1:I:183:PRO:HD3	1.76	0.49
1:K:57:ILE:HG13	1:K:63:VAL:HG21	1.94	0.49
1:K:172:LYS:HG3	1:L:179:GLU:OE1	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:104:PHE:O	1:L:105:LYS:HB2	2.11	0.49
1:A:150:VAL:HG13	1:C:180:GLY:HA2	1.93	0.49
1:B:71:ILE:O	1:B:72:SER:HB3	2.12	0.49
1:B:277:LYS:CE	1:B:278:VAL:H	2.25	0.49
1:E:50:PRO:O	1:E:53:LEU:HB3	2.11	0.49
1:F:12:ILE:HG22	1:F:13:ASN:N	2.27	0.49
1:H:98:PRO:O	1:H:99:VAL:HB	2.11	0.49
1:H:102:LYS:HG3	1:H:103:GLU:N	2.27	0.49
1:H:277:LYS:CE	1:H:278:VAL:H	2.25	0.49
1:I:71:ILE:O	1:I:72:SER:HB3	2.12	0.49
1:B:176:ASN:OD1	1:B:176:ASN:N	2.44	0.49
1:C:12:ILE:HG22	1:C:13:ASN:N	2.27	0.49
1:C:43:ASN:O	1:C:44:LEU:CB	2.60	0.49
1:C:123:ASN:ND2	1:C:261:ARG:HH21	2.09	0.49
1:C:178:TYR:H	1:C:178:TYR:HD2	1.58	0.49
1:H:12:ILE:HG22	1:H:13:ASN:N	2.28	0.49
1:J:60:PHE:O	1:J:60:PHE:CD1	2.64	0.49
1:K:123:ASN:O	1:K:124:ASN:OD1	2.30	0.49
1:A:130:THR:HG22	1:A:257:PHE:HE2	1.76	0.49
1:A:178:TYR:H	1:A:178:TYR:HD2	1.60	0.49
1:B:12:ILE:HG22	1:B:13:ASN:N	2.26	0.49
1:C:38:LEU:HD21	1:C:227:ILE:HD11	1.94	0.49
1:C:277:LYS:NZ	1:C:278:VAL:O	2.38	0.49
1:D:178:TYR:H	1:D:178:TYR:HD2	1.61	0.49
1:E:12:ILE:HG22	1:E:13:ASN:N	2.27	0.49
1:E:170:SER:C	1:E:171:LEU:O	2.55	0.49
1:E:178:TYR:H	1:E:178:TYR:HD2	1.60	0.49
1:G:222:MET:CE	1:G:227:ILE:HG21	2.40	0.49
1:L:277:LYS:CE	1:L:278:VAL:H	2.25	0.49
1:A:170:SER:C	1:A:171:LEU:O	2.55	0.49
1:B:186:PHE:CD2	1:B:196:ILE:HD11	2.46	0.49
1:C:174:VAL:O	1:C:177:GLN:HG3	2.12	0.49
1:D:50:PRO:O	1:D:54:GLU:HG3	2.12	0.49
1:F:59:GLN:O	1:F:60:PHE:CD1	2.66	0.49
1:F:178:TYR:H	1:F:178:TYR:HD2	1.61	0.49
1:F:277:LYS:CE	1:F:278:VAL:H	2.26	0.49
1:I:102:LYS:HG3	1:I:103:GLU:N	2.27	0.49
1:I:249:GLN:HB3	1:J:222:MET:HE2	1.95	0.49
1:B:209:LYS:NZ	1:B:209:LYS:HB3	2.27	0.49
1:D:50:PRO:O	1:D:53:LEU:HB3	2.13	0.49
1:F:174:VAL:O	1:F:177:GLN:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:11:SER:HB3	1:I:176:ASN:ND2	2.27	0.49
1:K:12:ILE:HG22	1:K:13:ASN:N	2.27	0.49
1:A:151:ASN:ND2	1:A:207:VAL:HG23	2.27	0.49
1:A:201:THR:O	1:A:201:THR:CG2	2.57	0.49
1:B:102:LYS:HG3	1:B:103:GLU:N	2.27	0.49
1:G:104:PHE:O	1:G:105:LYS:HB2	2.13	0.49
1:I:12:ILE:HG22	1:I:13:ASN:N	2.28	0.49
1:J:84:ARG:HD2	1:J:88:ASN:O	2.13	0.49
1:B:178:TYR:C	1:B:180:GLY:N	2.65	0.49
1:D:117:MET:CG	1:D:118:GLY:N	2.75	0.49
1:E:277:LYS:CE	1:E:278:VAL:H	2.26	0.49
1:F:71:ILE:O	1:F:72:SER:HB3	2.12	0.49
1:I:93:PHE:H	1:I:104:PHE:HB2	1.78	0.49
1:K:20:ARG:HG2	1:K:146:GLU:OE1	2.12	0.49
1:K:59:GLN:O	1:K:60:PHE:CD1	2.66	0.49
1:K:93:PHE:HB2	1:K:106:LEU:HD21	1.93	0.49
1:K:117:MET:CG	1:K:118:GLY:N	2.75	0.49
1:A:12:ILE:HG22	1:A:13:ASN:N	2.27	0.49
1:A:41:TRP:CE3	1:A:277:LYS:HE2	2.48	0.49
1:A:174:VAL:O	1:A:177:GLN:HG3	2.12	0.49
1:H:86:VAL:HA	1:I:99:VAL:HG11	1.93	0.49
1:I:38:LEU:HD21	1:I:227:ILE:HD11	1.93	0.49
1:L:176:ASN:OD1	1:L:176:ASN:N	2.46	0.49
1:B:168:GLN:HE22	1:B:169:LEU:HG	1.78	0.49
1:B:201:THR:HG23	1:C:159:VAL:CG1	2.32	0.49
1:C:154:ALA:HA	1:E:181:ASN:O	2.12	0.49
1:D:41:TRP:CE3	1:D:277:LYS:HE2	2.48	0.49
1:H:43:ASN:O	1:H:44:LEU:CB	2.60	0.49
1:H:50:PRO:O	1:H:53:LEU:HB3	2.13	0.49
1:J:170:SER:C	1:J:171:LEU:O	2.55	0.49
1:D:20:ARG:HG2	1:D:146:GLU:OE1	2.13	0.48
1:G:71:ILE:O	1:G:72:SER:HB3	2.12	0.48
1:J:130:THR:HG22	1:J:257:PHE:HE2	1.78	0.48
1:A:38:LEU:HD21	1:A:227:ILE:HD11	1.94	0.48
1:A:50:PRO:O	1:A:53:LEU:HB3	2.13	0.48
1:A:277:LYS:CE	1:A:278:VAL:H	2.26	0.48
1:B:101:GLN:O	1:B:102:LYS:HB2	2.13	0.48
1:B:178:TYR:H	1:B:178:TYR:HD2	1.61	0.48
1:B:248:GLU:HB2	1:C:282:TYR:CE1	2.48	0.48
1:E:154:ALA:HA	1:G:181:ASN:O	2.13	0.48
1:F:248:GLU:HG3	1:G:227:ILE:HG22	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:277:LYS:CE	1:G:278:VAL:H	2.26	0.48
1:H:169:LEU:HD13	1:H:173:GLN:OE1	2.13	0.48
1:H:178:TYR:H	1:H:178:TYR:HD2	1.61	0.48
1:L:123:ASN:ND2	1:L:261:ARG:HH21	2.11	0.48
1:E:71:ILE:O	1:E:72:SER:HB3	2.12	0.48
1:G:59:GLN:O	1:G:60:PHE:CD1	2.66	0.48
1:H:140:GLU:CD	1:I:145:LYS:HE2	2.38	0.48
1:K:41:TRP:HA	1:K:277:LYS:HD3	1.95	0.48
1:A:11:SER:CB	1:B:176:ASN:ND2	2.70	0.48
1:B:181:ASN:O	1:L:154:ALA:HA	2.14	0.48
1:C:110:ARG:CB	1:D:47:THR:CG2	2.91	0.48
1:F:283:ASP:O	1:F:284:ILE:CB	2.62	0.48
1:G:178:TYR:H	1:G:178:TYR:HD2	1.60	0.48
1:J:248:GLU:HG3	1:K:227:ILE:HG23	1.94	0.48
1:K:277:LYS:HE3	1:K:278:VAL:H	1.78	0.48
1:L:102:LYS:HG3	1:L:103:GLU:N	2.28	0.48
1:A:99:VAL:HG11	1:L:86:VAL:HA	1.95	0.48
1:D:182:ALA:H	1:D:183:PRO:HD3	1.76	0.48
1:E:209:LYS:NZ	1:E:209:LYS:HB3	2.28	0.48
1:G:57:ILE:HG13	1:G:63:VAL:HG21	1.95	0.48
1:H:104:PHE:O	1:H:105:LYS:HB2	2.14	0.48
1:K:222:MET:CE	1:K:227:ILE:HG21	2.41	0.48
1:L:41:TRP:HA	1:L:277:LYS:HD3	1.94	0.48
1:B:93:PHE:H	1:B:104:PHE:HB2	1.79	0.48
1:D:56:SER:O	1:D:59:GLN:O	2.31	0.48
1:E:59:GLN:O	1:E:60:PHE:CD1	2.66	0.48
1:F:50:PRO:O	1:F:53:LEU:HB3	2.14	0.48
1:H:176:ASN:N	1:H:176:ASN:OD1	2.47	0.48
1:J:59:GLN:O	1:J:60:PHE:CD1	2.67	0.48
1:K:56:SER:O	1:K:59:GLN:O	2.30	0.48
1:A:168:GLN:HE22	1:A:169:LEU:HG	1.77	0.48
1:A:262:GLU:OE2	1:A:278:VAL:HG13	2.14	0.48
1:E:84:ARG:HD2	1:E:88:ASN:O	2.14	0.48
1:I:248:GLU:HB3	1:J:282:TYR:CE2	2.48	0.48
1:J:41:TRP:CE3	1:J:277:LYS:HE2	2.48	0.48
1:J:151:ASN:ND2	1:J:207:VAL:HG23	2.28	0.48
1:F:248:GLU:CG	1:G:227:ILE:CG2	2.87	0.48
1:G:41:TRP:CE3	1:G:277:LYS:HE2	2.49	0.48
1:G:110:ARG:C	1:G:112:MET:H	2.22	0.48
1:G:172:LYS:HG3	1:H:179:GLU:OE1	2.14	0.48
1:H:57:ILE:HG13	1:H:63:VAL:HG21	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:274:LEU:HD13	1:H:274:LEU:C	2.39	0.48
1:I:168:GLN:HE22	1:I:169:LEU:HG	1.77	0.48
1:C:59:GLN:O	1:C:60:PHE:CD1	2.67	0.48
1:D:131:THR:O	1:D:135:GLU:HG3	2.14	0.48
1:E:154:ALA:CB	1:G:182:ALA:HB2	2.44	0.48
1:F:93:PHE:H	1:F:104:PHE:HB2	1.79	0.48
1:I:176:ASN:OD1	1:I:176:ASN:N	2.47	0.48
1:I:277:LYS:HE3	1:I:278:VAL:H	1.79	0.48
1:K:110:ARG:C	1:K:112:MET:N	2.72	0.48
1:A:176:ASN:OD1	1:A:176:ASN:N	2.46	0.48
1:A:179:GLU:C	1:A:181:ASN:N	2.68	0.48
1:B:20:ARG:HG2	1:B:146:GLU:OE1	2.14	0.48
1:B:62:TYR:HB3	1:B:63:VAL:H	1.31	0.48
1:B:123:ASN:O	1:B:124:ASN:OD1	2.32	0.48
1:C:283:ASP:O	1:C:284:ILE:CB	2.62	0.48
1:D:93:PHE:HB2	1:D:106:LEU:HD21	1.94	0.48
1:E:168:GLN:HE22	1:E:169:LEU:HG	1.78	0.48
1:H:60:PHE:O	1:H:60:PHE:CD1	2.67	0.48
1:H:93:PHE:H	1:H:104:PHE:HB2	1.79	0.48
1:I:154:ALA:HA	1:K:181:ASN:O	2.14	0.48
1:A:248:GLU:HG3	1:B:227:ILE:HG23	1.95	0.47
1:B:12:ILE:CG2	1:B:15:ILE:HB	2.44	0.47
1:B:72:SER:O	1:B:74:ILE:HG13	2.14	0.47
1:B:274:LEU:HD13	1:B:274:LEU:C	2.39	0.47
1:C:84:ARG:HD2	1:C:88:ASN:O	2.14	0.47
1:C:110:ARG:C	1:C:112:MET:N	2.72	0.47
1:D:104:PHE:O	1:D:105:LYS:HB2	2.14	0.47
1:F:84:ARG:HD2	1:F:88:ASN:O	2.13	0.47
1:I:154:ALA:CB	1:K:182:ALA:HB2	2.44	0.47
1:K:93:PHE:H	1:K:104:PHE:HB2	1.79	0.47
1:C:57:ILE:HG13	1:C:63:VAL:HG21	1.95	0.47
1:C:249:GLN:CB	1:D:222:MET:HE2	2.45	0.47
1:F:57:ILE:HG13	1:F:63:VAL:HG21	1.95	0.47
1:F:283:ASP:O	1:F:284:ILE:CG1	2.62	0.47
1:G:176:ASN:OD1	1:G:176:ASN:N	2.48	0.47
1:H:124:ASN:HD21	1:H:128:PHE:HB2	1.79	0.47
1:H:277:LYS:HE3	1:H:278:VAL:H	1.79	0.47
1:J:178:TYR:H	1:J:178:TYR:HD2	1.61	0.47
1:C:277:LYS:HE3	1:C:278:VAL:H	1.77	0.47
1:E:104:PHE:O	1:E:105:LYS:HB2	2.13	0.47
1:F:110:ARG:C	1:F:112:MET:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:151:ASN:ND2	1:F:207:VAL:HG23	2.27	0.47
1:G:62:TYR:HB3	1:G:63:VAL:H	1.31	0.47
1:G:170:SER:C	1:G:171:LEU:O	2.55	0.47
1:I:110:ARG:C	1:I:112:MET:H	2.22	0.47
1:J:104:PHE:O	1:J:105:LYS:HB2	2.15	0.47
1:K:182:ALA:H	1:K:183:PRO:HD3	1.77	0.47
1:A:131:THR:O	1:A:135:GLU:HG3	2.15	0.47
1:A:150:VAL:HG22	1:C:180:GLY:HA2	1.95	0.47
1:B:59:GLN:O	1:B:60:PHE:CD1	2.67	0.47
1:G:38:LEU:HD11	1:G:225:LEU:HB3	1.96	0.47
1:G:283:ASP:O	1:G:284:ILE:CB	2.63	0.47
1:J:262:GLU:OE2	1:J:278:VAL:HG13	2.14	0.47
1:K:176:ASN:N	1:K:176:ASN:OD1	2.48	0.47
1:B:277:LYS:HE3	1:B:278:VAL:H	1.80	0.47
1:D:38:LEU:HD11	1:D:225:LEU:HB3	1.96	0.47
1:D:60:PHE:O	1:D:60:PHE:CD1	2.68	0.47
1:D:205:TYR:C	1:D:205:TYR:CD2	2.92	0.47
1:D:277:LYS:HE3	1:D:278:VAL:H	1.79	0.47
1:D:283:ASP:O	1:D:284:ILE:CB	2.62	0.47
1:E:93:PHE:H	1:E:104:PHE:HB2	1.78	0.47
1:G:93:PHE:H	1:G:104:PHE:HB2	1.79	0.47
1:H:12:ILE:CG2	1:H:15:ILE:HB	2.44	0.47
1:I:12:ILE:CG2	1:I:15:ILE:HB	2.44	0.47
1:A:209:LYS:HD3	1:B:205:TYR:CE2	2.49	0.47
1:A:222:MET:CE	1:A:227:ILE:HG21	2.42	0.47
1:C:59:GLN:O	1:C:60:PHE:C	2.57	0.47
1:D:168:GLN:HB2	1:D:188:HIS:CE1	2.50	0.47
1:E:283:ASP:O	1:E:284:ILE:CB	2.62	0.47
1:F:170:SER:C	1:F:171:LEU:O	2.54	0.47
1:F:193:SER:C	1:F:195:SER:N	2.73	0.47
1:G:60:PHE:O	1:G:60:PHE:CD1	2.67	0.47
1:G:171:LEU:C	1:G:173:GLN:N	2.53	0.47
1:H:20:ARG:HG2	1:H:146:GLU:OE1	2.15	0.47
1:H:154:ALA:CA	1:J:182:ALA:HB2	2.44	0.47
1:I:58:HIS:ND1	1:I:130:THR:HG21	2.29	0.47
1:I:108:ASN:CG	1:I:108:ASN:O	2.55	0.47
1:J:12:ILE:CG2	1:J:15:ILE:HB	2.45	0.47
1:J:283:ASP:O	1:J:284:ILE:HG13	2.15	0.47
1:A:12:ILE:CG2	1:A:15:ILE:HB	2.44	0.47
1:A:193:SER:C	1:A:195:SER:H	2.22	0.47
1:A:283:ASP:O	1:A:284:ILE:CB	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:ILE:HG13	1:B:63:VAL:HG21	1.97	0.47
1:B:60:PHE:O	1:B:60:PHE:CD1	2.68	0.47
1:B:222:MET:CE	1:B:227:ILE:HG21	2.43	0.47
1:C:12:ILE:CG2	1:C:15:ILE:HB	2.44	0.47
1:D:57:ILE:HG12	1:D:63:VAL:HG21	1.96	0.47
1:D:62:TYR:HB3	1:D:63:VAL:H	1.31	0.47
1:E:12:ILE:CG2	1:E:15:ILE:HB	2.44	0.47
1:E:126:MET:HE1	1:F:36:TYR:HE1	1.79	0.47
1:E:176:ASN:N	1:E:176:ASN:OD1	2.47	0.47
1:F:222:MET:CE	1:F:227:ILE:HG21	2.44	0.47
1:G:174:VAL:O	1:G:177:GLN:HG3	2.14	0.47
1:I:59:GLN:O	1:I:60:PHE:CD1	2.67	0.47
1:I:209:LYS:H	1:I:209:LYS:HG2	1.38	0.47
1:I:248:GLU:HG3	1:J:227:ILE:HG23	1.97	0.47
1:J:50:PRO:O	1:J:53:LEU:HB3	2.14	0.47
1:J:126:MET:HE1	1:K:36:TYR:CE1	2.50	0.47
1:K:178:TYR:H	1:K:178:TYR:HD2	1.60	0.47
1:K:193:SER:C	1:K:195:SER:N	2.73	0.47
1:L:50:PRO:O	1:L:54:GLU:HG3	2.14	0.47
1:L:191:LEU:O	1:L:192:ASP:HB3	2.15	0.47
1:A:85:ASP:HB3	1:A:89:GLN:H	1.80	0.47
1:A:248:GLU:CD	1:B:227:ILE:HG23	2.40	0.47
1:B:193:SER:C	1:B:195:SER:N	2.73	0.47
1:C:60:PHE:O	1:C:60:PHE:CD1	2.67	0.47
1:C:110:ARG:C	1:C:112:MET:H	2.21	0.47
1:C:204:PRO:O	1:C:205:TYR:CB	2.63	0.47
1:C:283:ASP:O	1:C:284:ILE:CG1	2.63	0.47
1:D:93:PHE:H	1:D:104:PHE:HB2	1.79	0.47
1:F:117:MET:CG	1:F:118:GLY:N	2.76	0.47
1:I:11:SER:HB3	1:J:176:ASN:ND2	2.27	0.47
1:K:41:TRP:CE3	1:K:277:LYS:HE2	2.50	0.47
1:K:193:SER:C	1:K:195:SER:H	2.23	0.47
1:L:170:SER:C	1:L:171:LEU:O	2.56	0.47
1:A:104:PHE:O	1:A:105:LYS:HB2	2.14	0.47
1:A:204:PRO:O	1:A:205:TYR:CB	2.63	0.47
1:A:277:LYS:HE3	1:A:278:VAL:H	1.79	0.47
1:B:163:ALA:O	1:C:187:ALA:HA	2.15	0.47
1:C:50:PRO:O	1:C:53:LEU:HB3	2.15	0.47
1:E:274:LEU:HD13	1:E:274:LEU:C	2.40	0.47
1:I:274:LEU:HD13	1:I:274:LEU:C	2.39	0.47
1:K:170:SER:C	1:K:171:LEU:O	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:191:LEU:O	1:K:192:ASP:HB3	2.15	0.47
1:K:204:PRO:O	1:K:205:TYR:CB	2.62	0.47
1:L:104:PHE:O	1:L:105:LYS:CB	2.63	0.47
1:A:93:PHE:H	1:A:104:PHE:HB2	1.79	0.47
1:A:155:GLN:HG3	1:L:206:VAL:HG21	1.97	0.47
1:A:193:SER:C	1:A:195:SER:N	2.71	0.47
1:E:60:PHE:O	1:E:60:PHE:CD1	2.67	0.47
1:E:140:GLU:CD	1:F:145:LYS:HE2	2.40	0.47
1:F:283:ASP:O	1:F:284:ILE:HG13	2.14	0.47
1:I:41:TRP:HA	1:I:277:LYS:HD3	1.95	0.47
1:I:172:LYS:HG3	1:J:179:GLU:OE1	2.15	0.47
1:J:110:ARG:C	1:J:112:MET:H	2.23	0.47
1:J:277:LYS:CE	1:J:278:VAL:H	2.26	0.47
1:A:205:TYR:C	1:A:205:TYR:CD2	2.93	0.46
1:B:283:ASP:O	1:B:284:ILE:CB	2.63	0.46
1:C:93:PHE:H	1:C:104:PHE:HB2	1.79	0.46
1:C:176:ASN:N	1:C:176:ASN:OD1	2.48	0.46
1:D:84:ARG:HD2	1:D:88:ASN:O	2.15	0.46
1:D:193:SER:C	1:D:195:SER:N	2.73	0.46
1:E:151:ASN:ND2	1:E:207:VAL:HG23	2.26	0.46
1:G:20:ARG:HG2	1:G:146:GLU:OE1	2.15	0.46
1:G:283:ASP:O	1:G:284:ILE:HG13	2.15	0.46
1:J:93:PHE:H	1:J:104:PHE:HB2	1.80	0.46
1:C:222:MET:CE	1:C:227:ILE:HG21	2.43	0.46
1:C:283:ASP:O	1:C:284:ILE:HG13	2.15	0.46
1:F:20:ARG:HG2	1:F:146:GLU:OE1	2.16	0.46
1:F:104:PHE:O	1:F:105:LYS:HB2	2.14	0.46
1:F:158:PRO:O	1:F:159:VAL:CB	2.62	0.46
1:H:283:ASP:O	1:H:284:ILE:CB	2.62	0.46
1:I:209:LYS:HB2	1:J:205:TYR:OH	2.15	0.46
1:J:15:ILE:C	1:J:17:ARG:N	2.73	0.46
1:J:283:ASP:O	1:J:284:ILE:CB	2.64	0.46
1:K:12:ILE:CG2	1:K:15:ILE:HB	2.44	0.46
1:K:87:TYR:CE2	1:L:49:ASN:HB2	2.50	0.46
1:L:168:GLN:HE22	1:L:169:LEU:HG	1.78	0.46
1:A:274:LEU:HD13	1:A:274:LEU:C	2.40	0.46
1:B:84:ARG:HD2	1:B:88:ASN:O	2.15	0.46
1:B:104:PHE:O	1:B:105:LYS:CB	2.64	0.46
1:B:170:SER:C	1:B:171:LEU:O	2.58	0.46
1:C:20:ARG:HG2	1:C:146:GLU:OE1	2.16	0.46
1:E:110:ARG:C	1:E:112:MET:H	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:193:SER:C	1:F:195:SER:H	2.24	0.46
1:H:62:TYR:O	1:H:63:VAL:HB	2.15	0.46
1:I:222:MET:CE	1:I:227:ILE:HG21	2.45	0.46
1:I:283:ASP:O	1:I:284:ILE:HG13	2.16	0.46
1:J:15:ILE:C	1:J:17:ARG:H	2.22	0.46
1:J:223:THR:HG23	1:J:250:ILE:HG12	1.97	0.46
1:L:58:HIS:ND1	1:L:130:THR:HG21	2.31	0.46
1:L:151:ASN:ND2	1:L:207:VAL:HG23	2.30	0.46
1:L:205:TYR:C	1:L:205:TYR:CD2	2.93	0.46
1:C:57:ILE:N	1:C:63:VAL:HG21	2.31	0.46
1:D:274:LEU:HD13	1:D:274:LEU:C	2.41	0.46
1:F:43:ASN:O	1:F:44:LEU:CB	2.60	0.46
1:F:110:ARG:C	1:F:112:MET:H	2.22	0.46
1:H:39:PHE:HE1	1:H:258:LEU:HB2	1.80	0.46
1:A:20:ARG:HG2	1:A:146:GLU:OE1	2.14	0.46
1:C:104:PHE:O	1:C:105:LYS:CB	2.64	0.46
1:C:151:ASN:ND2	1:C:207:VAL:HG23	2.31	0.46
1:D:110:ARG:C	1:D:112:MET:H	2.23	0.46
1:D:110:ARG:C	1:D:112:MET:N	2.73	0.46
1:D:151:ASN:ND2	1:D:207:VAL:HG23	2.29	0.46
1:E:108:ASN:O	1:E:109:TYR:C	2.59	0.46
1:G:151:ASN:ND2	1:G:207:VAL:HG23	2.30	0.46
1:G:193:SER:C	1:G:195:SER:N	2.73	0.46
1:H:84:ARG:HD2	1:H:88:ASN:O	2.14	0.46
1:H:108:ASN:O	1:H:109:TYR:C	2.59	0.46
1:H:204:PRO:O	1:H:205:TYR:CB	2.63	0.46
1:K:62:TYR:HB3	1:K:63:VAL:H	1.31	0.46
1:K:110:ARG:C	1:K:112:MET:H	2.22	0.46
1:L:59:GLN:O	1:L:60:PHE:CD1	2.68	0.46
1:A:60:PHE:O	1:A:60:PHE:CD1	2.67	0.46
1:C:209:LYS:H	1:C:209:LYS:HG2	1.38	0.46
1:C:255:THR:HG21	1:D:281:ARG:HD3	1.98	0.46
1:G:274:LEU:HD13	1:G:274:LEU:C	2.41	0.46
1:G:277:LYS:HE3	1:G:278:VAL:H	1.80	0.46
1:J:193:SER:C	1:J:195:SER:H	2.23	0.46
1:J:209:LYS:H	1:J:209:LYS:HG2	1.36	0.46
1:K:274:LEU:HD13	1:K:274:LEU:C	2.40	0.46
1:K:283:ASP:O	1:K:284:ILE:CB	2.63	0.46
1:L:60:PHE:O	1:L:60:PHE:CD1	2.68	0.46
1:L:93:PHE:H	1:L:104:PHE:HB2	1.80	0.46
1:A:182:ALA:H	1:A:183:PRO:HD3	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:193:SER:C	1:C:195:SER:H	2.23	0.46
1:E:60:PHE:HA	1:E:129:PRO:HG3	1.97	0.46
1:G:84:ARG:HD2	1:G:88:ASN:O	2.15	0.46
1:G:110:ARG:C	1:G:112:MET:N	2.72	0.46
1:H:38:LEU:HD11	1:H:225:LEU:HB3	1.98	0.46
1:I:283:ASP:O	1:I:284:ILE:CG1	2.64	0.46
1:J:110:ARG:C	1:J:112:MET:N	2.74	0.46
1:K:283:ASP:O	1:K:284:ILE:CG1	2.64	0.46
1:B:172:LYS:NZ	1:C:177:GLN:HE22	2.13	0.46
1:B:204:PRO:O	1:B:205:TYR:CB	2.63	0.46
1:C:168:GLN:HB2	1:C:188:HIS:CE1	2.50	0.46
1:C:223:THR:HG23	1:C:250:ILE:HG12	1.97	0.46
1:D:170:SER:C	1:D:171:LEU:O	2.55	0.46
1:E:62:TYR:O	1:E:63:VAL:HB	2.16	0.46
1:F:204:PRO:O	1:F:205:TYR:CB	2.64	0.46
1:G:193:SER:C	1:G:195:SER:H	2.24	0.46
1:G:283:ASP:O	1:G:284:ILE:CG1	2.63	0.46
1:H:151:ASN:ND2	1:H:207:VAL:HG23	2.31	0.46
1:I:126:MET:HG3	1:J:55:LYS:NZ	2.31	0.46
1:I:193:SER:C	1:I:195:SER:N	2.73	0.46
1:J:101:GLN:O	1:J:102:LYS:HB2	2.15	0.46
1:B:38:LEU:O	1:B:39:PHE:CB	2.63	0.46
1:B:39:PHE:CA	1:B:280:PHE:O	2.64	0.46
1:D:15:ILE:C	1:D:17:ARG:H	2.24	0.46
1:D:158:PRO:O	1:D:159:VAL:CB	2.59	0.46
1:E:110:ARG:C	1:E:112:MET:N	2.73	0.46
1:F:154:ALA:CA	1:H:182:ALA:HB2	2.46	0.46
1:F:176:ASN:N	1:F:176:ASN:OD1	2.48	0.46
1:F:262:GLU:OE2	1:F:278:VAL:HG13	2.16	0.46
1:G:12:ILE:CG2	1:G:15:ILE:HB	2.45	0.46
1:G:143:GLU:OE2	1:H:153:ASN:ND2	2.44	0.46
1:H:205:TYR:C	1:H:205:TYR:CD2	2.94	0.46
1:I:20:ARG:HG2	1:I:146:GLU:OE1	2.16	0.46
1:J:277:LYS:HE3	1:J:278:VAL:H	1.80	0.46
1:J:283:ASP:O	1:J:284:ILE:CG1	2.64	0.46
1:K:15:ILE:C	1:K:17:ARG:N	2.74	0.46
1:L:110:ARG:C	1:L:112:MET:H	2.24	0.46
1:B:108:ASN:O	1:B:109:TYR:C	2.59	0.46
1:B:151:ASN:ND2	1:B:207:VAL:HG23	2.29	0.46
1:D:12:ILE:CG2	1:D:15:ILE:HB	2.45	0.46
1:D:59:GLN:O	1:D:60:PHE:CD1	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:248:GLU:CB	1:E:282:TYR:CZ	2.99	0.46
1:F:12:ILE:CG2	1:F:15:ILE:HB	2.44	0.46
1:F:191:LEU:O	1:F:192:ASP:HB3	2.15	0.46
1:H:58:HIS:ND1	1:H:130:THR:HG21	2.31	0.46
1:I:85:ASP:HB3	1:I:89:GLN:H	1.80	0.46
1:J:176:ASN:OD1	1:J:176:ASN:N	2.47	0.46
1:K:283:ASP:O	1:K:284:ILE:HG13	2.15	0.46
1:L:283:ASP:O	1:L:284:ILE:CB	2.63	0.46
1:A:39:PHE:CZ	1:A:257:PHE:HB2	2.51	0.45
1:D:144:LEU:HD13	1:D:214:LYS:HA	1.98	0.45
1:E:204:PRO:O	1:E:205:TYR:CB	2.63	0.45
1:G:108:ASN:O	1:G:109:TYR:C	2.59	0.45
1:G:168:GLN:HE22	1:G:169:LEU:HG	1.79	0.45
1:H:193:SER:C	1:H:195:SER:H	2.24	0.45
1:J:123:ASN:ND2	1:J:257:PHE:HD2	1.92	0.45
1:K:151:ASN:ND2	1:K:207:VAL:HG23	2.28	0.45
1:L:177:GLN:O	1:L:179:GLU:N	2.50	0.45
1:L:204:PRO:O	1:L:205:TYR:CB	2.63	0.45
1:A:15:ILE:C	1:A:17:ARG:N	2.74	0.45
1:A:84:ARG:HD2	1:A:88:ASN:O	2.16	0.45
1:B:105:LYS:HE2	1:B:114:GLU:OE1	2.17	0.45
1:B:193:SER:C	1:B:195:SER:H	2.24	0.45
1:F:101:GLN:O	1:F:102:LYS:HB2	2.16	0.45
1:G:85:ASP:HB3	1:G:89:GLN:H	1.81	0.45
1:G:154:ALA:HA	1:I:181:ASN:O	2.16	0.45
1:I:39:PHE:HE1	1:I:258:LEU:HB2	1.80	0.45
1:I:163:ALA:O	1:J:187:ALA:HA	2.16	0.45
1:I:177:GLN:O	1:I:179:GLU:N	2.49	0.45
1:J:57:ILE:N	1:J:63:VAL:HG21	2.31	0.45
1:J:205:TYR:C	1:J:205:TYR:CD2	2.93	0.45
1:L:12:ILE:CG2	1:L:15:ILE:HB	2.45	0.45
1:L:15:ILE:C	1:L:17:ARG:N	2.74	0.45
1:L:60:PHE:N	1:L:129:PRO:HB3	2.31	0.45
1:A:191:LEU:O	1:A:192:ASP:HB3	2.16	0.45
1:B:50:PRO:O	1:B:53:LEU:HB3	2.16	0.45
1:B:110:ARG:C	1:B:112:MET:H	2.23	0.45
1:C:193:SER:C	1:C:195:SER:N	2.73	0.45
1:F:284:ILE:O	1:F:284:ILE:HG22	2.16	0.45
1:H:72:SER:O	1:H:74:ILE:HG13	2.16	0.45
1:H:131:THR:O	1:H:135:GLU:HG3	2.17	0.45
1:I:15:ILE:C	1:I:17:ARG:N	2.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:205:TYR:C	1:I:205:TYR:CD2	2.94	0.45
1:J:71:ILE:CG2	1:J:74:ILE:HD11	2.45	0.45
1:K:84:ARG:HD2	1:K:88:ASN:O	2.16	0.45
1:L:101:GLN:O	1:L:102:LYS:HB2	2.16	0.45
1:L:209:LYS:H	1:L:209:LYS:HG2	1.39	0.45
1:L:277:LYS:HE3	1:L:278:VAL:H	1.81	0.45
1:A:193:SER:O	1:A:195:SER:N	2.50	0.45
1:C:159:VAL:HA	1:C:199:PHE:O	2.16	0.45
1:D:57:ILE:N	1:D:63:VAL:HG21	2.31	0.45
1:D:280:PHE:O	1:D:281:ARG:HB2	2.17	0.45
1:G:62:TYR:O	1:G:63:VAL:HB	2.17	0.45
1:I:117:MET:CG	1:I:118:GLY:N	2.78	0.45
1:I:193:SER:C	1:I:195:SER:H	2.24	0.45
1:J:39:PHE:HE1	1:J:258:LEU:HB2	1.82	0.45
1:J:62:TYR:HB3	1:J:63:VAL:H	1.31	0.45
1:J:85:ASP:HB3	1:J:89:GLN:H	1.81	0.45
1:K:60:PHE:O	1:K:60:PHE:CD1	2.69	0.45
1:K:140:GLU:CD	1:L:145:LYS:HE2	2.42	0.45
1:K:159:VAL:HA	1:K:199:PHE:O	2.16	0.45
1:A:110:ARG:C	1:A:112:MET:N	2.74	0.45
1:A:201:THR:CG2	1:B:159:VAL:HG11	2.33	0.45
1:A:204:PRO:O	1:A:205:TYR:HB3	2.16	0.45
1:B:57:ILE:N	1:B:63:VAL:HG21	2.32	0.45
1:B:110:ARG:C	1:B:112:MET:N	2.73	0.45
1:B:179:GLU:C	1:B:181:ASN:N	2.68	0.45
1:B:284:ILE:O	1:B:284:ILE:HG22	2.16	0.45
1:C:274:LEU:HD13	1:C:274:LEU:C	2.40	0.45
1:D:87:TYR:CE2	1:E:49:ASN:HB2	2.51	0.45
1:D:193:SER:C	1:D:195:SER:H	2.23	0.45
1:D:262:GLU:OE2	1:D:278:VAL:HG13	2.16	0.45
1:D:283:ASP:O	1:D:284:ILE:CG1	2.65	0.45
1:E:193:SER:C	1:E:195:SER:H	2.24	0.45
1:E:283:ASP:O	1:E:284:ILE:CG1	2.65	0.45
1:F:86:VAL:HA	1:G:99:VAL:CG1	2.45	0.45
1:H:179:GLU:C	1:H:181:ASN:N	2.68	0.45
1:I:191:LEU:O	1:I:192:ASP:HB3	2.17	0.45
1:J:191:LEU:O	1:J:192:ASP:HB3	2.15	0.45
1:K:101:GLN:O	1:K:102:LYS:HB2	2.17	0.45
1:K:177:GLN:O	1:K:179:GLU:N	2.49	0.45
1:B:283:ASP:O	1:B:284:ILE:HG13	2.17	0.45
1:D:62:TYR:O	1:D:63:VAL:HB	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:ILE:C	1:E:17:ARG:H	2.24	0.45
1:E:38:LEU:HD11	1:E:225:LEU:HB3	1.99	0.45
1:F:168:GLN:HB2	1:F:188:HIS:CE1	2.51	0.45
1:F:277:LYS:HE3	1:F:278:VAL:H	1.82	0.45
1:J:150:VAL:HG13	1:L:180:GLY:CA	2.43	0.45
1:K:15:ILE:C	1:K:17:ARG:H	2.23	0.45
1:L:274:LEU:HD13	1:L:274:LEU:C	2.41	0.45
1:A:177:GLN:HE22	1:L:172:LYS:NZ	2.14	0.45
1:C:110:ARG:HB3	1:D:47:THR:CG2	2.45	0.45
1:C:206:VAL:HG21	1:D:155:GLN:HG3	1.98	0.45
1:E:11:SER:HB3	1:F:176:ASN:ND2	2.32	0.45
1:E:39:PHE:CZ	1:E:257:PHE:HB2	2.52	0.45
1:F:248:GLU:OE1	1:G:227:ILE:HG23	2.16	0.45
1:G:205:TYR:C	1:G:205:TYR:CD2	2.95	0.45
1:I:280:PHE:O	1:I:281:ARG:HB2	2.17	0.45
1:K:204:PRO:O	1:K:205:TYR:HB3	2.17	0.45
1:C:101:GLN:O	1:C:102:LYS:HB2	2.15	0.45
1:C:262:GLU:OE2	1:C:278:VAL:HG13	2.17	0.45
1:E:191:LEU:O	1:E:192:ASP:HB3	2.16	0.45
1:F:274:LEU:HD13	1:F:274:LEU:C	2.41	0.45
1:H:110:ARG:C	1:H:112:MET:N	2.73	0.45
1:I:168:GLN:HB2	1:I:188:HIS:CE1	2.52	0.45
1:I:283:ASP:O	1:I:284:ILE:CB	2.63	0.45
1:J:38:LEU:HD11	1:J:225:LEU:HB3	1.98	0.45
1:J:113:LYS:HD2	1:J:113:LYS:O	2.17	0.45
1:A:15:ILE:C	1:A:17:ARG:H	2.24	0.45
1:A:283:ASP:O	1:A:284:ILE:CG1	2.65	0.45
1:B:151:ASN:O	1:B:154:ALA:HB3	2.17	0.45
1:H:39:PHE:CZ	1:H:257:PHE:HB2	2.51	0.45
1:H:191:LEU:O	1:H:192:ASP:HB3	2.17	0.45
1:H:213:GLN:O	1:H:216:ALA:HB3	2.17	0.45
1:I:15:ILE:C	1:I:17:ARG:H	2.24	0.45
1:J:193:SER:C	1:J:195:SER:N	2.72	0.45
1:K:85:ASP:HB3	1:K:89:GLN:H	1.82	0.45
1:K:104:PHE:O	1:K:105:LYS:HB2	2.16	0.45
1:K:108:ASN:O	1:K:109:TYR:C	2.59	0.45
1:L:110:ARG:C	1:L:112:MET:N	2.74	0.45
1:L:204:PRO:O	1:L:205:TYR:HB3	2.17	0.45
1:D:15:ILE:C	1:D:17:ARG:N	2.74	0.45
1:E:15:ILE:C	1:E:17:ARG:N	2.74	0.45
1:E:158:PRO:O	1:E:159:VAL:CB	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:284:ILE:O	1:G:284:ILE:HG22	2.17	0.45
1:I:110:ARG:C	1:I:112:MET:N	2.73	0.45
1:J:174:VAL:C	1:J:176:ASN:H	2.25	0.45
1:A:213:GLN:O	1:A:216:ALA:HB3	2.17	0.44
1:B:283:ASP:O	1:B:284:ILE:CG1	2.65	0.44
1:C:249:GLN:CG	1:D:222:MET:HE2	2.47	0.44
1:E:193:SER:C	1:E:195:SER:N	2.73	0.44
1:E:204:PRO:O	1:E:205:TYR:HB3	2.17	0.44
1:F:213:GLN:O	1:F:216:ALA:HB3	2.17	0.44
1:G:87:TYR:CE2	1:H:49:ASN:HB2	2.52	0.44
1:H:209:LYS:HB3	1:H:209:LYS:HZ3	1.82	0.44
1:I:284:ILE:O	1:I:284:ILE:HG22	2.16	0.44
1:K:213:GLN:O	1:K:216:ALA:HB3	2.18	0.44
1:L:71:ILE:CG2	1:L:74:ILE:HD11	2.47	0.44
1:A:280:PHE:O	1:A:281:ARG:HB2	2.17	0.44
1:A:283:ASP:O	1:A:284:ILE:HG13	2.17	0.44
1:B:150:VAL:HG22	1:D:180:GLY:HA2	1.99	0.44
1:B:280:PHE:O	1:B:281:ARG:HB2	2.17	0.44
1:C:158:PRO:O	1:C:159:VAL:CB	2.63	0.44
1:E:222:MET:CE	1:E:227:ILE:HG21	2.45	0.44
1:E:277:LYS:HE3	1:E:278:VAL:H	1.81	0.44
1:E:283:ASP:O	1:E:284:ILE:HG13	2.17	0.44
1:F:110:ARG:CB	1:G:47:THR:HG22	2.47	0.44
1:F:209:LYS:HB2	1:G:205:TYR:OH	2.16	0.44
1:G:72:SER:O	1:G:74:ILE:HG13	2.17	0.44
1:G:168:GLN:HB2	1:G:188:HIS:CE1	2.52	0.44
1:G:280:PHE:O	1:G:281:ARG:HB2	2.17	0.44
1:H:15:ILE:C	1:H:17:ARG:N	2.74	0.44
1:J:108:ASN:O	1:J:108:ASN:CG	2.59	0.44
1:J:259:LYS:O	1:J:263:GLU:HG3	2.17	0.44
1:A:57:ILE:HG13	1:A:63:VAL:HG21	1.99	0.44
1:A:101:GLN:O	1:A:102:LYS:HB2	2.17	0.44
1:A:187:ALA:HA	1:L:163:ALA:O	2.18	0.44
1:C:178:TYR:CD2	1:C:178:TYR:N	2.85	0.44
1:C:259:LYS:O	1:C:263:GLU:HG3	2.17	0.44
1:D:108:ASN:O	1:D:109:TYR:C	2.59	0.44
1:D:277:LYS:NZ	1:D:278:VAL:O	2.35	0.44
1:E:174:VAL:C	1:E:176:ASN:H	2.25	0.44
1:E:177:GLN:O	1:E:179:GLU:N	2.51	0.44
1:E:284:ILE:O	1:E:284:ILE:HG22	2.18	0.44
1:G:179:GLU:C	1:G:181:ASN:N	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:140:GLU:CD	1:J:145:LYS:HE2	2.42	0.44
1:L:193:SER:C	1:L:195:SER:H	2.25	0.44
1:A:57:ILE:N	1:A:63:VAL:HG21	2.32	0.44
1:A:168:GLN:HB2	1:A:188:HIS:CE1	2.52	0.44
1:B:168:GLN:HB2	1:B:188:HIS:CE1	2.53	0.44
1:C:57:ILE:HG12	1:C:63:VAL:HG21	1.99	0.44
1:E:205:TYR:C	1:E:205:TYR:CD2	2.96	0.44
1:F:108:ASN:O	1:F:109:TYR:C	2.60	0.44
1:F:130:THR:HG22	1:F:257:PHE:HE2	1.82	0.44
1:F:203:ALA:O	1:F:205:TYR:N	2.50	0.44
1:G:15:ILE:C	1:G:17:ARG:H	2.24	0.44
1:G:39:PHE:CZ	1:G:257:PHE:HB2	2.53	0.44
1:G:57:ILE:N	1:G:63:VAL:HG21	2.32	0.44
1:G:58:HIS:ND1	1:G:130:THR:HG21	2.32	0.44
1:I:62:TYR:O	1:I:63:VAL:HB	2.18	0.44
1:J:172:LYS:NZ	1:K:177:GLN:HE22	2.15	0.44
1:K:280:PHE:O	1:K:281:ARG:HB2	2.18	0.44
1:L:39:PHE:CZ	1:L:257:PHE:HB2	2.53	0.44
1:C:284:ILE:O	1:C:284:ILE:HG22	2.17	0.44
1:D:57:ILE:HG13	1:D:63:VAL:HG21	1.98	0.44
1:D:159:VAL:HA	1:D:199:PHE:O	2.17	0.44
1:E:39:PHE:HE1	1:E:258:LEU:HB2	1.82	0.44
1:G:15:ILE:C	1:G:17:ARG:N	2.75	0.44
1:H:110:ARG:C	1:H:112:MET:H	2.24	0.44
1:I:57:ILE:HG12	1:I:63:VAL:HG21	1.99	0.44
1:I:72:SER:O	1:I:74:ILE:HG13	2.18	0.44
1:J:61:GLY:O	1:J:62:TYR:C	2.60	0.44
1:J:151:ASN:HD21	1:J:205:TYR:HA	1.83	0.44
1:L:72:SER:O	1:L:74:ILE:HG13	2.17	0.44
1:A:108:ASN:O	1:A:109:TYR:C	2.60	0.44
1:A:110:ARG:C	1:A:112:MET:H	2.24	0.44
1:G:144:LEU:HD13	1:G:214:LYS:HA	1.99	0.44
1:J:193:SER:O	1:J:195:SER:N	2.50	0.44
1:K:38:LEU:HD11	1:K:225:LEU:HB3	1.98	0.44
1:C:38:LEU:HD11	1:C:225:LEU:HB3	2.00	0.44
1:C:280:PHE:O	1:C:281:ARG:HB2	2.18	0.44
1:D:191:LEU:O	1:D:192:ASP:HB3	2.18	0.44
1:D:204:PRO:O	1:D:205:TYR:CB	2.65	0.44
1:E:168:GLN:HB2	1:E:188:HIS:CE1	2.53	0.44
1:F:15:ILE:C	1:F:17:ARG:N	2.75	0.44
1:G:262:GLU:OE2	1:G:278:VAL:HG13	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:60:PHE:N	1:H:129:PRO:HB3	2.33	0.44
1:H:283:ASP:O	1:H:284:ILE:CG1	2.66	0.44
1:K:113:LYS:O	1:K:113:LYS:HD2	2.18	0.44
1:L:193:SER:C	1:L:195:SER:N	2.74	0.44
1:A:62:TYR:HB3	1:A:63:VAL:H	1.31	0.44
1:C:113:LYS:O	1:C:113:LYS:HD2	2.18	0.44
1:C:204:PRO:O	1:C:205:TYR:HB3	2.18	0.44
1:D:283:ASP:O	1:D:284:ILE:HG13	2.18	0.44
1:E:87:TYR:CE2	1:F:49:ASN:HB2	2.52	0.44
1:F:85:ASP:HB3	1:F:89:GLN:H	1.83	0.44
1:G:204:PRO:O	1:G:205:TYR:CB	2.66	0.44
1:H:204:PRO:O	1:H:205:TYR:HB3	2.18	0.44
1:I:84:ARG:HD2	1:I:88:ASN:O	2.17	0.44
1:J:163:ALA:O	1:K:187:ALA:HA	2.17	0.44
1:K:62:TYR:O	1:K:63:VAL:HB	2.18	0.44
1:L:131:THR:O	1:L:135:GLU:HG3	2.18	0.44
1:L:280:PHE:O	1:L:281:ARG:HB2	2.18	0.44
1:B:15:ILE:C	1:B:17:ARG:H	2.25	0.44
1:E:57:ILE:N	1:E:63:VAL:HG21	2.33	0.44
1:E:59:GLN:O	1:E:60:PHE:C	2.61	0.44
1:F:205:TYR:CD2	1:F:205:TYR:C	2.96	0.44
1:G:158:PRO:O	1:G:159:VAL:CB	2.62	0.44
1:H:57:ILE:N	1:H:63:VAL:HG21	2.32	0.44
1:H:193:SER:C	1:H:195:SER:N	2.73	0.44
1:H:284:ILE:HG22	1:H:284:ILE:O	2.17	0.44
1:J:39:PHE:CA	1:J:280:PHE:O	2.65	0.44
1:K:168:GLN:HB2	1:K:188:HIS:CE1	2.53	0.44
1:L:85:ASP:HB3	1:L:89:GLN:H	1.82	0.44
1:A:104:PHE:O	1:A:105:LYS:CB	2.65	0.43
1:A:269:ASN:CG	1:A:275:ASN:H	2.26	0.43
1:B:203:ALA:O	1:B:205:TYR:N	2.51	0.43
1:B:262:GLU:OE2	1:B:278:VAL:HG13	2.18	0.43
1:B:275:ASN:C	1:B:277:LYS:N	2.75	0.43
1:C:105:LYS:HE2	1:C:114:GLU:OE1	2.18	0.43
1:D:105:LYS:HE2	1:D:114:GLU:OE1	2.18	0.43
1:F:57:ILE:N	1:F:63:VAL:HG21	2.33	0.43
1:F:178:TYR:N	1:F:178:TYR:CD2	2.86	0.43
1:H:62:TYR:HB3	1:H:63:VAL:H	1.30	0.43
1:H:104:PHE:O	1:H:105:LYS:CB	2.66	0.43
1:I:113:LYS:HD2	1:I:113:LYS:O	2.18	0.43
1:K:104:PHE:O	1:K:105:LYS:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:LEU:HD11	1:B:121:ILE:HD12	2.00	0.43
1:C:150:VAL:HG13	1:E:180:GLY:CA	2.45	0.43
1:D:85:ASP:HB3	1:D:89:GLN:H	1.82	0.43
1:D:284:ILE:O	1:D:284:ILE:HG22	2.17	0.43
1:E:275:ASN:C	1:E:277:LYS:N	2.76	0.43
1:F:39:PHE:HE1	1:F:258:LEU:HB2	1.81	0.43
1:F:104:PHE:O	1:F:105:LYS:CB	2.65	0.43
1:G:104:PHE:O	1:G:105:LYS:CB	2.66	0.43
1:G:131:THR:O	1:G:135:GLU:HG3	2.18	0.43
1:I:178:TYR:CD2	1:I:178:TYR:N	2.86	0.43
1:L:213:GLN:O	1:L:216:ALA:HB3	2.18	0.43
1:A:177:GLN:O	1:A:179:GLU:N	2.51	0.43
1:B:62:TYR:O	1:B:63:VAL:HB	2.18	0.43
1:C:191:LEU:O	1:C:192:ASP:HB3	2.17	0.43
1:C:248:GLU:CD	1:D:227:ILE:CG2	2.83	0.43
1:D:101:GLN:O	1:D:102:LYS:HB2	2.18	0.43
1:D:213:GLN:O	1:D:216:ALA:HB3	2.18	0.43
1:E:20:ARG:HG2	1:E:146:GLU:OE1	2.18	0.43
1:E:104:PHE:O	1:E:105:LYS:CB	2.66	0.43
1:F:62:TYR:O	1:F:63:VAL:HB	2.18	0.43
1:G:213:GLN:O	1:G:216:ALA:HB3	2.19	0.43
1:H:15:ILE:C	1:H:17:ARG:H	2.24	0.43
1:H:168:GLN:HB2	1:H:188:HIS:CE1	2.53	0.43
1:I:39:PHE:CZ	1:I:257:PHE:HB2	2.53	0.43
1:I:60:PHE:O	1:I:60:PHE:CD1	2.69	0.43
1:I:262:GLU:OE2	1:I:278:VAL:HG13	2.18	0.43
1:J:276:VAL:O	1:J:277:LYS:C	2.60	0.43
1:L:15:ILE:C	1:L:17:ARG:H	2.24	0.43
1:L:57:ILE:HG12	1:L:63:VAL:HG21	1.99	0.43
1:L:222:MET:CE	1:L:227:ILE:HG21	2.44	0.43
1:A:60:PHE:HA	1:A:129:PRO:HG3	2.00	0.43
1:C:39:PHE:CZ	1:C:257:PHE:HB2	2.53	0.43
1:C:255:THR:O	1:C:256:VAL:C	2.62	0.43
1:D:113:LYS:HD2	1:D:113:LYS:O	2.19	0.43
1:D:178:TYR:CD2	1:D:178:TYR:N	2.87	0.43
1:F:39:PHE:CZ	1:F:257:PHE:HB2	2.53	0.43
1:G:163:ALA:O	1:H:187:ALA:HA	2.18	0.43
1:H:255:THR:O	1:H:256:VAL:C	2.62	0.43
1:H:262:GLU:OE2	1:H:278:VAL:HG13	2.18	0.43
1:I:71:ILE:CG2	1:I:74:ILE:HD11	2.48	0.43
1:I:105:LYS:HE2	1:I:114:GLU:OE1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:62:TYR:O	1:J:63:VAL:HB	2.19	0.43
1:J:275:ASN:C	1:J:277:LYS:N	2.76	0.43
1:L:283:ASP:O	1:L:284:ILE:CG1	2.66	0.43
1:A:178:TYR:CD2	1:A:178:TYR:N	2.87	0.43
1:B:61:GLY:O	1:B:62:TYR:C	2.61	0.43
1:B:85:ASP:HB3	1:B:89:GLN:HB2	2.00	0.43
1:B:193:SER:O	1:B:195:SER:N	2.51	0.43
1:C:66:TYR:CE2	1:C:68:ASP:HA	2.54	0.43
1:C:174:VAL:C	1:C:176:ASN:H	2.27	0.43
1:C:277:LYS:O	1:C:278:VAL:CB	2.67	0.43
1:D:71:ILE:CG2	1:D:74:ILE:HD11	2.48	0.43
1:D:72:SER:O	1:D:74:ILE:HG13	2.19	0.43
1:D:201:THR:O	1:D:201:THR:CG2	2.57	0.43
1:D:275:ASN:C	1:D:277:LYS:N	2.77	0.43
1:E:178:TYR:N	1:E:178:TYR:CD2	2.86	0.43
1:E:213:GLN:O	1:E:216:ALA:HB3	2.19	0.43
1:F:15:ILE:C	1:F:17:ARG:H	2.25	0.43
1:F:72:SER:O	1:F:74:ILE:HG13	2.18	0.43
1:F:280:PHE:O	1:F:281:ARG:HB2	2.18	0.43
1:G:105:LYS:HE2	1:G:114:GLU:OE1	2.19	0.43
1:G:151:ASN:HD21	1:G:205:TYR:HA	1.84	0.43
1:G:177:GLN:O	1:G:179:GLU:N	2.51	0.43
1:H:105:LYS:HE2	1:H:114:GLU:OE1	2.18	0.43
1:I:57:ILE:N	1:I:63:VAL:HG21	2.32	0.43
1:I:206:VAL:HG21	1:J:155:GLN:HG3	1.99	0.43
1:B:205:TYR:C	1:B:205:TYR:CD2	2.96	0.43
1:B:259:LYS:O	1:B:263:GLU:HG3	2.18	0.43
1:C:62:TYR:O	1:C:63:VAL:HB	2.17	0.43
1:F:131:THR:O	1:F:135:GLU:HG3	2.19	0.43
1:F:204:PRO:O	1:F:205:TYR:HB3	2.18	0.43
1:G:59:GLN:O	1:G:60:PHE:C	2.62	0.43
1:H:144:LEU:HD13	1:H:214:LYS:HA	2.00	0.43
1:I:51:SER:O	1:I:55:LYS:HG3	2.19	0.43
1:I:101:GLN:O	1:I:102:LYS:HB2	2.18	0.43
1:I:144:LEU:HD13	1:I:214:LYS:HA	2.01	0.43
1:I:164:ASN:C	1:I:164:ASN:HD22	2.26	0.43
1:I:204:PRO:O	1:I:205:TYR:CB	2.66	0.43
1:I:259:LYS:O	1:I:263:GLU:HG3	2.19	0.43
1:I:275:ASN:C	1:I:277:LYS:N	2.76	0.43
1:J:126:MET:HG3	1:K:55:LYS:NZ	2.34	0.43
1:J:203:ALA:O	1:J:205:TYR:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:275:ASN:C	1:L:277:LYS:N	2.77	0.43
1:L:284:ILE:O	1:L:284:ILE:HG22	2.16	0.43
1:A:71:ILE:CG2	1:A:74:ILE:HD11	2.49	0.43
1:B:204:PRO:O	1:B:205:TYR:HB3	2.18	0.43
1:C:130:THR:HG22	1:C:257:PHE:HE2	1.84	0.43
1:C:131:THR:O	1:C:135:GLU:HG3	2.18	0.43
1:C:276:VAL:O	1:C:277:LYS:C	2.62	0.43
1:C:283:ASP:O	1:C:284:ILE:HB	2.19	0.43
1:D:36:TYR:CD1	1:D:55:LYS:HD2	2.54	0.43
1:D:104:PHE:O	1:D:105:LYS:CB	2.66	0.43
1:E:72:SER:O	1:E:74:ILE:HG13	2.17	0.43
1:G:191:LEU:O	1:G:192:ASP:HB3	2.18	0.43
1:H:222:MET:CE	1:H:227:ILE:HG21	2.46	0.43
1:H:280:PHE:O	1:H:281:ARG:HB2	2.19	0.43
1:K:144:LEU:HD13	1:K:214:LYS:HA	2.00	0.43
1:L:59:GLN:O	1:L:60:PHE:C	2.62	0.43
1:L:62:TYR:O	1:L:63:VAL:HB	2.18	0.43
1:L:108:ASN:O	1:L:109:TYR:C	2.61	0.43
1:A:39:PHE:HE1	1:A:258:LEU:HB2	1.84	0.43
1:A:205:TYR:OH	1:L:209:LYS:HB2	2.19	0.43
1:C:108:ASN:O	1:C:109:TYR:C	2.61	0.43
1:C:205:TYR:CD2	1:C:205:TYR:C	2.97	0.43
1:F:60:PHE:O	1:F:60:PHE:CD1	2.70	0.43
1:F:126:MET:HE2	1:G:55:LYS:NZ	2.34	0.43
1:G:39:PHE:CA	1:G:280:PHE:O	2.67	0.43
1:H:85:ASP:HB3	1:H:89:GLN:HB2	2.01	0.43
1:H:151:ASN:HD21	1:H:205:TYR:HA	1.84	0.43
1:H:275:ASN:C	1:H:277:LYS:N	2.77	0.43
1:J:104:PHE:O	1:J:105:LYS:CB	2.67	0.43
1:J:105:LYS:HE2	1:J:114:GLU:OE1	2.19	0.43
1:J:131:THR:O	1:J:135:GLU:HG3	2.18	0.43
1:J:209:LYS:HD3	1:K:205:TYR:CE2	2.54	0.43
1:J:280:PHE:O	1:J:281:ARG:HB2	2.18	0.43
1:K:85:ASP:HB3	1:K:89:GLN:HB2	2.01	0.43
1:K:284:ILE:HG22	1:K:284:ILE:O	2.17	0.43
1:L:168:GLN:HB2	1:L:188:HIS:CE1	2.54	0.43
1:L:203:ALA:O	1:L:205:TYR:N	2.52	0.43
1:L:259:LYS:O	1:L:263:GLU:HG3	2.19	0.43
1:A:255:THR:O	1:A:256:VAL:C	2.62	0.43
1:C:15:ILE:C	1:C:17:ARG:H	2.25	0.43
1:C:103:GLU:C	1:C:104:PHE:HD1	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:280:PHE:O	1:E:281:ARG:HB2	2.18	0.43
1:F:38:LEU:HD11	1:F:225:LEU:HB3	2.00	0.43
1:F:249:GLN:CB	1:G:222:MET:HE2	2.47	0.43
1:G:248:GLU:HB3	1:H:282:TYR:CZ	2.54	0.43
1:I:104:PHE:O	1:I:105:LYS:CB	2.66	0.43
1:I:277:LYS:O	1:I:278:VAL:CB	2.67	0.43
1:J:284:ILE:O	1:J:284:ILE:HG22	2.18	0.43
1:K:57:ILE:N	1:K:63:VAL:HG21	2.33	0.43
1:A:72:SER:O	1:A:74:ILE:HG13	2.18	0.43
1:B:158:PRO:O	1:B:159:VAL:CB	2.60	0.43
1:C:39:PHE:HE1	1:C:258:LEU:HB2	1.83	0.43
1:C:108:ASN:O	1:C:108:ASN:CG	2.61	0.43
1:C:193:SER:O	1:C:195:SER:N	2.52	0.43
1:D:59:GLN:O	1:D:60:PHE:C	2.61	0.43
1:D:143:GLU:OE2	1:E:153:ASN:ND2	2.49	0.43
1:D:151:ASN:HD21	1:D:205:TYR:HA	1.84	0.43
1:D:174:VAL:C	1:D:176:ASN:H	2.27	0.43
1:E:62:TYR:HB3	1:E:63:VAL:H	1.31	0.43
1:F:275:ASN:C	1:F:277:LYS:N	2.76	0.43
1:J:182:ALA:H	1:J:183:PRO:HD3	1.79	0.43
1:K:105:LYS:HE2	1:K:114:GLU:OE1	2.19	0.43
1:K:209:LYS:HB3	1:K:209:LYS:HZ3	1.82	0.43
1:A:62:TYR:O	1:A:63:VAL:HB	2.19	0.42
1:A:126:MET:C	1:A:128:PHE:N	2.77	0.42
1:A:209:LYS:H	1:A:209:LYS:HG2	1.40	0.42
1:B:144:LEU:HD13	1:B:214:LYS:HA	2.00	0.42
1:B:174:VAL:C	1:B:176:ASN:H	2.27	0.42
1:B:275:ASN:C	1:B:277:LYS:H	2.27	0.42
1:B:277:LYS:O	1:B:278:VAL:CB	2.67	0.42
1:C:86:VAL:CA	1:D:99:VAL:HG11	2.43	0.42
1:D:39:PHE:HE1	1:D:258:LEU:HB2	1.83	0.42
1:E:101:GLN:O	1:E:102:LYS:HB2	2.19	0.42
1:E:283:ASP:O	1:E:284:ILE:HB	2.18	0.42
1:F:42:GLU:HB2	1:F:277:LYS:HB3	2.01	0.42
1:G:126:MET:HG3	1:H:55:LYS:HZ3	1.84	0.42
1:J:108:ASN:O	1:J:109:TYR:C	2.62	0.42
1:K:151:ASN:HD21	1:K:205:TYR:HA	1.84	0.42
1:L:105:LYS:HE2	1:L:114:GLU:OE1	2.19	0.42
1:L:255:THR:O	1:L:256:VAL:C	2.62	0.42
1:A:61:GLY:O	1:A:62:TYR:C	2.60	0.42
1:A:105:LYS:HE2	1:A:114:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ASN:O	1:A:154:ALA:HB3	2.19	0.42
1:A:209:LYS:O	1:A:210:LEU:C	2.59	0.42
1:C:15:ILE:C	1:C:17:ARG:N	2.75	0.42
1:E:131:THR:O	1:E:135:GLU:HG3	2.19	0.42
1:E:277:LYS:O	1:E:278:VAL:CB	2.68	0.42
1:F:223:THR:HG23	1:F:250:ILE:HG12	2.01	0.42
1:G:61:GLY:O	1:G:62:TYR:C	2.62	0.42
1:G:71:ILE:CG2	1:G:74:ILE:HD11	2.49	0.42
1:I:57:ILE:HG13	1:I:63:VAL:HG21	2.01	0.42
1:J:66:TYR:CE2	1:J:68:ASP:HA	2.54	0.42
1:J:277:LYS:O	1:J:278:VAL:CB	2.67	0.42
1:K:72:SER:O	1:K:74:ILE:HG13	2.19	0.42
1:K:277:LYS:NZ	1:K:278:VAL:O	2.36	0.42
1:L:174:VAL:C	1:L:176:ASN:H	2.26	0.42
1:A:203:ALA:O	1:A:205:TYR:N	2.52	0.42
1:B:15:ILE:C	1:B:17:ARG:N	2.75	0.42
1:B:59:GLN:O	1:B:60:PHE:C	2.61	0.42
1:C:62:TYR:HB3	1:C:63:VAL:H	1.32	0.42
1:C:177:GLN:O	1:C:179:GLU:N	2.52	0.42
1:C:209:LYS:HB2	1:D:205:TYR:CZ	2.54	0.42
1:C:275:ASN:C	1:C:277:LYS:N	2.77	0.42
1:E:262:GLU:OE2	1:E:278:VAL:HG13	2.18	0.42
1:G:101:GLN:O	1:G:102:LYS:HB2	2.19	0.42
1:G:178:TYR:N	1:G:178:TYR:CD2	2.86	0.42
1:H:177:GLN:O	1:H:179:GLU:N	2.52	0.42
1:H:283:ASP:O	1:H:284:ILE:HG13	2.18	0.42
1:I:131:THR:O	1:I:135:GLU:HG3	2.19	0.42
1:J:60:PHE:HA	1:J:129:PRO:HG3	2.00	0.42
1:J:168:GLN:HB2	1:J:188:HIS:CE1	2.54	0.42
1:K:178:TYR:CD2	1:K:178:TYR:N	2.87	0.42
1:K:265:CYS:O	1:K:266:GLU:C	2.62	0.42
1:A:284:ILE:O	1:A:284:ILE:HG22	2.19	0.42
1:B:85:ASP:HB3	1:B:89:GLN:H	1.84	0.42
1:B:178:TYR:N	1:B:178:TYR:CD2	2.87	0.42
1:B:201:THR:CG2	1:C:159:VAL:HG11	2.33	0.42
1:E:71:ILE:CG2	1:E:74:ILE:HD11	2.49	0.42
1:F:193:SER:O	1:F:195:SER:N	2.52	0.42
1:G:85:ASP:HB3	1:G:89:GLN:HB2	2.01	0.42
1:H:85:ASP:HB3	1:H:89:GLN:H	1.85	0.42
1:H:283:ASP:O	1:H:284:ILE:HB	2.19	0.42
1:I:109:TYR:O	1:I:110:ARG:HB2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:151:ASN:ND2	1:I:207:VAL:HG23	2.32	0.42
1:J:178:TYR:N	1:J:178:TYR:CD2	2.87	0.42
1:K:39:PHE:HE1	1:K:258:LEU:HB2	1.83	0.42
1:K:205:TYR:C	1:K:205:TYR:CD2	2.97	0.42
1:L:283:ASP:O	1:L:284:ILE:HG13	2.18	0.42
1:B:191:LEU:O	1:B:192:ASP:HB3	2.18	0.42
1:C:42:GLU:HB2	1:C:277:LYS:HB3	2.00	0.42
1:D:193:SER:O	1:D:195:SER:N	2.53	0.42
1:F:276:VAL:O	1:F:277:LYS:C	2.62	0.42
1:F:283:ASP:O	1:F:284:ILE:HB	2.20	0.42
1:H:172:LYS:HG3	1:I:179:GLU:OE1	2.19	0.42
1:I:39:PHE:CE1	1:I:258:LEU:HB2	2.54	0.42
1:I:172:LYS:NZ	1:J:177:GLN:HE22	2.17	0.42
1:I:255:THR:O	1:I:256:VAL:C	2.61	0.42
1:J:103:GLU:C	1:J:104:PHE:HD1	2.28	0.42
1:J:109:TYR:O	1:J:110:ARG:HB2	2.19	0.42
1:J:204:PRO:O	1:J:205:TYR:CB	2.66	0.42
1:J:213:GLN:O	1:J:216:ALA:HB3	2.20	0.42
1:K:39:PHE:CZ	1:K:257:PHE:HB2	2.54	0.42
1:L:103:GLU:C	1:L:104:PHE:HD1	2.28	0.42
1:L:277:LYS:O	1:L:278:VAL:CB	2.68	0.42
1:A:113:LYS:HD2	1:A:113:LYS:O	2.18	0.42
1:B:248:GLU:HB2	1:C:282:TYR:CD1	2.55	0.42
1:C:151:ASN:O	1:C:154:ALA:HB3	2.19	0.42
1:C:154:ALA:HB1	1:E:182:ALA:HB2	2.01	0.42
1:D:39:PHE:CZ	1:D:257:PHE:HB2	2.54	0.42
1:D:255:THR:O	1:D:256:VAL:C	2.62	0.42
1:E:85:ASP:HB3	1:E:89:GLN:H	1.85	0.42
1:E:105:LYS:HE2	1:E:114:GLU:OE1	2.19	0.42
1:E:113:LYS:HD2	1:E:113:LYS:O	2.20	0.42
1:G:269:ASN:CG	1:G:275:ASN:H	2.28	0.42
1:H:113:LYS:O	1:H:113:LYS:HD2	2.19	0.42
1:J:20:ARG:HG2	1:J:146:GLU:OE1	2.19	0.42
1:J:42:GLU:HB2	1:J:277:LYS:HB3	2.02	0.42
1:L:39:PHE:HE1	1:L:258:LEU:HB2	1.84	0.42
1:A:66:TYR:CE2	1:A:68:ASP:HA	2.55	0.42
1:A:172:LYS:HG3	1:B:179:GLU:OE1	2.20	0.42
1:A:259:LYS:O	1:A:263:GLU:HG3	2.19	0.42
1:A:271:LEU:C	1:A:272:TYR:CD1	2.98	0.42
1:A:276:VAL:O	1:A:277:LYS:C	2.63	0.42
1:B:58:HIS:ND1	1:B:130:THR:HG21	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:276:VAL:O	1:D:277:LYS:C	2.62	0.42
1:E:38:LEU:O	1:E:39:PHE:HB2	2.20	0.42
1:F:174:VAL:C	1:F:176:ASN:H	2.27	0.42
1:F:201:THR:CG2	1:G:159:VAL:HG11	2.27	0.42
1:I:276:VAL:O	1:I:277:LYS:C	2.61	0.42
1:J:144:LEU:HD13	1:J:214:LYS:HA	2.01	0.42
1:K:103:GLU:C	1:K:104:PHE:HD1	2.28	0.42
1:K:131:THR:O	1:K:135:GLU:HG3	2.20	0.42
1:K:163:ALA:O	1:L:187:ALA:HA	2.20	0.42
1:B:38:LEU:HD11	1:B:225:LEU:HB3	2.01	0.42
1:B:131:THR:O	1:B:135:GLU:HG3	2.19	0.42
1:C:209:LYS:HB3	1:C:209:LYS:HZ2	1.84	0.42
1:D:172:LYS:HG3	1:E:179:GLU:OE1	2.19	0.42
1:D:209:LYS:HB3	1:D:209:LYS:HZ3	1.84	0.42
1:E:265:CYS:O	1:E:266:GLU:C	2.63	0.42
1:F:151:ASN:HD21	1:F:205:TYR:HA	1.84	0.42
1:G:53:LEU:HD11	1:G:121:ILE:HD12	2.02	0.42
1:H:42:GLU:HB2	1:H:277:LYS:HB3	2.01	0.42
1:H:164:ASN:C	1:H:164:ASN:HD22	2.28	0.42
1:I:61:GLY:O	1:I:62:TYR:C	2.63	0.42
1:J:117:MET:HB2	1:J:271:LEU:HD11	2.02	0.42
1:K:143:GLU:OE2	1:L:153:ASN:ND2	2.51	0.42
1:L:144:LEU:HD13	1:L:214:LYS:HA	2.02	0.42
1:L:269:ASN:CG	1:L:275:ASN:H	2.28	0.42
1:A:151:ASN:HD21	1:A:205:TYR:HA	1.85	0.42
1:C:85:ASP:HB3	1:C:89:GLN:H	1.85	0.42
1:D:259:LYS:O	1:D:263:GLU:HG3	2.20	0.42
1:D:265:CYS:O	1:D:266:GLU:C	2.63	0.42
1:E:39:PHE:CA	1:E:280:PHE:O	2.68	0.42
1:F:103:GLU:C	1:F:104:PHE:HD1	2.28	0.42
1:F:172:LYS:HG3	1:G:179:GLU:OE1	2.20	0.42
1:G:66:TYR:CE2	1:G:68:ASP:HA	2.54	0.42
1:G:193:SER:O	1:G:195:SER:N	2.53	0.42
1:H:39:PHE:CA	1:H:280:PHE:O	2.66	0.42
1:I:38:LEU:HD11	1:I:225:LEU:HB3	2.01	0.42
1:I:174:VAL:C	1:I:176:ASN:H	2.27	0.42
1:K:193:SER:O	1:K:195:SER:N	2.52	0.42
1:K:262:GLU:OE2	1:K:278:VAL:HG13	2.20	0.42
1:K:276:VAL:O	1:K:277:LYS:C	2.62	0.42
1:A:143:GLU:O	1:A:147:ILE:HG13	2.20	0.42
1:A:277:LYS:O	1:A:278:VAL:CB	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:VAL:HA	1:C:99:VAL:HG11	2.01	0.42
1:B:103:GLU:C	1:B:104:PHE:HD1	2.28	0.42
1:B:213:GLN:O	1:B:216:ALA:HB3	2.19	0.42
1:C:102:LYS:HG3	1:C:103:GLU:H	1.85	0.42
1:D:283:ASP:O	1:D:284:ILE:HB	2.19	0.42
1:E:58:HIS:ND1	1:E:130:THR:HG21	2.35	0.42
1:F:177:GLN:O	1:F:179:GLU:N	2.53	0.42
1:F:259:LYS:HD2	1:G:281:ARG:NH1	2.35	0.42
1:G:39:PHE:HE1	1:G:258:LEU:HB2	1.84	0.42
1:G:140:GLU:CD	1:H:145:LYS:HE2	2.45	0.42
1:H:178:TYR:CD2	1:H:178:TYR:N	2.88	0.42
1:I:66:TYR:CE2	1:I:68:ASP:HA	2.55	0.42
1:I:108:ASN:ND2	1:I:270:GLU:HB3	2.35	0.42
1:I:213:GLN:O	1:I:216:ALA:HB3	2.20	0.42
1:K:165:ASP:HB3	1:K:167:ASN:ND2	2.35	0.42
1:A:104:PHE:HB3	1:A:105:LYS:H	1.54	0.41
1:B:39:PHE:HE1	1:B:258:LEU:HB2	1.85	0.41
1:B:177:GLN:O	1:B:179:GLU:N	2.53	0.41
1:C:72:SER:O	1:C:74:ILE:HG13	2.19	0.41
1:F:66:TYR:CE2	1:F:68:ASP:HA	2.55	0.41
1:H:103:GLU:C	1:H:104:PHE:HD1	2.28	0.41
1:H:259:LYS:O	1:H:263:GLU:HG3	2.20	0.41
1:L:164:ASN:HD22	1:L:164:ASN:C	2.27	0.41
1:A:57:ILE:HG23	1:A:123:ASN:HB2	2.01	0.41
1:A:59:GLN:O	1:A:60:PHE:C	2.63	0.41
1:A:150:VAL:HG13	1:C:180:GLY:O	2.20	0.41
1:B:39:PHE:CZ	1:B:257:PHE:HB2	2.55	0.41
1:B:57:ILE:HG12	1:B:63:VAL:HG21	2.02	0.41
1:B:71:ILE:CG2	1:B:74:ILE:HD11	2.49	0.41
1:B:98:PRO:O	1:B:99:VAL:CB	2.68	0.41
1:B:113:LYS:HD2	1:B:113:LYS:O	2.20	0.41
1:B:143:GLU:O	1:B:147:ILE:HG13	2.20	0.41
1:C:53:LEU:HD11	1:C:121:ILE:HD12	2.02	0.41
1:C:85:ASP:HB3	1:C:89:GLN:HB2	2.02	0.41
1:C:109:TYR:O	1:C:110:ARG:HB2	2.20	0.41
1:C:110:ARG:NH2	1:D:72:SER:CB	2.67	0.41
1:D:42:GLU:HB2	1:D:277:LYS:HB3	2.02	0.41
1:E:209:LYS:H	1:E:209:LYS:HG2	1.38	0.41
1:F:108:ASN:O	1:F:108:ASN:CG	2.62	0.41
1:G:113:LYS:HD2	1:G:113:LYS:O	2.19	0.41
1:G:204:PRO:O	1:G:205:TYR:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:39:PHE:CA	1:I:280:PHE:O	2.68	0.41
1:I:193:SER:O	1:I:195:SER:N	2.53	0.41
1:J:49:ASN:HD22	1:J:50:PRO:N	2.18	0.41
1:K:283:ASP:O	1:K:284:ILE:HB	2.20	0.41
1:B:117:MET:HB2	1:B:271:LEU:HD11	2.02	0.41
1:D:53:LEU:HD11	1:D:121:ILE:HD12	2.03	0.41
1:D:57:ILE:HG12	1:D:63:VAL:CG2	2.50	0.41
1:D:87:TYR:CZ	1:E:49:ASN:N	2.85	0.41
1:E:151:ASN:HD21	1:E:205:TYR:HA	1.84	0.41
1:E:193:SER:O	1:E:195:SER:N	2.53	0.41
1:E:255:THR:O	1:E:256:VAL:C	2.63	0.41
1:E:275:ASN:C	1:E:277:LYS:H	2.28	0.41
1:F:277:LYS:O	1:F:278:VAL:CB	2.68	0.41
1:G:87:TYR:CZ	1:H:49:ASN:N	2.82	0.41
1:H:57:ILE:HG12	1:H:63:VAL:HG21	2.01	0.41
1:H:174:VAL:C	1:H:176:ASN:H	2.27	0.41
1:H:275:ASN:C	1:H:277:LYS:H	2.29	0.41
1:I:151:ASN:O	1:I:152:GLN:C	2.63	0.41
1:J:265:CYS:O	1:J:266:GLU:C	2.63	0.41
1:K:38:LEU:O	1:K:39:PHE:CB	2.68	0.41
1:K:108:ASN:ND2	1:K:270:GLU:HB3	2.35	0.41
1:L:39:PHE:CA	1:L:280:PHE:O	2.67	0.41
1:L:113:LYS:HD2	1:L:113:LYS:O	2.20	0.41
1:L:178:TYR:CD2	1:L:178:TYR:N	2.86	0.41
1:B:255:THR:O	1:B:256:VAL:C	2.64	0.41
1:D:39:PHE:CA	1:D:280:PHE:O	2.68	0.41
1:D:85:ASP:HB3	1:D:89:GLN:HB2	2.01	0.41
1:E:85:ASP:HB3	1:E:89:GLN:HB2	2.01	0.41
1:E:159:VAL:HA	1:E:199:PHE:O	2.21	0.41
1:E:203:ALA:O	1:E:205:TYR:N	2.53	0.41
1:F:249:GLN:NE2	1:G:222:MET:HG3	2.34	0.41
1:F:259:LYS:O	1:F:263:GLU:HG3	2.19	0.41
1:G:57:ILE:HG12	1:G:63:VAL:HG21	2.02	0.41
1:J:204:PRO:O	1:J:205:TYR:HB3	2.21	0.41
1:K:71:ILE:CG2	1:K:74:ILE:HD11	2.51	0.41
1:K:259:LYS:O	1:K:263:GLU:HG3	2.20	0.41
1:A:61:GLY:O	1:A:62:TYR:O	2.38	0.41
1:A:180:GLY:HA2	1:K:150:VAL:HG22	2.01	0.41
1:A:280:PHE:O	1:A:281:ARG:CB	2.68	0.41
1:B:276:VAL:O	1:B:277:LYS:C	2.63	0.41
1:C:144:LEU:HD13	1:C:214:LYS:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:87:TYR:HB3	1:G:52:PHE:CD1	2.55	0.41
1:F:105:LYS:HE2	1:F:114:GLU:OE1	2.20	0.41
1:F:165:ASP:HB3	1:F:167:ASN:ND2	2.35	0.41
1:G:42:GLU:HB2	1:G:277:LYS:HB3	2.02	0.41
1:G:174:VAL:C	1:G:176:ASN:H	2.28	0.41
1:H:154:ALA:HB1	1:J:182:ALA:HB2	2.03	0.41
1:H:163:ALA:O	1:I:187:ALA:HA	2.21	0.41
1:H:170:SER:O	1:H:171:LEU:O	2.38	0.41
1:J:165:ASP:HB3	1:J:167:ASN:ND2	2.35	0.41
1:K:39:PHE:CA	1:K:280:PHE:O	2.67	0.41
1:K:59:GLN:O	1:K:60:PHE:C	2.64	0.41
1:K:143:GLU:O	1:K:147:ILE:HG13	2.21	0.41
1:K:275:ASN:C	1:K:277:LYS:N	2.76	0.41
1:L:265:CYS:O	1:L:266:GLU:C	2.64	0.41
1:L:276:VAL:O	1:L:277:LYS:C	2.63	0.41
1:A:39:PHE:CA	1:A:280:PHE:O	2.67	0.41
1:A:145:LYS:HE2	1:L:140:GLU:CD	2.45	0.41
1:B:49:ASN:HD22	1:B:50:PRO:N	2.18	0.41
1:B:164:ASN:HD22	1:B:164:ASN:C	2.29	0.41
1:D:66:TYR:CE2	1:D:68:ASP:HA	2.56	0.41
1:D:87:TYR:OH	1:E:48:ILE:CA	2.43	0.41
1:D:269:ASN:CG	1:D:275:ASN:H	2.27	0.41
1:G:102:LYS:HG3	1:G:103:GLU:H	1.85	0.41
1:G:280:PHE:O	1:G:281:ARG:CB	2.69	0.41
1:H:154:ALA:HA	1:J:181:ASN:O	2.20	0.41
1:H:209:LYS:HD3	1:I:205:TYR:CE2	2.55	0.41
1:H:276:VAL:O	1:H:277:LYS:C	2.64	0.41
1:J:39:PHE:CZ	1:J:257:PHE:HB2	2.55	0.41
1:J:255:THR:O	1:J:256:VAL:C	2.62	0.41
1:K:66:TYR:CE2	1:K:68:ASP:HA	2.56	0.41
1:K:108:ASN:O	1:K:108:ASN:CG	2.63	0.41
1:K:164:ASN:C	1:K:164:ASN:HD22	2.29	0.41
1:K:174:VAL:C	1:K:176:ASN:H	2.28	0.41
1:L:85:ASP:HB3	1:L:89:GLN:HB2	2.02	0.41
1:A:108:ASN:ND2	1:A:270:GLU:HB3	2.35	0.41
1:B:283:ASP:O	1:B:284:ILE:HB	2.20	0.41
1:D:126:MET:HE1	1:E:36:TYR:CE1	2.56	0.41
1:D:282:TYR:CG	1:D:283:ASP:N	2.89	0.41
1:E:209:LYS:O	1:E:210:LEU:C	2.63	0.41
1:F:11:SER:HB3	1:G:176:ASN:HD22	1.85	0.41
1:F:113:LYS:HD2	1:F:113:LYS:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:255:THR:O	1:F:256:VAL:C	2.63	0.41
1:H:74:ILE:HG22	1:H:75:ALA:N	2.36	0.41
1:H:165:ASP:HB3	1:H:167:ASN:ND2	2.36	0.41
1:H:188:HIS:HB3	1:H:191:LEU:HG	2.03	0.41
1:I:151:ASN:HD21	1:I:205:TYR:HA	1.85	0.41
1:J:38:LEU:O	1:J:39:PHE:CB	2.69	0.41
1:J:154:ALA:HB1	1:L:182:ALA:HB2	2.01	0.41
1:K:53:LEU:HD11	1:K:121:ILE:HD12	2.02	0.41
1:A:38:LEU:O	1:A:39:PHE:HB2	2.21	0.41
1:A:49:ASN:HA	1:A:50:PRO:HD2	1.95	0.41
1:A:275:ASN:C	1:A:277:LYS:N	2.78	0.41
1:B:269:ASN:CG	1:B:275:ASN:H	2.28	0.41
1:D:117:MET:HB2	1:D:271:LEU:HD11	2.03	0.41
1:D:280:PHE:O	1:D:281:ARG:CB	2.69	0.41
1:E:66:TYR:CE2	1:E:68:ASP:HA	2.55	0.41
1:G:103:GLU:C	1:G:104:PHE:HD1	2.28	0.41
1:G:277:LYS:NZ	1:G:278:VAL:O	2.36	0.41
1:I:85:ASP:HB3	1:I:89:GLN:HB2	2.03	0.41
1:K:209:LYS:H	1:K:209:LYS:HG2	1.36	0.41
1:L:57:ILE:N	1:L:63:VAL:HG21	2.35	0.41
1:L:66:TYR:CE2	1:L:68:ASP:HA	2.55	0.41
1:L:283:ASP:O	1:L:284:ILE:HB	2.20	0.41
1:A:85:ASP:HB3	1:A:89:GLN:HB2	2.02	0.41
1:A:87:TYR:OH	1:B:48:ILE:HA	2.21	0.41
1:A:269:ASN:ND2	1:A:275:ASN:H	2.18	0.41
1:B:282:TYR:CG	1:B:283:ASP:N	2.89	0.41
1:C:61:GLY:O	1:C:62:TYR:C	2.64	0.41
1:C:71:ILE:CG2	1:C:74:ILE:HD11	2.50	0.41
1:C:188:HIS:HB3	1:C:191:LEU:HG	2.03	0.41
1:C:269:ASN:CG	1:C:275:ASN:H	2.28	0.41
1:D:60:PHE:N	1:D:129:PRO:HB3	2.35	0.41
1:D:108:ASN:ND2	1:D:270:GLU:HB3	2.36	0.41
1:D:177:GLN:O	1:D:179:GLU:N	2.54	0.41
1:D:269:ASN:ND2	1:D:275:ASN:H	2.19	0.41
1:E:124:ASN:HD21	1:E:128:PHE:HB2	1.86	0.41
1:F:86:VAL:HG13	1:G:100:TYR:HB2	2.03	0.41
1:F:164:ASN:HD22	1:F:164:ASN:C	2.29	0.41
1:G:203:ALA:O	1:G:205:TYR:N	2.53	0.41
1:G:283:ASP:O	1:G:284:ILE:HB	2.20	0.41
1:H:61:GLY:O	1:H:62:TYR:C	2.64	0.41
1:H:71:ILE:CG2	1:H:74:ILE:HD11	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:104:PHE:HB3	1:H:105:LYS:H	1.56	0.41
1:H:109:TYR:O	1:H:110:ARG:HB2	2.21	0.41
1:H:151:ASN:O	1:H:152:GLN:C	2.62	0.41
1:H:193:SER:O	1:H:195:SER:N	2.54	0.41
1:H:209:LYS:O	1:H:212:ALA:HB3	2.21	0.41
1:I:154:ALA:CA	1:K:182:ALA:HB2	2.49	0.41
1:I:204:PRO:O	1:I:205:TYR:HB3	2.20	0.41
1:I:280:PHE:O	1:I:281:ARG:CB	2.69	0.41
1:J:72:SER:O	1:J:74:ILE:HG13	2.20	0.41
1:J:177:GLN:O	1:J:179:GLU:N	2.54	0.41
1:K:34:LEU:HD23	1:K:34:LEU:HA	1.97	0.41
1:K:57:ILE:HG23	1:K:123:ASN:HB2	2.00	0.41
1:K:269:ASN:CG	1:K:275:ASN:H	2.28	0.41
1:L:61:GLY:O	1:L:62:TYR:C	2.63	0.41
1:L:108:ASN:O	1:L:108:ASN:CG	2.61	0.41
1:L:151:ASN:O	1:L:154:ALA:HB3	2.20	0.41
1:B:108:ASN:ND2	1:B:270:GLU:HB3	2.36	0.41
1:C:57:ILE:HG12	1:C:63:VAL:CG2	2.52	0.41
1:C:151:ASN:HD21	1:C:205:TYR:HA	1.85	0.41
1:E:57:ILE:HG12	1:E:63:VAL:HG21	2.02	0.41
1:F:209:LYS:HB2	1:G:205:TYR:CZ	2.55	0.41
1:F:265:CYS:O	1:F:266:GLU:C	2.63	0.41
1:G:57:ILE:HA	1:G:61:GLY:O	2.21	0.41
1:H:108:ASN:ND2	1:H:270:GLU:HB3	2.36	0.41
1:H:269:ASN:CG	1:H:275:ASN:H	2.28	0.41
1:I:103:GLU:C	1:I:104:PHE:HD1	2.29	0.41
1:A:42:GLU:HB2	1:A:277:LYS:HB3	2.02	0.40
1:A:126:MET:HE2	1:B:55:LYS:NZ	2.36	0.40
1:A:174:VAL:C	1:A:176:ASN:H	2.29	0.40
1:D:103:GLU:C	1:D:104:PHE:HD1	2.28	0.40
1:G:265:CYS:O	1:G:266:GLU:C	2.62	0.40
1:H:265:CYS:O	1:H:266:GLU:C	2.63	0.40
1:I:269:ASN:CG	1:I:275:ASN:H	2.29	0.40
1:K:102:LYS:HG3	1:K:103:GLU:H	1.85	0.40
1:K:271:LEU:C	1:K:272:TYR:CD1	3.00	0.40
1:K:275:ASN:C	1:K:277:LYS:H	2.29	0.40
1:L:165:ASP:HB3	1:L:167:ASN:ND2	2.36	0.40
1:A:188:HIS:HB3	1:A:191:LEU:HG	2.03	0.40
1:B:280:PHE:O	1:B:281:ARG:CB	2.69	0.40
1:D:78:GLY:HA3	1:D:95:ALA:HA	2.04	0.40
1:E:103:GLU:C	1:E:104:PHE:HD1	2.28	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:108:ASN:O	1:E:108:ASN:CG	2.64	0.40
1:E:276:VAL:O	1:E:277:LYS:C	2.63	0.40
1:F:61:GLY:O	1:F:62:TYR:C	2.64	0.40
1:F:109:TYR:O	1:F:110:ARG:HB2	2.22	0.40
1:F:126:MET:C	1:F:128:PHE:N	2.76	0.40
1:G:275:ASN:C	1:G:277:LYS:N	2.77	0.40
1:G:282:TYR:CG	1:G:283:ASP:N	2.88	0.40
1:H:66:TYR:CE2	1:H:68:ASP:HA	2.56	0.40
1:H:101:GLN:O	1:H:102:LYS:HB2	2.19	0.40
1:H:172:LYS:NZ	1:I:177:GLN:HE22	2.19	0.40
1:J:53:LEU:HD11	1:J:121:ILE:HD12	2.02	0.40
1:K:255:THR:O	1:K:256:VAL:C	2.64	0.40
1:A:38:LEU:HD11	1:A:225:LEU:HB3	2.02	0.40
1:A:103:GLU:C	1:A:104:PHE:HD1	2.28	0.40
1:A:109:TYR:O	1:A:110:ARG:HB2	2.20	0.40
1:A:144:LEU:HD13	1:A:214:LYS:HA	2.03	0.40
1:A:283:ASP:O	1:A:284:ILE:HB	2.20	0.40
1:B:61:GLY:O	1:B:62:TYR:O	2.39	0.40
1:D:61:GLY:O	1:D:62:TYR:C	2.63	0.40
1:D:109:TYR:O	1:D:110:ARG:HB2	2.21	0.40
1:D:203:ALA:O	1:D:205:TYR:N	2.55	0.40
1:E:39:PHE:CE1	1:E:258:LEU:HB2	2.57	0.40
1:F:269:ASN:CG	1:F:275:ASN:H	2.29	0.40
1:G:255:THR:O	1:G:256:VAL:C	2.62	0.40
1:G:276:VAL:O	1:G:277:LYS:C	2.63	0.40
1:J:59:GLN:O	1:J:60:PHE:C	2.63	0.40
1:K:42:GLU:CD	1:K:279:LYS:HE2	2.47	0.40
1:L:98:PRO:O	1:L:99:VAL:CB	2.69	0.40
1:L:158:PRO:O	1:L:159:VAL:CB	2.64	0.40
1:A:265:CYS:O	1:A:266:GLU:C	2.62	0.40
1:B:42:GLU:HB2	1:B:277:LYS:HB3	2.04	0.40
1:B:165:ASP:HB3	1:B:167:ASN:ND2	2.36	0.40
1:C:74:ILE:HG22	1:C:75:ALA:N	2.37	0.40
1:C:126:MET:C	1:C:128:PHE:N	2.74	0.40
1:C:165:ASP:HB3	1:C:167:ASN:ND2	2.36	0.40
1:C:275:ASN:C	1:C:277:LYS:H	2.30	0.40
1:D:151:ASN:O	1:D:154:ALA:HB3	2.22	0.40
1:D:277:LYS:O	1:D:278:VAL:CB	2.69	0.40
1:E:61:GLY:O	1:E:62:TYR:C	2.64	0.40
1:F:71:ILE:CG2	1:F:74:ILE:HD11	2.51	0.40
1:F:128:PHE:HA	1:F:129:PRO:HD3	1.97	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:172:LYS:NZ	1:G:177:GLN:HE22	2.19	0.40
1:F:209:LYS:HB3	1:F:209:LYS:HZ2	1.86	0.40
1:G:108:ASN:O	1:G:108:ASN:CG	2.63	0.40
1:G:169:LEU:HD22	1:G:173:GLN:CD	2.46	0.40
1:H:271:LEU:C	1:H:272:TYR:CD1	2.99	0.40
1:H:277:LYS:O	1:H:278:VAL:CB	2.68	0.40
1:J:102:LYS:HG3	1:J:103:GLU:H	1.86	0.40
1:J:283:ASP:O	1:J:284:ILE:HB	2.22	0.40
1:K:179:GLU:C	1:K:181:ASN:N	2.69	0.40
1:K:209:LYS:O	1:K:210:LEU:C	2.63	0.40
1:B:180:GLY:CA	1:L:150:VAL:HG13	2.47	0.40
1:C:117:MET:HB2	1:C:271:LEU:HD11	2.04	0.40
1:D:204:PRO:O	1:D:205:TYR:HB3	2.21	0.40
1:E:108:ASN:ND2	1:E:270:GLU:HB3	2.36	0.40
1:F:108:ASN:ND2	1:F:270:GLU:HB3	2.37	0.40
1:F:144:LEU:HD13	1:F:214:LYS:HA	2.02	0.40
1:F:275:ASN:C	1:F:277:LYS:H	2.30	0.40
1:G:109:TYR:O	1:G:110:ARG:HB2	2.21	0.40
1:G:154:ALA:HB1	1:I:182:ALA:HB2	2.02	0.40
1:I:271:LEU:C	1:I:272:TYR:CD1	2.99	0.40
1:J:61:GLY:O	1:J:62:TYR:O	2.39	0.40
1:K:61:GLY:O	1:K:62:TYR:C	2.64	0.40
1:L:123:ASN:C	1:L:123:ASN:HD22	2.28	0.40
1:L:151:ASN:HD21	1:L:205:TYR:HA	1.86	0.40
1:L:275:ASN:C	1:L:277:LYS:H	2.28	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:TYR:OH	1:I:62:TYR:OH[3_445]	2.12	0.08

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	B	253/309 (82%)	182 (72%)	37 (15%)	34 (13%)	0	1
1	C	253/309 (82%)	179 (71%)	40 (16%)	34 (13%)	0	1
1	D	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	E	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	F	253/309 (82%)	180 (71%)	38 (15%)	35 (14%)	0	1
1	G	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	H	253/309 (82%)	180 (71%)	38 (15%)	35 (14%)	0	1
1	I	253/309 (82%)	181 (72%)	37 (15%)	35 (14%)	0	1
1	J	253/309 (82%)	182 (72%)	37 (15%)	34 (13%)	0	1
1	K	253/309 (82%)	181 (72%)	39 (15%)	33 (13%)	0	1
1	L	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
All	All	3036/3708 (82%)	2170 (72%)	456 (15%)	410 (14%)	0	1

All (410) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	TYR
1	A	105	LYS
1	A	107	TYR
1	A	113	LYS
1	A	117	MET
1	A	127	ALA
1	A	181	ASN
1	A	182	ALA
1	A	279	LYS
1	A	281	ARG
1	A	284	ILE
1	B	61	GLY
1	B	62	TYR
1	B	105	LYS
1	B	107	TYR
1	B	113	LYS
1	B	117	MET
1	B	127	ALA
1	B	181	ASN

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Mol	Chain	Res	Type
1	B	182	ALA
1	B	183	PRO
1	B	279	LYS
1	B	281	ARG
1	B	284	ILE
1	C	62	TYR
1	C	105	LYS
1	C	107	TYR
1	C	113	LYS
1	C	117	MET
1	C	127	ALA
1	C	181	ASN
1	C	182	ALA
1	C	183	PRO
1	C	279	LYS
1	C	281	ARG
1	C	284	ILE
1	D	61	GLY
1	D	62	TYR
1	D	105	LYS
1	D	107	TYR
1	D	113	LYS
1	D	117	MET
1	D	127	ALA
1	D	181	ASN
1	D	182	ALA
1	D	183	PRO
1	D	279	LYS
1	D	281	ARG
1	D	284	ILE
1	E	61	GLY
1	E	62	TYR
1	E	105	LYS
1	E	107	TYR
1	E	113	LYS
1	E	117	MET
1	E	127	ALA
1	E	181	ASN
1	E	182	ALA
1	E	279	LYS
1	E	281	ARG
1	E	284	ILE

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Mol	Chain	Res	Type
1	F	61	GLY
1	F	62	TYR
1	F	105	LYS
1	F	107	TYR
1	F	113	LYS
1	F	117	MET
1	F	127	ALA
1	F	181	ASN
1	F	182	ALA
1	F	183	PRO
1	F	279	LYS
1	F	281	ARG
1	F	284	ILE
1	G	61	GLY
1	G	62	TYR
1	G	105	LYS
1	G	107	TYR
1	G	113	LYS
1	G	117	MET
1	G	127	ALA
1	G	181	ASN
1	G	182	ALA
1	G	183	PRO
1	G	279	LYS
1	G	281	ARG
1	G	284	ILE
1	H	61	GLY
1	H	62	TYR
1	H	105	LYS
1	H	107	TYR
1	H	113	LYS
1	H	117	MET
1	H	127	ALA
1	H	181	ASN
1	H	182	ALA
1	H	279	LYS
1	H	281	ARG
1	H	284	ILE
1	I	61	GLY
1	I	62	TYR
1	I	105	LYS
1	I	107	TYR

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Mol	Chain	Res	Type
1	I	113	LYS
1	I	117	MET
1	I	127	ALA
1	I	181	ASN
1	I	182	ALA
1	I	279	LYS
1	I	281	ARG
1	I	284	ILE
1	J	61	GLY
1	J	62	TYR
1	J	105	LYS
1	J	107	TYR
1	J	113	LYS
1	J	117	MET
1	J	127	ALA
1	J	181	ASN
1	J	182	ALA
1	J	277	LYS
1	J	279	LYS
1	J	281	ARG
1	J	284	ILE
1	K	61	GLY
1	K	62	TYR
1	K	105	LYS
1	K	107	TYR
1	K	113	LYS
1	K	117	MET
1	K	127	ALA
1	K	181	ASN
1	K	182	ALA
1	K	279	LYS
1	K	281	ARG
1	K	284	ILE
1	L	61	GLY
1	L	62	TYR
1	L	105	LYS
1	L	107	TYR
1	L	113	LYS
1	L	117	MET
1	L	127	ALA
1	L	181	ASN
1	L	182	ALA

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Mol	Chain	Res	Type
1	L	279	LYS
1	L	281	ARG
1	L	284	ILE
1	A	60	PHE
1	A	61	GLY
1	A	63	VAL
1	A	109	TYR
1	A	110	ARG
1	A	126	MET
1	A	171	LEU
1	A	178	TYR
1	A	180	GLY
1	A	183	PRO
1	A	204	PRO
1	A	277	LYS
1	A	278	VAL
1	B	60	PHE
1	B	63	VAL
1	B	109	TYR
1	B	110	ARG
1	B	124	ASN
1	B	126	MET
1	B	171	LEU
1	B	178	TYR
1	B	180	GLY
1	B	204	PRO
1	B	277	LYS
1	B	278	VAL
1	C	60	PHE
1	C	61	GLY
1	C	63	VAL
1	C	109	TYR
1	C	110	ARG
1	C	124	ASN
1	C	126	MET
1	C	171	LEU
1	C	178	TYR
1	C	180	GLY
1	C	204	PRO
1	C	277	LYS
1	C	278	VAL
1	D	60	PHE

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Mol	Chain	Res	Type
1	D	63	VAL
1	D	109	TYR
1	D	110	ARG
1	D	124	ASN
1	D	126	MET
1	D	171	LEU
1	D	178	TYR
1	D	180	GLY
1	D	204	PRO
1	D	277	LYS
1	D	278	VAL
1	E	60	PHE
1	E	63	VAL
1	E	109	TYR
1	E	110	ARG
1	E	124	ASN
1	E	126	MET
1	E	171	LEU
1	E	178	TYR
1	E	180	GLY
1	E	183	PRO
1	E	204	PRO
1	E	277	LYS
1	E	278	VAL
1	F	60	PHE
1	F	63	VAL
1	F	109	TYR
1	F	110	ARG
1	F	124	ASN
1	F	126	MET
1	F	171	LEU
1	F	178	TYR
1	F	180	GLY
1	F	204	PRO
1	F	277	LYS
1	F	278	VAL
1	G	60	PHE
1	G	63	VAL
1	G	109	TYR
1	G	110	ARG
1	G	124	ASN
1	G	126	MET

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Mol	Chain	Res	Type
1	G	171	LEU
1	G	178	TYR
1	G	180	GLY
1	G	204	PRO
1	G	277	LYS
1	G	278	VAL
1	H	60	PHE
1	H	63	VAL
1	H	109	TYR
1	H	110	ARG
1	H	124	ASN
1	H	126	MET
1	H	171	LEU
1	H	178	TYR
1	H	180	GLY
1	H	183	PRO
1	H	204	PRO
1	H	277	LYS
1	H	278	VAL
1	I	60	PHE
1	I	63	VAL
1	I	109	TYR
1	I	110	ARG
1	I	124	ASN
1	I	126	MET
1	I	171	LEU
1	I	178	TYR
1	I	180	GLY
1	I	183	PRO
1	I	204	PRO
1	I	277	LYS
1	I	278	VAL
1	J	60	PHE
1	J	63	VAL
1	J	109	TYR
1	J	110	ARG
1	J	124	ASN
1	J	126	MET
1	J	171	LEU
1	J	178	TYR
1	J	180	GLY
1	J	183	PRO

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Mol	Chain	Res	Type
1	J	204	PRO
1	J	278	VAL
1	K	60	PHE
1	K	63	VAL
1	K	109	TYR
1	K	110	ARG
1	K	124	ASN
1	K	126	MET
1	K	171	LEU
1	K	178	TYR
1	K	180	GLY
1	K	183	PRO
1	K	204	PRO
1	K	277	LYS
1	K	278	VAL
1	L	60	PHE
1	L	63	VAL
1	L	109	TYR
1	L	110	ARG
1	L	126	MET
1	L	171	LEU
1	L	178	TYR
1	L	180	GLY
1	L	183	PRO
1	L	204	PRO
1	L	277	LYS
1	L	278	VAL
1	A	124	ASN
1	A	272	TYR
1	B	283	ASP
1	C	172	LYS
1	C	272	TYR
1	C	283	ASP
1	D	172	LYS
1	D	272	TYR
1	D	283	ASP
1	E	172	LYS
1	F	172	LYS
1	F	272	TYR
1	F	283	ASP
1	G	172	LYS
1	G	283	ASP

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Mol	Chain	Res	Type
1	H	172	LYS
1	H	272	TYR
1	I	172	LYS
1	I	272	TYR
1	I	283	ASP
1	J	172	LYS
1	J	272	TYR
1	J	283	ASP
1	K	272	TYR
1	K	283	ASP
1	L	124	ASN
1	A	44	LEU
1	A	172	LYS
1	A	192	ASP
1	A	205	TYR
1	A	283	ASP
1	B	44	LEU
1	B	172	LYS
1	B	192	ASP
1	B	205	TYR
1	B	272	TYR
1	C	39	PHE
1	C	44	LEU
1	C	159	VAL
1	C	192	ASP
1	C	205	TYR
1	D	44	LEU
1	D	159	VAL
1	D	192	ASP
1	D	205	TYR
1	E	44	LEU
1	E	159	VAL
1	E	192	ASP
1	E	205	TYR
1	E	272	TYR
1	E	283	ASP
1	F	44	LEU
1	F	192	ASP
1	G	44	LEU
1	G	192	ASP
1	G	205	TYR
1	G	272	TYR

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Mol	Chain	Res	Type
1	H	44	LEU
1	H	159	VAL
1	H	192	ASP
1	H	205	TYR
1	H	283	ASP
1	I	44	LEU
1	I	192	ASP
1	I	205	TYR
1	J	44	LEU
1	J	192	ASP
1	J	205	TYR
1	K	44	LEU
1	K	172	LYS
1	K	192	ASP
1	K	205	TYR
1	L	44	LEU
1	L	172	LYS
1	L	192	ASP
1	L	205	TYR
1	L	272	TYR
1	L	283	ASP
1	A	114	GLU
1	A	159	VAL
1	B	159	VAL
1	D	114	GLU
1	E	114	GLU
1	F	39	PHE
1	F	159	VAL
1	F	205	TYR
1	G	114	GLU
1	G	159	VAL
1	I	159	VAL
1	J	159	VAL
1	K	159	VAL
1	L	159	VAL
1	A	99	VAL
1	B	208	ASP
1	C	99	VAL
1	E	99	VAL
1	F	99	VAL
1	F	114	GLU
1	G	99	VAL

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Mol	Chain	Res	Type
1	H	99	VAL
1	H	114	GLU
1	H	208	ASP
1	I	39	PHE
1	I	99	VAL
1	I	208	ASP
1	J	114	GLU
1	K	99	VAL
1	L	39	PHE
1	L	99	VAL
1	B	99	VAL
1	D	99	VAL
1	J	99	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	B	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	C	229/277 (83%)	216 (94%)	13 (6%)	18	51
1	D	229/277 (83%)	216 (94%)	13 (6%)	18	51
1	E	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	F	229/277 (83%)	216 (94%)	13 (6%)	18	51
1	G	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	H	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	I	229/277 (83%)	216 (94%)	13 (6%)	18	51
1	J	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	K	229/277 (83%)	215 (94%)	14 (6%)	17	49
1	L	229/277 (83%)	215 (94%)	14 (6%)	17	49
All	All	2748/3324 (83%)	2584 (94%)	164 (6%)	17	50

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	101	GLN
1	A	113	LYS
1	A	115	GLU
1	A	160	LEU
1	A	164	ASN
1	A	178	TYR
1	A	196	ILE
1	A	204	PRO
1	A	209	LYS
1	A	213	GLN
1	A	261	ARG
1	A	271	LEU
1	A	277	LYS
1	B	49	ASN
1	B	101	GLN
1	B	113	LYS
1	B	115	GLU
1	B	160	LEU
1	B	164	ASN
1	B	178	TYR
1	B	196	ILE
1	B	204	PRO
1	B	209	LYS
1	B	213	GLN
1	B	261	ARG
1	B	271	LEU
1	B	277	LYS
1	C	49	ASN
1	C	101	GLN
1	C	113	LYS
1	C	115	GLU
1	C	160	LEU
1	C	164	ASN
1	C	178	TYR
1	C	196	ILE
1	C	204	PRO
1	C	209	LYS
1	C	213	GLN
1	C	271	LEU
1	C	277	LYS
1	D	49	ASN

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Mol	Chain	Res	Type
1	D	101	GLN
1	D	113	LYS
1	D	115	GLU
1	D	160	LEU
1	D	164	ASN
1	D	178	TYR
1	D	196	ILE
1	D	204	PRO
1	D	209	LYS
1	D	213	GLN
1	D	271	LEU
1	D	277	LYS
1	E	49	ASN
1	E	101	GLN
1	E	113	LYS
1	E	115	GLU
1	E	160	LEU
1	E	164	ASN
1	E	178	TYR
1	E	196	ILE
1	E	204	PRO
1	E	209	LYS
1	E	213	GLN
1	E	261	ARG
1	E	271	LEU
1	E	277	LYS
1	F	49	ASN
1	F	101	GLN
1	F	113	LYS
1	F	115	GLU
1	F	160	LEU
1	F	164	ASN
1	F	178	TYR
1	F	196	ILE
1	F	204	PRO
1	F	209	LYS
1	F	213	GLN
1	F	271	LEU
1	F	277	LYS
1	G	49	ASN
1	G	101	GLN
1	G	113	LYS

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Mol	Chain	Res	Type
1	G	115	GLU
1	G	160	LEU
1	G	164	ASN
1	G	178	TYR
1	G	196	ILE
1	G	204	PRO
1	G	209	LYS
1	G	213	GLN
1	G	261	ARG
1	G	271	LEU
1	G	277	LYS
1	H	49	ASN
1	H	101	GLN
1	H	113	LYS
1	H	115	GLU
1	H	160	LEU
1	H	164	ASN
1	H	178	TYR
1	H	196	ILE
1	H	204	PRO
1	H	209	LYS
1	H	213	GLN
1	H	261	ARG
1	H	271	LEU
1	H	277	LYS
1	I	49	ASN
1	I	101	GLN
1	I	113	LYS
1	I	115	GLU
1	I	160	LEU
1	I	164	ASN
1	I	178	TYR
1	I	196	ILE
1	I	204	PRO
1	I	209	LYS
1	I	213	GLN
1	I	271	LEU
1	I	277	LYS
1	J	49	ASN
1	J	101	GLN
1	J	113	LYS
1	J	115	GLU

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Mol	Chain	Res	Type
1	J	160	LEU
1	J	164	ASN
1	J	178	TYR
1	J	196	ILE
1	J	204	PRO
1	J	209	LYS
1	J	213	GLN
1	J	261	ARG
1	J	271	LEU
1	J	277	LYS
1	K	49	ASN
1	K	101	GLN
1	K	113	LYS
1	K	115	GLU
1	K	160	LEU
1	K	164	ASN
1	K	178	TYR
1	K	196	ILE
1	K	204	PRO
1	K	209	LYS
1	K	213	GLN
1	K	261	ARG
1	K	271	LEU
1	K	277	LYS
1	L	49	ASN
1	L	101	GLN
1	L	113	LYS
1	L	115	GLU
1	L	143	GLU
1	L	160	LEU
1	L	164	ASN
1	L	178	TYR
1	L	196	ILE
1	L	204	PRO
1	L	209	LYS
1	L	213	GLN
1	L	271	LEU
1	L	277	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (198) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	21	ASN
1	A	29	ASN
1	A	32	GLN
1	A	43	ASN
1	A	49	ASN
1	A	123	ASN
1	A	124	ASN
1	A	151	ASN
1	A	152	GLN
1	A	166	ASN
1	A	167	ASN
1	A	168	GLN
1	A	173	GLN
1	A	177	GLN
1	A	188	HIS
1	B	16	GLN
1	B	21	ASN
1	B	29	ASN
1	B	32	GLN
1	B	43	ASN
1	B	49	ASN
1	B	108	ASN
1	B	123	ASN
1	B	124	ASN
1	B	151	ASN
1	B	152	GLN
1	B	155	GLN
1	B	164	ASN
1	B	166	ASN
1	B	167	ASN
1	B	168	GLN
1	B	173	GLN
1	B	177	GLN
1	B	188	HIS
1	C	32	GLN
1	C	43	ASN
1	C	49	ASN
1	C	123	ASN
1	C	124	ASN
1	C	151	ASN
1	C	152	GLN
1	C	155	GLN

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Mol	Chain	Res	Type
1	C	166	ASN
1	C	167	ASN
1	C	168	GLN
1	C	173	GLN
1	C	177	GLN
1	C	188	HIS
1	D	21	ASN
1	D	29	ASN
1	D	32	GLN
1	D	43	ASN
1	D	49	ASN
1	D	59	GLN
1	D	108	ASN
1	D	123	ASN
1	D	151	ASN
1	D	152	GLN
1	D	155	GLN
1	D	166	ASN
1	D	167	ASN
1	D	168	GLN
1	D	173	GLN
1	D	177	GLN
1	D	188	HIS
1	E	21	ASN
1	E	29	ASN
1	E	32	GLN
1	E	43	ASN
1	E	49	ASN
1	E	123	ASN
1	E	124	ASN
1	E	151	ASN
1	E	152	GLN
1	E	155	GLN
1	E	166	ASN
1	E	167	ASN
1	E	168	GLN
1	E	173	GLN
1	E	177	GLN
1	E	188	HIS
1	F	21	ASN
1	F	29	ASN
1	F	32	GLN

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Mol	Chain	Res	Type
1	F	43	ASN
1	F	49	ASN
1	F	108	ASN
1	F	123	ASN
1	F	124	ASN
1	F	151	ASN
1	F	152	GLN
1	F	155	GLN
1	F	166	ASN
1	F	167	ASN
1	F	168	GLN
1	F	173	GLN
1	F	177	GLN
1	F	188	HIS
1	G	21	ASN
1	G	29	ASN
1	G	32	GLN
1	G	43	ASN
1	G	49	ASN
1	G	123	ASN
1	G	124	ASN
1	G	151	ASN
1	G	152	GLN
1	G	166	ASN
1	G	167	ASN
1	G	168	GLN
1	G	173	GLN
1	G	177	GLN
1	G	188	HIS
1	H	21	ASN
1	H	29	ASN
1	H	32	GLN
1	H	43	ASN
1	H	49	ASN
1	H	108	ASN
1	H	123	ASN
1	H	124	ASN
1	H	151	ASN
1	H	152	GLN
1	H	155	GLN
1	H	164	ASN
1	H	166	ASN

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Mol	Chain	Res	Type
1	H	167	ASN
1	H	168	GLN
1	H	173	GLN
1	H	177	GLN
1	H	188	HIS
1	I	21	ASN
1	I	29	ASN
1	I	32	GLN
1	I	43	ASN
1	I	49	ASN
1	I	123	ASN
1	I	124	ASN
1	I	151	ASN
1	I	152	GLN
1	I	155	GLN
1	I	166	ASN
1	I	167	ASN
1	I	168	GLN
1	I	173	GLN
1	I	177	GLN
1	I	188	HIS
1	J	21	ASN
1	J	29	ASN
1	J	32	GLN
1	J	43	ASN
1	J	49	ASN
1	J	123	ASN
1	J	124	ASN
1	J	151	ASN
1	J	152	GLN
1	J	155	GLN
1	J	166	ASN
1	J	167	ASN
1	J	168	GLN
1	J	173	GLN
1	J	177	GLN
1	J	188	HIS
1	K	21	ASN
1	K	29	ASN
1	K	32	GLN
1	K	43	ASN
1	K	49	ASN

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Mol	Chain	Res	Type
1	K	123	ASN
1	K	124	ASN
1	K	151	ASN
1	K	152	GLN
1	K	155	GLN
1	K	166	ASN
1	K	167	ASN
1	K	168	GLN
1	K	173	GLN
1	K	177	GLN
1	K	188	HIS
1	L	21	ASN
1	L	29	ASN
1	L	32	GLN
1	L	43	ASN
1	L	49	ASN
1	L	108	ASN
1	L	123	ASN
1	L	124	ASN
1	L	151	ASN
1	L	152	GLN
1	L	155	GLN
1	L	164	ASN
1	L	166	ASN
1	L	167	ASN
1	L	168	GLN
1	L	173	GLN
1	L	177	GLN
1	L	188	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	257/309 (83%)	0.74	43 (16%)	4 3	18, 45, 98, 120	0
1	B	257/309 (83%)	0.94	54 (21%)	2 2	18, 52, 97, 121	0
1	C	257/309 (83%)	1.06	62 (24%)	2 2	21, 55, 100, 124	0
1	D	257/309 (83%)	1.01	52 (20%)	3 2	20, 58, 109, 127	0
1	E	257/309 (83%)	1.23	68 (26%)	1 1	23, 72, 113, 123	0
1	F	257/309 (83%)	1.06	64 (24%)	2 2	19, 61, 104, 120	0
1	G	257/309 (83%)	0.94	49 (19%)	3 2	21, 57, 102, 127	0
1	H	257/309 (83%)	1.06	55 (21%)	2 2	17, 64, 111, 124	0
1	I	257/309 (83%)	0.86	51 (19%)	3 2	19, 46, 90, 116	0
1	J	257/309 (83%)	0.64	36 (14%)	6 5	22, 43, 87, 115	0
1	K	257/309 (83%)	0.84	52 (20%)	3 2	17, 53, 96, 127	0
1	L	257/309 (83%)	0.72	44 (17%)	4 3	19, 48, 98, 116	0
All	All	3084/3708 (83%)	0.93	630 (20%)	3 2	17, 53, 106, 127	0

All (630) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	182	ALA	8.9
1	C	109	TYR	7.9
1	I	272	TYR	7.7
1	J	109	TYR	7.6
1	G	182	ALA	7.3
1	A	182	ALA	6.9
1	J	182	ALA	6.8
1	E	111	ASP	6.7
1	L	12	ILE	6.7
1	I	109	TYR	6.6
1	I	111	ASP	6.3

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Mol	Chain	Res	Type	RSRZ
1	H	182	ALA	6.2
1	F	109	TYR	6.1
1	D	276	VAL	6.1
1	H	111	ASP	6.0
1	E	169	LEU	5.9
1	G	12	ILE	5.8
1	C	182	ALA	5.8
1	D	285	VAL	5.8
1	I	285	VAL	5.8
1	G	276	VAL	5.7
1	K	111	ASP	5.7
1	G	277	LYS	5.6
1	L	272	TYR	5.5
1	B	273	GLY	5.3
1	H	11	SER	5.3
1	H	72	SER	5.2
1	B	272	TYR	5.2
1	C	272	TYR	5.1
1	C	285	VAL	5.0
1	I	182	ALA	5.0
1	A	272	TYR	5.0
1	B	12	ILE	4.9
1	J	272	TYR	4.9
1	F	72	SER	4.9
1	H	285	VAL	4.9
1	I	276	VAL	4.9
1	H	108	ASN	4.9
1	D	182	ALA	4.9
1	E	182	ALA	4.9
1	A	11	SER	4.8
1	B	181	ASN	4.8
1	H	277	LYS	4.8
1	F	181	ASN	4.7
1	C	85	ASP	4.7
1	E	11	SER	4.7
1	L	182	ALA	4.7
1	J	276	VAL	4.6
1	D	168	GLN	4.6
1	L	284	ILE	4.6
1	C	276	VAL	4.6
1	I	181	ASN	4.6
1	D	101	GLN	4.6

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Mol	Chain	Res	Type	RSRZ
1	K	277	LYS	4.5
1	H	181	ASN	4.5
1	L	109	TYR	4.5
1	B	108	ASN	4.4
1	I	13	ASN	4.4
1	B	111	ASP	4.4
1	A	276	VAL	4.4
1	H	272	TYR	4.4
1	B	182	ALA	4.3
1	I	170	SER	4.3
1	K	12	ILE	4.3
1	J	111	ASP	4.3
1	B	169	LEU	4.3
1	B	61	GLY	4.3
1	F	111	ASP	4.3
1	H	12	ILE	4.3
1	J	181	ASN	4.2
1	L	115	GLU	4.2
1	K	16	GLN	4.2
1	K	273	GLY	4.2
1	I	108	ASN	4.2
1	E	70	VAL	4.2
1	H	270	GLU	4.2
1	H	276	VAL	4.2
1	E	118	GLY	4.2
1	D	13	ASN	4.1
1	F	85	ASP	4.1
1	A	54	GLU	4.1
1	K	168	GLN	4.1
1	F	169	LEU	4.1
1	F	110	ARG	4.1
1	F	18	GLN	4.1
1	B	283	ASP	4.1
1	C	169	LEU	4.1
1	B	13	ASN	4.0
1	J	275	ASN	4.0
1	K	276	VAL	4.0
1	C	194	ASP	4.0
1	D	16	GLN	4.0
1	K	170	SER	4.0
1	L	16	GLN	4.0
1	C	277	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	F	108	ASN	4.0
1	B	284	ILE	4.0
1	D	111	ASP	4.0
1	B	277	LYS	4.0
1	D	112	MET	4.0
1	F	112	MET	4.0
1	C	72	SER	4.0
1	F	282	TYR	4.0
1	H	70	VAL	3.9
1	A	16	GLN	3.9
1	C	273	GLY	3.9
1	L	61	GLY	3.9
1	E	88	ASN	3.9
1	H	169	LEU	3.9
1	L	111	ASP	3.9
1	G	273	GLY	3.9
1	B	16	GLN	3.9
1	C	43	ASN	3.9
1	L	108	ASN	3.9
1	B	167	ASN	3.9
1	G	13	ASN	3.9
1	K	181	ASN	3.9
1	A	273	GLY	3.9
1	F	247	ASP	3.9
1	J	194	ASP	3.9
1	E	285	VAL	3.8
1	A	115	GLU	3.8
1	D	179	GLU	3.8
1	D	12	ILE	3.8
1	H	273	GLY	3.8
1	K	169	LEU	3.8
1	D	277	LYS	3.8
1	H	112	MET	3.8
1	F	180	GLY	3.8
1	F	97	SER	3.8
1	H	170	SER	3.8
1	B	107	TYR	3.8
1	K	176	ASN	3.7
1	C	247	ASP	3.7
1	A	109	TYR	3.7
1	C	178	TYR	3.7
1	D	272	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	F	179	GLU	3.7
1	J	112	MET	3.7
1	A	170	SER	3.7
1	B	54	GLU	3.7
1	H	109	TYR	3.7
1	A	180	GLY	3.7
1	D	85	ASP	3.6
1	G	270	GLU	3.6
1	E	179	GLU	3.6
1	E	176	ASN	3.6
1	I	275	ASN	3.6
1	J	12	ILE	3.6
1	D	178	TYR	3.6
1	F	11	SER	3.6
1	B	88	ASN	3.5
1	D	115	GLU	3.5
1	B	178	TYR	3.5
1	D	181	ASN	3.5
1	E	108	ASN	3.5
1	F	13	ASN	3.5
1	I	12	ILE	3.5
1	B	70	VAL	3.5
1	G	63	VAL	3.5
1	C	181	ASN	3.5
1	F	107	TYR	3.5
1	G	61	GLY	3.5
1	I	277	LYS	3.5
1	A	169	LEU	3.5
1	F	106	LEU	3.5
1	H	284	ILE	3.5
1	I	97	SER	3.5
1	I	169	LEU	3.5
1	H	20	ARG	3.5
1	D	61	GLY	3.5
1	A	284	ILE	3.5
1	E	277	LYS	3.4
1	G	21	ASN	3.4
1	K	13	ASN	3.4
1	L	13	ASN	3.4
1	D	273	GLY	3.4
1	B	90	ALA	3.4
1	E	177	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	12	ILE	3.4
1	A	277	LYS	3.4
1	A	285	VAL	3.4
1	J	285	VAL	3.4
1	F	43	ASN	3.4
1	J	108	ASN	3.4
1	C	168	GLN	3.4
1	F	283	ASP	3.4
1	F	285	VAL	3.4
1	B	110	ARG	3.4
1	H	110	ARG	3.4
1	E	275	ASN	3.4
1	L	181	ASN	3.4
1	F	277	LYS	3.4
1	H	114	GLU	3.4
1	K	109	TYR	3.4
1	A	61	GLY	3.4
1	I	273	GLY	3.4
1	G	112	MET	3.4
1	I	112	MET	3.4
1	E	168	GLN	3.4
1	H	13	ASN	3.4
1	A	85	ASP	3.4
1	K	284	ILE	3.4
1	E	83	GLN	3.4
1	G	16	GLN	3.4
1	E	124	ASN	3.3
1	E	181	ASN	3.3
1	F	176	ASN	3.3
1	D	270	GLU	3.3
1	E	63	VAL	3.3
1	E	112	MET	3.3
1	B	166	ASN	3.3
1	E	86	VAL	3.3
1	F	276	VAL	3.3
1	L	70	VAL	3.3
1	J	115	GLU	3.3
1	E	61	GLY	3.3
1	F	170	SER	3.3
1	B	84	ARG	3.3
1	A	168	GLN	3.3
1	H	101	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	278	VAL	3.3
1	B	285	VAL	3.3
1	K	285	VAL	3.3
1	A	176	ASN	3.3
1	K	208	ASP	3.2
1	C	12	ILE	3.2
1	E	272	TYR	3.2
1	K	97	SER	3.2
1	F	194	ASP	3.2
1	D	284	ILE	3.2
1	C	110	ARG	3.2
1	C	177	GLN	3.2
1	E	91	THR	3.2
1	G	283	ASP	3.2
1	A	18	GLN	3.2
1	C	56	SER	3.2
1	D	173	GLN	3.2
1	E	97	SER	3.2
1	L	170	SER	3.2
1	L	177	GLN	3.2
1	I	194	ASP	3.2
1	F	182	ALA	3.2
1	F	61	GLY	3.2
1	G	11	SER	3.2
1	G	72	SER	3.2
1	G	89	GLN	3.2
1	G	168	GLN	3.2
1	I	110	ARG	3.1
1	C	117	MET	3.1
1	C	95	ALA	3.1
1	H	95	ALA	3.1
1	I	270	GLU	3.1
1	H	63	VAL	3.1
1	G	109	TYR	3.1
1	L	283	ASP	3.1
1	F	54	GLU	3.1
1	A	178	TYR	3.1
1	C	282	TYR	3.1
1	C	269	ASN	3.1
1	J	88	ASN	3.1
1	L	15	ILE	3.1
1	H	106	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	194	ASP	3.1
1	A	12	ILE	3.1
1	I	177	GLN	3.1
1	E	82	GLY	3.1
1	H	278	VAL	3.1
1	E	54	GLU	3.1
1	G	115	GLU	3.1
1	I	113	LYS	3.1
1	H	269	ASN	3.0
1	L	285	VAL	3.0
1	C	11	SER	3.0
1	H	194	ASP	3.0
1	H	283	ASP	3.0
1	I	127	ALA	3.0
1	H	21	ASN	3.0
1	I	168	GLN	3.0
1	A	111	ASP	3.0
1	K	272	TYR	3.0
1	J	176	ASN	3.0
1	L	168	GLN	3.0
1	L	276	VAL	3.0
1	F	56	SER	3.0
1	C	267	LYS	3.0
1	E	115	GLU	3.0
1	E	72	SER	3.0
1	I	72	SER	3.0
1	F	116	ASP	3.0
1	B	278	VAL	3.0
1	C	54	GLU	2.9
1	D	109	TYR	2.9
1	L	62	TYR	2.9
1	E	273	GLY	2.9
1	G	194	ASP	2.9
1	H	48	ILE	2.9
1	D	269	ASN	2.9
1	A	113	LYS	2.9
1	I	115	GLU	2.9
1	C	107	TYR	2.9
1	K	63	VAL	2.9
1	G	180	GLY	2.9
1	F	168	GLN	2.9
1	I	68	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	K	177	GLN	2.9
1	C	112	MET	2.9
1	A	181	ASN	2.9
1	D	17	ARG	2.9
1	A	194	ASP	2.9
1	D	283	ASP	2.9
1	A	108	ASN	2.9
1	H	251	GLU	2.9
1	B	180	GLY	2.9
1	B	179	GLU	2.9
1	D	263	GLU	2.9
1	D	275	ASN	2.9
1	E	123	ASN	2.9
1	J	43	ASN	2.9
1	L	176	ASN	2.9
1	L	179	GLU	2.9
1	J	18	GLN	2.8
1	I	85	ASP	2.8
1	C	248	GLU	2.8
1	F	14	GLU	2.8
1	K	263	GLU	2.8
1	E	13	ASN	2.8
1	K	88	ASN	2.8
1	B	109	TYR	2.8
1	F	272	TYR	2.8
1	E	98	PRO	2.8
1	F	86	VAL	2.8
1	G	179	GLU	2.8
1	F	123	ASN	2.8
1	G	181	ASN	2.8
1	I	43	ASN	2.8
1	G	272	TYR	2.8
1	I	178	TYR	2.8
1	K	62	TYR	2.8
1	B	83	GLN	2.8
1	L	169	LEU	2.8
1	D	124	ASN	2.8
1	G	15	ILE	2.8
1	G	88	ASN	2.8
1	H	275	ASN	2.8
1	L	18	GLN	2.8
1	E	84	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	J	277	LYS	2.8
1	L	85	ASP	2.8
1	H	61	GLY	2.8
1	C	123	ASN	2.8
1	G	178	TYR	2.8
1	E	89	GLN	2.8
1	B	115	GLU	2.8
1	D	103	GLU	2.8
1	E	270	GLU	2.8
1	K	275	ASN	2.7
1	B	276	VAL	2.7
1	C	16	GLN	2.7
1	C	18	GLN	2.7
1	G	169	LEU	2.7
1	A	114	GLU	2.7
1	E	14	GLU	2.7
1	J	283	ASP	2.7
1	H	178	TYR	2.7
1	C	127	ALA	2.7
1	E	92	VAL	2.7
1	G	54	GLU	2.7
1	E	95	ALA	2.7
1	E	16	GLN	2.7
1	F	173	GLN	2.7
1	L	178	TYR	2.7
1	A	275	ASN	2.7
1	F	275	ASN	2.7
1	I	164	ASN	2.7
1	D	104	PHE	2.7
1	J	266	GLU	2.7
1	D	63	VAL	2.7
1	F	178	TYR	2.7
1	F	278	VAL	2.7
1	G	99	VAL	2.7
1	H	271	LEU	2.7
1	K	86	VAL	2.7
1	K	283	ASP	2.7
1	F	117	MET	2.6
1	C	20	ARG	2.6
1	B	170	SER	2.6
1	A	107	TYR	2.6
1	E	178	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	15	ILE	2.6
1	K	247	ASP	2.6
1	A	13	ASN	2.6
1	D	18	GLN	2.6
1	D	113	LYS	2.6
1	K	108	ASN	2.6
1	E	180	GLY	2.6
1	B	248	GLU	2.6
1	H	91	THR	2.6
1	C	278	VAL	2.6
1	F	113	LYS	2.6
1	J	284	ILE	2.6
1	C	111	ASP	2.6
1	G	85	ASP	2.6
1	C	108	ASN	2.6
1	G	177	GLN	2.6
1	D	82	GLY	2.6
1	G	266	GLU	2.6
1	G	278	VAL	2.6
1	G	110	ARG	2.6
1	E	15	ILE	2.6
1	G	107	TYR	2.6
1	C	126	MET	2.6
1	H	69	PRO	2.6
1	D	165	ASP	2.6
1	F	273	GLY	2.6
1	E	271	LEU	2.6
1	L	54	GLU	2.6
1	F	95	ALA	2.6
1	F	87	TYR	2.6
1	J	61	GLY	2.6
1	L	107	TYR	2.5
1	G	173	GLN	2.5
1	B	86	VAL	2.5
1	B	275	ASN	2.5
1	D	43	ASN	2.5
1	E	194	ASP	2.5
1	F	269	ASN	2.5
1	I	247	ASP	2.5
1	J	247	ASP	2.5
1	K	54	GLU	2.5
1	K	115	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	46	PRO	2.5
1	I	107	TYR	2.5
1	H	16	GLN	2.5
1	L	113	LYS	2.5
1	C	88	ASN	2.5
1	C	164	ASN	2.5
1	F	248	GLU	2.5
1	I	167	ASN	2.5
1	I	176	ASN	2.5
1	K	85	ASP	2.5
1	A	179	GLU	2.5
1	C	13	ASN	2.5
1	J	153	ASN	2.5
1	K	61	GLY	2.5
1	F	265	CYS	2.5
1	L	266	GLU	2.5
1	A	112	MET	2.5
1	D	176	ASN	2.5
1	E	110	ARG	2.5
1	J	274	LEU	2.5
1	D	180	GLY	2.5
1	F	284	ILE	2.4
1	I	11	SER	2.4
1	C	17	ARG	2.4
1	C	165	ASP	2.4
1	D	116	ASP	2.4
1	E	68	ASP	2.4
1	H	123	ASN	2.4
1	D	15	ILE	2.4
1	F	12	ILE	2.4
1	G	170	SER	2.4
1	L	14	GLU	2.4
1	L	260	SER	2.4
1	I	95	ALA	2.4
1	H	18	GLN	2.4
1	A	104	PHE	2.4
1	C	97	SER	2.4
1	C	176	ASN	2.4
1	E	49	ASN	2.4
1	A	283	ASP	2.4
1	E	278	VAL	2.4
1	L	63	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	J	178	TYR	2.4
1	D	110	ARG	2.4
1	G	114	GLU	2.4
1	I	54	GLU	2.4
1	I	63	VAL	2.4
1	K	69	PRO	2.4
1	D	88	ASN	2.4
1	C	87	TYR	2.4
1	E	85	ASP	2.4
1	L	277	LYS	2.4
1	D	177	GLN	2.4
1	I	16	GLN	2.4
1	C	179	GLU	2.4
1	C	98	PRO	2.4
1	I	180	GLY	2.3
1	A	62	TYR	2.3
1	B	85	ASP	2.3
1	D	62	TYR	2.3
1	K	15	ILE	2.3
1	I	283	ASP	2.3
1	B	89	GLN	2.3
1	H	168	GLN	2.3
1	E	279	LYS	2.3
1	C	284	ILE	2.3
1	E	90	ALA	2.3
1	D	282	TYR	2.3
1	E	107	TYR	2.3
1	C	271	LEU	2.3
1	B	249	GLN	2.3
1	I	179	GLU	2.3
1	F	63	VAL	2.3
1	J	113	LYS	2.3
1	A	110	ARG	2.3
1	E	56	SER	2.3
1	E	284	ILE	2.3
1	E	133	THR	2.3
1	A	117	MET	2.3
1	B	117	MET	2.3
1	I	104	PHE	2.3
1	B	68	ASP	2.3
1	C	283	ASP	2.3
1	H	68	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	251	GLU	2.3
1	C	270	GLU	2.3
1	K	179	GLU	2.3
1	K	270	GLU	2.3
1	B	20	ARG	2.3
1	E	20	ARG	2.3
1	D	170	SER	2.3
1	D	107	TYR	2.3
1	H	176	ASN	2.3
1	B	173	GLN	2.3
1	C	83	GLN	2.3
1	E	283	ASP	2.3
1	J	168	GLN	2.3
1	L	247	ASP	2.3
1	H	179	GLU	2.3
1	F	69	PRO	2.3
1	H	50	PRO	2.3
1	E	274	LEU	2.3
1	K	11	SER	2.3
1	C	116	ASP	2.3
1	L	194	ASP	2.3
1	I	15	ILE	2.2
1	K	274	LEU	2.2
1	C	62	TYR	2.2
1	F	66	TYR	2.2
1	G	62	TYR	2.2
1	H	107	TYR	2.2
1	G	84	ARG	2.2
1	F	101	GLN	2.2
1	K	74	ILE	2.2
1	D	118	GLY	2.2
1	E	254	GLY	2.2
1	K	107	TYR	2.2
1	B	21	ASN	2.2
1	L	251	GLU	2.2
1	E	96	ALA	2.2
1	C	113	LYS	2.2
1	G	70	VAL	2.2
1	B	260	SER	2.2
1	E	18	GLN	2.2
1	F	177	GLN	2.2
1	L	69	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	273	GLY	2.2
1	B	104	PHE	2.2
1	F	99	VAL	2.2
1	G	81	SER	2.2
1	I	74	ILE	2.2
1	J	72	SER	2.2
1	E	266	GLU	2.2
1	F	115	GLU	2.2
1	K	42	GLU	2.2
1	C	63	VAL	2.1
1	H	282	TYR	2.1
1	F	71	ILE	2.1
1	K	112	MET	2.1
1	F	127	ALA	2.1
1	B	176	ASN	2.1
1	F	98	PRO	2.1
1	G	20	ARG	2.1
1	K	180	GLY	2.1
1	A	247	ASP	2.1
1	C	106	LEU	2.1
1	I	18	GLN	2.1
1	E	50	PRO	2.1
1	J	179	GLU	2.1
1	L	72	SER	2.1
1	H	49	ASN	2.1
1	J	104	PHE	2.1
1	J	278	VAL	2.1
1	G	74	ILE	2.1
1	B	101	GLN	2.1
1	I	83	GLN	2.1
1	J	54	GLU	2.1
1	B	193	SER	2.1
1	A	123	ASN	2.1
1	K	167	ASN	2.1
1	K	219	ASN	2.1
1	L	123	ASN	2.1
1	C	68	ASP	2.1
1	I	271	LEU	2.1
1	B	264	ALA	2.1
1	I	96	ALA	2.1
1	K	101	GLN	2.1
1	F	189	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	263	GLU	2.1
1	G	123	ASN	2.1
1	K	123	ASN	2.1
1	L	84	ARG	2.1
1	K	194	ASP	2.1
1	B	87	TYR	2.1
1	D	87	TYR	2.1
1	B	168	GLN	2.1
1	C	61	GLY	2.1
1	L	173	GLN	2.1
1	D	114	GLU	2.1
1	E	129	PRO	2.1
1	H	45	PRO	2.1
1	H	183	PRO	2.1
1	A	21	ASN	2.0
1	G	275	ASN	2.0
1	F	165	ASP	2.0
1	K	104	PHE	2.0
1	I	189	GLU	2.0
1	J	170	SER	2.0
1	C	21	ASN	2.0
1	E	117	MET	2.0
1	J	123	ASN	2.0
1	E	109	TYR	2.0
1	K	282	TYR	2.0
1	G	265	CYS	2.0
1	H	104	PHE	2.0
1	H	180	GLY	2.0
1	A	177	GLN	2.0
1	K	183	PRO	2.0
1	J	169	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.