



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:33 PM UTC

PDB ID : 3EHZ / pdb_00003ehz
Title : X-ray structure of the pentameric ligand gated ion channel of *Gloeobacter violaceus* (GLIC) in a presumptive open conformation
Authors : Hilf, R.J.C.; Dutzler, R.
Deposited on : 2008-09-15
Resolution : 3.10 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

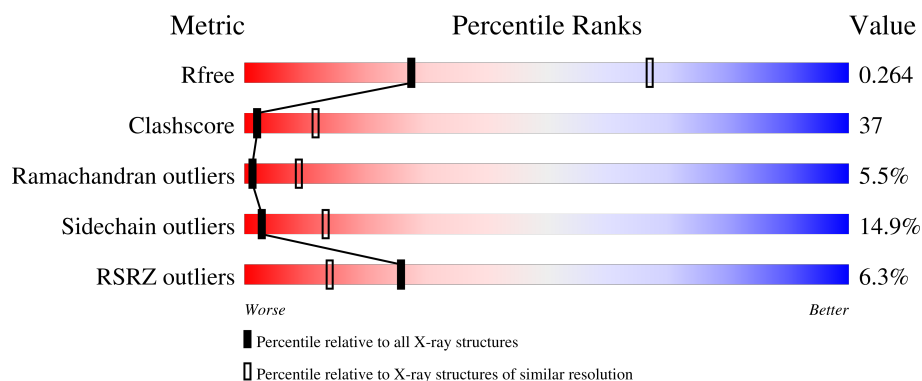
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	317	5% 39% 44% 13% ..
1	B	317	4% 38% 46% 12% ..
1	C	317	7% 42% 42% 13% ..
1	D	317	9% 41% 44% 11% ..
1	E	317	6% 40% 44% 13% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12652 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 Glr4197 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2521	1662	403	452	4			
1	B	310	Total	C	N	O	S	0	0	0
			2521	1662	403	452	4			
1	C	310	Total	C	N	O	S	0	0	0
			2521	1662	403	452	4			
1	D	310	Total	C	N	O	S	0	0	0
			2521	1662	403	452	4			
1	E	310	Total	C	N	O	S	0	0	0
			2521	1662	403	452	4			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q7NDN8
A	1	GLN	-	expression tag	UNP Q7NDN8
A	2	ASP	-	expression tag	UNP Q7NDN8
A	3	MET	-	expression tag	UNP Q7NDN8
A	4	VAL	-	expression tag	UNP Q7NDN8
A	5	SER	-	expression tag	UNP Q7NDN8
A	6	PRO	-	expression tag	UNP Q7NDN8
B	0	GLY	-	expression tag	UNP Q7NDN8
B	1	GLN	-	expression tag	UNP Q7NDN8
B	2	ASP	-	expression tag	UNP Q7NDN8
B	3	MET	-	expression tag	UNP Q7NDN8
B	4	VAL	-	expression tag	UNP Q7NDN8
B	5	SER	-	expression tag	UNP Q7NDN8
B	6	PRO	-	expression tag	UNP Q7NDN8
C	0	GLY	-	expression tag	UNP Q7NDN8
C	1	GLN	-	expression tag	UNP Q7NDN8
C	2	ASP	-	expression tag	UNP Q7NDN8
C	3	MET	-	expression tag	UNP Q7NDN8
C	4	VAL	-	expression tag	UNP Q7NDN8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	5	SER	-	expression tag	UNP Q7NDN8
C	6	PRO	-	expression tag	UNP Q7NDN8
D	0	GLY	-	expression tag	UNP Q7NDN8
D	1	GLN	-	expression tag	UNP Q7NDN8
D	2	ASP	-	expression tag	UNP Q7NDN8
D	3	MET	-	expression tag	UNP Q7NDN8
D	4	VAL	-	expression tag	UNP Q7NDN8
D	5	SER	-	expression tag	UNP Q7NDN8
D	6	PRO	-	expression tag	UNP Q7NDN8
E	0	GLY	-	expression tag	UNP Q7NDN8
E	1	GLN	-	expression tag	UNP Q7NDN8
E	2	ASP	-	expression tag	UNP Q7NDN8
E	3	MET	-	expression tag	UNP Q7NDN8
E	4	VAL	-	expression tag	UNP Q7NDN8
E	5	SER	-	expression tag	UNP Q7NDN8
E	6	PRO	-	expression tag	UNP Q7NDN8

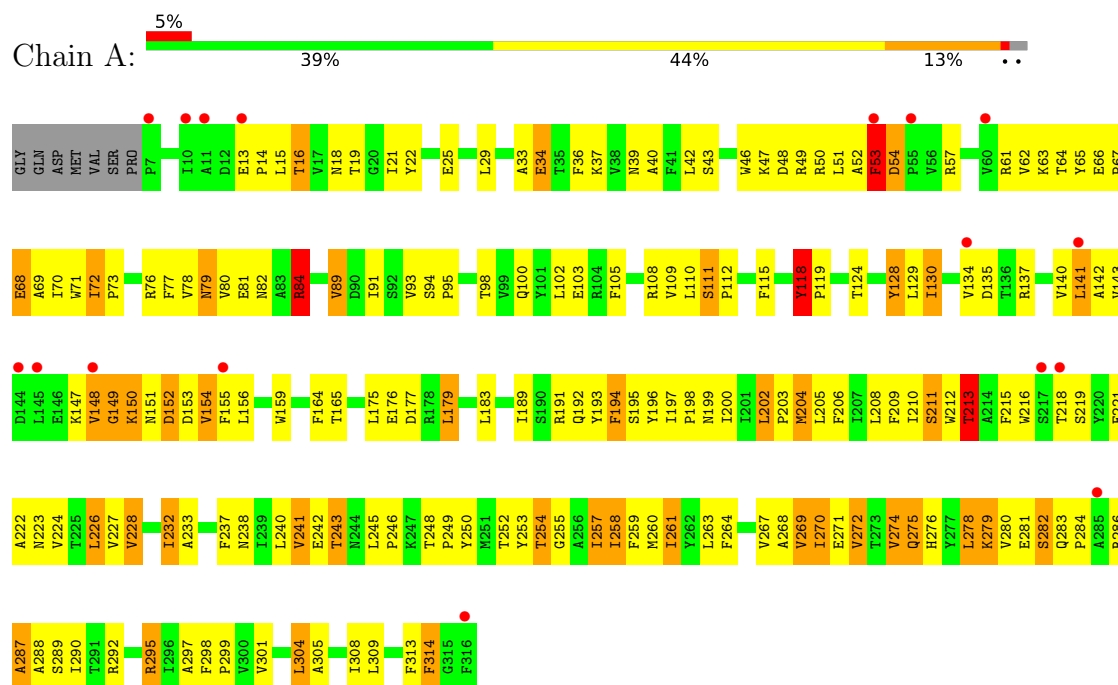
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	8	Total O 8 8	0	0
2	B	9	Total O 9 9	0	0
2	C	11	Total O 11 11	0	0
2	D	10	Total O 10 10	0	0
2	E	9	Total O 9 9	0	0

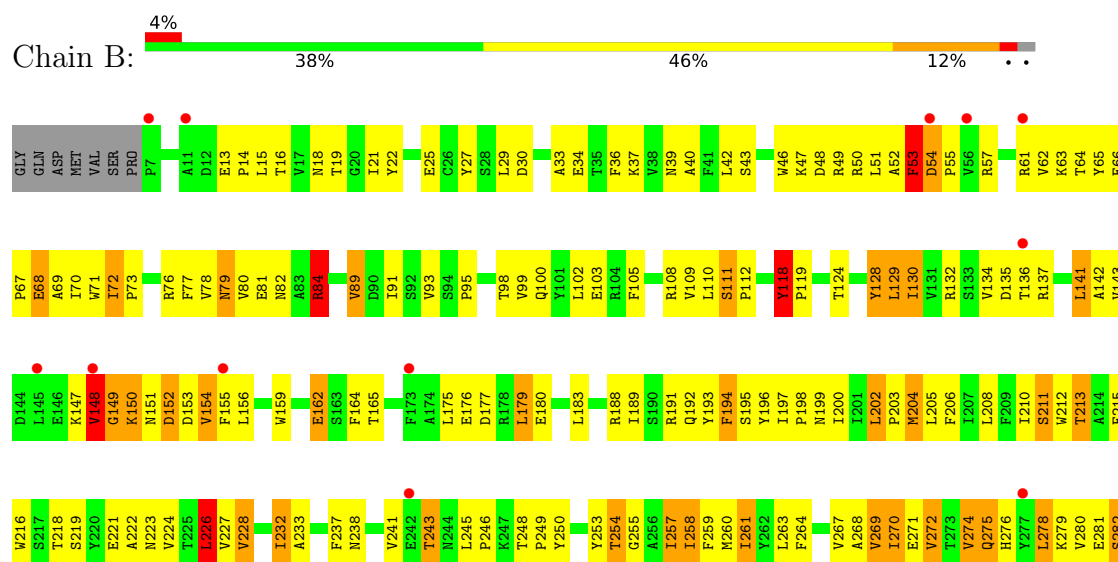
3 Residue-property plots

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

• Molecule 1: Glr4197 protein



• Molecule 1: Glr4197 protein

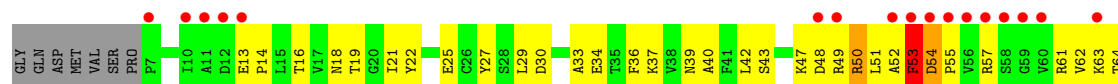




• Molecule 1: Glr4197 protein

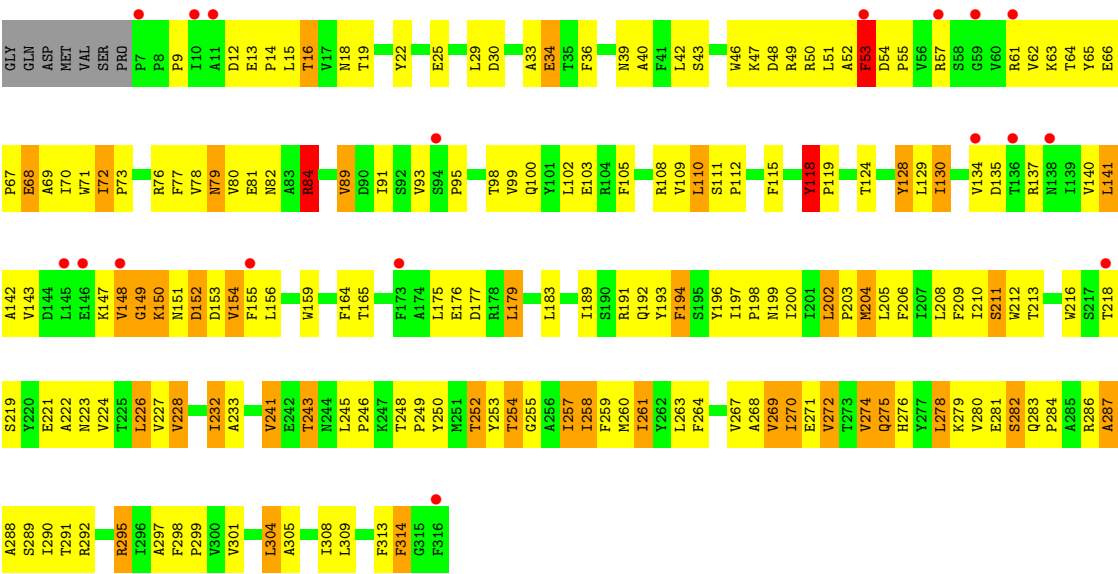


• Molecule 1: Glr4197 protein



• Molecule 1: Glr4197 protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	179.22Å 132.86Å 161.42Å 90.00° 102.19° 90.00°	Depositor
Resolution (Å)	19.97 – 3.10 19.97 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.97-3.10) 99.1 (19.97-3.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 3.11Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.238 , 0.266 0.238 , 0.264	Depositor DCC
R_{free} test set	3368 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	77.1	Xtriage
Anisotropy	0.296	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 65.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12652	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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	0.62	0/2589	1.00	12/3535 (0.3%)
1	B	0.61	0/2589	0.99	11/3535 (0.3%)
1	C	0.62	0/2589	1.00	12/3535 (0.3%)
1	D	0.63	0/2589	0.99	11/3535 (0.3%)
1	E	0.63	0/2589	0.99	8/3535 (0.2%)
All	All	0.62	0/12945	0.99	54/17675 (0.3%)

There are no bond length outliers.

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128	TYR	N-CA-C	7.42	122.42	111.96
1	E	128	TYR	N-CA-C	7.36	122.34	111.96
1	C	128	TYR	N-CA-C	7.35	122.32	111.96
1	B	128	TYR	N-CA-C	7.19	122.10	111.96
1	D	128	TYR	N-CA-C	6.89	121.68	111.96
1	E	53	PHE	N-CA-C	6.65	120.14	109.83
1	B	53	PHE	N-CA-C	6.60	120.06	109.83
1	A	118	TYR	CA-C-N	-6.59	112.20	119.19
1	A	118	TYR	C-N-CA	-6.59	112.20	119.19
1	C	53	PHE	N-CA-C	6.42	119.78	109.83
1	D	111	SER	CA-C-N	6.42	126.38	119.76
1	D	111	SER	C-N-CA	6.42	126.38	119.76
1	A	213	THR	N-CA-C	-6.40	104.57	112.38
1	C	118	TYR	CA-C-N	-6.33	112.48	119.19
1	C	118	TYR	C-N-CA	-6.33	112.48	119.19
1	D	53	PHE	N-CA-C	6.33	119.63	109.83
1	A	53	PHE	N-CA-C	6.29	119.58	109.83
1	C	111	SER	CA-C-N	6.23	126.18	119.76
1	C	111	SER	C-N-CA	6.23	126.18	119.76
1	E	111	SER	CA-C-N	6.19	126.13	119.76
1	E	111	SER	C-N-CA	6.19	126.13	119.76
1	C	152	ASP	N-CA-C	-6.13	106.47	112.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	118	TYR	CA-C-N	-6.06	112.77	119.19
1	D	118	TYR	C-N-CA	-6.06	112.77	119.19
1	B	118	TYR	CA-C-N	-5.97	112.86	119.19
1	B	118	TYR	C-N-CA	-5.97	112.86	119.19
1	A	152	ASP	N-CA-C	-5.92	106.69	112.97
1	D	213	THR	N-CA-C	-5.86	105.23	112.38
1	E	152	ASP	N-CA-C	-5.84	106.78	112.97
1	A	111	SER	CA-C-N	5.82	125.75	119.76
1	A	111	SER	C-N-CA	5.82	125.75	119.76
1	B	111	SER	CA-C-N	5.66	125.59	119.76
1	B	111	SER	C-N-CA	5.66	125.59	119.76
1	D	54	ASP	CA-C-N	5.61	126.85	119.84
1	D	54	ASP	C-N-CA	5.61	126.85	119.84
1	E	118	TYR	CA-C-N	-5.56	113.30	119.19
1	E	118	TYR	C-N-CA	-5.56	113.30	119.19
1	B	152	ASP	N-CA-C	-5.55	107.09	112.97
1	A	135	ASP	N-CA-C	-5.53	106.37	114.39
1	D	135	ASP	N-CA-C	-5.50	106.42	114.39
1	C	135	ASP	N-CA-C	-5.45	106.49	114.39
1	D	152	ASP	N-CA-C	-5.42	107.23	112.97
1	C	213	THR	N-CA-C	-5.30	105.92	112.38
1	A	279	LYS	N-CA-C	-5.25	105.94	114.09
1	C	279	LYS	N-CA-C	-5.24	106.67	114.64
1	B	54	ASP	CA-C-N	5.20	126.33	119.84
1	B	54	ASP	C-N-CA	5.20	126.33	119.84
1	B	213	THR	N-CA-C	-5.17	106.07	112.38
1	E	135	ASP	N-CA-C	-5.17	106.89	114.39
1	A	54	ASP	CA-C-N	5.06	126.17	119.84
1	A	54	ASP	C-N-CA	5.06	126.17	119.84
1	C	245	LEU	CA-C-N	5.03	125.04	120.21
1	C	245	LEU	C-N-CA	5.03	125.04	120.21
1	B	135	ASP	N-CA-C	-5.01	107.13	114.39

There are no chirality outliers.

There are no planarity outliers.

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	2521	0	2537	198	0
1	B	2521	0	2537	200	0
1	C	2521	0	2537	195	0
1	D	2521	0	2537	195	0
1	E	2521	0	2537	190	0
2	A	8	0	0	0	0
2	B	9	0	0	0	0
2	C	11	0	0	0	0
2	D	10	0	0	0	0
2	E	9	0	0	0	0
All	All	12652	0	12685	948	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (948) 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:D:22:TYR:HA	1:D:149:GLY:HA2	1.43	0.99
1:B:13:GLU:HB3	1:B:14:PRO:HD2	1.47	0.97
1:C:22:TYR:HA	1:C:149:GLY:HA2	1.46	0.97
1:B:22:TYR:HA	1:B:149:GLY:HA2	1.43	0.96
1:C:13:GLU:HB3	1:C:14:PRO:HD2	1.48	0.96
1:E:22:TYR:HA	1:E:149:GLY:HA2	1.47	0.95
1:E:13:GLU:HB3	1:E:14:PRO:HD2	1.47	0.95
1:B:147:LYS:C	1:B:149:GLY:H	1.76	0.94
1:D:13:GLU:HB3	1:D:14:PRO:HD2	1.47	0.93
1:A:22:TYR:HA	1:A:149:GLY:HA2	1.47	0.93
1:E:147:LYS:C	1:E:149:GLY:H	1.76	0.93
1:A:13:GLU:HB3	1:A:14:PRO:HD2	1.48	0.92
1:A:147:LYS:C	1:A:149:GLY:H	1.78	0.92
1:E:151:ASN:HD22	1:E:152:ASP:H	1.17	0.92
1:A:151:ASN:HD22	1:A:152:ASP:H	1.18	0.91
1:D:22:TYR:HA	1:D:149:GLY:CA	2.00	0.91
1:A:77:PHE:CD1	1:A:84:ARG:HD2	2.05	0.91
1:C:147:LYS:C	1:C:149:GLY:H	1.77	0.90
1:E:77:PHE:CD1	1:E:84:ARG:HD2	2.08	0.89
1:B:22:TYR:HA	1:B:149:GLY:CA	2.01	0.89
1:C:77:PHE:CD1	1:C:84:ARG:HD2	2.07	0.89
1:D:54:ASP:HB2	1:D:57:ARG:HB2	1.52	0.89
1:B:78:VAL:HG22	1:B:130:ILE:HG12	1.55	0.88
1:D:77:PHE:CD1	1:D:84:ARG:HD2	2.07	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:ASN:HD22	1:C:152:ASP:H	1.20	0.88
1:D:84:ARG:HB2	1:D:84:ARG:HH11	1.39	0.88
1:E:141:LEU:HD23	1:E:142:ALA:H	1.40	0.88
1:C:54:ASP:HB2	1:C:57:ARG:HB2	1.56	0.87
1:E:84:ARG:HH11	1:E:84:ARG:HB2	1.40	0.87
1:E:22:TYR:HA	1:E:149:GLY:CA	2.04	0.87
1:B:77:PHE:CD1	1:B:84:ARG:HD2	2.09	0.87
1:E:54:ASP:HB2	1:E:57:ARG:HB2	1.57	0.87
1:B:249:PRO:HD2	1:B:250:TYR:CD1	2.10	0.86
1:E:197:ILE:HB	1:E:198:PRO:HD3	1.58	0.86
1:D:197:ILE:HB	1:D:198:PRO:HD3	1.57	0.86
1:B:151:ASN:HD22	1:B:152:ASP:H	1.21	0.86
1:E:249:PRO:HD2	1:E:250:TYR:CD1	2.11	0.86
1:D:77:PHE:HD1	1:D:84:ARG:HD2	1.41	0.86
1:A:249:PRO:HD2	1:A:250:TYR:CD1	2.11	0.86
1:B:54:ASP:HB2	1:B:57:ARG:HB2	1.57	0.85
1:A:22:TYR:HA	1:A:149:GLY:CA	2.05	0.85
1:D:147:LYS:C	1:D:149:GLY:H	1.79	0.85
1:C:249:PRO:HD2	1:C:250:TYR:CD1	2.12	0.85
1:D:151:ASN:HD22	1:D:152:ASP:H	1.21	0.85
1:C:22:TYR:HA	1:C:149:GLY:CA	2.05	0.85
1:B:141:LEU:HD23	1:B:142:ALA:H	1.42	0.84
1:C:197:ILE:HB	1:C:198:PRO:HD3	1.58	0.84
1:D:249:PRO:HD2	1:D:250:TYR:CD1	2.13	0.84
1:D:84:ARG:HB2	1:D:84:ARG:NH1	1.93	0.84
1:C:79:ASN:HD22	1:C:79:ASN:H	1.26	0.83
1:D:141:LEU:HD23	1:D:142:ALA:H	1.41	0.83
1:D:78:VAL:HG22	1:D:130:ILE:HG12	1.60	0.83
1:B:197:ILE:HB	1:B:198:PRO:HD3	1.59	0.83
1:C:84:ARG:HB2	1:C:84:ARG:HH11	1.44	0.83
1:A:78:VAL:HG22	1:A:130:ILE:HG12	1.61	0.83
1:A:54:ASP:HB2	1:A:57:ARG:HB2	1.59	0.82
1:E:84:ARG:HB2	1:E:84:ARG:NH1	1.95	0.82
1:D:79:ASN:H	1:D:79:ASN:HD22	1.26	0.82
1:A:84:ARG:HH11	1:A:84:ARG:HB2	1.43	0.82
1:E:78:VAL:HG22	1:E:130:ILE:HG12	1.60	0.82
1:C:77:PHE:HD1	1:C:84:ARG:HD2	1.45	0.82
1:A:84:ARG:HB2	1:A:84:ARG:NH1	1.95	0.82
1:A:77:PHE:HD1	1:A:84:ARG:HD2	1.42	0.81
1:A:79:ASN:HD22	1:A:79:ASN:H	1.25	0.81
1:D:84:ARG:HH11	1:D:84:ARG:CB	1.94	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:149:GLY:O	1:D:150:LYS:HB2	1.81	0.81
1:E:84:ARG:HH11	1:E:84:ARG:CB	1.93	0.81
1:B:79:ASN:H	1:B:79:ASN:HD22	1.25	0.81
1:C:78:VAL:HG22	1:C:130:ILE:HG12	1.63	0.81
1:B:80:VAL:HG12	1:B:82:ASN:O	1.80	0.81
1:A:197:ILE:HB	1:A:198:PRO:HD3	1.61	0.81
1:A:76:ARG:NH2	1:A:130:ILE:HD12	1.96	0.80
1:B:149:GLY:O	1:B:150:LYS:HB2	1.79	0.80
1:A:141:LEU:HD23	1:A:142:ALA:H	1.46	0.79
1:C:84:ARG:HB2	1:C:84:ARG:NH1	1.97	0.79
1:B:84:ARG:HH11	1:B:84:ARG:HB2	1.45	0.79
1:D:128:TYR:O	1:D:129:LEU:HB2	1.83	0.79
1:A:84:ARG:HH11	1:A:84:ARG:CB	1.95	0.79
1:E:80:VAL:HG12	1:E:82:ASN:O	1.83	0.79
1:C:149:GLY:O	1:C:150:LYS:HB2	1.81	0.79
1:B:77:PHE:HD1	1:B:84:ARG:HD2	1.44	0.79
1:E:149:GLY:O	1:E:150:LYS:HB2	1.81	0.79
1:E:76:ARG:NH2	1:E:130:ILE:HD12	1.98	0.79
1:E:79:ASN:HD22	1:E:79:ASN:H	1.30	0.79
1:B:84:ARG:HB2	1:B:84:ARG:NH1	1.98	0.78
1:D:80:VAL:HG12	1:D:82:ASN:O	1.82	0.78
1:E:77:PHE:HD1	1:E:84:ARG:HD2	1.45	0.78
1:D:48:ASP:O	1:D:51:LEU:HD23	1.82	0.78
1:D:76:ARG:NH2	1:D:130:ILE:HD12	1.99	0.78
1:A:149:GLY:O	1:A:150:LYS:HB2	1.81	0.78
1:B:13:GLU:HB3	1:B:14:PRO:CD	2.13	0.78
1:A:128:TYR:O	1:A:129:LEU:HB2	1.84	0.77
1:C:76:ARG:NH2	1:C:130:ILE:HD12	1.99	0.77
1:B:76:ARG:NH2	1:B:130:ILE:HD12	1.98	0.77
1:C:80:VAL:HG12	1:C:82:ASN:O	1.84	0.77
1:C:141:LEU:HD23	1:C:142:ALA:H	1.47	0.77
1:C:13:GLU:HB3	1:C:14:PRO:CD	2.14	0.77
1:A:13:GLU:HB3	1:A:14:PRO:CD	2.14	0.77
1:A:80:VAL:HG12	1:A:82:ASN:O	1.85	0.77
1:E:13:GLU:HB3	1:E:14:PRO:CD	2.14	0.77
1:D:13:GLU:HB3	1:D:14:PRO:CD	2.14	0.76
1:C:84:ARG:HH11	1:C:84:ARG:CB	1.97	0.76
1:E:128:TYR:O	1:E:129:LEU:HB2	1.84	0.76
1:B:84:ARG:HH11	1:B:84:ARG:CB	1.99	0.76
1:A:208:LEU:O	1:A:211:SER:HB3	1.87	0.75
1:C:48:ASP:O	1:C:51:LEU:HD23	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:282:SER:C	1:C:284:PRO:HD3	2.11	0.74
1:C:128:TYR:O	1:C:129:LEU:HB2	1.87	0.74
1:E:282:SER:C	1:E:284:PRO:HD3	2.12	0.74
1:B:147:LYS:C	1:B:149:GLY:N	2.46	0.74
1:E:208:LEU:O	1:E:211:SER:HB3	1.88	0.74
1:B:282:SER:C	1:B:284:PRO:HD3	2.13	0.74
1:B:208:LEU:O	1:B:211:SER:HB3	1.87	0.73
1:E:48:ASP:O	1:E:51:LEU:HD23	1.88	0.72
1:D:253:TYR:HA	1:D:313:PHE:CE2	2.24	0.72
1:D:208:LEU:O	1:D:211:SER:HB3	1.89	0.72
1:E:249:PRO:HD2	1:E:250:TYR:HD1	1.53	0.72
1:D:282:SER:C	1:D:284:PRO:HD3	2.14	0.72
1:D:77:PHE:H	1:D:84:ARG:HD3	1.55	0.72
1:A:151:ASN:HD22	1:A:152:ASP:N	1.87	0.72
1:D:249:PRO:HD2	1:D:250:TYR:HD1	1.54	0.72
1:A:282:SER:C	1:A:284:PRO:HD3	2.14	0.72
1:B:128:TYR:O	1:B:129:LEU:HB2	1.90	0.72
1:E:147:LYS:HE2	1:E:165:THR:HA	1.72	0.72
1:A:249:PRO:HD2	1:A:250:TYR:HD1	1.54	0.71
1:A:147:LYS:HE2	1:A:165:THR:HA	1.72	0.71
1:E:151:ASN:HD22	1:E:152:ASP:N	1.87	0.71
1:E:66:GLU:HG3	1:E:67:PRO:HD2	1.72	0.71
1:B:66:GLU:HG3	1:B:67:PRO:HD2	1.73	0.70
1:B:249:PRO:HD2	1:B:250:TYR:HD1	1.53	0.70
1:A:48:ASP:O	1:A:51:LEU:HD23	1.91	0.70
1:A:253:TYR:HA	1:A:313:PHE:CE2	2.26	0.70
1:C:208:LEU:O	1:C:211:SER:HB3	1.92	0.70
1:E:253:TYR:HA	1:E:313:PHE:CE2	2.25	0.70
1:E:151:ASN:ND2	1:E:152:ASP:H	1.89	0.70
1:A:77:PHE:H	1:A:84:ARG:HD3	1.56	0.70
1:D:42:LEU:HB3	1:D:103:GLU:HG2	1.72	0.70
1:A:151:ASN:ND2	1:A:152:ASP:H	1.90	0.70
1:B:76:ARG:HH22	1:B:130:ILE:HD12	1.57	0.70
1:C:253:TYR:HA	1:C:313:PHE:CE2	2.26	0.69
1:B:48:ASP:O	1:B:51:LEU:HD23	1.90	0.69
1:E:275:GLN:O	1:E:275:GLN:HG2	1.91	0.69
1:C:77:PHE:H	1:C:84:ARG:HD3	1.57	0.69
1:D:151:ASN:HD22	1:D:152:ASP:N	1.90	0.69
1:C:151:ASN:HD22	1:C:152:ASP:N	1.90	0.69
1:B:80:VAL:CG1	1:B:82:ASN:O	2.40	0.69
1:B:202:LEU:HD12	1:C:259:PHE:CZ	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:42:LEU:HB3	1:E:103:GLU:HG2	1.75	0.69
1:A:76:ARG:HH22	1:A:130:ILE:HD12	1.57	0.69
1:C:151:ASN:ND2	1:C:152:ASP:H	1.91	0.68
1:B:275:GLN:HG2	1:B:275:GLN:O	1.93	0.68
1:B:253:TYR:HA	1:B:313:PHE:CE2	2.27	0.68
1:C:275:GLN:O	1:C:275:GLN:HG2	1.93	0.68
1:B:77:PHE:H	1:B:84:ARG:HD3	1.57	0.68
1:C:249:PRO:HD2	1:C:250:TYR:HD1	1.55	0.68
1:C:147:LYS:HE2	1:C:165:THR:HA	1.74	0.68
1:A:42:LEU:HB3	1:A:103:GLU:HG2	1.77	0.67
1:E:76:ARG:HH22	1:E:130:ILE:HD12	1.57	0.67
1:B:151:ASN:HD22	1:B:152:ASP:N	1.90	0.67
1:D:147:LYS:HE2	1:D:165:THR:HA	1.76	0.67
1:D:276:HIS:O	1:D:280:VAL:HG22	1.95	0.67
1:E:80:VAL:CG1	1:E:82:ASN:O	2.42	0.67
1:B:151:ASN:ND2	1:B:152:ASP:H	1.92	0.67
1:A:147:LYS:C	1:A:149:GLY:N	2.48	0.67
1:B:147:LYS:HE2	1:B:165:THR:HA	1.75	0.67
1:A:80:VAL:CG1	1:A:82:ASN:O	2.43	0.67
1:E:77:PHE:H	1:E:84:ARG:HD3	1.60	0.67
1:D:66:GLU:HG3	1:D:67:PRO:HD2	1.77	0.67
1:E:147:LYS:C	1:E:149:GLY:N	2.47	0.67
1:B:260:MET:HE2	1:B:309:LEU:HD22	1.76	0.66
1:C:66:GLU:HG3	1:C:67:PRO:HD2	1.76	0.66
1:A:267:VAL:HA	1:A:270:ILE:HB	1.77	0.66
1:A:276:HIS:O	1:A:280:VAL:HG22	1.95	0.66
1:B:276:HIS:O	1:B:280:VAL:HG22	1.96	0.66
1:C:42:LEU:HB3	1:C:103:GLU:HG2	1.76	0.66
1:E:276:HIS:O	1:E:280:VAL:HG22	1.95	0.66
1:D:54:ASP:HB2	1:D:57:ARG:CB	2.24	0.66
1:D:202:LEU:HD12	1:E:259:PHE:HZ	1.61	0.66
1:B:202:LEU:HD12	1:C:259:PHE:HZ	1.59	0.66
1:C:80:VAL:CG1	1:C:82:ASN:O	2.44	0.66
1:E:53:PHE:O	1:E:53:PHE:CD1	2.49	0.66
1:B:42:LEU:HB3	1:B:103:GLU:HG2	1.76	0.66
1:B:53:PHE:O	1:B:53:PHE:CD1	2.48	0.66
1:D:76:ARG:HH22	1:D:130:ILE:HD12	1.59	0.66
1:A:297:ALA:O	1:A:301:VAL:HG23	1.95	0.65
1:C:54:ASP:HB2	1:C:57:ARG:CB	2.26	0.65
1:C:267:VAL:HA	1:C:270:ILE:HB	1.78	0.65
1:D:65:TYR:CG	1:D:70:ILE:HD11	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:GLN:O	1:A:275:GLN:HG2	1.94	0.65
1:C:65:TYR:CG	1:C:70:ILE:HD11	2.31	0.65
1:D:80:VAL:CG1	1:D:82:ASN:O	2.43	0.65
1:A:53:PHE:O	1:A:53:PHE:CD1	2.49	0.65
1:D:260:MET:HE2	1:D:309:LEU:HD22	1.77	0.65
1:A:66:GLU:HG3	1:A:67:PRO:HD2	1.78	0.65
1:D:267:VAL:HA	1:D:270:ILE:HB	1.78	0.65
1:D:151:ASN:ND2	1:D:152:ASP:H	1.92	0.65
1:D:275:GLN:O	1:D:275:GLN:HG2	1.95	0.65
1:B:267:VAL:HA	1:B:270:ILE:HB	1.77	0.65
1:D:202:LEU:HD12	1:E:259:PHE:CZ	2.31	0.65
1:A:260:MET:HE2	1:A:309:LEU:HD22	1.78	0.65
1:B:54:ASP:HB2	1:B:57:ARG:CB	2.27	0.64
1:B:65:TYR:CG	1:B:70:ILE:HD11	2.31	0.64
1:C:53:PHE:O	1:C:53:PHE:CD1	2.51	0.64
1:C:276:HIS:O	1:C:280:VAL:HG22	1.96	0.64
1:E:54:ASP:HB2	1:E:57:ARG:CB	2.27	0.64
1:E:276:HIS:C	1:E:278:LEU:H	2.05	0.64
1:C:274:VAL:C	1:C:276:HIS:H	2.05	0.64
1:B:159:TRP:CE3	1:B:189:ILE:HD12	2.32	0.64
1:C:76:ARG:HH22	1:C:130:ILE:HD12	1.61	0.64
1:D:274:VAL:C	1:D:276:HIS:H	2.06	0.64
1:A:54:ASP:HB2	1:A:57:ARG:CB	2.28	0.64
1:C:297:ALA:O	1:C:301:VAL:HG23	1.98	0.64
1:E:65:TYR:CG	1:E:70:ILE:HD11	2.31	0.64
1:D:147:LYS:C	1:D:149:GLY:N	2.49	0.63
1:E:297:ALA:O	1:E:301:VAL:HG23	1.99	0.63
1:B:297:ALA:O	1:B:301:VAL:HG23	1.98	0.63
1:E:260:MET:HE2	1:E:309:LEU:HD22	1.79	0.63
1:D:53:PHE:CD1	1:D:53:PHE:O	2.52	0.63
1:C:147:LYS:C	1:C:149:GLY:N	2.47	0.62
1:C:276:HIS:C	1:C:278:LEU:H	2.07	0.62
1:A:274:VAL:C	1:A:276:HIS:H	2.06	0.62
1:B:274:VAL:C	1:B:276:HIS:H	2.05	0.62
1:B:276:HIS:C	1:B:278:LEU:H	2.07	0.62
1:D:276:HIS:C	1:D:278:LEU:H	2.07	0.62
1:C:283:GLN:HE21	1:C:286:ARG:HB2	1.65	0.62
1:D:22:TYR:HA	1:D:149:GLY:HA3	1.82	0.62
1:E:267:VAL:HA	1:E:270:ILE:HB	1.79	0.62
1:E:274:VAL:C	1:E:276:HIS:H	2.08	0.62
1:C:260:MET:HE2	1:C:309:LEU:HD22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:TYR:CG	1:A:70:ILE:HD11	2.34	0.62
1:E:281:GLU:O	1:E:283:GLN:N	2.31	0.62
1:C:159:TRP:CE3	1:C:189:ILE:HD12	2.35	0.61
1:A:276:HIS:C	1:A:278:LEU:H	2.08	0.61
1:E:40:ALA:HB3	1:E:105:PHE:CZ	2.35	0.61
1:B:53:PHE:O	1:B:53:PHE:HD1	1.83	0.61
1:A:53:PHE:O	1:A:53:PHE:HD1	1.84	0.61
1:A:159:TRP:CE3	1:A:189:ILE:HD12	2.35	0.61
1:E:53:PHE:O	1:E:53:PHE:HD1	1.84	0.61
1:B:89:VAL:HG11	1:B:102:LEU:HD23	1.82	0.60
1:B:267:VAL:HG23	1:B:298:PHE:CZ	2.36	0.60
1:B:212:TRP:HZ3	1:B:264:PHE:HD2	1.49	0.60
1:D:283:GLN:HE21	1:D:286:ARG:HB2	1.65	0.60
1:D:297:ALA:O	1:D:301:VAL:HG23	1.99	0.60
1:D:281:GLU:O	1:D:283:GLN:N	2.31	0.60
1:E:89:VAL:HG11	1:E:102:LEU:HD23	1.83	0.60
1:E:283:GLN:HE21	1:E:286:ARG:HB2	1.66	0.60
1:C:40:ALA:HB3	1:C:105:PHE:CZ	2.37	0.60
1:D:159:TRP:CE3	1:D:189:ILE:HD12	2.36	0.60
1:E:212:TRP:HZ3	1:E:264:PHE:HD2	1.49	0.60
1:A:40:ALA:HB3	1:A:105:PHE:CZ	2.37	0.60
1:A:202:LEU:HD12	1:B:259:PHE:HZ	1.66	0.60
1:B:147:LYS:O	1:B:149:GLY:N	2.34	0.60
1:B:281:GLU:O	1:B:283:GLN:N	2.30	0.60
1:A:281:GLU:O	1:A:283:GLN:N	2.32	0.59
1:B:100:GLN:HE21	1:B:100:GLN:HA	1.66	0.59
1:D:267:VAL:HG23	1:D:298:PHE:CZ	2.37	0.59
1:D:278:LEU:HD21	1:D:286:ARG:HB3	1.84	0.59
1:A:283:GLN:HE21	1:A:286:ARG:HB2	1.68	0.59
1:C:267:VAL:HG23	1:C:298:PHE:CZ	2.38	0.59
1:A:255:GLY:O	1:A:258:ILE:HG22	2.02	0.59
1:C:278:LEU:HD21	1:C:286:ARG:HB3	1.85	0.59
1:E:278:LEU:HD21	1:E:286:ARG:HB3	1.84	0.59
1:A:259:PHE:CZ	1:E:202:LEU:HD12	2.38	0.59
1:B:53:PHE:HD1	1:B:53:PHE:C	2.11	0.59
1:B:283:GLN:HE21	1:B:286:ARG:HB2	1.66	0.59
1:E:283:GLN:N	1:E:284:PRO:HD3	2.18	0.59
1:A:202:LEU:HD12	1:B:259:PHE:CZ	2.37	0.59
1:A:212:TRP:HZ3	1:A:264:PHE:HD2	1.51	0.59
1:E:254:THR:O	1:E:258:ILE:HB	2.03	0.59
1:E:255:GLY:O	1:E:258:ILE:HG22	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:ILE:HG23	1:C:269:VAL:HG11	1.85	0.59
1:B:254:THR:O	1:B:258:ILE:HB	2.02	0.59
1:C:53:PHE:O	1:C:53:PHE:HD1	1.86	0.58
1:E:53:PHE:HD1	1:E:53:PHE:C	2.11	0.58
1:C:283:GLN:N	1:C:284:PRO:HD3	2.17	0.58
1:D:212:TRP:HZ3	1:D:264:PHE:HD2	1.50	0.58
1:C:241:VAL:C	1:C:243:THR:H	2.12	0.58
1:C:255:GLY:O	1:C:258:ILE:HG22	2.03	0.58
1:E:147:LYS:O	1:E:149:GLY:N	2.36	0.58
1:C:151:ASN:O	1:C:154:VAL:HG22	2.04	0.58
1:A:283:GLN:N	1:A:284:PRO:HD3	2.19	0.58
1:B:283:GLN:N	1:B:284:PRO:HD3	2.19	0.58
1:E:100:GLN:HA	1:E:100:GLN:HE21	1.68	0.58
1:A:267:VAL:HG23	1:A:298:PHE:CZ	2.39	0.57
1:A:278:LEU:HD21	1:A:286:ARG:HB3	1.85	0.57
1:C:254:THR:O	1:C:258:ILE:HB	2.03	0.57
1:D:283:GLN:N	1:D:284:PRO:HD3	2.18	0.57
1:A:53:PHE:HD1	1:A:53:PHE:C	2.12	0.57
1:C:212:TRP:HZ3	1:C:264:PHE:HD2	1.50	0.57
1:E:159:TRP:CE3	1:E:189:ILE:HD12	2.39	0.57
1:A:77:PHE:HD1	1:A:84:ARG:CD	2.16	0.57
1:D:100:GLN:HE21	1:D:100:GLN:HA	1.69	0.57
1:A:259:PHE:HZ	1:E:202:LEU:HD12	1.69	0.57
1:D:53:PHE:O	1:D:53:PHE:HD1	1.87	0.57
1:A:100:GLN:HE21	1:A:100:GLN:HA	1.69	0.57
1:A:254:THR:O	1:A:258:ILE:HB	2.04	0.57
1:D:255:GLY:O	1:D:258:ILE:HG22	2.05	0.57
1:A:271:GLU:O	1:A:272:VAL:C	2.48	0.57
1:B:53:PHE:CD1	1:B:53:PHE:C	2.82	0.57
1:B:255:GLY:O	1:B:258:ILE:HG22	2.05	0.57
1:C:53:PHE:CD1	1:C:53:PHE:C	2.83	0.57
1:E:267:VAL:HG23	1:E:298:PHE:CZ	2.39	0.57
1:D:271:GLU:OE2	1:D:272:VAL:N	2.38	0.56
1:B:151:ASN:O	1:B:154:VAL:HG22	2.06	0.56
1:C:53:PHE:HD1	1:C:53:PHE:C	2.13	0.56
1:C:202:LEU:HD12	1:D:259:PHE:CZ	2.41	0.56
1:D:29:LEU:HD23	1:D:29:LEU:C	2.29	0.56
1:E:70:ILE:HG22	1:E:71:TRP:O	2.05	0.56
1:B:29:LEU:HD23	1:B:29:LEU:C	2.31	0.56
1:D:286:ARG:O	1:D:289:SER:HB3	2.06	0.56
1:B:271:GLU:O	1:B:272:VAL:C	2.49	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:LYS:O	1:C:149:GLY:N	2.37	0.56
1:E:22:TYR:HA	1:E:149:GLY:HA3	1.86	0.56
1:B:286:ARG:O	1:B:289:SER:HB3	2.04	0.56
1:B:89:VAL:CG1	1:B:102:LEU:HD23	2.36	0.56
1:C:271:GLU:OE2	1:C:272:VAL:N	2.39	0.56
1:D:200:ILE:O	1:D:204:MET:HB2	2.06	0.56
1:A:53:PHE:CD1	1:A:53:PHE:C	2.83	0.56
1:A:147:LYS:O	1:A:149:GLY:N	2.38	0.56
1:D:53:PHE:CD1	1:D:53:PHE:C	2.84	0.56
1:D:147:LYS:O	1:D:149:GLY:N	2.39	0.56
1:E:53:PHE:CD1	1:E:53:PHE:C	2.82	0.56
1:C:155:PHE:CE1	1:D:112:PRO:HB3	2.41	0.56
1:D:53:PHE:HD1	1:D:53:PHE:C	2.14	0.56
1:A:29:LEU:C	1:A:29:LEU:HD23	2.32	0.55
1:A:33:ALA:O	1:A:34:GLU:HB2	2.06	0.55
1:D:40:ALA:HB3	1:D:105:PHE:CZ	2.41	0.55
1:C:89:VAL:HG11	1:C:102:LEU:HD23	1.88	0.55
1:C:281:GLU:O	1:C:283:GLN:N	2.32	0.55
1:D:216:TRP:CE2	1:D:295:ARG:HD3	2.42	0.55
1:A:54:ASP:HB2	1:A:57:ARG:CG	2.36	0.55
1:B:200:ILE:O	1:B:204:MET:HB2	2.06	0.55
1:E:151:ASN:O	1:E:154:VAL:HG22	2.05	0.55
1:A:79:ASN:H	1:A:79:ASN:ND2	2.02	0.55
1:B:179:LEU:HD12	1:B:179:LEU:C	2.32	0.55
1:E:241:VAL:C	1:E:243:THR:H	2.13	0.55
1:C:54:ASP:HB2	1:C:57:ARG:CG	2.36	0.55
1:D:254:THR:O	1:D:258:ILE:HB	2.06	0.55
1:E:208:LEU:HD13	1:E:261:ILE:HG23	1.89	0.55
1:A:151:ASN:O	1:A:154:VAL:HG22	2.07	0.55
1:A:200:ILE:O	1:A:204:MET:HB2	2.07	0.55
1:B:54:ASP:HB2	1:B:57:ARG:CG	2.36	0.55
1:B:70:ILE:HG22	1:B:71:TRP:O	2.06	0.55
1:D:241:VAL:C	1:D:243:THR:H	2.13	0.55
1:E:200:ILE:O	1:E:204:MET:HB2	2.06	0.55
1:E:54:ASP:HB2	1:E:57:ARG:CG	2.37	0.55
1:E:271:GLU:O	1:E:272:VAL:C	2.50	0.55
1:A:216:TRP:CE2	1:A:295:ARG:HD3	2.42	0.55
1:D:54:ASP:HB2	1:D:57:ARG:CG	2.37	0.55
1:D:281:GLU:C	1:D:283:GLN:H	2.15	0.55
1:E:29:LEU:C	1:E:29:LEU:HD23	2.32	0.55
1:C:216:TRP:CE2	1:C:295:ARG:HD3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:271:GLU:O	1:C:272:VAL:C	2.49	0.55
1:D:179:LEU:HD12	1:D:179:LEU:C	2.32	0.55
1:A:271:GLU:OE2	1:A:272:VAL:N	2.40	0.54
1:A:286:ARG:O	1:A:289:SER:HB3	2.07	0.54
1:B:79:ASN:H	1:B:79:ASN:ND2	2.01	0.54
1:B:281:GLU:C	1:B:283:GLN:H	2.14	0.54
1:C:224:VAL:O	1:C:228:VAL:HB	2.07	0.54
1:E:281:GLU:C	1:E:283:GLN:H	2.15	0.54
1:E:286:ARG:O	1:E:289:SER:HB3	2.06	0.54
1:B:278:LEU:HD21	1:B:286:ARG:HB3	1.90	0.54
1:D:18:ASN:HB3	1:D:143:VAL:HG23	1.89	0.54
1:E:248:THR:HB	1:E:250:TYR:CE1	2.42	0.54
1:A:36:PHE:CE1	1:A:109:VAL:HB	2.43	0.54
1:A:241:VAL:C	1:A:243:THR:H	2.15	0.54
1:C:200:ILE:O	1:C:204:MET:HB2	2.07	0.54
1:E:216:TRP:CE2	1:E:295:ARG:HD3	2.42	0.54
1:B:248:THR:HB	1:B:250:TYR:CE1	2.43	0.54
1:D:77:PHE:HD1	1:D:84:ARG:CD	2.16	0.54
1:E:89:VAL:CG1	1:E:102:LEU:HD23	2.37	0.54
1:D:314:PHE:CD1	1:D:314:PHE:N	2.76	0.54
1:E:314:PHE:CD1	1:E:314:PHE:N	2.76	0.54
1:A:18:ASN:HB3	1:A:143:VAL:HG23	1.89	0.54
1:A:179:LEU:C	1:A:179:LEU:HD12	2.33	0.54
1:A:257:ILE:O	1:A:261:ILE:HG12	2.07	0.54
1:C:202:LEU:HD12	1:D:259:PHE:HZ	1.73	0.54
1:C:281:GLU:C	1:C:283:GLN:H	2.16	0.54
1:D:53:PHE:O	1:D:54:ASP:C	2.50	0.54
1:D:210:ILE:HG23	1:E:269:VAL:HG11	1.89	0.54
1:B:216:TRP:CE2	1:B:295:ARG:HD3	2.42	0.54
1:D:271:GLU:O	1:D:272:VAL:C	2.52	0.54
1:D:298:PHE:HB2	1:D:299:PRO:HD3	1.91	0.53
1:E:271:GLU:OE2	1:E:272:VAL:N	2.41	0.53
1:B:271:GLU:OE2	1:B:272:VAL:N	2.40	0.53
1:D:248:THR:HB	1:D:250:TYR:CE1	2.43	0.53
1:E:33:ALA:O	1:E:34:GLU:HB2	2.08	0.53
1:E:298:PHE:HB2	1:E:299:PRO:HD3	1.90	0.53
1:A:155:PHE:CE1	1:B:112:PRO:HB3	2.43	0.53
1:D:89:VAL:HG11	1:D:102:LEU:HD23	1.90	0.53
1:A:22:TYR:HA	1:A:149:GLY:HA3	1.87	0.53
1:B:40:ALA:HB3	1:B:105:PHE:CZ	2.43	0.53
1:D:151:ASN:O	1:D:154:VAL:HG22	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118:TYR:CD1	1:E:118:TYR:C	2.84	0.53
1:A:25:GLU:HB2	1:A:39:ASN:HB3	1.91	0.53
1:E:77:PHE:HD1	1:E:84:ARG:CD	2.17	0.53
1:C:18:ASN:HB3	1:C:143:VAL:HG23	1.89	0.53
1:D:25:GLU:HB2	1:D:39:ASN:HB3	1.91	0.53
1:A:248:THR:HB	1:A:250:TYR:CE1	2.43	0.53
1:A:314:PHE:CD1	1:A:314:PHE:N	2.77	0.53
1:C:29:LEU:C	1:C:29:LEU:HD23	2.33	0.53
1:C:100:GLN:HE21	1:C:100:GLN:HA	1.73	0.53
1:C:287:ALA:O	1:C:289:SER:N	2.42	0.53
1:D:70:ILE:HG22	1:D:71:TRP:O	2.09	0.53
1:C:286:ARG:O	1:C:289:SER:HB3	2.08	0.53
1:E:49:ARG:C	1:E:51:LEU:H	2.17	0.53
1:E:179:LEU:C	1:E:179:LEU:HD12	2.34	0.53
1:E:219:SER:OG	1:E:222:ALA:HB3	2.09	0.53
1:A:89:VAL:HG11	1:A:102:LEU:HD23	1.91	0.53
1:D:278:LEU:HD23	1:D:287:ALA:HB2	1.91	0.53
1:E:278:LEU:HD23	1:E:287:ALA:HB2	1.91	0.53
1:C:179:LEU:C	1:C:179:LEU:HD12	2.34	0.52
1:E:79:ASN:H	1:E:79:ASN:ND2	2.05	0.52
1:A:281:GLU:C	1:A:283:GLN:H	2.15	0.52
1:C:278:LEU:HD23	1:C:287:ALA:HB2	1.90	0.52
1:E:287:ALA:O	1:E:289:SER:N	2.42	0.52
1:C:314:PHE:CD1	1:C:314:PHE:N	2.77	0.52
1:C:248:THR:HB	1:C:250:TYR:CE1	2.45	0.52
1:B:53:PHE:O	1:B:54:ASP:C	2.53	0.52
1:D:54:ASP:CB	1:D:57:ARG:HB2	2.33	0.52
1:A:193:TYR:O	1:A:194:PHE:HB2	2.09	0.52
1:B:22:TYR:HA	1:B:149:GLY:HA3	1.85	0.52
1:B:241:VAL:C	1:B:243:THR:H	2.16	0.52
1:D:118:TYR:CD1	1:D:118:TYR:C	2.87	0.52
1:C:49:ARG:C	1:C:51:LEU:H	2.17	0.52
1:C:70:ILE:HG22	1:C:71:TRP:O	2.10	0.52
1:C:77:PHE:HD1	1:C:84:ARG:CD	2.19	0.52
1:A:298:PHE:HB2	1:A:299:PRO:HD3	1.92	0.52
1:C:245:LEU:HD12	1:C:246:PRO:HD2	1.92	0.52
1:C:257:ILE:O	1:C:261:ILE:HG12	2.10	0.52
1:A:76:ARG:O	1:A:129:LEU:HA	2.09	0.52
1:A:287:ALA:O	1:A:289:SER:N	2.43	0.52
1:A:149:GLY:O	1:A:150:LYS:CB	2.57	0.51
1:E:18:ASN:HB3	1:E:143:VAL:HG23	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:GLU:HB2	1:E:39:ASN:HB3	1.91	0.51
1:A:70:ILE:HG22	1:A:71:TRP:O	2.09	0.51
1:A:118:TYR:CD1	1:A:118:TYR:C	2.87	0.51
1:B:49:ARG:C	1:B:51:LEU:H	2.18	0.51
1:C:298:PHE:HB2	1:C:299:PRO:HD3	1.91	0.51
1:A:278:LEU:HD23	1:A:287:ALA:HB2	1.93	0.51
1:B:298:PHE:HB2	1:B:299:PRO:HD3	1.92	0.51
1:E:147:LYS:O	1:E:147:LYS:HG2	2.11	0.51
1:A:274:VAL:O	1:A:276:HIS:N	2.42	0.51
1:D:89:VAL:CG1	1:D:102:LEU:HD23	2.41	0.51
1:A:193:TYR:C	1:A:193:TYR:CD2	2.89	0.51
1:C:147:LYS:O	1:C:147:LYS:HG2	2.11	0.51
1:A:13:GLU:CB	1:A:14:PRO:CD	2.87	0.51
1:D:33:ALA:O	1:D:34:GLU:HB2	2.11	0.51
1:E:151:ASN:ND2	1:E:152:ASP:N	2.55	0.51
1:A:150:LYS:CG	1:A:154:VAL:HG21	2.41	0.51
1:A:208:LEU:HD13	1:A:261:ILE:HG23	1.92	0.51
1:B:278:LEU:HD23	1:B:287:ALA:HB2	1.92	0.51
1:E:13:GLU:CB	1:E:14:PRO:CD	2.86	0.51
1:B:314:PHE:N	1:B:314:PHE:CD1	2.77	0.51
1:D:49:ARG:C	1:D:51:LEU:H	2.19	0.51
1:E:276:HIS:C	1:E:278:LEU:N	2.69	0.51
1:A:224:VAL:O	1:A:228:VAL:HB	2.10	0.50
1:B:22:TYR:CA	1:B:149:GLY:HA2	2.29	0.50
1:B:77:PHE:HD1	1:B:84:ARG:CD	2.19	0.50
1:B:193:TYR:O	1:B:194:PHE:HB2	2.10	0.50
1:B:208:LEU:HD13	1:B:261:ILE:HG23	1.93	0.50
1:C:22:TYR:HA	1:C:149:GLY:HA3	1.89	0.50
1:D:208:LEU:HD13	1:D:261:ILE:HG23	1.92	0.50
1:A:245:LEU:HD12	1:A:246:PRO:HD2	1.93	0.50
1:C:25:GLU:HB2	1:C:39:ASN:HB3	1.92	0.50
1:C:193:TYR:O	1:C:194:PHE:HB2	2.10	0.50
1:D:68:GLU:CD	1:D:68:GLU:N	2.68	0.50
1:D:193:TYR:O	1:D:194:PHE:HB2	2.10	0.50
1:E:34:GLU:OE2	1:E:112:PRO:HA	2.10	0.50
1:C:34:GLU:OE2	1:C:112:PRO:HA	2.11	0.50
1:C:76:ARG:O	1:C:129:LEU:HA	2.12	0.50
1:B:219:SER:OG	1:B:222:ALA:HB3	2.11	0.50
1:C:53:PHE:O	1:C:54:ASP:C	2.55	0.50
1:C:241:VAL:C	1:C:243:THR:N	2.69	0.50
1:E:70:ILE:HD13	1:E:70:ILE:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ARG:C	1:A:51:LEU:H	2.19	0.50
1:C:150:LYS:CG	1:C:154:VAL:HG21	2.42	0.50
1:D:155:PHE:CE1	1:E:112:PRO:HB3	2.47	0.50
1:A:53:PHE:O	1:A:54:ASP:C	2.55	0.50
1:A:219:SER:OG	1:A:222:ALA:HB3	2.11	0.50
1:C:54:ASP:CB	1:C:57:ARG:HB2	2.36	0.50
1:D:155:PHE:CZ	1:E:112:PRO:HB3	2.46	0.50
1:D:257:ILE:O	1:D:261:ILE:HG12	2.10	0.50
1:C:72:ILE:HG22	1:C:73:PRO:HD2	1.94	0.50
1:E:53:PHE:O	1:E:54:ASP:C	2.53	0.50
1:A:269:VAL:HG11	1:E:210:ILE:HG23	1.94	0.50
1:B:150:LYS:HG2	1:B:154:VAL:HG21	1.94	0.50
1:B:224:VAL:O	1:B:228:VAL:HB	2.12	0.50
1:C:118:TYR:CD1	1:C:118:TYR:C	2.88	0.50
1:D:193:TYR:CD2	1:D:193:TYR:C	2.90	0.50
1:D:219:SER:OG	1:D:222:ALA:HB3	2.12	0.50
1:B:54:ASP:HB2	1:B:57:ARG:HG3	1.94	0.49
1:B:274:VAL:O	1:B:276:HIS:N	2.41	0.49
1:D:76:ARG:O	1:D:129:LEU:HA	2.12	0.49
1:E:241:VAL:C	1:E:243:THR:N	2.69	0.49
1:B:118:TYR:CD1	1:B:118:TYR:C	2.86	0.49
1:A:15:LEU:HD11	1:A:46:TRP:HB2	1.94	0.49
1:A:54:ASP:HB2	1:A:57:ARG:HG3	1.93	0.49
1:A:54:ASP:CB	1:A:57:ARG:HB2	2.39	0.49
1:A:268:ALA:O	1:A:272:VAL:HG22	2.11	0.49
1:B:274:VAL:C	1:B:276:HIS:N	2.70	0.49
1:D:147:LYS:O	1:D:147:LYS:HG2	2.12	0.49
1:B:287:ALA:O	1:B:289:SER:N	2.46	0.49
1:B:68:GLU:N	1:B:68:GLU:CD	2.70	0.49
1:C:219:SER:OG	1:C:222:ALA:HB3	2.13	0.49
1:E:245:LEU:HD12	1:E:246:PRO:HD2	1.95	0.49
1:A:68:GLU:N	1:A:68:GLU:CD	2.71	0.49
1:B:48:ASP:HB3	1:B:51:LEU:HD21	1.95	0.49
1:B:245:LEU:HD12	1:B:246:PRO:HD2	1.93	0.49
1:B:257:ILE:O	1:B:261:ILE:HG12	2.11	0.49
1:D:287:ALA:O	1:D:289:SER:N	2.46	0.49
1:C:36:PHE:CE1	1:C:109:VAL:HB	2.47	0.49
1:A:274:VAL:C	1:A:276:HIS:N	2.71	0.49
1:C:33:ALA:O	1:C:34:GLU:HB2	2.12	0.49
1:C:79:ASN:H	1:C:79:ASN:ND2	2.02	0.49
1:C:287:ALA:C	1:C:289:SER:N	2.71	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:274:VAL:O	1:E:276:HIS:N	2.45	0.49
1:A:89:VAL:CG1	1:A:102:LEU:HD23	2.43	0.49
1:C:274:VAL:C	1:C:276:HIS:N	2.71	0.49
1:D:224:VAL:O	1:D:228:VAL:HB	2.13	0.49
1:D:245:LEU:HD12	1:D:246:PRO:HD2	1.95	0.49
1:A:40:ALA:HB3	1:A:105:PHE:CE1	2.48	0.48
1:B:147:LYS:O	1:B:147:LYS:HG2	2.13	0.48
1:C:54:ASP:HB2	1:C:57:ARG:HG3	1.94	0.48
1:E:40:ALA:HB3	1:E:105:PHE:CE1	2.48	0.48
1:E:76:ARG:O	1:E:129:LEU:HA	2.12	0.48
1:B:268:ALA:O	1:B:272:VAL:HG22	2.14	0.48
1:E:224:VAL:O	1:E:228:VAL:HB	2.13	0.48
1:B:25:GLU:HB2	1:B:39:ASN:HB3	1.94	0.48
1:C:282:SER:C	1:C:284:PRO:CD	2.86	0.48
1:A:57:ARG:HE	1:A:57:ARG:HA	1.79	0.48
1:B:34:GLU:OE2	1:B:112:PRO:HA	2.14	0.48
1:C:68:GLU:N	1:C:68:GLU:CD	2.71	0.48
1:E:54:ASP:HB2	1:E:57:ARG:HG3	1.94	0.48
1:A:151:ASN:ND2	1:A:152:ASP:N	2.56	0.48
1:A:287:ALA:C	1:A:289:SER:N	2.72	0.48
1:B:18:ASN:HB3	1:B:143:VAL:HG23	1.96	0.48
1:B:33:ALA:O	1:B:34:GLU:HB2	2.12	0.48
1:B:155:PHE:CZ	1:C:112:PRO:HB3	2.48	0.48
1:C:89:VAL:CG1	1:C:102:LEU:HD23	2.42	0.48
1:C:150:LYS:HG2	1:C:154:VAL:HG21	1.96	0.48
1:C:193:TYR:O	1:C:194:PHE:CB	2.61	0.48
1:E:54:ASP:CB	1:E:57:ARG:HB2	2.37	0.48
1:E:141:LEU:HD23	1:E:142:ALA:N	2.19	0.48
1:E:193:TYR:O	1:E:194:PHE:HB2	2.12	0.48
1:A:72:ILE:HG22	1:A:73:PRO:HD2	1.95	0.48
1:B:141:LEU:HD23	1:B:142:ALA:N	2.20	0.48
1:B:151:ASN:ND2	1:B:152:ASP:N	2.58	0.48
1:E:36:PHE:CE1	1:E:109:VAL:HB	2.49	0.48
1:E:150:LYS:CG	1:E:154:VAL:HG21	2.43	0.48
1:E:257:ILE:O	1:E:261:ILE:HG12	2.14	0.48
1:B:19:THR:HA	1:B:43:SER:O	2.13	0.48
1:D:137:ARG:HA	1:D:137:ARG:HD3	1.75	0.48
1:A:19:THR:HA	1:A:43:SER:O	2.13	0.48
1:A:147:LYS:O	1:A:147:LYS:HG2	2.13	0.48
1:B:76:ARG:O	1:B:129:LEU:HA	2.14	0.48
1:B:241:VAL:C	1:B:243:THR:N	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:19:THR:HA	1:C:43:SER:O	2.14	0.48
1:E:193:TYR:O	1:E:194:PHE:CB	2.62	0.48
1:B:13:GLU:CB	1:B:14:PRO:CD	2.85	0.48
1:B:150:LYS:CG	1:B:154:VAL:HG21	2.44	0.48
1:C:194:PHE:C	1:C:196:TYR:N	2.70	0.48
1:C:276:HIS:C	1:C:278:LEU:N	2.71	0.48
1:D:22:TYR:CA	1:D:149:GLY:HA2	2.29	0.48
1:D:149:GLY:O	1:D:150:LYS:CB	2.59	0.48
1:D:193:TYR:O	1:D:194:PHE:CB	2.62	0.48
1:D:274:VAL:O	1:D:276:HIS:N	2.44	0.48
1:E:19:THR:HA	1:E:43:SER:O	2.14	0.48
1:E:150:LYS:HG2	1:E:154:VAL:HG21	1.96	0.48
1:A:193:TYR:O	1:A:194:PHE:CB	2.62	0.47
1:D:54:ASP:HB2	1:D:57:ARG:HG3	1.96	0.47
1:D:276:HIS:C	1:D:278:LEU:N	2.71	0.47
1:B:270:ILE:HD13	1:B:270:ILE:HA	1.71	0.47
1:D:194:PHE:C	1:D:196:TYR:N	2.70	0.47
1:B:193:TYR:C	1:B:193:TYR:CD2	2.92	0.47
1:C:208:LEU:HD13	1:C:261:ILE:HG23	1.97	0.47
1:C:268:ALA:O	1:C:272:VAL:HG22	2.15	0.47
1:D:19:THR:HA	1:D:43:SER:O	2.14	0.47
1:D:212:TRP:CE3	1:D:298:PHE:HD1	2.32	0.47
1:B:70:ILE:N	1:B:70:ILE:HD13	2.29	0.47
1:E:84:ARG:NH1	1:E:84:ARG:CB	2.66	0.47
1:A:196:TYR:CD1	1:A:196:TYR:N	2.83	0.47
1:C:155:PHE:CZ	1:D:112:PRO:HB3	2.49	0.47
1:D:36:PHE:CE1	1:D:109:VAL:HB	2.50	0.47
1:D:61:ARG:HG2	1:D:62:VAL:HG23	1.96	0.47
1:A:112:PRO:HB3	1:E:155:PHE:CE1	2.49	0.47
1:A:276:HIS:C	1:A:278:LEU:N	2.72	0.47
1:B:137:ARG:HD2	1:B:179:LEU:HG	1.96	0.47
1:C:49:ARG:O	1:C:51:LEU:N	2.48	0.47
1:A:48:ASP:HB3	1:A:51:LEU:HD21	1.97	0.47
1:A:194:PHE:C	1:A:196:TYR:N	2.71	0.47
1:C:48:ASP:HB3	1:C:51:LEU:HD21	1.97	0.47
1:C:193:TYR:C	1:C:193:TYR:CD2	2.92	0.47
1:C:274:VAL:O	1:C:276:HIS:N	2.43	0.47
1:E:193:TYR:CD2	1:E:193:TYR:C	2.92	0.47
1:E:194:PHE:C	1:E:196:TYR:N	2.70	0.47
1:E:268:ALA:O	1:E:272:VAL:HG22	2.14	0.47
1:E:282:SER:C	1:E:284:PRO:CD	2.86	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:TYR:N	1:C:196:TYR:CD1	2.83	0.47
1:D:150:LYS:CG	1:D:154:VAL:HG21	2.45	0.47
1:E:147:LYS:O	1:E:147:LYS:CG	2.63	0.47
1:E:270:ILE:HA	1:E:270:ILE:HD13	1.68	0.47
1:A:70:ILE:HD13	1:A:70:ILE:N	2.29	0.47
1:A:141:LEU:HD23	1:A:142:ALA:N	2.24	0.47
1:A:232:ILE:HG22	1:A:233:ALA:N	2.29	0.47
1:B:62:VAL:HG13	1:B:93:VAL:O	2.15	0.47
1:B:194:PHE:C	1:B:196:TYR:N	2.71	0.47
1:C:61:ARG:HG2	1:C:62:VAL:HG23	1.97	0.47
1:D:81:GLU:HG3	1:D:108:ARG:HG3	1.96	0.47
1:E:49:ARG:O	1:E:51:LEU:N	2.48	0.47
1:E:118:TYR:HB3	1:E:119:PRO:HD3	1.96	0.47
1:A:210:ILE:HG23	1:B:269:VAL:HG11	1.97	0.47
1:C:226:LEU:HA	1:C:226:LEU:HD22	1.71	0.47
1:D:72:ILE:HG22	1:D:73:PRO:HD2	1.96	0.47
1:A:137:ARG:HA	1:A:137:ARG:HD3	1.72	0.46
1:B:271:GLU:O	1:B:274:VAL:N	2.48	0.46
1:C:147:LYS:O	1:C:147:LYS:CG	2.63	0.46
1:D:34:GLU:OE2	1:D:112:PRO:HA	2.14	0.46
1:E:15:LEU:HD11	1:E:46:TRP:HB2	1.97	0.46
1:B:196:TYR:N	1:B:196:TYR:CD1	2.84	0.46
1:C:212:TRP:CE3	1:C:298:PHE:HD1	2.33	0.46
1:D:141:LEU:HD23	1:D:142:ALA:N	2.20	0.46
1:D:147:LYS:O	1:D:147:LYS:CG	2.63	0.46
1:A:305:ALA:O	1:A:309:LEU:HB2	2.15	0.46
1:E:48:ASP:HB3	1:E:51:LEU:HD21	1.96	0.46
1:E:212:TRP:CE3	1:E:298:PHE:HD1	2.32	0.46
1:E:287:ALA:C	1:E:289:SER:N	2.71	0.46
1:A:205:LEU:O	1:A:206:PHE:C	2.58	0.46
1:B:257:ILE:O	1:B:261:ILE:CG1	2.64	0.46
1:D:118:TYR:HB3	1:D:119:PRO:HD3	1.98	0.46
1:D:151:ASN:ND2	1:D:152:ASP:N	2.58	0.46
1:E:62:VAL:HG13	1:E:93:VAL:O	2.16	0.46
1:A:42:LEU:HB3	1:A:103:GLU:CG	2.45	0.46
1:A:137:ARG:HD2	1:A:179:LEU:HG	1.96	0.46
1:B:150:LYS:HB3	1:B:150:LYS:HE2	1.70	0.46
1:C:111:SER:HA	1:C:112:PRO:HD2	1.78	0.46
1:C:118:TYR:HB3	1:C:119:PRO:HD3	1.95	0.46
1:D:65:TYR:CD1	1:D:70:ILE:HD11	2.51	0.46
1:E:274:VAL:HG12	1:E:275:GLN:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:THR:HG22	1:A:279:LYS:HE2	1.98	0.46
1:B:49:ARG:O	1:B:51:LEU:N	2.49	0.46
1:B:305:ALA:O	1:B:309:LEU:HB2	2.16	0.46
1:C:15:LEU:HD11	1:C:46:TRP:HB2	1.97	0.46
1:C:40:ALA:HB3	1:C:105:PHE:CE1	2.50	0.46
1:D:70:ILE:N	1:D:70:ILE:HD13	2.30	0.46
1:B:199:ASN:O	1:B:200:ILE:HD13	2.16	0.46
1:B:304:LEU:O	1:B:308:ILE:HG12	2.16	0.46
1:C:57:ARG:HE	1:C:57:ARG:HA	1.80	0.46
1:C:155:PHE:HB3	1:C:156:LEU:H	1.58	0.46
1:D:48:ASP:HB3	1:D:51:LEU:HD21	1.97	0.46
1:A:61:ARG:HG2	1:A:62:VAL:HG23	1.98	0.46
1:E:72:ILE:HG22	1:E:73:PRO:HD2	1.98	0.46
1:E:196:TYR:N	1:E:196:TYR:CD1	2.84	0.46
1:B:276:HIS:C	1:B:278:LEU:N	2.71	0.46
1:C:81:GLU:HG3	1:C:108:ARG:HG3	1.98	0.46
1:D:68:GLU:CD	1:D:68:GLU:H	2.23	0.46
1:D:150:LYS:HE2	1:D:150:LYS:HB3	1.73	0.46
1:A:147:LYS:O	1:A:147:LYS:CG	2.64	0.46
1:B:193:TYR:O	1:B:194:PHE:CB	2.62	0.46
1:B:282:SER:C	1:B:284:PRO:CD	2.87	0.46
1:C:191:ARG:HG3	1:C:192:GLN:N	2.31	0.46
1:D:150:LYS:HG2	1:D:154:VAL:HG21	1.97	0.46
1:E:57:ARG:HE	1:E:57:ARG:HA	1.81	0.46
1:E:68:GLU:N	1:E:68:GLU:CD	2.73	0.46
1:A:94:SER:OG	1:A:95:PRO:HD2	2.16	0.45
1:B:54:ASP:CB	1:B:57:ARG:HB2	2.37	0.45
1:B:274:VAL:HG12	1:B:275:GLN:N	2.31	0.45
1:D:270:ILE:HD13	1:D:270:ILE:HA	1.68	0.45
1:D:287:ALA:C	1:D:289:SER:N	2.73	0.45
1:B:36:PHE:CE1	1:B:109:VAL:HB	2.51	0.45
1:B:65:TYR:CD1	1:B:70:ILE:HD11	2.50	0.45
1:B:309:LEU:HD12	1:B:309:LEU:HA	1.75	0.45
1:C:149:GLY:O	1:C:150:LYS:CB	2.58	0.45
1:E:65:TYR:CD1	1:E:70:ILE:HD11	2.52	0.45
1:A:191:ARG:HG3	1:A:192:GLN:N	2.32	0.45
1:A:212:TRP:CE3	1:A:298:PHE:HD1	2.34	0.45
1:A:257:ILE:O	1:A:261:ILE:CG1	2.64	0.45
1:A:271:GLU:O	1:A:274:VAL:N	2.49	0.45
1:B:15:LEU:HD11	1:B:46:TRP:HB2	1.99	0.45
1:D:304:LEU:O	1:D:308:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:PHE:CE1	1:C:112:PRO:HB3	2.51	0.45
1:D:53:PHE:CE1	1:D:95:PRO:HA	2.52	0.45
1:D:223:ASN:HB3	1:D:272:VAL:HG11	1.99	0.45
1:D:241:VAL:C	1:D:243:THR:N	2.70	0.45
1:A:34:GLU:OE2	1:A:112:PRO:HA	2.15	0.45
1:A:155:PHE:CZ	1:B:112:PRO:HB3	2.51	0.45
1:B:287:ALA:C	1:B:289:SER:N	2.73	0.45
1:D:268:ALA:O	1:D:272:VAL:HG22	2.16	0.45
1:B:81:GLU:HG3	1:B:108:ARG:HG3	1.99	0.45
1:C:70:ILE:HD13	1:C:70:ILE:N	2.31	0.45
1:E:149:GLY:O	1:E:164:PHE:HD1	2.00	0.45
1:E:305:ALA:O	1:E:309:LEU:HB2	2.17	0.45
1:A:150:LYS:HG2	1:A:154:VAL:HG21	1.97	0.45
1:B:57:ARG:HE	1:B:57:ARG:HA	1.81	0.45
1:B:72:ILE:HG22	1:B:73:PRO:HD2	1.98	0.45
1:C:22:TYR:CA	1:C:149:GLY:HA2	2.32	0.45
1:B:232:ILE:HG22	1:B:233:ALA:N	2.32	0.45
1:C:304:LEU:O	1:C:308:ILE:HG12	2.16	0.45
1:E:218:THR:HG22	1:E:279:LYS:HE2	1.99	0.45
1:A:49:ARG:O	1:A:51:LEU:N	2.50	0.45
1:B:226:LEU:HA	1:B:226:LEU:HD22	1.68	0.45
1:C:128:TYR:O	1:C:183:LEU:O	2.35	0.45
1:C:137:ARG:HD2	1:C:179:LEU:HG	1.99	0.45
1:E:304:LEU:O	1:E:308:ILE:HG12	2.17	0.45
1:A:274:VAL:HG12	1:A:275:GLN:N	2.32	0.44
1:B:47:LYS:HD2	1:B:49:ARG:HH21	1.81	0.44
1:E:151:ASN:C	1:E:153:ASP:H	2.25	0.44
1:E:155:PHE:HB3	1:E:156:LEU:H	1.60	0.44
1:A:81:GLU:HG3	1:A:108:ARG:HG3	1.99	0.44
1:A:150:LYS:HB3	1:A:150:LYS:HE2	1.73	0.44
1:B:155:PHE:HB3	1:B:156:LEU:H	1.58	0.44
1:C:274:VAL:HG12	1:C:275:GLN:N	2.32	0.44
1:D:57:ARG:HE	1:D:57:ARG:HA	1.81	0.44
1:A:241:VAL:C	1:A:243:THR:N	2.71	0.44
1:A:304:LEU:O	1:A:308:ILE:HG12	2.16	0.44
1:B:42:LEU:HB3	1:B:103:GLU:CG	2.45	0.44
1:D:305:ALA:O	1:D:309:LEU:HB2	2.16	0.44
1:B:197:ILE:HB	1:B:198:PRO:CD	2.41	0.44
1:D:62:VAL:HG13	1:D:93:VAL:O	2.17	0.44
1:E:53:PHE:CE2	1:E:63:LYS:HB3	2.53	0.44
1:B:212:TRP:CE3	1:B:298:PHE:HD1	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:ASN:C	1:C:153:ASP:H	2.25	0.44
1:A:223:ASN:HB3	1:A:272:VAL:HG11	2.00	0.44
1:D:22:TYR:CD1	1:D:149:GLY:HA2	2.52	0.44
1:A:118:TYR:HB3	1:A:119:PRO:HD3	1.99	0.44
1:D:212:TRP:HB2	1:D:215:PHE:CE1	2.53	0.44
1:A:65:TYR:CD1	1:A:70:ILE:HD11	2.52	0.44
1:A:155:PHE:HB3	1:A:156:LEU:H	1.59	0.44
1:B:53:PHE:CE1	1:B:95:PRO:HA	2.53	0.44
1:B:212:TRP:CZ3	1:B:264:PHE:HD2	2.33	0.44
1:D:210:ILE:O	1:D:213:THR:HB	2.17	0.44
1:E:22:TYR:CD1	1:E:149:GLY:HA2	2.53	0.44
1:E:137:ARG:HD3	1:E:137:ARG:HA	1.77	0.44
1:E:232:ILE:HG22	1:E:233:ALA:N	2.32	0.44
1:E:274:VAL:C	1:E:276:HIS:N	2.73	0.44
1:B:147:LYS:O	1:B:147:LYS:CG	2.66	0.44
1:C:62:VAL:HG13	1:C:93:VAL:O	2.18	0.44
1:C:205:LEU:O	1:C:206:PHE:C	2.61	0.43
1:C:218:THR:HG22	1:C:279:LYS:HE2	2.00	0.43
1:C:287:ALA:C	1:C:289:SER:H	2.26	0.43
1:E:202:LEU:O	1:E:203:PRO:C	2.61	0.43
1:A:53:PHE:CE1	1:A:95:PRO:HA	2.53	0.43
1:B:53:PHE:CE2	1:B:63:LYS:HB3	2.53	0.43
1:D:27:TYR:HB3	1:E:110:LEU:HD11	2.00	0.43
1:E:271:GLU:O	1:E:274:VAL:N	2.51	0.43
1:A:175:LEU:O	1:A:176:GLU:HB2	2.17	0.43
1:B:68:GLU:CD	1:B:68:GLU:H	2.25	0.43
1:B:137:ARG:HA	1:B:137:ARG:HD3	1.78	0.43
1:C:37:LYS:HG2	1:C:108:ARG:HB3	1.99	0.43
1:C:65:TYR:CD1	1:C:70:ILE:HD11	2.52	0.43
1:C:149:GLY:O	1:C:164:PHE:HD1	2.01	0.43
1:D:253:TYR:CA	1:D:313:PHE:CE2	3.00	0.43
1:E:47:LYS:HD2	1:E:49:ARG:HH21	1.82	0.43
1:E:226:LEU:HA	1:E:226:LEU:HD22	1.67	0.43
1:A:52:ALA:HA	1:A:95:PRO:O	2.18	0.43
1:A:309:LEU:HD12	1:A:309:LEU:HA	1.79	0.43
1:B:61:ARG:HG2	1:B:62:VAL:HG23	2.01	0.43
1:C:271:GLU:O	1:C:274:VAL:N	2.51	0.43
1:D:13:GLU:CB	1:D:14:PRO:CD	2.87	0.43
1:D:314:PHE:N	1:D:314:PHE:HD1	2.16	0.43
1:E:205:LEU:O	1:E:206:PHE:C	2.62	0.43
1:E:209:PHE:O	1:E:210:ILE:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:TYR:CD1	1:A:149:GLY:HA2	2.53	0.43
1:D:212:TRP:HB2	1:D:215:PHE:CD1	2.53	0.43
1:D:216:TRP:CH2	1:D:295:ARG:HB3	2.53	0.43
1:E:137:ARG:HD2	1:E:179:LEU:HG	1.99	0.43
1:E:199:ASN:O	1:E:200:ILE:HD13	2.19	0.43
1:E:216:TRP:CH2	1:E:295:ARG:HB3	2.54	0.43
1:E:223:ASN:O	1:E:227:VAL:HG23	2.19	0.43
1:E:287:ALA:C	1:E:289:SER:H	2.27	0.43
1:A:298:PHE:CB	1:A:299:PRO:HD3	2.49	0.43
1:B:118:TYR:HB3	1:B:119:PRO:HD3	2.00	0.43
1:C:212:TRP:CZ3	1:C:264:PHE:HD2	2.35	0.43
1:C:53:PHE:CE2	1:C:63:LYS:HB3	2.54	0.43
1:C:199:ASN:O	1:C:200:ILE:HD13	2.19	0.43
1:C:305:ALA:O	1:C:309:LEU:HB2	2.17	0.43
1:D:30:ASP:HB3	1:D:33:ALA:HB3	2.00	0.43
1:D:132:ARG:HA	1:D:180:GLU:HG2	2.01	0.43
1:D:237:PHE:O	1:D:238:ASN:C	2.60	0.43
1:D:274:VAL:HG12	1:D:275:GLN:N	2.33	0.43
1:E:128:TYR:O	1:E:183:LEU:O	2.37	0.43
1:A:37:LYS:HG2	1:A:108:ARG:HB3	2.01	0.43
1:A:287:ALA:C	1:A:289:SER:H	2.26	0.43
1:B:22:TYR:CD1	1:B:149:GLY:HA2	2.54	0.43
1:B:149:GLY:O	1:B:150:LYS:CB	2.57	0.43
1:C:52:ALA:HA	1:C:95:PRO:O	2.18	0.43
1:D:40:ALA:HB3	1:D:105:PHE:CE1	2.53	0.43
1:D:49:ARG:O	1:D:51:LEU:N	2.51	0.43
1:D:218:THR:HG22	1:D:279:LYS:HE2	2.01	0.43
1:E:9:PRO:HB3	1:E:48:ASP:OD1	2.18	0.43
1:A:151:ASN:C	1:A:153:ASP:H	2.27	0.43
1:D:205:LEU:O	1:D:206:PHE:C	2.62	0.43
1:E:53:PHE:CE1	1:E:95:PRO:HA	2.54	0.43
1:E:257:ILE:O	1:E:261:ILE:CG1	2.67	0.43
1:A:111:SER:HA	1:A:112:PRO:HD2	1.78	0.43
1:A:115:PHE:O	1:A:252:THR:HG22	2.19	0.43
1:C:53:PHE:CE1	1:C:95:PRO:HA	2.54	0.43
1:C:94:SER:OG	1:C:95:PRO:HD2	2.19	0.43
1:E:61:ARG:HG2	1:E:62:VAL:HG23	2.01	0.43
1:E:298:PHE:CB	1:E:299:PRO:HD3	2.49	0.43
1:A:62:VAL:HG13	1:A:93:VAL:O	2.18	0.42
1:A:140:VAL:CG2	1:A:183:LEU:HG	2.49	0.42
1:B:30:ASP:HB3	1:B:33:ALA:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:ASN:ND2	1:C:152:ASP:N	2.57	0.42
1:D:128:TYR:O	1:D:183:LEU:O	2.37	0.42
1:D:191:ARG:HG3	1:D:192:GLN:N	2.33	0.42
1:B:49:ARG:C	1:B:51:LEU:N	2.77	0.42
1:B:191:ARG:HG3	1:B:192:GLN:N	2.34	0.42
1:B:202:LEU:O	1:B:203:PRO:C	2.61	0.42
1:C:257:ILE:O	1:C:261:ILE:CG1	2.67	0.42
1:D:199:ASN:O	1:D:200:ILE:HD13	2.19	0.42
1:D:202:LEU:HD22	1:D:202:LEU:HA	1.94	0.42
1:D:257:ILE:O	1:D:261:ILE:CG1	2.67	0.42
1:D:282:SER:C	1:D:284:PRO:CD	2.88	0.42
1:E:42:LEU:HB3	1:E:103:GLU:CG	2.48	0.42
1:A:202:LEU:O	1:A:203:PRO:C	2.60	0.42
1:B:52:ALA:HA	1:B:95:PRO:O	2.19	0.42
1:B:218:THR:HG22	1:B:279:LYS:HE2	2.01	0.42
1:C:27:TYR:HB3	1:D:110:LEU:HD11	2.01	0.42
1:C:232:ILE:HG22	1:C:233:ALA:N	2.34	0.42
1:E:42:LEU:O	1:E:102:LEU:HD12	2.19	0.42
1:E:115:PHE:O	1:E:252:THR:HG22	2.19	0.42
1:E:191:ARG:HG3	1:E:192:GLN:N	2.34	0.42
1:A:128:TYR:O	1:A:183:LEU:O	2.37	0.42
1:B:27:TYR:HB3	1:C:110:LEU:HD11	2.02	0.42
1:C:68:GLU:CD	1:C:68:GLU:H	2.27	0.42
1:C:79:ASN:HD22	1:C:79:ASN:N	2.05	0.42
1:D:196:TYR:N	1:D:196:TYR:CD1	2.85	0.42
1:A:53:PHE:CE2	1:A:63:LYS:HB3	2.54	0.42
1:A:226:LEU:HD23	1:B:224:VAL:HB	2.01	0.42
1:C:65:TYR:CD2	1:C:70:ILE:HD11	2.54	0.42
1:C:223:ASN:HB3	1:C:272:VAL:HG11	2.00	0.42
1:C:298:PHE:CB	1:C:299:PRO:HD3	2.48	0.42
1:E:204:MET:HE2	1:E:204:MET:HB3	1.93	0.42
1:B:21:ILE:O	1:B:149:GLY:HA3	2.19	0.42
1:D:42:LEU:O	1:D:102:LEU:HD12	2.19	0.42
1:D:47:LYS:HD2	1:D:49:ARG:HH21	1.85	0.42
1:D:137:ARG:HD2	1:D:179:LEU:HG	2.02	0.42
1:D:271:GLU:O	1:D:274:VAL:N	2.52	0.42
1:E:52:ALA:HA	1:E:95:PRO:O	2.20	0.42
1:E:65:TYR:CD2	1:E:70:ILE:HD11	2.54	0.42
1:C:25:GLU:OE1	1:C:25:GLU:HA	2.20	0.42
1:C:49:ARG:C	1:C:51:LEU:N	2.77	0.42
1:D:274:VAL:C	1:D:276:HIS:N	2.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:49:ARG:C	1:E:51:LEU:N	2.77	0.42
1:E:81:GLU:HG3	1:E:108:ARG:HG3	2.00	0.42
1:B:283:GLN:N	1:B:284:PRO:CD	2.83	0.42
1:D:21:ILE:O	1:D:149:GLY:HA3	2.19	0.42
1:D:70:ILE:HG22	1:D:71:TRP:N	2.34	0.42
1:D:298:PHE:CB	1:D:299:PRO:HD3	2.48	0.42
1:A:210:ILE:O	1:A:213:THR:HB	2.19	0.42
1:A:282:SER:C	1:A:284:PRO:CD	2.88	0.42
1:B:195:SER:O	1:B:199:ASN:HB2	2.20	0.42
1:B:237:PHE:O	1:B:238:ASN:C	2.59	0.42
1:C:47:LYS:HD2	1:C:49:ARG:HH21	1.85	0.42
1:D:212:TRP:CZ3	1:D:264:PHE:HD2	2.34	0.42
1:B:77:PHE:H	1:B:84:ARG:CD	2.29	0.42
1:B:223:ASN:HB3	1:B:272:VAL:HG11	2.00	0.42
1:C:210:ILE:O	1:C:213:THR:HB	2.20	0.42
1:C:226:LEU:HD23	1:D:224:VAL:HB	2.01	0.42
1:A:22:TYR:CA	1:A:149:GLY:HA2	2.34	0.41
1:A:47:LYS:HD2	1:A:49:ARG:HH21	1.84	0.41
1:B:37:LYS:HE3	1:B:108:ARG:HD2	2.02	0.41
1:B:205:LEU:O	1:B:206:PHE:C	2.62	0.41
1:B:275:GLN:O	1:B:275:GLN:CG	2.67	0.41
1:C:141:LEU:HD23	1:C:142:ALA:N	2.26	0.41
1:C:283:GLN:N	1:C:284:PRO:CD	2.82	0.41
1:E:314:PHE:N	1:E:314:PHE:HD1	2.17	0.41
1:A:202:LEU:HD22	1:A:202:LEU:HA	1.87	0.41
1:A:224:VAL:HB	1:E:226:LEU:HD23	2.02	0.41
1:A:242:GLU:O	1:A:242:GLU:HG2	2.20	0.41
1:A:77:PHE:H	1:A:84:ARG:CD	2.29	0.41
1:A:270:ILE:HD13	1:A:270:ILE:HA	1.67	0.41
1:D:195:SER:O	1:D:199:ASN:HB2	2.20	0.41
1:D:232:ILE:HG22	1:D:233:ALA:N	2.35	0.41
1:D:281:GLU:C	1:D:283:GLN:N	2.78	0.41
1:D:287:ALA:C	1:D:289:SER:H	2.28	0.41
1:B:128:TYR:O	1:B:183:LEU:O	2.38	0.41
1:B:298:PHE:CB	1:B:299:PRO:HD3	2.50	0.41
1:D:50:ARG:O	1:D:50:ARG:HG2	2.20	0.41
1:D:149:GLY:O	1:D:164:PHE:HD1	2.02	0.41
1:A:149:GLY:O	1:A:164:PHE:HD1	2.03	0.41
1:A:212:TRP:HB2	1:A:215:PHE:CD1	2.56	0.41
1:A:281:GLU:C	1:A:283:GLN:N	2.78	0.41
1:C:202:LEU:O	1:C:203:PRO:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:ALA:HB1	1:D:95:PRO:O	2.21	0.41
1:D:283:GLN:N	1:D:284:PRO:CD	2.83	0.41
1:E:54:ASP:HA	1:E:55:PRO:HD2	1.89	0.41
1:E:253:TYR:HB2	1:E:313:PHE:HD2	1.86	0.41
1:A:68:GLU:CD	1:A:68:GLU:H	2.28	0.41
1:B:148:VAL:O	1:B:149:GLY:C	2.64	0.41
1:B:149:GLY:O	1:B:164:PHE:HD1	2.03	0.41
1:C:137:ARG:HA	1:C:137:ARG:HD3	1.74	0.41
1:C:270:ILE:HD13	1:C:270:ILE:HA	1.70	0.41
1:D:25:GLU:OE1	1:D:25:GLU:HA	2.21	0.41
1:D:84:ARG:NH1	1:D:84:ARG:CB	2.66	0.41
1:A:21:ILE:O	1:A:149:GLY:HA3	2.20	0.41
1:A:195:SER:O	1:A:199:ASN:HB2	2.20	0.41
1:B:132:ARG:HA	1:B:180:GLU:HG2	2.02	0.41
1:D:197:ILE:HB	1:D:198:PRO:CD	2.40	0.41
1:E:175:LEU:O	1:E:176:GLU:HB2	2.20	0.41
1:A:84:ARG:NH1	1:A:84:ARG:CB	2.66	0.41
1:A:209:PHE:O	1:A:210:ILE:C	2.63	0.41
1:A:226:LEU:HA	1:A:226:LEU:HD22	1.73	0.41
1:B:111:SER:HA	1:B:112:PRO:HD2	1.80	0.41
1:B:216:TRP:CH2	1:B:295:ARG:HB3	2.55	0.41
1:B:287:ALA:C	1:B:289:SER:H	2.28	0.41
1:C:77:PHE:H	1:C:84:ARG:CD	2.30	0.41
1:C:195:SER:O	1:C:199:ASN:HB2	2.21	0.41
1:C:196:TYR:N	1:C:196:TYR:HD1	2.18	0.41
1:C:281:GLU:C	1:C:283:GLN:N	2.79	0.41
1:A:15:LEU:HD12	1:A:16:THR:N	2.36	0.41
1:A:253:TYR:CA	1:A:313:PHE:CE2	3.01	0.41
1:A:314:PHE:N	1:A:314:PHE:HD1	2.19	0.41
1:B:54:ASP:HA	1:B:55:PRO:HD2	1.88	0.41
1:B:151:ASN:C	1:B:153:ASP:H	2.28	0.41
1:B:175:LEU:O	1:B:176:GLU:HB2	2.20	0.41
1:B:223:ASN:O	1:B:227:VAL:HG23	2.20	0.41
1:C:286:ARG:O	1:C:287:ALA:C	2.63	0.41
1:D:53:PHE:CE2	1:D:63:LYS:HB3	2.55	0.41
1:D:77:PHE:H	1:D:84:ARG:CD	2.27	0.41
1:D:151:ASN:C	1:D:153:ASP:H	2.29	0.41
1:D:309:LEU:HA	1:D:309:LEU:HD12	1.75	0.41
1:E:196:TYR:N	1:E:196:TYR:HD1	2.19	0.41
1:A:237:PHE:O	1:A:238:ASN:C	2.62	0.41
1:B:196:TYR:N	1:B:196:TYR:HD1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:226:LEU:HD23	1:C:224:VAL:HB	2.03	0.41
1:E:30:ASP:HB3	1:E:33:ALA:HB3	2.02	0.41
1:A:223:ASN:O	1:A:227:VAL:HG23	2.21	0.40
1:B:25:GLU:OE1	1:B:25:GLU:HA	2.22	0.40
1:B:40:ALA:HB3	1:B:105:PHE:CE1	2.56	0.40
1:B:212:TRP:HB2	1:B:215:PHE:CD1	2.56	0.40
1:D:37:LYS:HG2	1:D:108:ARG:HB3	2.02	0.40
1:A:212:TRP:HB2	1:A:215:PHE:CE1	2.56	0.40
1:C:15:LEU:HD12	1:C:16:THR:N	2.36	0.40
1:D:115:PHE:O	1:D:252:THR:HG22	2.22	0.40
1:A:283:GLN:N	1:A:284:PRO:CD	2.83	0.40
1:C:116:ARG:HG3	1:C:250:TYR:CD2	2.57	0.40
1:E:15:LEU:HD12	1:E:16:THR:N	2.37	0.40
1:E:76:ARG:HH12	1:E:130:ILE:HD11	1.86	0.40
1:B:162:GLU:HB2	1:B:188:ARG:O	2.21	0.40
1:C:42:LEU:O	1:C:102:LEU:HD12	2.22	0.40
1:C:223:ASN:O	1:C:227:VAL:HG23	2.21	0.40
1:C:253:TYR:CA	1:C:313:PHE:CE2	3.01	0.40
1:C:275:GLN:O	1:C:275:GLN:CG	2.67	0.40
1:C:253:TYR:HB2	1:C:313:PHE:HD2	1.86	0.40
1:E:253:TYR:CA	1:E:313:PHE:CE2	3.01	0.40
1:E:283:GLN:N	1:E:284:PRO:CD	2.82	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	308/317 (97%)	239 (78%)	52 (17%)	17 (6%)	1	9
1	B	308/317 (97%)	243 (79%)	49 (16%)	16 (5%)	1	10
1	C	308/317 (97%)	242 (79%)	48 (16%)	18 (6%)	1	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	308/317 (97%)	244 (79%)	47 (15%)	17 (6%)	1	9
1	E	308/317 (97%)	243 (79%)	48 (16%)	17 (6%)	1	9
All	All	1540/1585 (97%)	1211 (79%)	244 (16%)	85 (6%)	1	9

All (85) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	ARG
1	A	118	TYR
1	A	148	VAL
1	A	150	LYS
1	A	194	PHE
1	A	275	GLN
1	B	50	ARG
1	B	118	TYR
1	B	148	VAL
1	B	150	LYS
1	B	194	PHE
1	B	275	GLN
1	C	50	ARG
1	C	118	TYR
1	C	148	VAL
1	C	150	LYS
1	C	194	PHE
1	C	275	GLN
1	D	50	ARG
1	D	118	TYR
1	D	148	VAL
1	D	150	LYS
1	D	194	PHE
1	D	275	GLN
1	E	50	ARG
1	E	118	TYR
1	E	148	VAL
1	E	150	LYS
1	E	194	PHE
1	E	275	GLN
1	A	69	ALA
1	A	287	ALA
1	B	69	ALA
1	B	287	ALA

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Mol	Chain	Res	Type
1	C	69	ALA
1	C	287	ALA
1	D	69	ALA
1	D	287	ALA
1	E	69	ALA
1	E	287	ALA
1	A	84	ARG
1	A	240	LEU
1	A	288	ALA
1	A	295	ARG
1	B	84	ARG
1	C	84	ARG
1	D	84	ARG
1	E	84	ARG
1	E	288	ALA
1	B	226	LEU
1	B	282	SER
1	B	288	ALA
1	C	149	GLY
1	C	282	SER
1	C	288	ALA
1	D	282	SER
1	D	288	ALA
1	E	282	SER
1	E	295	ARG
1	A	34	GLU
1	A	278	LEU
1	B	149	GLY
1	B	278	LEU
1	C	226	LEU
1	C	271	GLU
1	C	278	LEU
1	C	295	ARG
1	D	226	LEU
1	D	278	LEU
1	E	34	GLU
1	E	149	GLY
1	E	278	LEU
1	A	149	GLY
1	A	282	SER
1	B	129	LEU
1	C	34	GLU

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Mol	Chain	Res	Type
1	D	149	GLY
1	D	295	ARG
1	E	291	THR
1	B	290	ILE
1	D	55	PRO
1	D	290	ILE
1	E	290	ILE
1	C	290	ILE
1	A	290	ILE

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	278/284 (98%)	237 (85%)	41 (15%)	3	14
1	B	278/284 (98%)	235 (84%)	43 (16%)	2	12
1	C	278/284 (98%)	239 (86%)	39 (14%)	3	15
1	D	278/284 (98%)	239 (86%)	39 (14%)	3	15
1	E	278/284 (98%)	233 (84%)	45 (16%)	2	11
All	All	1390/1420 (98%)	1183 (85%)	207 (15%)	3	13

All (207) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	53	PHE
1	A	64	THR
1	A	68	GLU
1	A	72	ILE
1	A	79	ASN
1	A	84	ARG
1	A	89	VAL
1	A	91	ILE
1	A	98	THR

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Mol	Chain	Res	Type
1	A	110	LEU
1	A	124	THR
1	A	130	ILE
1	A	134	VAL
1	A	141	LEU
1	A	148	VAL
1	A	154	VAL
1	A	177	ASP
1	A	179	LEU
1	A	202	LEU
1	A	204	MET
1	A	211	SER
1	A	213	THR
1	A	221	GLU
1	A	226	LEU
1	A	228	VAL
1	A	232	ILE
1	A	241	VAL
1	A	243	THR
1	A	254	THR
1	A	257	ILE
1	A	258	ILE
1	A	261	ILE
1	A	263	LEU
1	A	269	VAL
1	A	270	ILE
1	A	272	VAL
1	A	274	VAL
1	A	292	ARG
1	A	304	LEU
1	A	314	PHE
1	B	16	THR
1	B	53	PHE
1	B	64	THR
1	B	68	GLU
1	B	72	ILE
1	B	79	ASN
1	B	84	ARG
1	B	89	VAL
1	B	91	ILE
1	B	98	THR
1	B	99	VAL

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Mol	Chain	Res	Type
1	B	110	LEU
1	B	124	THR
1	B	130	ILE
1	B	134	VAL
1	B	136	THR
1	B	141	LEU
1	B	148	VAL
1	B	154	VAL
1	B	162	GLU
1	B	177	ASP
1	B	179	LEU
1	B	202	LEU
1	B	204	MET
1	B	211	SER
1	B	213	THR
1	B	221	GLU
1	B	226	LEU
1	B	228	VAL
1	B	232	ILE
1	B	243	THR
1	B	254	THR
1	B	257	ILE
1	B	258	ILE
1	B	261	ILE
1	B	263	LEU
1	B	269	VAL
1	B	270	ILE
1	B	272	VAL
1	B	274	VAL
1	B	290	ILE
1	B	292	ARG
1	B	314	PHE
1	C	16	THR
1	C	53	PHE
1	C	64	THR
1	C	68	GLU
1	C	72	ILE
1	C	79	ASN
1	C	84	ARG
1	C	89	VAL
1	C	91	ILE
1	C	98	THR

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Mol	Chain	Res	Type
1	C	99	VAL
1	C	110	LEU
1	C	124	THR
1	C	130	ILE
1	C	134	VAL
1	C	141	LEU
1	C	148	VAL
1	C	154	VAL
1	C	177	ASP
1	C	179	LEU
1	C	202	LEU
1	C	204	MET
1	C	211	SER
1	C	213	THR
1	C	221	GLU
1	C	226	LEU
1	C	228	VAL
1	C	232	ILE
1	C	243	THR
1	C	254	THR
1	C	257	ILE
1	C	258	ILE
1	C	263	LEU
1	C	269	VAL
1	C	270	ILE
1	C	272	VAL
1	C	274	VAL
1	C	292	ARG
1	C	314	PHE
1	D	16	THR
1	D	53	PHE
1	D	64	THR
1	D	68	GLU
1	D	72	ILE
1	D	79	ASN
1	D	84	ARG
1	D	89	VAL
1	D	91	ILE
1	D	98	THR
1	D	99	VAL
1	D	110	LEU
1	D	124	THR

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Mol	Chain	Res	Type
1	D	130	ILE
1	D	134	VAL
1	D	141	LEU
1	D	148	VAL
1	D	154	VAL
1	D	177	ASP
1	D	179	LEU
1	D	202	LEU
1	D	204	MET
1	D	211	SER
1	D	213	THR
1	D	221	GLU
1	D	226	LEU
1	D	228	VAL
1	D	232	ILE
1	D	243	THR
1	D	254	THR
1	D	257	ILE
1	D	258	ILE
1	D	263	LEU
1	D	269	VAL
1	D	270	ILE
1	D	272	VAL
1	D	274	VAL
1	D	292	ARG
1	D	314	PHE
1	E	12	ASP
1	E	16	THR
1	E	53	PHE
1	E	64	THR
1	E	68	GLU
1	E	72	ILE
1	E	79	ASN
1	E	84	ARG
1	E	89	VAL
1	E	91	ILE
1	E	98	THR
1	E	99	VAL
1	E	110	LEU
1	E	124	THR
1	E	130	ILE
1	E	134	VAL

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Mol	Chain	Res	Type
1	E	140	VAL
1	E	141	LEU
1	E	148	VAL
1	E	154	VAL
1	E	177	ASP
1	E	179	LEU
1	E	202	LEU
1	E	204	MET
1	E	211	SER
1	E	213	THR
1	E	221	GLU
1	E	226	LEU
1	E	228	VAL
1	E	232	ILE
1	E	241	VAL
1	E	243	THR
1	E	252	THR
1	E	254	THR
1	E	257	ILE
1	E	258	ILE
1	E	261	ILE
1	E	263	LEU
1	E	269	VAL
1	E	270	ILE
1	E	272	VAL
1	E	274	VAL
1	E	292	ARG
1	E	304	LEU
1	E	314	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	100	GLN
1	A	123	GLN
1	A	151	ASN
1	A	283	GLN
1	B	79	ASN
1	B	100	GLN
1	B	123	GLN
1	B	151	ASN

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Mol	Chain	Res	Type
1	B	283	GLN
1	C	79	ASN
1	C	100	GLN
1	C	123	GLN
1	C	151	ASN
1	C	283	GLN
1	D	79	ASN
1	D	100	GLN
1	D	123	GLN
1	D	151	ASN
1	D	234	HIS
1	D	283	GLN
1	E	79	ASN
1	E	100	GLN
1	E	123	GLN
1	E	151	ASN
1	E	283	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	310/317 (97%)	0.34	17 (5%)	30 16	56, 83, 126, 163	0
1	B	310/317 (97%)	0.28	14 (4%)	38 20	57, 83, 125, 163	0
1	C	310/317 (97%)	0.29	21 (6%)	23 12	58, 82, 126, 164	0
1	D	310/317 (97%)	0.44	28 (9%)	15 8	57, 83, 124, 163	0
1	E	310/317 (97%)	0.34	18 (5%)	29 16	57, 82, 125, 164	0
All	All	1550/1585 (97%)	0.34	98 (6%)	26 14	56, 83, 126, 164	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	55	PRO	6.5
1	D	57	ARG	5.4
1	B	148	VAL	5.2
1	D	11	ALA	4.5
1	A	11	ALA	4.5
1	B	7	PRO	4.4
1	D	7	PRO	4.4
1	C	11	ALA	4.0
1	C	7	PRO	3.9
1	B	11	ALA	3.8
1	E	11	ALA	3.6
1	C	10	ILE	3.6
1	A	134	VAL	3.6
1	E	145	LEU	3.6
1	E	7	PRO	3.5
1	A	145	LEU	3.5
1	C	316	PHE	3.4
1	A	7	PRO	3.4
1	A	53	PHE	3.4
1	E	134	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	148	VAL	3.3
1	E	148	VAL	3.3
1	D	60	VAL	3.2
1	D	95	PRO	3.1
1	D	54	ASP	3.1
1	D	145	LEU	3.1
1	E	146	GLU	3.1
1	A	148	VAL	3.1
1	C	219	SER	3.0
1	D	316	PHE	3.0
1	E	173	PHE	3.0
1	A	218	THR	3.0
1	D	96	ASP	2.9
1	D	315	GLY	2.9
1	E	218	THR	2.9
1	C	55	PRO	2.8
1	E	155	PHE	2.8
1	B	56	VAL	2.8
1	C	13	GLU	2.8
1	D	97	GLY	2.8
1	D	53	PHE	2.8
1	D	49	ARG	2.8
1	D	59	GLY	2.7
1	A	316	PHE	2.7
1	D	12	ASP	2.7
1	C	134	VAL	2.7
1	B	173	PHE	2.7
1	A	144	ASP	2.7
1	C	218	THR	2.7
1	E	136	THR	2.7
1	C	173	PHE	2.6
1	A	13	GLU	2.6
1	B	61	ARG	2.6
1	B	136	THR	2.6
1	A	155	PHE	2.5
1	E	316	PHE	2.5
1	A	55	PRO	2.5
1	C	217	SER	2.5
1	C	56	VAL	2.5
1	E	53	PHE	2.5
1	D	52	ALA	2.4
1	B	54	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	10	ILE	2.4
1	D	58	SER	2.4
1	C	61	ARG	2.4
1	A	60	VAL	2.4
1	D	56	VAL	2.4
1	D	173	PHE	2.4
1	E	94	SER	2.4
1	C	138	ASN	2.4
1	C	87	ASP	2.4
1	D	138	ASN	2.3
1	C	53	PHE	2.3
1	B	285	ALA	2.3
1	D	10	ILE	2.3
1	B	242	GLU	2.3
1	A	285	ALA	2.3
1	C	145	LEU	2.3
1	B	316	PHE	2.2
1	E	59	GLY	2.2
1	E	57	ARG	2.2
1	E	61	ARG	2.2
1	C	58	SER	2.2
1	C	148	VAL	2.2
1	E	10	ILE	2.2
1	A	141	LEU	2.2
1	D	63	LYS	2.2
1	D	48	ASP	2.2
1	E	138	ASN	2.1
1	D	218	THR	2.1
1	B	277	TYR	2.1
1	B	155	PHE	2.1
1	C	12	ASP	2.1
1	A	217	SER	2.1
1	B	145	LEU	2.1
1	D	13	GLU	2.1
1	D	275	GLN	2.1
1	C	142	ALA	2.0

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

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.