



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 05:21 PM GMT

PDB ID : 2C9M
Title : STRUCTURE OF (SR) CALCIUM-ATPASE IN THE CA2E1 STATE
SOLVED IN A P1 CRYSTAL FORM.
Authors : Lund Jensen, A.-M.; Sorensen, T.L.-M.; Olesen, C.; Moller, J.V.; Nissen, P.
Deposited on : 2005-12-13
Resolution : 3.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

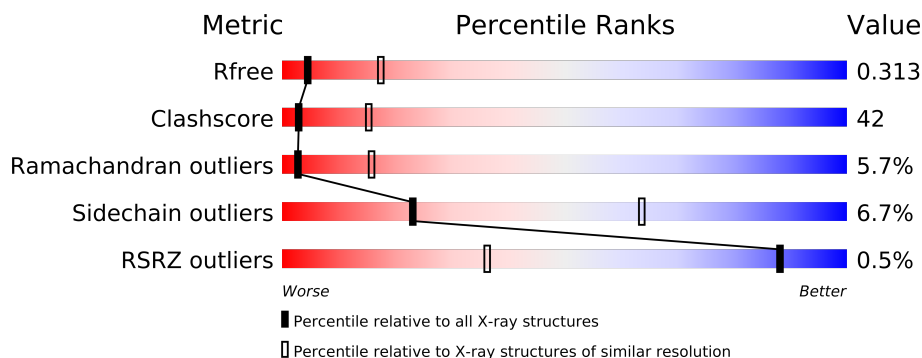
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.00 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}	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	994	
1	B	994	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	CA	B	996	-	X
3	K	B	997	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15351 atoms, of which 0 are hydrogen and 0 are deuterium.

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 SARCOPLASMIC/ENDOPLASMICRETICULUM CALCIUM ATPASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	994	Total	C	N	O	S	0	0	0
			7670	4876	1287	1450	57			
1	B	994	Total	C	N	O	S	0	0	0
			7670	4876	1287	1450	57			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Ca	0	0
			3	3		
2	A	4	Total	Ca	0	0
			4	4		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	K	0	0
			1	1		
3	A	1	Total	K	0	0
			1	1		

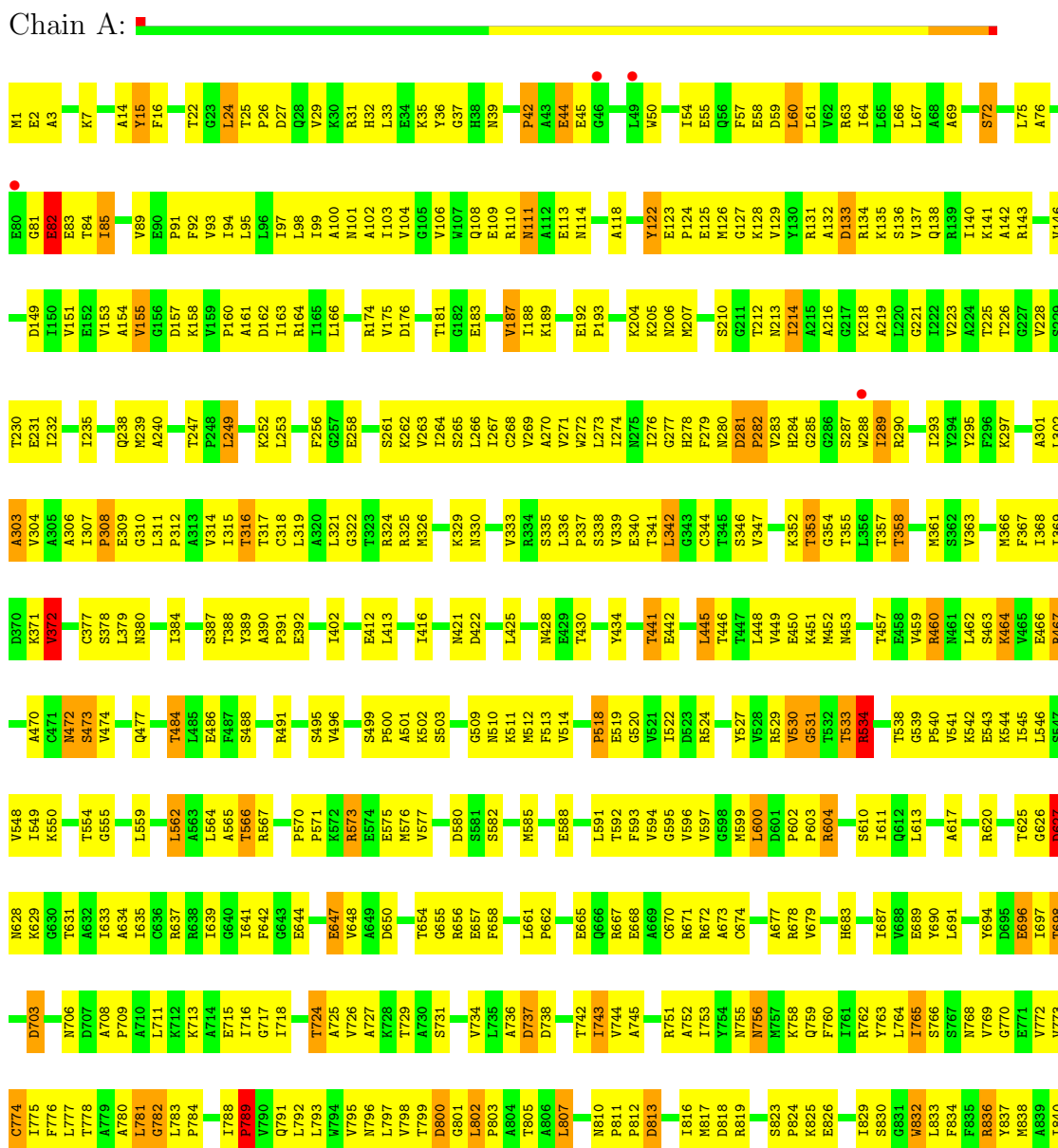
- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

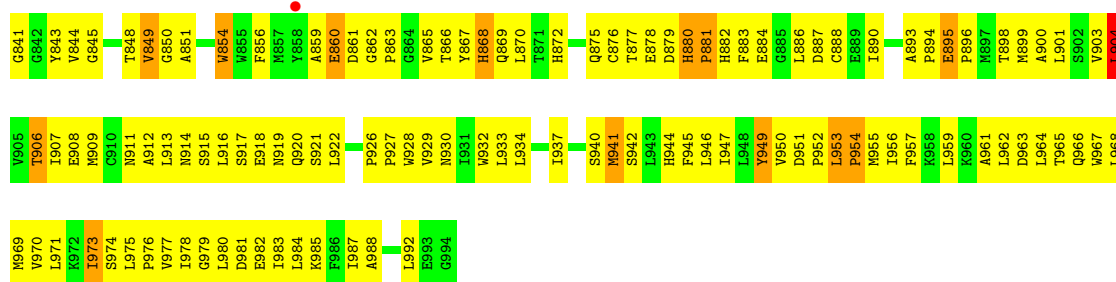
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	A	1	Total	Cl	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

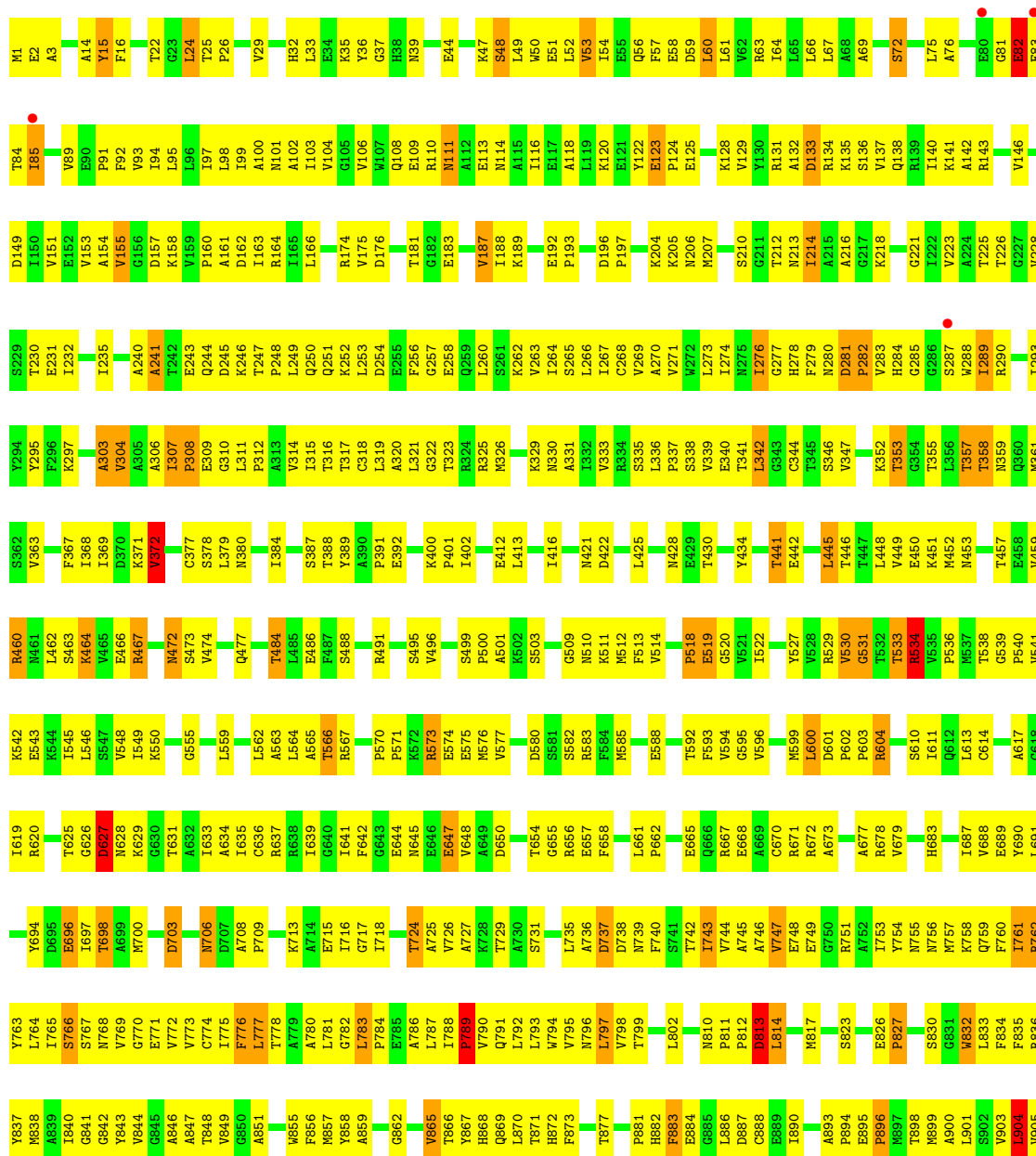
• Molecule 1: SARCOPLASMIC/ENDOPLASMICRETICULUM CALCIUM ATPASE 1





• Molecule 1: SARCOPLASMIC/ENDOPLASMICRETICULUM CALCIUM ATPASE 1

Chain B:



K969	V970	L971	K972	L973	S974	L975	P976	V977	L978	G979	L980	D981	E982	L983	L984	K985	P986	L987	A988	L992	E993	G994																																
T906	E908	M909	G910	N911	L912	L913	N914	S915	L916	S917	E918	N919	Q920	N921	S922	P926	W928	V929	N930	W932	L933	L934	L937	G938	L939	S940	M941	S942	L943	L944	F945	L946	L947	L948	Y949	P950	D951	P952	L953	P954	M955	L956	P957	K958	L959	K960	A961	L962	D963	L964	T965	Q966	W967	L968

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.95Å 81.28Å 131.01Å 97.64° 99.94° 95.22°	Depositor
Resolution (Å)	15.00 – 3.00 23.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	80.4 (15.00-3.00) 80.2 (23.79-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.99Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.266 , 0.317 0.261 , 0.313	Depositor DCC
R_{free} test set	1064 reflections (2.61%)	DCC
Wilson B-factor (Å ²)	75.2	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 35.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 45320 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	15351	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, CA, CL

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	0.49	1/7811 (0.0%)	0.72	2/10592 (0.0%)
1	B	0.48	0/7811	0.71	1/10592 (0.0%)
All	All	0.48	1/15622 (0.0%)	0.72	3/21184 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	674	CYS	CB-SG	-6.05	1.72	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	GLU	CA-CB-CG	5.91	126.40	113.40
1	A	800	ASP	N-CA-C	-5.73	95.52	111.00
1	B	82	GLU	CA-CB-CG	5.44	125.36	113.40

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7670	0	7764	632	0
1	B	7670	0	7766	677	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	1	0
4	B	1	0	0	0	0
All	All	15351	0	15530	1309	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 42.

All (1309) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:830:SER:HB3	1:B:833:LEU:HB2	1.40	1.03
1:A:372:VAL:HG13	1:A:377:CYS:HB3	1.44	0.99
1:A:263:VAL:HG12	1:A:267:ILE:HD11	1.44	0.97
1:B:372:VAL:HG13	1:B:377:CYS:HB3	1.46	0.97
1:B:559:LEU:HD23	1:B:600:LEU:HB3	1.47	0.95
1:A:559:LEU:HD23	1:A:600:LEU:HB3	1.47	0.95
1:B:47:LYS:HB3	1:B:51:GLU:HB3	1.46	0.94
1:A:214:ILE:HD13	1:A:214:ILE:H	1.33	0.94
1:B:263:VAL:HG12	1:B:267:ILE:HD11	1.48	0.93
1:A:658:PHE:HA	1:A:661:LEU:HD12	1.49	0.93
1:A:629:LYS:O	1:A:633:ILE:HG13	1.70	0.92
1:B:907:ILE:HD12	1:B:974:SER:HA	1.50	0.92
1:B:767:SER:HB3	1:B:911:ASN:HD22	1.36	0.91
1:B:658:PHE:HA	1:B:661:LEU:HD12	1.50	0.91
1:B:129:VAL:HG12	1:B:151:VAL:HG22	1.50	0.90
1:A:24:LEU:HD13	1:A:149:ASP:HA	1.51	0.90
1:A:759:GLN:HE21	1:A:917:SER:HA	1.35	0.90
1:B:214:ILE:HD13	1:B:214:ILE:H	1.37	0.90
1:A:755:ASN:O	1:A:759:GLN:HG3	1.72	0.90
1:B:904:LEU:O	1:B:907:ILE:HG22	1.70	0.90
1:B:756:ASN:HA	1:B:759:GLN:HE21	1.37	0.89
1:B:980:LEU:HA	1:B:983:ILE:HD12	1.53	0.89
1:B:629:LYS:O	1:B:633:ILE:HG13	1.73	0.88
1:A:904:LEU:O	1:A:907:ILE:HG22	1.74	0.87
1:A:679:VAL:HG13	1:A:683:HIS:HB2	1.55	0.87
1:B:567:ARG:HD3	1:B:570:PRO:HA	1.57	0.87
1:B:24:LEU:HD13	1:B:149:ASP:HA	1.54	0.87
1:A:773:VAL:CG2	1:A:845:GLY:HA3	2.05	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:783:LEU:HD13	1:B:870:LEU:HD11	1.55	0.87
1:A:773:VAL:HG23	1:A:845:GLY:HA3	1.55	0.86
1:B:679:VAL:HG13	1:B:683:HIS:HB2	1.56	0.86
1:B:311:LEU:HB3	1:B:312:PRO:HD3	1.58	0.86
1:A:567:ARG:HD3	1:A:570:PRO:HA	1.56	0.86
1:B:530:VAL:HG12	1:B:531:GLY:H	1.39	0.86
1:A:530:VAL:HG12	1:A:531:GLY:H	1.41	0.86
1:B:920:GLN:O	1:B:985:LYS:HD3	1.76	0.86
1:B:319:LEU:HD11	1:B:339:VAL:CG2	2.06	0.85
1:B:319:LEU:HD11	1:B:339:VAL:HG21	1.57	0.85
1:A:783:LEU:HD22	1:A:784:PRO:HD2	1.57	0.85
1:A:813:ASP:OD1	1:A:917:SER:HB2	1.76	0.85
1:A:42:PRO:HG2	1:A:44:GLU:OE1	1.77	0.84
1:A:769:VAL:HG13	1:A:841:GLY:HA3	1.58	0.84
1:B:798:VAL:HG13	1:B:940:SER:HB3	1.59	0.84
1:A:788:ILE:HG12	1:A:791:GLN:NE2	1.92	0.84
1:A:980:LEU:HA	1:A:983:ILE:HD12	1.59	0.83
1:B:886:LEU:HD11	1:B:890:ILE:HD11	1.58	0.83
1:B:767:SER:HB3	1:B:911:ASN:ND2	1.93	0.82
1:A:844:VAL:HG12	1:A:907:ILE:HG12	1.61	0.82
1:B:767:SER:CB	1:B:911:ASN:HD22	1.93	0.81
1:A:679:VAL:CG1	1:A:683:HIS:HB2	2.10	0.81
1:A:311:LEU:HB3	1:A:312:PRO:HD3	1.62	0.81
1:A:125:GLU:HB3	1:A:142:ALA:HB2	1.61	0.81
1:A:907:ILE:HD12	1:A:974:SER:HA	1.63	0.81
1:B:775:ILE:HD11	1:B:787:LEU:HD12	1.62	0.81
1:A:920:GLN:O	1:A:985:LYS:HD3	1.81	0.81
1:A:193:PRO:HD3	4:A:1000:CL:CL	2.18	0.80
1:A:125:GLU:CD	1:A:158:LYS:HB3	2.03	0.79
1:B:679:VAL:CG1	1:B:683:HIS:HB2	2.12	0.79
1:A:759:GLN:NE2	1:A:917:SER:HA	1.97	0.79
1:B:798:VAL:O	1:B:909:MET:HE1	1.82	0.79
1:A:881:PRO:HG2	1:A:882:HIS:H	1.45	0.79
1:A:111:ASN:HD22	1:A:111:ASN:H	1.31	0.79
1:B:49:LEU:HB3	1:B:254:ASP:HB3	1.64	0.78
1:B:111:ASN:H	1:B:111:ASN:HD22	1.32	0.78
1:A:756:ASN:HA	1:A:759:GLN:OE1	1.83	0.78
1:B:276:ILE:HA	1:B:279:PHE:CE2	2.18	0.78
1:A:802:LEU:HB3	1:A:803:PRO:HD3	1.65	0.78
1:B:907:ILE:HA	1:B:974:SER:HB3	1.64	0.77
1:A:102:ALA:O	1:A:106:VAL:HG22	1.83	0.77
1:B:573:ARG:HG3	1:B:573:ARG:HH11	1.50	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:102:ALA:O	1:B:106:VAL:HG22	1.83	0.77
1:A:276:ILE:HA	1:A:279:PHE:CE2	2.20	0.77
1:B:580:ASP:OD2	1:B:582:SER:HB3	1.85	0.77
1:B:887:ASP:HB2	1:B:890:ILE:HG23	1.64	0.77
1:A:580:ASP:OD2	1:A:582:SER:HB3	1.84	0.76
1:B:814:LEU:HG	1:B:920:GLN:HE21	1.49	0.76
1:B:794:TRP:HD1	1:B:901:LEU:HD11	1.49	0.76
1:B:278:HIS:HA	1:B:281:ASP:OD2	1.86	0.76
1:A:811:PRO:HG2	1:A:929:VAL:HG12	1.67	0.76
1:A:565:ALA:HA	1:A:594:VAL:HG23	1.67	0.76
1:A:769:VAL:O	1:A:773:VAL:HG13	1.85	0.75
1:A:125:GLU:OE2	1:A:158:LYS:HB3	1.86	0.75
1:B:565:ALA:HA	1:B:594:VAL:HG23	1.69	0.75
1:B:795:VAL:HG13	1:B:904:LEU:HG	1.69	0.75
1:A:347:VAL:HG22	1:A:620:ARG:HB2	1.69	0.75
1:A:129:VAL:HG12	1:A:151:VAL:HG22	1.66	0.75
1:A:75:LEU:HD12	1:A:76:ALA:N	2.01	0.75
1:B:811:PRO:HG2	1:B:929:VAL:HG12	1.69	0.75
1:B:318:CYS:SG	1:B:756:ASN:HB3	2.27	0.74
1:A:573:ARG:HH11	1:A:573:ARG:HG3	1.50	0.74
1:A:267:ILE:HG21	1:A:772:VAL:HG11	1.69	0.74
1:B:928:TRP:HA	1:B:934:LEU:HD11	1.69	0.74
1:A:697:ILE:HA	1:A:715:GLU:HG2	1.68	0.74
1:A:278:HIS:HA	1:A:281:ASP:OD2	1.88	0.74
1:A:763:TYR:HB2	1:A:915:SER:OG	1.88	0.74
1:A:907:ILE:HA	1:A:974:SER:HB3	1.69	0.73
1:B:314:VAL:HG21	1:B:760:PHE:CE2	2.23	0.73
1:A:387:SER:HB3	1:A:602:PRO:CG	2.19	0.73
1:B:441:THR:HG22	1:B:599:MET:SD	2.28	0.73
1:B:75:LEU:HD12	1:B:76:ALA:N	2.02	0.73
1:B:678:ARG:HH11	1:B:678:ARG:HG3	1.54	0.73
1:B:161:ALA:HA	1:B:210:SER:HB2	1.70	0.72
1:B:697:ILE:HA	1:B:715:GLU:HG2	1.70	0.72
1:B:962:LEU:HB3	1:B:966:GLN:HB3	1.71	0.72
1:B:95:LEU:O	1:B:99:ILE:HG12	1.90	0.72
1:B:941:MET:HA	1:B:941:MET:CE	2.18	0.72
1:A:175:VAL:HG22	1:A:214:ILE:HG22	1.72	0.72
1:A:678:ARG:HG3	1:A:678:ARG:HH11	1.55	0.72
1:A:941:MET:CE	1:A:941:MET:HA	2.19	0.72
1:A:825:LYS:HG3	1:A:826:GLU:H	1.55	0.72
1:A:446:THR:O	1:A:449:VAL:HG22	1.89	0.72
1:B:788:ILE:HB	1:B:789:PRO:HD2	1.71	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:95:LEU:O	1:A:99:ILE:HG12	1.90	0.71
1:A:823:SER:HB2	1:A:825:LYS:HG2	1.71	0.71
1:B:310:GLY:O	1:B:314:VAL:HG23	1.90	0.71
1:A:100:ALA:HA	1:A:103:ILE:HG22	1.72	0.71
1:B:756:ASN:HA	1:B:759:GLN:NE2	2.06	0.71
1:A:367:PHE:CD2	1:A:379:LEU:HD13	2.25	0.71
1:B:769:VAL:HG12	1:B:841:GLY:HA3	1.71	0.71
1:B:367:PHE:CD2	1:B:379:LEU:HD13	2.25	0.71
1:A:559:LEU:CD2	1:A:600:LEU:HB3	2.20	0.71
1:B:175:VAL:HG22	1:B:214:ILE:HG22	1.73	0.71
1:B:840:ILE:HD13	1:B:980:LEU:HD23	1.73	0.71
1:B:763:TYR:HB2	1:B:915:SER:OG	1.91	0.71
1:B:347:VAL:CG2	1:B:696:GLU:HG2	2.20	0.71
1:B:617:ALA:HB1	1:B:751:ARG:HH12	1.54	0.70
1:A:416:ILE:HD11	1:A:594:VAL:HG21	1.73	0.70
1:A:449:VAL:HG21	1:A:472:ASN:ND2	2.06	0.70
1:B:267:ILE:HG21	1:B:772:VAL:HG11	1.73	0.70
1:A:281:ASP:HB3	1:A:282:PRO:HD2	1.73	0.70
1:A:988:ALA:HA	1:A:992:LEU:HD12	1.73	0.70
1:A:310:GLY:O	1:A:314:VAL:HG23	1.91	0.70
1:A:319:LEU:HD11	1:A:339:VAL:CG2	2.22	0.70
1:B:988:ALA:HA	1:B:992:LEU:HD12	1.74	0.70
1:A:111:ASN:N	1:A:111:ASN:HD22	1.88	0.70
1:B:346:SER:OG	1:B:696:GLU:HG3	1.91	0.70
1:A:2:GLU:CD	1:A:3:ALA:H	1.94	0.70
1:A:926:PRO:O	1:A:929:VAL:HG23	1.91	0.70
1:B:755:ASN:O	1:B:759:GLN:HG3	1.92	0.69
1:B:281:ASP:HB3	1:B:282:PRO:HD2	1.73	0.69
1:B:2:GLU:CD	1:B:3:ALA:H	1.95	0.69
1:B:918:GLU:C	1:B:919:ASN:HD22	1.94	0.69
1:A:25:THR:HG22	1:A:132:ALA:HB2	1.73	0.69
1:B:926:PRO:O	1:B:929:VAL:HG23	1.93	0.69
1:B:899:MET:HG2	1:B:962:LEU:HD21	1.73	0.69
1:B:917:SER:OG	1:B:920:GLN:HB2	1.91	0.69
1:B:111:ASN:N	1:B:111:ASN:HD22	1.89	0.69
1:B:347:VAL:HG22	1:B:620:ARG:HB2	1.74	0.69
1:A:962:LEU:HB3	1:A:966:GLN:HB3	1.74	0.69
1:A:122:TYR:O	1:A:124:PRO:HD3	1.93	0.69
1:B:783:LEU:CD1	1:B:870:LEU:HD11	2.23	0.68
1:B:100:ALA:HA	1:B:103:ILE:HG22	1.74	0.68
1:A:459:VAL:HA	1:A:462:LEU:HD12	1.74	0.68
1:A:361:MET:HE3	1:A:599:MET:HB2	1.75	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:311:LEU:HA	1:A:760:PHE:CE1	2.28	0.68
1:A:342:LEU:HD12	1:A:716:ILE:HD13	1.73	0.68
1:B:319:LEU:CD1	1:B:339:VAL:HG21	2.22	0.68
1:B:416:ILE:HD11	1:B:594:VAL:HG21	1.74	0.68
1:B:832:TRP:O	1:B:835:PHE:HB3	1.94	0.68
1:B:628:ASN:HB3	1:B:678:ARG:HH22	1.58	0.68
1:A:647:GLU:H	1:A:647:GLU:CD	1.97	0.68
1:B:446:THR:O	1:B:449:VAL:HG22	1.92	0.67
1:B:47:LYS:HD3	1:B:51:GLU:O	1.95	0.67
1:A:336:LEU:N	1:A:337:PRO:HD2	2.09	0.67
1:B:559:LEU:CD2	1:B:600:LEU:HB3	2.22	0.67
1:B:25:THR:HG22	1:B:132:ALA:HB2	1.75	0.67
1:A:326:MET:CE	1:A:333:VAL:HG21	2.25	0.67
1:A:742:THR:O	1:A:745:ALA:N	2.27	0.67
1:A:778:THR:HG22	1:A:849:VAL:HG13	1.76	0.67
1:A:811:PRO:HG2	1:A:929:VAL:CG1	2.24	0.67
1:B:359:ASN:HA	1:B:601:ASP:OD1	1.94	0.67
1:B:459:VAL:HA	1:B:462:LEU:HD12	1.77	0.67
1:B:671:ARG:HB3	1:B:694:TYR:CE2	2.30	0.67
1:B:662:PRO:HD2	1:B:665:GLU:HB2	1.76	0.67
1:B:387:SER:HB3	1:B:602:PRO:CG	2.24	0.67
1:B:336:LEU:N	1:B:337:PRO:HD2	2.10	0.67
1:A:271:VAL:HA	1:A:274:ILE:HG12	1.76	0.67
1:B:647:GLU:CD	1:B:647:GLU:H	1.98	0.67
1:A:631:THR:O	1:A:634:ALA:HB3	1.95	0.67
1:A:918:GLU:C	1:A:919:ASN:HD22	1.98	0.67
1:A:308:PRO:HB2	1:A:764:LEU:HD12	1.76	0.66
1:A:928:TRP:HA	1:A:934:LEU:HD11	1.77	0.66
1:B:539:GLY:N	1:B:540:PRO:HD2	2.10	0.66
1:B:306:ALA:O	1:B:768:ASN:ND2	2.28	0.66
1:A:975:LEU:N	1:A:976:PRO:HD2	2.11	0.66
1:A:100:ALA:HB1	1:A:797:LEU:HD11	1.77	0.66
1:A:210:SER:HB3	1:A:230:THR:HG21	1.76	0.66
1:A:54:ILE:HD12	1:A:55:GLU:N	2.10	0.66
1:A:662:PRO:HD2	1:A:665:GLU:HB2	1.78	0.66
1:A:81:GLY:C	1:A:82:GLU:OE1	2.35	0.66
1:B:210:SER:HB3	1:B:230:THR:HG21	1.78	0.66
1:A:441:THR:HG22	1:A:599:MET:SD	2.36	0.66
1:A:412:GLU:OE1	1:A:529:ARG:HD2	1.95	0.66
1:B:944:HIS:O	1:B:947:ILE:HG22	1.95	0.65
1:B:357:THR:HA	1:B:603:PRO:HA	1.77	0.65
1:A:899:MET:HG2	1:A:962:LEU:HD21	1.77	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:230:THR:CG2	1:A:232:ILE:HG22	2.26	0.65
1:A:161:ALA:HA	1:A:210:SER:HB2	1.76	0.65
1:B:361:MET:HE3	1:B:599:MET:HB2	1.78	0.65
1:B:347:VAL:HG23	1:B:696:GLU:HG2	1.77	0.65
1:A:162:ASP:OD1	1:A:230:THR:HG23	1.96	0.65
1:A:50:TRP:HB2	1:A:55:GLU:CD	2.16	0.65
1:B:495:SER:HB3	1:B:514:VAL:HA	1.78	0.65
1:A:317:THR:HG22	1:A:321:LEU:HD12	1.77	0.65
1:B:975:LEU:N	1:B:976:PRO:HD2	2.12	0.65
1:B:317:THR:HG22	1:B:321:LEU:HD12	1.79	0.65
1:A:319:LEU:HD11	1:A:339:VAL:HG21	1.78	0.65
1:A:442:GLU:O	1:A:445:LEU:HB2	1.96	0.65
1:B:271:VAL:HA	1:B:274:ILE:HG12	1.78	0.65
1:A:495:SER:HB3	1:A:514:VAL:HA	1.78	0.65
1:A:941:MET:HE2	1:A:941:MET:HA	1.78	0.65
1:A:539:GLY:N	1:A:540:PRO:HD2	2.12	0.65
1:A:944:HIS:O	1:A:947:ILE:HG22	1.96	0.65
1:A:100:ALA:CB	1:A:797:LEU:HD11	2.27	0.65
1:B:893:ALA:O	1:B:896:PRO:HD2	1.96	0.65
1:B:342:LEU:HD12	1:B:716:ILE:HD13	1.79	0.65
1:B:442:GLU:O	1:B:445:LEU:HB2	1.97	0.65
1:A:82:GLU:N	1:A:82:GLU:OE1	2.30	0.65
1:B:267:ILE:CG2	1:B:772:VAL:HG11	2.28	0.64
1:B:783:LEU:HD13	1:B:870:LEU:CD1	2.26	0.64
1:B:82:GLU:OE1	1:B:82:GLU:N	2.30	0.64
1:B:775:ILE:CD1	1:B:787:LEU:HD12	2.27	0.64
1:B:898:THR:OG1	1:B:959:LEU:HA	1.97	0.64
1:B:49:LEU:HB3	1:B:254:ASP:CB	2.28	0.64
1:B:230:THR:CG2	1:B:232:ILE:HG22	2.26	0.64
1:A:628:ASN:HB3	1:A:678:ARG:HH22	1.62	0.64
1:B:610:SER:HB3	1:B:744:VAL:HG21	1.79	0.64
1:A:770:GLY:HA2	1:A:841:GLY:O	1.96	0.64
1:B:759:GLN:OE1	1:B:917:SER:HA	1.96	0.64
1:A:347:VAL:CG2	1:A:696:GLU:HG2	2.27	0.64
1:B:883:PHE:O	1:B:884:GLU:HG2	1.97	0.64
1:B:518:PRO:O	1:B:522:ILE:HG12	1.98	0.64
1:B:962:LEU:HB3	1:B:966:GLN:CB	2.28	0.64
1:A:770:GLY:HA3	1:A:844:VAL:CG2	2.28	0.64
1:B:941:MET:HA	1:B:941:MET:HE2	1.79	0.64
1:B:449:VAL:HG21	1:B:472:ASN:ND2	2.12	0.64
1:A:413:LEU:C	1:A:413:LEU:HD23	2.17	0.64
1:B:962:LEU:HA	1:B:966:GLN:OE1	1.97	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:162:ASP:OD1	1:B:230:THR:HG23	1.97	0.64
1:B:1:MET:O	1:B:1:MET:HG3	1.98	0.64
1:A:263:VAL:O	1:A:267:ILE:HG13	1.97	0.64
1:A:629:LYS:HD2	1:A:657:GLU:OE1	1.98	0.64
1:A:459:VAL:HG23	1:A:460:ARG:H	1.61	0.64
1:B:895:GLU:N	1:B:896:PRO:HD2	2.13	0.64
1:A:467:ARG:HG2	1:A:467:ARG:HH11	1.62	0.64
1:A:798:VAL:HG13	1:A:940:SER:HB3	1.78	0.64
1:A:559:LEU:HD21	1:A:600:LEU:HD13	1.80	0.63
1:A:762:ARG:HG3	1:A:837:TYR:CE1	2.33	0.63
1:B:60:LEU:O	1:B:60:LEU:HD12	1.98	0.63
1:B:907:ILE:CA	1:B:974:SER:HB3	2.29	0.63
1:B:886:LEU:HD11	1:B:890:ILE:CD1	2.29	0.63
1:B:766:SER:O	1:B:769:VAL:HG12	1.97	0.63
1:B:628:ASN:HD21	1:B:631:THR:HG23	1.63	0.63
1:A:449:VAL:CG2	1:A:472:ASN:ND2	2.61	0.63
1:B:894:PRO:HG2	1:B:895:GLU:OE2	1.99	0.63
1:A:679:VAL:HG13	1:A:683:HIS:CB	2.26	0.63
1:A:946:LEU:C	1:A:946:LEU:HD23	2.19	0.63
1:A:843:TYR:OH	1:A:976:PRO:HG2	1.99	0.63
1:B:870:LEU:C	1:B:870:LEU:HD12	2.19	0.63
1:B:330:ASN:HB3	1:B:736:ALA:HB3	1.79	0.63
1:B:631:THR:O	1:B:634:ALA:HB3	1.99	0.63
1:A:118:ALA:HB1	1:A:324:ARG:HE	1.63	0.63
1:B:25:THR:O	1:B:29:VAL:HG23	1.98	0.63
1:B:946:LEU:C	1:B:946:LEU:HD23	2.20	0.63
1:B:467:ARG:HH11	1:B:467:ARG:HG2	1.64	0.62
1:B:658:PHE:HA	1:B:661:LEU:CD1	2.26	0.62
1:B:326:MET:CE	1:B:333:VAL:HG21	2.28	0.62
1:B:230:THR:HG21	1:B:232:ILE:HG22	1.81	0.62
1:A:97:ILE:HG21	1:A:793:LEU:HB3	1.82	0.62
1:A:610:SER:HB3	1:A:744:VAL:HG21	1.81	0.62
1:B:412:GLU:OE1	1:B:529:ARG:HD2	1.99	0.62
1:A:708:ALA:HB3	1:A:709:PRO:HD3	1.80	0.62
1:A:25:THR:O	1:A:29:VAL:HG23	1.98	0.62
1:B:559:LEU:HD21	1:B:600:LEU:HD13	1.81	0.62
1:A:230:THR:HG21	1:A:232:ILE:HG22	1.82	0.62
1:B:957:PHE:O	1:B:959:LEU:HG	1.99	0.62
1:A:369:ILE:N	1:A:369:ILE:HD12	2.13	0.62
1:A:962:LEU:HB3	1:A:966:GLN:CB	2.30	0.62
1:A:947:ILE:HG12	1:A:957:PHE:CE2	2.34	0.62
1:B:683:HIS:O	1:B:687:ILE:HG13	2.00	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:230:THR:HG22	1:A:232:ILE:H	1.64	0.62
1:A:264:ILE:HA	1:A:267:ILE:HD12	1.81	0.62
1:A:100:ALA:HA	1:A:103:ILE:CG2	2.30	0.62
1:B:413:LEU:C	1:B:413:LEU:HD23	2.20	0.62
1:B:212:THR:HG22	1:B:213:ASN:N	2.15	0.62
1:A:330:ASN:HB3	1:A:736:ALA:HB3	1.81	0.61
1:B:742:THR:O	1:B:745:ALA:N	2.33	0.61
1:A:658:PHE:HA	1:A:661:LEU:CD1	2.27	0.61
1:B:679:VAL:HG13	1:B:683:HIS:CB	2.28	0.61
1:B:639:ILE:HD11	1:B:641:ILE:HD12	1.83	0.61
1:A:326:MET:HE3	1:A:333:VAL:HG21	1.82	0.61
1:B:369:ILE:HD12	1:B:369:ILE:N	2.15	0.61
1:A:24:LEU:HD22	1:A:149:ASP:HB3	1.82	0.61
1:A:898:THR:OG1	1:A:959:LEU:HA	2.00	0.61
1:A:769:VAL:CG1	1:A:841:GLY:HA3	2.28	0.61
1:A:448:LEU:O	1:A:452:MET:HG3	2.00	0.61
1:B:836:ARG:HD3	1:B:984:LEU:HD12	1.82	0.61
1:A:263:VAL:HG12	1:A:267:ILE:CD1	2.25	0.61
1:B:214:ILE:H	1:B:214:ILE:CD1	2.13	0.61
1:A:367:PHE:CE1	1:A:596:VAL:HB	2.36	0.61
1:A:907:ILE:CA	1:A:974:SER:HB3	2.31	0.61
1:A:57:PHE:O	1:A:61:LEU:HG	2.01	0.61
1:A:953:LEU:H	1:A:954:PRO:HD2	1.65	0.61
1:A:947:ILE:HG12	1:A:957:PHE:CD2	2.36	0.61
1:B:843:TYR:O	1:B:846:ALA:HB3	2.00	0.60
1:B:484:THR:HB	1:B:496:VAL:HG12	1.81	0.60
1:B:449:VAL:CG2	1:B:472:ASN:ND2	2.63	0.60
1:A:962:LEU:HA	1:A:966:GLN:OE1	2.01	0.60
1:B:459:VAL:HG23	1:B:460:ARG:H	1.65	0.60
1:B:263:VAL:O	1:B:267:ILE:HG13	2.00	0.60
1:A:271:VAL:C	1:A:273:LEU:H	2.05	0.60
1:A:50:TRP:HB2	1:A:55:GLU:OE2	2.01	0.60
1:A:518:PRO:O	1:A:522:ILE:HG12	2.02	0.60
1:B:93:VAL:HB	1:B:790:VAL:HG11	1.83	0.60
1:B:708:ALA:HB3	1:B:709:PRO:HD3	1.82	0.60
1:A:650:ASP:HB2	1:A:672:ARG:NH2	2.16	0.60
1:B:834:PHE:O	1:B:838:MET:HG2	2.01	0.60
1:A:917:SER:OG	1:A:920:GLN:HB2	2.01	0.60
1:A:347:VAL:HG23	1:A:696:GLU:HG2	1.82	0.60
1:A:1:MET:HG3	1:A:1:MET:O	2.02	0.60
1:B:118:ALA:C	1:B:120:LYS:H	2.04	0.60
1:A:214:ILE:H	1:A:214:ILE:CD1	2.11	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:628:ASN:HD21	1:A:631:THR:HG23	1.66	0.60
1:A:957:PHE:O	1:A:959:LEU:HG	2.01	0.60
1:A:642:PHE:CD2	1:A:648:VAL:HG11	2.36	0.60
1:B:100:ALA:HA	1:B:103:ILE:CG2	2.32	0.60
1:B:788:ILE:HB	1:B:789:PRO:CD	2.31	0.60
1:A:484:THR:HB	1:A:496:VAL:HG12	1.84	0.60
1:A:212:THR:HG22	1:A:213:ASN:N	2.16	0.60
1:B:762:ARG:CZ	1:B:836:ARG:NH1	2.64	0.60
1:A:683:HIS:O	1:A:687:ILE:HG13	2.01	0.60
1:B:462:LEU:HD22	1:B:466:GLU:HB3	1.84	0.60
1:B:726:VAL:HG13	1:B:727:ALA:N	2.16	0.60
1:A:780:ALA:C	1:A:782:GLY:H	2.05	0.60
1:A:346:SER:OG	1:A:696:GLU:HG3	2.01	0.59
1:A:387:SER:HB3	1:A:602:PRO:HG3	1.83	0.59
1:A:94:ILE:HD12	1:A:95:LEU:N	2.17	0.59
1:A:671:ARG:HB3	1:A:694:TYR:CE2	2.37	0.59
1:A:689:GLU:HB2	1:A:713:LYS:HZ3	1.68	0.59
1:B:116:ILE:HD13	1:B:320:ALA:HB2	1.84	0.59
1:A:249:LEU:O	1:A:253:LEU:HB2	2.02	0.59
1:A:372:VAL:HG13	1:A:377:CYS:CB	2.25	0.59
1:B:947:ILE:HG12	1:B:957:PHE:CE2	2.37	0.59
1:A:311:LEU:HA	1:A:760:PHE:HE1	1.65	0.59
1:B:367:PHE:CE2	1:B:379:LEU:HD13	2.38	0.59
1:A:22:THR:HG22	1:A:135:LYS:NZ	2.18	0.59
1:A:758:LYS:HE3	1:A:833:LEU:HD21	1.84	0.59
1:B:134:ARG:HH11	1:B:134:ARG:HG3	1.67	0.59
1:A:355:THR:HA	1:A:738:ASP:O	2.02	0.59
1:B:629:LYS:HD2	1:B:657:GLU:OE1	2.02	0.59
1:B:52:LEU:HD12	1:B:56:GLN:OE1	2.03	0.59
1:A:697:ILE:HG23	1:A:715:GLU:HG2	1.85	0.59
1:A:60:LEU:O	1:A:60:LEU:HD12	2.03	0.59
1:B:24:LEU:HD22	1:B:149:ASP:HB3	1.85	0.59
1:A:367:PHE:CE2	1:A:379:LEU:HD13	2.37	0.59
1:B:22:THR:HG22	1:B:135:LYS:NZ	2.18	0.59
1:B:725:ALA:O	1:B:729:THR:HG23	2.03	0.59
1:B:953:LEU:H	1:B:954:PRO:HD2	1.68	0.59
1:A:223:VAL:HG11	1:A:226:THR:HG22	1.85	0.58
1:B:530:VAL:O	1:B:531:GLY:C	2.41	0.58
1:B:654:THR:HA	1:B:677:ALA:O	2.03	0.58
1:B:131:ARG:HG3	1:B:131:ARG:HH11	1.67	0.58
1:A:600:LEU:O	1:A:600:LEU:HD23	2.03	0.58
1:B:603:PRO:HB3	1:B:639:ILE:HG22	1.83	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:230:THR:HG22	1:B:232:ILE:H	1.67	0.58
1:A:825:LYS:HG3	1:A:826:GLU:N	2.17	0.58
1:B:264:ILE:HA	1:B:267:ILE:HD12	1.84	0.58
1:B:788:ILE:HG12	1:B:791:GLN:HG3	1.86	0.58
1:B:94:ILE:HD12	1:B:95:LEU:N	2.18	0.58
1:B:271:VAL:C	1:B:273:LEU:H	2.07	0.58
1:B:212:THR:CG2	1:B:213:ASN:N	2.67	0.58
1:B:650:ASP:HB2	1:B:672:ARG:NH2	2.18	0.58
1:B:50:TRP:CZ2	1:B:311:LEU:HD23	2.38	0.58
1:B:154:ALA:O	1:B:214:ILE:HD11	2.03	0.58
1:B:223:VAL:HG11	1:B:226:THR:HG22	1.85	0.58
1:B:794:TRP:HE1	1:B:944:HIS:HD1	1.52	0.58
1:A:879:ASP:C	1:A:881:PRO:HD3	2.24	0.58
1:B:282:PRO:O	1:B:284:HIS:N	2.37	0.58
1:B:770:GLY:CA	1:B:841:GLY:O	2.52	0.58
1:B:573:ARG:HG3	1:B:573:ARG:NH1	2.17	0.58
1:B:57:PHE:O	1:B:61:LEU:HG	2.04	0.58
1:A:726:VAL:HG13	1:A:727:ALA:N	2.18	0.58
1:A:867:TYR:C	1:A:869:GLN:H	2.07	0.58
1:B:933:LEU:O	1:B:937:ILE:HG13	2.04	0.58
1:B:762:ARG:NH2	1:B:918:GLU:O	2.37	0.57
1:B:900:ALA:O	1:B:903:VAL:N	2.36	0.57
1:A:140:ILE:HD12	1:A:141:LYS:H	1.69	0.57
1:B:39:ASN:HB3	1:B:143:ARG:HA	1.86	0.57
1:B:847:ALA:HB1	1:B:973:ILE:HD12	1.85	0.57
1:B:244:GLN:HE21	1:B:247:THR:CG2	2.17	0.57
1:B:947:ILE:HG12	1:B:957:PHE:CD2	2.40	0.57
1:B:146:VAL:O	1:B:149:ASP:OD2	2.22	0.57
1:A:39:ASN:HB3	1:A:143:ARG:HA	1.86	0.57
1:A:539:GLY:O	1:A:543:GLU:HG2	2.04	0.57
1:A:134:ARG:HH11	1:A:134:ARG:HG3	1.67	0.57
1:A:462:LEU:HD22	1:A:466:GLU:HB3	1.85	0.57
1:B:474:VAL:HA	1:B:477:GLN:HE21	1.70	0.57
1:A:770:GLY:O	1:A:773:VAL:HG22	2.04	0.57
1:B:530:VAL:HG12	1:B:531:GLY:N	2.16	0.57
1:A:69:ALA:HA	1:A:297:LYS:HZ1	1.69	0.57
1:B:116:ILE:CD1	1:B:320:ALA:HB2	2.35	0.57
1:A:639:ILE:HD11	1:A:641:ILE:HD12	1.87	0.57
1:B:308:PRO:HB3	1:B:764:LEU:HG	1.87	0.57
1:B:263:VAL:HG12	1:B:267:ILE:CD1	2.28	0.57
1:A:783:LEU:CD2	1:A:784:PRO:HD2	2.31	0.57
1:A:125:GLU:OE1	1:A:158:LYS:HB3	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:950:VAL:O	1:A:954:PRO:HD2	2.05	0.57
1:B:567:ARG:HD3	1:B:570:PRO:CA	2.32	0.57
1:A:800:ASP:O	1:A:802:LEU:N	2.37	0.57
1:B:367:PHE:HA	1:B:380:ASN:O	2.04	0.57
1:B:539:GLY:O	1:B:543:GLU:HG2	2.05	0.57
1:B:353:THR:O	1:B:353:THR:CG2	2.53	0.57
1:A:843:TYR:C	1:A:843:TYR:CD2	2.78	0.57
1:A:879:ASP:O	1:A:880:HIS:HB2	2.04	0.57
1:A:867:TYR:O	1:A:869:GLN:N	2.38	0.57
1:B:762:ARG:CZ	1:B:836:ARG:HH12	2.18	0.57
1:B:812:PRO:O	1:B:813:ASP:O	2.23	0.57
1:B:448:LEU:O	1:B:452:MET:HG3	2.05	0.57
1:A:763:TYR:CE1	1:A:912:ALA:HB2	2.40	0.56
1:B:336:LEU:O	1:B:339:VAL:HG22	2.05	0.56
1:B:279:PHE:HE1	1:B:295:TYR:HB2	1.69	0.56
1:A:950:VAL:HG12	1:A:952:PRO:HD2	1.87	0.56
1:A:573:ARG:NH1	1:A:573:ARG:HG3	2.17	0.56
1:B:881:PRO:HD2	1:B:883:PHE:HE2	1.69	0.56
1:A:836:ARG:HH11	1:A:836:ARG:CG	2.17	0.56
1:B:950:VAL:O	1:B:954:PRO:HD2	2.05	0.56
1:A:33:LEU:O	1:A:37:GLY:N	2.38	0.56
1:A:488:SER:OG	1:A:491:ARG:NH1	2.39	0.56
1:A:137:VAL:HG12	1:A:138:GLN:N	2.20	0.56
1:A:154:ALA:O	1:A:214:ILE:HD11	2.06	0.56
1:A:770:GLY:HA3	1:A:844:VAL:HG23	1.88	0.56
1:A:335:SER:OG	1:A:337:PRO:HG2	2.05	0.56
1:A:131:ARG:HG3	1:A:131:ARG:HH11	1.71	0.56
1:B:628:ASN:HD21	1:B:631:THR:CG2	2.17	0.56
1:B:240:ALA:O	1:B:241:ALA:C	2.44	0.56
1:A:834:PHE:O	1:A:838:MET:HG2	2.06	0.56
1:A:968:LEU:HD23	1:A:968:LEU:O	2.05	0.56
1:B:968:LEU:HD23	1:B:968:LEU:O	2.05	0.56
1:A:282:PRO:O	1:A:284:HIS:N	2.39	0.56
1:A:988:ALA:CA	1:A:992:LEU:HD12	2.35	0.56
1:A:900:ALA:O	1:A:903:VAL:N	2.38	0.56
1:A:50:TRP:HB2	1:A:55:GLU:OE1	2.04	0.56
1:A:428:ASN:OD1	1:A:430:THR:HB	2.04	0.56
1:A:25:THR:HB	1:A:26:PRO:HD2	1.87	0.56
1:A:903:VAL:HA	1:A:970:VAL:HG13	1.88	0.56
1:A:66:LEU:HD12	1:A:94:ILE:HD11	1.86	0.56
1:B:950:VAL:HG12	1:B:952:PRO:HD2	1.87	0.56
1:B:137:VAL:HG12	1:B:138:GLN:H	1.70	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:832:TRP:CZ2	1:A:988:ALA:HB2	2.41	0.56
1:A:146:VAL:O	1:A:149:ASP:OD2	2.24	0.56
1:B:260:LEU:HD11	1:B:765:ILE:HD11	1.88	0.56
1:A:137:VAL:HG12	1:A:138:GLN:H	1.71	0.56
1:A:774:CYS:SG	1:A:775:ILE:N	2.79	0.56
1:B:899:MET:O	1:B:903:VAL:HG23	2.05	0.55
1:B:306:ALA:HA	1:B:768:ASN:HD21	1.70	0.55
1:B:777:LEU:HA	1:B:780:ALA:HB3	1.87	0.55
1:B:325:ARG:NH1	1:B:812:PRO:HG3	2.21	0.55
1:A:962:LEU:CD2	1:A:966:GLN:HB3	2.37	0.55
1:A:567:ARG:HD3	1:A:570:PRO:CA	2.31	0.55
1:B:89:VAL:O	1:B:93:VAL:HG23	2.06	0.55
1:A:389:TYR:HB3	1:A:425:LEU:HD21	1.88	0.55
1:B:372:VAL:HG13	1:B:377:CYS:CB	2.28	0.55
1:B:66:LEU:HD12	1:B:94:ILE:HD11	1.86	0.55
1:A:628:ASN:HD21	1:A:631:THR:CG2	2.20	0.55
1:B:367:PHE:CE1	1:B:596:VAL:HB	2.42	0.55
1:A:329:LYS:O	1:A:330:ASN:HB2	2.06	0.55
1:B:771:GLU:O	1:B:775:ILE:HG12	2.06	0.55
1:B:814:LEU:HG	1:B:920:GLN:NE2	2.20	0.55
1:A:192:GLU:HB3	1:A:193:PRO:HD2	1.88	0.55
1:B:276:ILE:HA	1:B:279:PHE:CD2	2.41	0.55
1:B:25:THR:HB	1:B:26:PRO:HD2	1.88	0.55
1:A:872:HIS:O	1:A:875:GLN:HG2	2.06	0.55
1:A:325:ARG:NH1	1:A:812:PRO:HG3	2.21	0.55
1:A:851:ALA:CB	1:A:903:VAL:HG21	2.37	0.55
1:B:137:VAL:HG12	1:B:138:GLN:N	2.21	0.55
1:B:69:ALA:HA	1:B:297:LYS:HZ1	1.72	0.55
1:B:428:ASN:OD1	1:B:430:THR:HB	2.07	0.55
1:A:913:LEU:HD22	1:A:927:PRO:HB3	1.89	0.55
1:A:128:LYS:O	1:A:151:VAL:HG13	2.07	0.55
1:B:855:TRP:CZ2	1:B:895:GLU:HB2	2.42	0.55
1:A:212:THR:CG2	1:A:213:ASN:N	2.70	0.55
1:B:903:VAL:HA	1:B:970:VAL:HG13	1.89	0.55
1:A:530:VAL:HG12	1:A:531:GLY:N	2.19	0.55
1:B:81:GLY:C	1:B:82:GLU:OE1	2.45	0.55
1:A:153:VAL:O	1:A:218:LYS:HA	2.06	0.55
1:A:725:ALA:O	1:A:729:THR:HG23	2.07	0.55
1:B:54:ILE:HG23	1:B:307:ILE:CG2	2.37	0.55
1:B:697:ILE:HG23	1:B:715:GLU:HG2	1.89	0.54
1:A:823:SER:CB	1:A:825:LYS:HG2	2.37	0.54
1:B:748:GLU:HB2	1:B:817:MET:SD	2.47	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:737:ASP:OD1	1:A:737:ASP:N	2.40	0.54
1:B:988:ALA:CA	1:B:992:LEU:HD12	2.37	0.54
1:B:413:LEU:HG	1:B:564:LEU:CD1	2.37	0.54
1:A:302:LEU:HA	1:A:792:LEU:HD13	1.89	0.54
1:A:880:HIS:N	1:A:881:PRO:CD	2.71	0.54
1:B:628:ASN:HA	1:B:678:ARG:NH1	2.22	0.54
1:B:140:ILE:HD12	1:B:141:LYS:H	1.73	0.54
1:A:474:VAL:HA	1:A:477:GLN:HE21	1.71	0.54
1:B:571:PRO:HG2	1:B:576:MET:SD	2.48	0.54
1:A:513:PHE:CD1	1:A:566:THR:HG23	2.42	0.54
1:B:389:TYR:HB3	1:B:425:LEU:HD21	1.89	0.54
1:B:315:ILE:HG12	1:B:757:MET:HG3	1.90	0.54
1:A:367:PHE:O	1:A:368:ILE:HG23	2.08	0.54
1:B:724:THR:HB	1:B:726:VAL:HG12	1.88	0.54
1:B:488:SER:OG	1:B:491:ARG:NH1	2.41	0.54
1:B:840:ILE:HG22	1:B:841:GLY:N	2.23	0.54
1:B:562:LEU:O	1:B:596:VAL:HG13	2.07	0.54
1:A:836:ARG:HD3	1:A:984:LEU:CD1	2.38	0.54
1:B:355:THR:HA	1:B:738:ASP:O	2.07	0.54
1:B:155:VAL:HG13	1:B:216:ALA:HA	1.88	0.54
1:B:962:LEU:CD2	1:B:966:GLN:HB3	2.38	0.54
1:A:276:ILE:HA	1:A:279:PHE:CD2	2.42	0.54
1:A:724:THR:HB	1:A:726:VAL:HG12	1.89	0.54
1:A:155:VAL:HG13	1:A:216:ALA:HA	1.89	0.54
1:B:826:GLU:O	1:B:827:PRO:O	2.26	0.54
1:A:214:ILE:N	1:A:214:ILE:HD13	2.14	0.54
1:B:50:TRP:CE3	1:B:257:GLY:HA3	2.42	0.54
1:A:678:ARG:NH1	1:A:678:ARG:HG3	2.22	0.54
1:A:176:ASP:O	1:A:212:THR:HG23	2.07	0.54
1:B:794:TRP:HZ2	1:B:944:HIS:HA	1.72	0.54
1:A:571:PRO:HG2	1:A:576:MET:SD	2.48	0.54
1:B:726:VAL:HG13	1:B:727:ALA:H	1.72	0.54
1:A:726:VAL:HG13	1:A:727:ALA:H	1.72	0.54
1:B:192:GLU:HB3	1:B:193:PRO:HD2	1.90	0.54
1:A:164:ARG:HA	1:A:207:MET:SD	2.48	0.54
1:B:153:VAL:O	1:B:218:LYS:HA	2.07	0.54
1:B:308:PRO:CB	1:B:764:LEU:HG	2.38	0.53
1:B:903:VAL:HG22	1:B:973:ILE:HG21	1.90	0.53
1:A:755:ASN:OD1	1:A:819:ARG:NH2	2.40	0.53
1:B:920:GLN:HA	1:B:920:GLN:OE1	2.08	0.53
1:B:765:ILE:HG21	1:B:837:TYR:HD2	1.73	0.53
1:B:53:VAL:O	1:B:53:VAL:HG12	2.08	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:628:ASN:HA	1:A:678:ARG:NH1	2.23	0.53
1:A:627:ASP:O	1:A:678:ARG:HG2	2.09	0.53
1:A:903:VAL:CG2	1:A:973:ILE:HG21	2.39	0.53
1:B:176:ASP:O	1:B:212:THR:HG23	2.08	0.53
1:A:264:ILE:O	1:A:266:LEU:N	2.42	0.53
1:A:654:THR:HA	1:A:677:ALA:O	2.09	0.53
1:B:104:VAL:HG21	1:B:797:LEU:HD11	1.91	0.53
1:A:89:VAL:O	1:A:93:VAL:HG23	2.07	0.53
1:B:322:GLY:HA3	1:B:753:ILE:HD11	1.91	0.53
1:B:513:PHE:CD1	1:B:566:THR:HG23	2.44	0.53
1:A:788:ILE:HB	1:A:789:PRO:HD2	1.90	0.53
1:A:279:PHE:HE1	1:A:295:TYR:HB2	1.72	0.53
1:A:751:ARG:CB	1:A:816:ILE:HD11	2.38	0.53
1:B:326:MET:HE3	1:B:333:VAL:HG21	1.89	0.53
1:B:82:GLU:HB2	1:B:83:GLU:OE1	2.09	0.53
1:B:794:TRP:CZ2	1:B:944:HIS:HA	2.43	0.53
1:B:2:GLU:CD	1:B:3:ALA:N	2.62	0.53
1:B:98:LEU:HA	1:B:101:ASN:HD22	1.72	0.53
1:A:110:ARG:HH11	1:A:110:ARG:HG3	1.73	0.53
1:B:762:ARG:NH2	1:B:836:ARG:HH12	2.07	0.53
1:A:916:LEU:HD11	1:A:927:PRO:HA	1.91	0.53
1:A:358:THR:HG23	1:A:602:PRO:O	2.08	0.53
1:B:656:ARG:HG2	1:B:656:ARG:HH11	1.73	0.53
1:A:367:PHE:HA	1:A:380:ASN:O	2.09	0.53
1:B:836:ARG:HD3	1:B:984:LEU:CD1	2.40	0.52
1:A:880:HIS:HA	1:A:883:PHE:CD2	2.45	0.52
1:B:123:GLU:O	1:B:123:GLU:HG2	2.09	0.52
1:B:154:ALA:O	1:B:214:ILE:CG1	2.58	0.52
1:B:913:LEU:HD22	1:B:927:PRO:HB3	1.91	0.52
1:B:246:LYS:HA	1:B:251:GLN:HG3	1.90	0.52
1:A:98:LEU:HA	1:A:101:ASN:HD22	1.73	0.52
1:B:867:TYR:CG	1:B:868:HIS:N	2.78	0.52
1:B:799:THR:HB	1:B:908:GLU:OE1	2.09	0.52
1:B:369:ILE:HA	1:B:379:LEU:HD23	1.91	0.52
1:A:459:VAL:HG23	1:A:460:ARG:N	2.23	0.52
1:B:459:VAL:HG23	1:B:460:ARG:N	2.25	0.52
1:A:765:ILE:HG21	1:A:837:TYR:CD2	2.44	0.52
1:B:311:LEU:HB3	1:B:312:PRO:CD	2.34	0.52
1:B:49:LEU:HB3	1:B:254:ASP:CG	2.30	0.52
1:A:336:LEU:O	1:A:339:VAL:HG22	2.09	0.52
1:A:742:THR:O	1:A:743:ILE:C	2.48	0.52
1:B:228:VAL:O	1:B:228:VAL:HG22	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:920:GLN:HA	1:A:920:GLN:OE1	2.10	0.52
1:B:522:ILE:HD12	1:B:545:ILE:HG21	1.92	0.52
1:A:69:ALA:O	1:A:91:PRO:HG3	2.10	0.52
1:A:72:SER:HA	1:A:293:ILE:CD1	2.39	0.52
1:B:627:ASP:O	1:B:678:ARG:HG2	2.10	0.52
1:A:2:GLU:CD	1:A:3:ALA:N	2.62	0.52
1:B:895:GLU:OE2	1:B:960:LYS:HG2	2.10	0.52
1:B:600:LEU:HD23	1:B:600:LEU:O	2.09	0.52
1:B:916:LEU:HD11	1:B:927:PRO:HA	1.91	0.52
1:B:290:ARG:O	1:B:293:ILE:HG12	2.09	0.52
1:A:844:VAL:HG23	1:A:845:GLY:H	1.74	0.52
1:A:975:LEU:N	1:A:976:PRO:CD	2.73	0.52
1:A:825:LYS:CG	1:A:826:GLU:H	2.21	0.52
1:B:620:ARG:NH2	1:B:670:CYS:O	2.42	0.52
1:B:862:GLY:O	1:B:865:VAL:HG13	2.10	0.52
1:A:252:LYS:NZ	1:A:826:GLU:O	2.40	0.51
1:B:763:TYR:CE1	1:B:912:ALA:HB2	2.45	0.51
1:B:100:ALA:O	1:B:104:VAL:HG23	2.10	0.51
1:B:747:VAL:HG12	1:B:748:GLU:N	2.25	0.51
1:A:264:ILE:C	1:A:266:LEU:H	2.14	0.51
1:B:787:LEU:HD13	1:B:792:LEU:HD23	1.91	0.51
1:B:335:SER:OG	1:B:337:PRO:HG2	2.09	0.51
1:B:668:GLU:OE2	1:B:671:ARG:NH1	2.40	0.51
1:B:174:ARG:HA	1:B:187:VAL:O	2.11	0.51
1:B:402:ILE:O	1:B:402:ILE:HD12	2.10	0.51
1:A:384:ILE:HD12	1:A:384:ILE:N	2.25	0.51
1:A:559:LEU:CD2	1:A:600:LEU:HD13	2.40	0.51
1:A:763:TYR:CD1	1:A:912:ALA:HA	2.45	0.51
1:A:762:ARG:HG3	1:A:837:TYR:HE1	1.75	0.51
1:A:530:VAL:O	1:A:531:GLY:C	2.49	0.51
1:A:795:VAL:HG22	1:A:901:LEU:CD1	2.40	0.51
1:B:887:ASP:CB	1:B:890:ILE:HG23	2.36	0.51
1:B:717:GLY:O	1:B:731:SER:HB2	2.11	0.51
1:B:784:PRO:HA	1:B:873:PHE:CE2	2.46	0.51
1:A:791:GLN:O	1:A:795:VAL:HG23	2.11	0.51
1:A:363:VAL:HG11	1:A:448:LEU:HD22	1.93	0.51
1:B:72:SER:O	1:B:75:LEU:HG	2.08	0.51
1:A:467:ARG:HH11	1:A:467:ARG:CG	2.24	0.51
1:A:836:ARG:NH1	1:A:836:ARG:HG2	2.24	0.51
1:B:214:ILE:N	1:B:214:ILE:HD13	2.17	0.51
1:B:367:PHE:O	1:B:368:ILE:HG23	2.10	0.51
1:A:903:VAL:HG22	1:A:973:ILE:HG21	1.92	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:110:ARG:HG3	1:B:110:ARG:HH11	1.75	0.51
1:A:69:ALA:HA	1:A:297:LYS:NZ	2.25	0.51
1:A:100:ALA:O	1:A:104:VAL:HG23	2.11	0.51
1:A:319:LEU:CD1	1:A:339:VAL:HG21	2.40	0.51
1:B:753:ILE:HG22	1:B:753:ILE:O	2.11	0.51
1:A:840:ILE:HD11	1:A:981:ASP:HB2	1.93	0.51
1:A:44:GLU:OE2	1:A:45:GLU:HG3	2.11	0.51
1:B:347:VAL:HG21	1:B:696:GLU:HG2	1.90	0.51
1:A:122:TYR:O	1:A:124:PRO:CD	2.59	0.51
1:A:270:ALA:O	1:A:274:ILE:HG23	2.11	0.51
1:B:249:LEU:O	1:B:252:LYS:N	2.43	0.51
1:A:881:PRO:HG2	1:A:882:HIS:N	2.21	0.51
1:B:49:LEU:HD21	1:B:258:GLU:OE1	2.11	0.51
1:B:883:PHE:HD2	1:B:883:PHE:H	1.58	0.51
1:B:975:LEU:N	1:B:976:PRO:CD	2.74	0.50
1:A:950:VAL:C	1:A:952:PRO:HD2	2.31	0.50
1:B:116:ILE:HG22	1:B:116:ILE:O	2.10	0.50
1:B:157:ASP:O	1:B:214:ILE:HD13	2.12	0.50
1:B:154:ALA:O	1:B:214:ILE:HG13	2.11	0.50
1:B:256:PHE:C	1:B:258:GLU:H	2.15	0.50
1:B:269:VAL:O	1:B:269:VAL:HG12	2.12	0.50
1:B:315:ILE:O	1:B:317:THR:N	2.45	0.50
1:A:843:TYR:HE2	1:A:907:ILE:HD11	1.75	0.50
1:A:881:PRO:CG	1:A:882:HIS:H	2.19	0.50
1:A:111:ASN:ND2	1:A:111:ASN:H	2.05	0.50
1:A:522:ILE:HD12	1:A:545:ILE:HG21	1.92	0.50
1:B:963:ASP:N	1:B:966:GLN:HB2	2.27	0.50
1:B:49:LEU:HD23	1:B:254:ASP:HB3	1.93	0.50
1:A:833:LEU:O	1:A:836:ARG:HB3	2.11	0.50
1:A:737:ASP:O	1:A:738:ASP:HB2	2.12	0.50
1:A:491:ARG:HD3	1:A:585:MET:HA	1.92	0.50
1:A:258:GLU:O	1:A:262:LYS:HG2	2.12	0.50
1:A:752:ALA:N	1:A:816:ILE:HD11	2.27	0.50
1:B:484:THR:CB	1:B:496:VAL:HG12	2.42	0.50
1:A:72:SER:O	1:A:75:LEU:HG	2.09	0.50
1:B:69:ALA:O	1:B:91:PRO:HG3	2.12	0.50
1:B:357:THR:HG23	1:B:601:ASP:OD2	2.12	0.50
1:B:347:VAL:HB	1:B:698:THR:HG23	1.93	0.50
1:A:54:ILE:CG2	1:A:261:SER:HB3	2.41	0.50
1:B:953:LEU:O	1:B:955:MET:N	2.44	0.50
1:B:363:VAL:HG11	1:B:448:LEU:HD22	1.94	0.50
1:B:921:SER:HA	1:B:982:GLU:OE2	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:848:THR:C	1:A:850:GLY:H	2.15	0.50
1:A:157:ASP:O	1:A:214:ILE:HD13	2.12	0.50
1:B:903:VAL:CG2	1:B:973:ILE:HG21	2.42	0.50
1:A:907:ILE:CG2	1:A:908:GLU:N	2.75	0.50
1:B:104:VAL:HG13	1:B:802:LEU:CD2	2.41	0.50
1:B:353:THR:O	1:B:353:THR:HG22	2.12	0.50
1:B:642:PHE:CD2	1:B:648:VAL:HG11	2.46	0.50
1:A:907:ILE:HG23	1:A:908:GLU:N	2.27	0.50
1:B:870:LEU:O	1:B:873:PHE:HB3	2.12	0.50
1:B:111:ASN:H	1:B:111:ASN:ND2	2.06	0.50
1:B:368:ILE:HG22	1:B:595:GLY:HA3	1.94	0.50
1:A:290:ARG:O	1:A:293:ILE:HG12	2.11	0.50
1:B:387:SER:HB3	1:B:602:PRO:HG3	1.93	0.50
1:A:988:ALA:CB	1:A:992:LEU:HD12	2.41	0.50
1:A:798:VAL:O	1:A:909:MET:HE1	2.11	0.50
1:A:164:ARG:CZ	1:A:206:ASN:HD22	2.25	0.50
1:A:832:TRP:CZ3	1:A:992:LEU:HD11	2.47	0.49
1:A:777:LEU:O	1:A:781:LEU:HG	2.11	0.49
1:B:907:ILE:HG23	1:B:908:GLU:N	2.27	0.49
1:A:347:VAL:HB	1:A:698:THR:HG23	1.94	0.49
1:B:72:SER:HA	1:B:293:ILE:CD1	2.41	0.49
1:A:963:ASP:N	1:A:966:GLN:HB2	2.27	0.49
1:B:718:ILE:HD13	1:B:743:ILE:HG12	1.94	0.49
1:B:491:ARG:HD3	1:B:585:MET:HA	1.93	0.49
1:A:239:MET:HG3	1:A:240:ALA:H	1.77	0.49
1:A:123:GLU:OE2	1:A:734:VAL:HG21	2.12	0.49
1:B:559:LEU:CD2	1:B:600:LEU:HD13	2.41	0.49
1:A:369:ILE:HA	1:A:379:LEU:HD23	1.94	0.49
1:A:620:ARG:NH2	1:A:691:LEU:HD21	2.27	0.49
1:B:122:TYR:O	1:B:124:PRO:N	2.45	0.49
1:A:463:SER:O	1:A:466:GLU:HB2	2.12	0.49
1:B:342:LEU:HD12	1:B:716:ILE:CD1	2.41	0.49
1:B:742:THR:O	1:B:743:ILE:C	2.51	0.49
1:A:953:LEU:N	1:A:954:PRO:HD2	2.27	0.49
1:A:953:LEU:O	1:A:955:MET:N	2.44	0.49
1:A:836:ARG:HH11	1:A:836:ARG:HG2	1.77	0.49
1:A:228:VAL:HG22	1:A:228:VAL:O	2.12	0.49
1:B:264:ILE:O	1:B:266:LEU:N	2.46	0.49
1:A:342:LEU:HD12	1:A:716:ILE:CD1	2.40	0.49
1:B:258:GLU:O	1:B:262:LYS:HG2	2.13	0.49
1:B:104:VAL:HG13	1:B:802:LEU:HD21	1.93	0.49
1:A:780:ALA:O	1:A:782:GLY:N	2.43	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:269:VAL:O	1:A:269:VAL:HG12	2.13	0.49
1:B:264:ILE:C	1:B:266:LEU:H	2.16	0.49
1:B:49:LEU:O	1:B:53:VAL:HG23	2.12	0.49
1:B:678:ARG:HG3	1:B:678:ARG:NH1	2.20	0.49
1:A:333:VAL:HG11	1:A:339:VAL:CG1	2.43	0.49
1:B:495:SER:CB	1:B:514:VAL:HG22	2.43	0.49
1:A:668:GLU:OE2	1:A:671:ARG:NH1	2.42	0.49
1:A:603:PRO:HB3	1:A:639:ILE:HG22	1.95	0.49
1:B:188:ILE:HG22	1:B:189:LYS:N	2.27	0.49
1:A:154:ALA:O	1:A:214:ILE:CG1	2.61	0.49
1:A:799:THR:HG21	1:A:908:GLU:HB2	1.93	0.49
1:B:783:LEU:HD13	1:B:784:PRO:HD3	1.95	0.49
1:B:333:VAL:HG11	1:B:339:VAL:CG1	2.43	0.49
1:B:893:ALA:C	1:B:896:PRO:HD2	2.33	0.49
1:B:577:VAL:O	1:B:577:VAL:HG23	2.13	0.49
1:A:770:GLY:HA3	1:A:844:VAL:HG21	1.92	0.49
1:B:463:SER:O	1:B:466:GLU:HB2	2.12	0.49
1:A:204:LYS:O	1:A:206:ASN:N	2.43	0.49
1:B:122:TYR:O	1:B:123:GLU:C	2.50	0.49
1:A:188:ILE:HG22	1:A:189:LYS:N	2.27	0.49
1:A:906:THR:HG22	1:A:974:SER:CB	2.42	0.49
1:A:784:PRO:HG3	1:A:856:PHE:CE2	2.47	0.49
1:A:287:SER:HB3	1:A:290:ARG:HD3	1.95	0.49
1:A:353:THR:O	1:A:353:THR:CG2	2.61	0.49
1:A:530:VAL:HB	1:A:533:THR:OG1	2.12	0.48
1:A:369:ILE:N	1:A:369:ILE:CD1	2.76	0.48
1:A:289:ILE:O	1:A:293:ILE:HG23	2.13	0.48
1:B:69:ALA:HA	1:B:297:LYS:NZ	2.27	0.48
1:B:635:ILE:O	1:B:639:ILE:HG12	2.13	0.48
1:B:620:ARG:NH2	1:B:691:LEU:HD21	2.28	0.48
1:A:949:TYR:CD1	1:A:949:TYR:N	2.81	0.48
1:A:509:GLY:O	1:A:511:LYS:HG2	2.13	0.48
1:A:111:ASN:N	1:A:111:ASN:ND2	2.60	0.48
1:A:823:SER:C	1:A:825:LYS:H	2.16	0.48
1:A:463:SER:OG	1:A:466:GLU:HG3	2.13	0.48
1:A:230:THR:HG22	1:A:232:ILE:HG22	1.94	0.48
1:A:163:ILE:CD1	1:A:223:VAL:HG22	2.43	0.48
1:B:737:ASP:OD1	1:B:737:ASP:N	2.35	0.48
1:B:287:SER:HB3	1:B:290:ARG:HD3	1.95	0.48
1:B:289:ILE:O	1:B:293:ILE:HG23	2.13	0.48
1:B:270:ALA:O	1:B:274:ILE:HG23	2.14	0.48
1:B:794:TRP:CH2	1:B:943:LEU:O	2.66	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:134:ARG:HG3	1:B:134:ARG:NH1	2.29	0.48
1:B:823:SER:HB2	1:B:826:GLU:HB2	1.94	0.48
1:A:204:LYS:C	1:A:206:ASN:H	2.15	0.48
1:B:164:ARG:HA	1:B:207:MET:SD	2.53	0.48
1:B:384:ILE:N	1:B:384:ILE:HD12	2.29	0.48
1:B:869:GLN:HA	1:B:871:THR:HG22	1.94	0.48
1:B:756:ASN:CA	1:B:759:GLN:HE21	2.18	0.48
1:B:887:ASP:HB2	1:B:890:ILE:CG2	2.40	0.48
1:B:293:ILE:O	1:B:297:LYS:HG3	2.13	0.48
1:B:33:LEU:O	1:B:37:GLY:N	2.42	0.48
1:A:859:ALA:O	1:A:861:ASP:N	2.47	0.48
1:A:264:ILE:HD13	1:A:267:ILE:HD12	1.95	0.48
1:B:539:GLY:N	1:B:540:PRO:CD	2.75	0.48
1:A:642:PHE:CG	1:A:648:VAL:HG11	2.48	0.48
1:B:737:ASP:O	1:B:738:ASP:HB2	2.14	0.48
1:A:459:VAL:O	1:A:462:LEU:N	2.43	0.48
1:B:953:LEU:C	1:B:955:MET:H	2.17	0.48
1:A:625:THR:OG1	1:A:626:GLY:N	2.46	0.48
1:A:247:THR:HB	1:A:340:GLU:OE1	2.13	0.48
1:B:280:ASN:OD1	1:B:281:ASP:N	2.47	0.48
1:A:368:ILE:HG22	1:A:595:GLY:HA3	1.96	0.48
1:A:921:SER:HA	1:A:982:GLU:OE2	2.13	0.48
1:B:843:TYR:CD2	1:B:843:TYR:C	2.87	0.48
1:B:288:TRP:HD1	1:B:289:ILE:HG13	1.78	0.48
1:B:631:THR:O	1:B:635:ILE:HG13	2.13	0.48
1:B:540:PRO:O	1:B:543:GLU:HB2	2.14	0.48
1:B:134:ARG:HG2	1:B:136:SER:H	1.79	0.48
1:B:22:THR:HG22	1:B:135:LYS:HZ3	1.79	0.48
1:B:163:ILE:CD1	1:B:223:VAL:HG22	2.44	0.48
1:A:134:ARG:HG3	1:A:134:ARG:NH1	2.29	0.48
1:A:854:TRP:O	1:A:859:ALA:HB2	2.13	0.48
1:B:762:ARG:O	1:B:762:ARG:HG2	2.14	0.48
1:A:315:ILE:O	1:A:317:THR:N	2.47	0.48
1:B:263:VAL:O	1:B:264:ILE:C	2.53	0.48
1:B:899:MET:HG2	1:B:962:LEU:CD2	2.42	0.48
1:A:369:ILE:CD1	1:A:593:PHE:HE1	2.26	0.48
1:A:280:ASN:OD1	1:A:281:ASP:N	2.47	0.48
1:A:124:PRO:O	1:A:126:MET:HG2	2.14	0.48
1:A:1:MET:HB2	1:A:16:PHE:CZ	2.48	0.48
1:A:868:HIS:C	1:A:870:LEU:H	2.17	0.48
1:A:865:VAL:HG12	1:A:866:THR:N	2.28	0.48
1:B:264:ILE:HD13	1:B:267:ILE:HD12	1.95	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:214:ILE:O	1:B:214:ILE:HG12	2.13	0.47
1:B:325:ARG:NH1	1:B:749:GLU:OE1	2.47	0.47
1:B:811:PRO:HG2	1:B:929:VAL:CG1	2.43	0.47
1:A:539:GLY:N	1:A:540:PRO:CD	2.77	0.47
1:B:950:VAL:C	1:B:952:PRO:HD2	2.34	0.47
1:B:501:ALA:C	1:B:503:SER:H	2.17	0.47
1:B:949:TYR:N	1:B:949:TYR:CD1	2.82	0.47
1:B:689:GLU:HB2	1:B:713:LYS:HZ3	1.79	0.47
1:A:256:PHE:C	1:A:258:GLU:H	2.17	0.47
1:B:530:VAL:HB	1:B:533:THR:OG1	2.13	0.47
1:B:111:ASN:N	1:B:111:ASN:ND2	2.61	0.47
1:B:745:ALA:O	1:B:746:ALA:C	2.52	0.47
1:B:953:LEU:O	1:B:956:ILE:N	2.48	0.47
1:A:84:THR:O	1:A:85:ILE:HB	2.14	0.47
1:A:322:GLY:HA3	1:A:753:ILE:HD11	1.96	0.47
1:B:794:TRP:HH2	1:B:943:LEU:O	1.97	0.47
1:B:979:GLY:O	1:B:983:ILE:HG13	2.14	0.47
1:B:798:VAL:O	1:B:909:MET:CE	2.57	0.47
1:A:311:LEU:HB3	1:A:312:PRO:CD	2.38	0.47
1:A:797:LEU:O	1:A:797:LEU:HD23	2.13	0.47
1:A:371:LYS:O	1:A:377:CYS:HB2	2.14	0.47
1:B:794:TRP:HE1	1:B:944:HIS:CE1	2.31	0.47
1:A:538:THR:HB	1:A:540:PRO:HD2	1.97	0.47
1:A:491:ARG:HE	1:A:588:GLU:CD	2.18	0.47
1:B:826:GLU:HA	1:B:827:PRO:HD2	1.66	0.47
1:B:717:GLY:C	1:B:731:SER:HB2	2.35	0.47
1:B:509:GLY:O	1:B:511:LYS:HG2	2.13	0.47
1:A:15:TYR:CD1	1:A:15:TYR:O	2.67	0.47
1:A:751:ARG:C	1:A:816:ILE:HD11	2.34	0.47
1:B:887:ASP:O	1:B:890:ILE:HG12	2.14	0.47
1:B:369:ILE:CD1	1:B:593:PHE:HE1	2.27	0.47
1:A:895:GLU:N	1:A:896:PRO:HD2	2.29	0.47
1:B:306:ALA:C	1:B:768:ASN:HD21	2.16	0.47
1:B:271:VAL:HG22	1:B:776:PHE:HE1	1.78	0.47
1:A:953:LEU:C	1:A:955:MET:H	2.18	0.47
1:B:756:ASN:HD21	1:B:810:ASN:HB2	1.80	0.47
1:B:50:TRP:C	1:B:52:LEU:H	2.18	0.47
1:A:293:ILE:O	1:A:297:LYS:HG3	2.14	0.47
1:B:748:GLU:HG3	1:B:817:MET:HG2	1.96	0.47
1:B:245:ASP:OD1	1:B:246:LYS:N	2.47	0.47
1:A:886:LEU:O	1:A:886:LEU:HD12	2.14	0.47
1:B:549:ILE:HG22	1:B:549:ILE:O	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:857:MET:HE3	1:B:858:TYR:HE1	1.79	0.47
1:A:263:VAL:CG1	1:A:267:ILE:HD11	2.31	0.47
1:B:786:ALA:O	1:B:787:LEU:HG	2.15	0.47
1:A:449:VAL:O	1:A:453:ASN:N	2.37	0.47
1:B:467:ARG:CG	1:B:467:ARG:HH11	2.25	0.47
1:B:413:LEU:HG	1:B:564:LEU:HD12	1.96	0.47
1:A:577:VAL:HG23	1:A:577:VAL:O	2.15	0.47
1:B:369:ILE:CD1	1:B:369:ILE:N	2.77	0.47
1:A:288:TRP:HD1	1:A:289:ILE:HG13	1.79	0.47
1:B:271:VAL:HG22	1:B:776:PHE:CE1	2.50	0.47
1:A:467:ARG:HD2	1:A:467:ARG:O	2.15	0.47
1:A:953:LEU:O	1:A:956:ILE:N	2.48	0.47
1:A:484:THR:CB	1:A:496:VAL:HG12	2.45	0.47
1:B:303:ALA:O	1:B:306:ALA:N	2.45	0.47
1:A:413:LEU:O	1:A:413:LEU:HD23	2.15	0.47
1:B:474:VAL:HA	1:B:477:GLN:NE2	2.30	0.47
1:A:470:ALA:O	1:A:473:SER:N	2.48	0.47
1:A:876:CYS:C	1:A:888:CYS:SG	2.92	0.47
1:B:963:ASP:H	1:B:966:GLN:HB2	1.79	0.47
1:B:129:VAL:CG1	1:B:151:VAL:HG22	2.35	0.47
1:B:253:LEU:HD21	1:B:315:ILE:HD11	1.97	0.47
1:A:763:TYR:CD2	1:A:764:LEU:HD23	2.50	0.47
1:A:496:VAL:O	1:A:512:MET:HA	2.15	0.47
1:B:109:GLU:O	1:B:113:GLU:HG2	2.15	0.47
1:B:161:ALA:CA	1:B:210:SER:HB2	2.41	0.47
1:A:54:ILE:C	1:A:54:ILE:HD12	2.35	0.47
1:B:895:GLU:N	1:B:896:PRO:CD	2.78	0.47
1:B:953:LEU:N	1:B:954:PRO:HD2	2.29	0.47
1:A:247:THR:CB	1:A:340:GLU:OE1	2.62	0.46
1:A:895:GLU:H	1:A:895:GLU:CD	2.05	0.46
1:A:963:ASP:H	1:A:966:GLN:HB2	1.79	0.46
1:B:434:TYR:OH	1:B:464:LYS:HG3	2.15	0.46
1:A:933:LEU:O	1:A:937:ILE:HG13	2.14	0.46
1:B:658:PHE:CA	1:B:661:LEU:HD12	2.35	0.46
1:B:913:LEU:O	1:B:922:LEU:HD21	2.15	0.46
1:B:1:MET:HB2	1:B:16:PHE:CZ	2.49	0.46
1:A:836:ARG:HD3	1:A:984:LEU:HD13	1.96	0.46
1:B:247:THR:H	1:B:251:GLN:CG	2.28	0.46
1:B:400:LYS:HA	1:B:401:PRO:HD3	1.81	0.46
1:A:354:GLY:O	1:A:604:ARG:HD2	2.15	0.46
1:B:836:ARG:HH11	1:B:836:ARG:HG2	1.80	0.46
1:B:840:ILE:O	1:B:843:TYR:N	2.49	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:496:VAL:O	1:B:512:MET:HA	2.15	0.46
1:B:538:THR:HB	1:B:540:PRO:HD2	1.98	0.46
1:A:949:TYR:HD1	1:A:949:TYR:N	2.13	0.46
1:A:859:ALA:O	1:A:860:GLU:C	2.53	0.46
1:B:352:LYS:HD2	1:B:635:ILE:HG21	1.97	0.46
1:A:474:VAL:HA	1:A:477:GLN:NE2	2.31	0.46
1:A:341:THR:O	1:A:344:CYS:N	2.34	0.46
1:B:614:CYS:HB3	1:B:619:ILE:HB	1.97	0.46
1:B:988:ALA:CB	1:B:992:LEU:HD12	2.44	0.46
1:B:837:TYR:HD1	1:B:837:TYR:H	1.64	0.46
1:A:867:TYR:CG	1:A:868:HIS:N	2.83	0.46
1:B:140:ILE:HG13	1:B:141:LYS:N	2.31	0.46
1:B:204:LYS:C	1:B:206:ASN:H	2.18	0.46
1:B:774:CYS:SG	1:B:848:THR:HG21	2.56	0.46
1:B:906:THR:HG21	1:B:970:VAL:HG12	1.98	0.46
1:B:974:SER:C	1:B:976:PRO:HD2	2.36	0.46
1:A:751:ARG:NH2	1:A:819:ARG:O	2.44	0.46
1:A:285:GLY:HA3	1:A:290:ARG:CZ	2.46	0.46
1:A:895:GLU:OE1	1:A:895:GLU:N	2.25	0.46
1:A:140:ILE:HG13	1:A:141:LYS:N	2.31	0.46
1:A:637:ARG:HA	1:A:642:PHE:O	2.15	0.46
1:A:238:GLN:HG3	1:A:238:GLN:O	2.16	0.46
1:A:154:ALA:O	1:A:214:ILE:HG13	2.15	0.46
1:B:907:ILE:CG2	1:B:908:GLU:N	2.78	0.46
1:B:306:ALA:HA	1:B:768:ASN:ND2	2.31	0.46
1:A:134:ARG:HG2	1:A:136:SER:H	1.80	0.46
1:B:795:VAL:CG1	1:B:904:LEU:HG	2.42	0.46
1:B:911:ASN:O	1:B:914:ASN:HB2	2.16	0.46
1:B:230:THR:HG22	1:B:232:ILE:HG22	1.96	0.46
1:A:122:TYR:C	1:A:124:PRO:HD3	2.35	0.46
1:B:14:ALA:O	1:B:16:PHE:N	2.49	0.46
1:B:442:GLU:O	1:B:445:LEU:N	2.48	0.46
1:B:413:LEU:O	1:B:413:LEU:HD23	2.16	0.46
1:B:637:ARG:HA	1:B:642:PHE:O	2.16	0.46
1:B:341:THR:O	1:B:344:CYS:N	2.35	0.46
1:B:84:THR:O	1:B:85:ILE:HB	2.16	0.46
1:B:788:ILE:CB	1:B:789:PRO:CD	2.93	0.46
1:A:25:THR:HG22	1:A:132:ALA:CB	2.43	0.46
1:B:157:ASP:HB2	1:B:214:ILE:HD11	1.98	0.46
1:B:843:TYR:CD2	1:B:844:VAL:N	2.83	0.46
1:B:953:LEU:C	1:B:955:MET:N	2.69	0.46
1:B:869:GLN:OE1	1:B:872:HIS:HD2	1.99	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:527:TYR:CD1	1:B:534:ARG:HD3	2.51	0.46
1:A:844:VAL:HG23	1:A:845:GLY:N	2.30	0.45
1:A:823:SER:O	1:A:826:GLU:HG2	2.15	0.45
1:A:459:VAL:O	1:A:460:ARG:C	2.55	0.45
1:A:540:PRO:O	1:A:543:GLU:HB2	2.16	0.45
1:B:855:TRP:CE3	1:B:856:PHE:HA	2.51	0.45
1:B:625:THR:OG1	1:B:626:GLY:N	2.49	0.45
1:A:829:ILE:HD13	1:A:837:TYR:CE2	2.51	0.45
1:A:352:LYS:HE2	1:A:627:ASP:OD1	2.16	0.45
1:A:230:THR:HG22	1:A:232:ILE:N	2.29	0.45
1:A:510:ASN:O	1:A:511:LYS:HD3	2.17	0.45
1:B:158:LYS:O	1:B:160:PRO:HD3	2.17	0.45
1:B:15:TYR:CD1	1:B:15:TYR:O	2.69	0.45
1:A:656:ARG:HH11	1:A:656:ARG:HG2	1.81	0.45
1:B:788:ILE:HG12	1:B:791:GLN:CG	2.46	0.45
1:B:798:VAL:CG1	1:B:940:SER:HB3	2.39	0.45
1:A:562:LEU:O	1:A:596:VAL:HG13	2.16	0.45
1:A:82:GLU:HB2	1:A:83:GLU:H	1.43	0.45
1:A:501:ALA:C	1:A:503:SER:H	2.19	0.45
1:A:263:VAL:O	1:A:264:ILE:C	2.55	0.45
1:B:154:ALA:O	1:B:214:ILE:CD1	2.64	0.45
1:B:769:VAL:CG1	1:B:841:GLY:HA3	2.43	0.45
1:B:770:GLY:HA3	1:B:841:GLY:O	2.15	0.45
1:A:75:LEU:HD12	1:A:76:ALA:CB	2.46	0.45
1:B:230:THR:HG22	1:B:232:ILE:N	2.30	0.45
1:A:449:VAL:CG2	1:A:450:GLU:N	2.79	0.45
1:A:108:GLN:HB3	1:A:805:THR:OG1	2.15	0.45
1:A:718:ILE:HD13	1:A:743:ILE:HG12	1.99	0.45
1:B:274:ILE:HD13	1:B:776:PHE:CZ	2.51	0.45
1:B:637:ARG:HD3	1:B:644:GLU:O	2.17	0.45
1:A:877:THR:O	1:A:878:GLU:HB3	2.16	0.45
1:B:903:VAL:HG13	1:B:973:ILE:CG2	2.46	0.45
1:B:759:GLN:C	1:B:761:ILE:N	2.68	0.45
1:A:783:LEU:HD22	1:A:784:PRO:CD	2.39	0.45
1:A:662:PRO:O	1:A:665:GLU:N	2.42	0.45
1:A:413:LEU:HG	1:A:564:LEU:CD1	2.47	0.45
1:B:949:TYR:N	1:B:949:TYR:HD1	2.13	0.45
1:A:974:SER:C	1:A:976:PRO:HD2	2.37	0.45
1:A:895:GLU:O	1:A:899:MET:N	2.49	0.45
1:B:855:TRP:O	1:B:859:ALA:HB2	2.16	0.45
1:B:110:ARG:O	1:B:114:ASN:N	2.49	0.45
1:B:869:GLN:C	1:B:871:THR:N	2.67	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:766:SER:O	1:A:769:VAL:HG12	2.17	0.45
1:B:326:MET:HE1	1:B:333:VAL:HG21	1.97	0.45
1:B:352:LYS:HE2	1:B:627:ASP:OD1	2.16	0.45
1:B:467:ARG:HA	1:B:467:ARG:HD2	1.64	0.45
1:B:85:ILE:HG22	1:B:85:ILE:O	2.17	0.45
1:A:303:ALA:O	1:A:304:VAL:C	2.55	0.45
1:A:157:ASP:HB2	1:A:214:ILE:HD11	1.99	0.45
1:B:633:ILE:O	1:B:636:CYS:HB2	2.17	0.45
1:B:50:TRP:CE3	1:B:257:GLY:CA	3.00	0.45
1:B:75:LEU:HD12	1:B:76:ALA:CB	2.47	0.45
1:B:449:VAL:O	1:B:453:ASN:N	2.36	0.45
1:A:22:THR:HG22	1:A:135:LYS:HZ1	1.81	0.45
1:B:66:LEU:HD12	1:B:94:ILE:CD1	2.47	0.45
1:A:66:LEU:HD12	1:A:94:ILE:CD1	2.47	0.45
1:A:100:ALA:CA	1:A:103:ILE:HG22	2.43	0.45
1:B:650:ASP:N	1:B:650:ASP:OD1	2.50	0.45
1:A:527:TYR:O	1:A:592:THR:HA	2.17	0.45
1:A:549:ILE:O	1:A:549:ILE:HG22	2.17	0.45
1:B:799:THR:HG21	1:B:908:GLU:HB2	1.99	0.45
1:B:980:LEU:HA	1:B:983:ILE:CD1	2.37	0.45
1:A:140:ILE:CD1	1:A:141:LYS:H	2.30	0.45
1:B:131:ARG:NH1	1:B:131:ARG:HG3	2.30	0.45
1:A:110:ARG:O	1:A:114:ASN:N	2.49	0.45
1:B:231:GLU:HA	1:B:231:GLU:OE1	2.16	0.45
1:A:109:GLU:O	1:A:113:GLU:HG2	2.16	0.45
1:B:794:TRP:NE1	1:B:944:HIS:ND1	2.63	0.44
1:A:899:MET:SD	1:A:962:LEU:HD22	2.57	0.44
1:B:662:PRO:O	1:B:665:GLU:N	2.42	0.44
1:B:303:ALA:O	1:B:304:VAL:C	2.56	0.44
1:B:491:ARG:HE	1:B:588:GLU:CD	2.21	0.44
1:B:204:LYS:O	1:B:206:ASN:N	2.47	0.44
1:B:773:VAL:HG21	1:B:842:GLY:HA2	1.99	0.44
1:A:927:PRO:O	1:A:934:LEU:HD21	2.17	0.44
1:B:247:THR:H	1:B:251:GLN:HG2	1.81	0.44
1:A:884:GLU:C	1:A:886:LEU:H	2.20	0.44
1:A:85:ILE:O	1:A:85:ILE:HG22	2.17	0.44
1:A:717:GLY:O	1:A:731:SER:HB2	2.18	0.44
1:B:977:VAL:HG13	1:B:978:ILE:N	2.32	0.44
1:B:611:ILE:HD13	1:B:641:ILE:HG13	2.00	0.44
1:A:637:ARG:HD3	1:A:644:GLU:O	2.17	0.44
1:A:35:LYS:HE3	1:A:36:TYR:CZ	2.53	0.44
1:B:832:TRP:CH2	1:B:992:LEU:HD11	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:767:SER:CB	1:B:911:ASN:ND2	2.64	0.44
1:A:39:ASN:HB3	1:A:142:ALA:O	2.17	0.44
1:A:271:VAL:C	1:A:273:LEU:N	2.70	0.44
1:A:953:LEU:C	1:A:955:MET:N	2.70	0.44
1:B:249:LEU:O	1:B:250:GLN:C	2.56	0.44
1:A:402:ILE:HD12	1:A:402:ILE:O	2.16	0.44
1:B:771:GLU:O	1:B:774:CYS:HB3	2.17	0.44
1:B:315:ILE:CG1	1:B:757:MET:HG3	2.48	0.44
1:A:977:VAL:HG13	1:A:978:ILE:N	2.33	0.44
1:A:631:THR:O	1:A:635:ILE:HG13	2.17	0.44
1:A:899:MET:O	1:A:903:VAL:HG23	2.17	0.44
1:A:778:THR:HG22	1:A:849:VAL:CG1	2.47	0.44
1:B:459:VAL:O	1:B:460:ARG:C	2.56	0.44
1:B:893:ALA:O	1:B:896:PRO:CG	2.66	0.44
1:A:390:ALA:HA	1:A:391:PRO:HD3	1.89	0.44
1:B:765:ILE:HG21	1:B:837:TYR:CD2	2.53	0.44
1:A:158:LYS:O	1:A:160:PRO:HD3	2.18	0.44
1:A:810:ASN:OD1	1:A:916:LEU:HD23	2.18	0.44
1:A:823:SER:C	1:A:825:LYS:N	2.70	0.44
1:A:527:TYR:CD1	1:A:534:ARG:HD3	2.52	0.44
1:A:214:ILE:HG12	1:A:214:ILE:O	2.16	0.44
1:B:97:ILE:HG21	1:B:793:LEU:HB3	1.99	0.44
1:A:445:LEU:O	1:A:448:LEU:HB3	2.18	0.44
1:A:737:ASP:O	1:A:738:ASP:CB	2.65	0.44
1:B:39:ASN:HB3	1:B:142:ALA:O	2.17	0.44
1:A:548:VAL:C	1:A:550:LYS:N	2.71	0.44
1:B:755:ASN:HA	1:B:758:LYS:HB2	2.00	0.44
1:B:765:ILE:HG22	1:B:766:SER:N	2.33	0.44
1:A:449:VAL:HG23	1:A:450:GLU:N	2.33	0.44
1:B:763:TYR:CD1	1:B:912:ALA:HA	2.52	0.44
1:B:617:ALA:HB1	1:B:751:ARG:NH1	2.26	0.44
1:A:836:ARG:NH1	1:A:836:ARG:CG	2.78	0.44
1:B:128:LYS:HD2	1:B:137:VAL:HG11	2.00	0.44
1:B:392:GLU:O	1:B:451:LYS:HE2	2.18	0.44
1:B:778:THR:HG22	1:B:849:VAL:HG13	1.99	0.44
1:A:338:SER:C	1:A:340:GLU:N	2.71	0.44
1:B:264:ILE:HA	1:B:267:ILE:CD1	2.47	0.44
1:A:764:LEU:O	1:A:765:ILE:C	2.55	0.44
1:B:48:SER:HB2	1:B:254:ASP:OD1	2.17	0.44
1:A:962:LEU:HD23	1:A:966:GLN:HB3	2.00	0.44
1:B:881:PRO:O	1:B:882:HIS:HB2	2.18	0.44
1:A:869:GLN:NE2	1:A:872:HIS:CD2	2.86	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:847:ALA:O	1:B:851:ALA:HB2	2.18	0.43
1:A:906:THR:CG2	1:A:974:SER:HB2	2.48	0.43
1:A:512:MET:HB2	1:A:567:ARG:HB3	1.99	0.43
1:B:285:GLY:HA3	1:B:290:ARG:CZ	2.48	0.43
1:B:446:THR:HG23	1:B:472:ASN:ND2	2.33	0.43
1:B:25:THR:HG22	1:B:132:ALA:CB	2.44	0.43
1:B:539:GLY:H	1:B:540:PRO:HD2	1.82	0.43
1:A:110:ARG:NH1	1:A:110:ARG:HG3	2.33	0.43
1:B:836:ARG:NH1	1:B:836:ARG:HG2	2.33	0.43
1:A:97:ILE:O	1:A:100:ALA:N	2.51	0.43
1:B:893:ALA:O	1:B:896:PRO:CD	2.63	0.43
1:B:706:ASN:HA	1:B:706:ASN:HD22	1.55	0.43
1:A:166:LEU:HG	1:A:221:GLY:HA2	1.99	0.43
1:A:841:GLY:HA2	1:A:844:VAL:CG2	2.49	0.43
1:A:832:TRP:CH2	1:A:992:LEU:HD11	2.53	0.43
1:A:650:ASP:OD1	1:A:650:ASP:N	2.51	0.43
1:A:388:THR:OG1	1:A:389:TYR:N	2.51	0.43
1:A:617:ALA:HB2	1:A:817:MET:O	2.18	0.43
1:A:499:SER:O	1:A:500:PRO:C	2.57	0.43
1:B:542:LYS:O	1:B:546:LEU:HD12	2.19	0.43
1:A:131:ARG:NH1	1:A:131:ARG:HG3	2.32	0.43
1:A:679:VAL:HG13	1:A:683:HIS:ND1	2.33	0.43
1:B:565:ALA:HB2	1:B:593:PHE:HA	2.00	0.43
1:B:66:LEU:C	1:B:66:LEU:HD23	2.38	0.43
1:B:355:THR:HG22	1:B:740:PHE:HB2	2.01	0.43
1:A:239:MET:HG3	1:A:240:ALA:N	2.33	0.43
1:A:542:LYS:O	1:A:546:LEU:HD12	2.18	0.43
1:B:196:ASP:HA	1:B:197:PRO:HD2	1.92	0.43
1:A:311:LEU:CA	1:A:760:PHE:HE1	2.31	0.43
1:B:378:SER:O	1:B:379:LEU:HD23	2.19	0.43
1:A:894:PRO:HD2	1:A:895:GLU:OE1	2.19	0.43
1:A:893:ALA:HA	1:A:894:PRO:HD3	1.80	0.43
1:B:449:VAL:CG2	1:B:450:GLU:N	2.81	0.43
1:B:164:ARG:CZ	1:B:206:ASN:HD22	2.32	0.43
1:A:930:ASN:C	1:A:930:ASN:OD1	2.57	0.43
1:A:253:LEU:HD21	1:A:315:ILE:HD11	2.01	0.43
1:A:768:ASN:O	1:A:769:VAL:C	2.54	0.43
1:B:358:THR:HG23	1:B:602:PRO:O	2.18	0.43
1:A:899:MET:HG2	1:A:962:LEU:CD2	2.46	0.43
1:A:780:ALA:C	1:A:782:GLY:N	2.70	0.43
1:B:32:HIS:O	1:B:36:TYR:HD2	2.01	0.43
1:B:832:TRP:CZ3	1:B:992:LEU:HD11	2.54	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:317:THR:O	1:B:318:CYS:C	2.57	0.43
1:A:932:TRP:HD1	1:A:932:TRP:H	1.67	0.43
1:B:942:SER:C	1:B:944:HIS:N	2.72	0.43
1:B:573:ARG:O	1:B:573:ARG:HD3	2.19	0.43
1:B:100:ALA:CA	1:B:103:ILE:HG22	2.45	0.43
1:A:830:SER:O	1:A:833:LEU:N	2.51	0.43
1:B:945:PHE:HE1	1:B:967:TRP:CZ2	2.36	0.43
1:A:264:ILE:HA	1:A:267:ILE:CD1	2.47	0.43
1:A:467:ARG:NH1	1:A:467:ARG:CG	2.82	0.43
1:B:248:PRO:O	1:B:252:LYS:HB2	2.19	0.43
1:A:181:THR:C	1:A:183:GLU:H	2.22	0.43
1:B:798:VAL:O	1:B:798:VAL:HG12	2.19	0.42
1:A:913:LEU:O	1:A:922:LEU:HD21	2.19	0.42
1:A:378:SER:O	1:A:379:LEU:HD23	2.19	0.42
1:B:97:ILE:O	1:B:100:ALA:N	2.52	0.42
1:B:83:GLU:O	1:B:83:GLU:HG2	2.19	0.42
1:B:118:ALA:C	1:B:120:LYS:N	2.72	0.42
1:A:911:ASN:O	1:A:914:ASN:HB2	2.19	0.42
1:B:58:GLU:OE1	1:B:309:GLU:OE2	2.37	0.42
1:B:125:GLU:HA	1:B:125:GLU:OE1	2.18	0.42
1:B:688:VAL:HG23	1:B:700:MET:HE1	2.01	0.42
1:B:832:TRP:CD1	1:B:833:LEU:N	2.87	0.42
1:A:654:THR:HG23	1:A:657:GLU:OE1	2.18	0.42
1:A:346:SER:C	1:A:347:VAL:HG23	2.40	0.42
1:B:228:VAL:CG2	1:B:228:VAL:O	2.67	0.42
1:B:548:VAL:C	1:B:550:LYS:N	2.71	0.42
1:B:166:LEU:HG	1:B:221:GLY:HA2	2.01	0.42
1:B:762:ARG:NE	1:B:836:ARG:NH1	2.67	0.42
1:A:154:ALA:O	1:A:214:ILE:CD1	2.67	0.42
1:A:975:LEU:HA	1:A:975:LEU:HD12	1.90	0.42
1:B:679:VAL:HG13	1:B:683:HIS:ND1	2.34	0.42
1:B:691:LEU:HD23	1:B:691:LEU:HA	1.82	0.42
1:A:268:CYS:C	1:A:270:ALA:H	2.22	0.42
1:B:271:VAL:CG2	1:B:776:PHE:HE1	2.32	0.42
1:A:14:ALA:O	1:A:16:PHE:N	2.52	0.42
1:A:829:ILE:HD13	1:A:837:TYR:HE2	1.84	0.42
1:A:974:SER:O	1:A:977:VAL:HG12	2.18	0.42
1:A:887:ASP:O	1:A:890:ILE:HG22	2.20	0.42
1:A:434:TYR:OH	1:A:464:LYS:HG3	2.19	0.42
1:B:59:ASP:O	1:B:63:ARG:HG3	2.19	0.42
1:A:249:LEU:HB2	1:A:340:GLU:CD	2.40	0.42
1:B:755:ASN:O	1:B:756:ASN:C	2.56	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:679:VAL:HG13	1:A:683:HIS:CG	2.54	0.42
1:A:825:LYS:CG	1:A:826:GLU:N	2.81	0.42
1:B:329:LYS:O	1:B:330:ASN:HB2	2.19	0.42
1:B:116:ILE:O	1:B:116:ILE:CG2	2.67	0.42
1:B:656:ARG:HG2	1:B:656:ARG:NH1	2.34	0.42
1:B:123:GLU:HA	1:B:124:PRO:HD2	1.76	0.42
1:B:402:ILE:HD12	1:B:402:ILE:C	2.40	0.42
1:A:865:VAL:O	1:A:866:THR:HG23	2.20	0.42
1:A:945:PHE:HE1	1:A:967:TRP:CZ2	2.37	0.42
1:A:317:THR:O	1:A:318:CYS:C	2.58	0.42
1:B:346:SER:C	1:B:347:VAL:HG23	2.40	0.42
1:B:449:VAL:HG23	1:B:450:GLU:N	2.35	0.42
1:A:83:GLU:O	1:A:83:GLU:HG2	2.19	0.42
1:B:271:VAL:C	1:B:273:LEU:N	2.72	0.42
1:A:867:TYR:C	1:A:869:GLN:N	2.72	0.42
1:A:353:THR:O	1:A:353:THR:HG22	2.20	0.42
1:A:753:ILE:HG22	1:A:753:ILE:O	2.20	0.42
1:A:303:ALA:O	1:A:306:ALA:N	2.50	0.42
1:B:499:SER:O	1:B:500:PRO:C	2.57	0.42
1:B:181:THR:C	1:B:183:GLU:H	2.23	0.42
1:A:711:LEU:HD23	1:A:711:LEU:HA	1.84	0.42
1:B:899:MET:SD	1:B:962:LEU:HD22	2.60	0.42
1:B:974:SER:O	1:B:977:VAL:HG12	2.19	0.42
1:A:762:ARG:CG	1:A:837:TYR:CE1	3.01	0.42
1:A:851:ALA:HB2	1:A:903:VAL:HG21	2.01	0.42
1:B:306:ALA:CA	1:B:768:ASN:HD21	2.33	0.42
1:B:35:LYS:HE3	1:B:36:TYR:CZ	2.55	0.42
1:A:765:ILE:HG21	1:A:837:TYR:HD2	1.85	0.42
1:B:512:MET:HB2	1:B:567:ARG:HB3	2.02	0.42
1:B:336:LEU:N	1:B:337:PRO:CD	2.81	0.42
1:A:335:SER:O	1:A:336:LEU:C	2.58	0.42
1:A:495:SER:CB	1:A:514:VAL:HG22	2.50	0.42
1:A:798:VAL:CG1	1:A:940:SER:HB3	2.48	0.42
1:B:964:LEU:O	1:B:968:LEU:HB2	2.19	0.42
1:B:833:LEU:O	1:B:836:ARG:HB3	2.20	0.42
1:A:54:ILE:HG22	1:A:261:SER:HB3	2.01	0.42
1:A:946:LEU:O	1:A:946:LEU:HD23	2.19	0.42
1:B:574:GLU:C	1:B:576:MET:H	2.22	0.42
1:B:110:ARG:HG3	1:B:110:ARG:NH1	2.35	0.42
1:B:510:ASN:O	1:B:511:LYS:HD3	2.19	0.42
1:B:231:GLU:O	1:B:235:ILE:HG12	2.20	0.42
1:B:276:ILE:HG12	1:B:279:PHE:HE2	1.85	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:347:VAL:HG21	1:A:696:GLU:HG2	1.98	0.42
1:A:2:GLU:CG	1:A:3:ALA:N	2.83	0.42
1:B:495:SER:HB3	1:B:514:VAL:HG22	2.01	0.42
1:B:388:THR:OG1	1:B:389:TYR:N	2.53	0.42
1:A:174:ARG:HA	1:A:187:VAL:O	2.20	0.42
1:A:667:ARG:HA	1:A:690:TYR:CD1	2.55	0.42
1:B:932:TRP:H	1:B:932:TRP:HD1	1.68	0.42
1:A:267:ILE:HG21	1:A:772:VAL:CG1	2.46	0.41
1:B:267:ILE:HG13	1:B:267:ILE:H	1.73	0.41
1:A:24:LEU:HD13	1:A:149:ASP:CA	2.37	0.41
1:B:94:ILE:HG22	1:B:790:VAL:HG12	2.01	0.41
1:A:66:LEU:HD23	1:A:66:LEU:C	2.40	0.41
1:A:126:MET:HA	1:A:140:ILE:O	2.19	0.41
1:B:100:ALA:HB1	1:B:797:LEU:HD21	2.02	0.41
1:B:642:PHE:CG	1:B:648:VAL:HG11	2.55	0.41
1:B:688:VAL:HG23	1:B:700:MET:CE	2.50	0.41
1:A:27:ASP:O	1:A:31:ARG:HB2	2.20	0.41
1:A:795:VAL:CG2	1:A:901:LEU:CD1	2.98	0.41
1:B:573:ARG:NH1	1:B:573:ARG:CG	2.83	0.41
1:A:276:ILE:HG12	1:A:279:PHE:HE2	1.85	0.41
1:B:811:PRO:HA	1:B:812:PRO:HD3	1.82	0.41
1:B:927:PRO:O	1:B:934:LEU:HD21	2.19	0.41
1:A:573:ARG:HD3	1:A:573:ARG:O	2.20	0.41
1:A:336:LEU:N	1:A:337:PRO:CD	2.81	0.41
1:A:335:SER:C	1:A:337:PRO:HD2	2.40	0.41
1:B:859:ALA:HB1	1:B:862:GLY:HA3	2.01	0.41
1:A:392:GLU:O	1:A:451:LYS:HE2	2.20	0.41
1:A:59:ASP:O	1:A:63:ARG:HG3	2.20	0.41
1:B:352:LYS:CD	1:B:635:ILE:HG21	2.51	0.41
1:B:89:VAL:HA	1:B:92:PHE:HD2	1.85	0.41
1:A:903:VAL:HG13	1:A:973:ILE:CG2	2.50	0.41
1:B:268:CYS:C	1:B:270:ALA:H	2.23	0.41
1:B:855:TRP:CE3	1:B:856:PHE:N	2.89	0.41
1:A:231:GLU:O	1:A:235:ILE:HG12	2.20	0.41
1:B:754:TYR:CE2	1:B:758:LYS:HG3	2.55	0.41
1:B:311:LEU:HA	1:B:760:PHE:CE1	2.55	0.41
1:B:760:PHE:O	1:B:760:PHE:CG	2.73	0.41
1:B:926:PRO:HB2	1:B:928:TRP:CE2	2.55	0.41
1:B:358:THR:HG22	1:B:604:ARG:HA	2.01	0.41
1:A:352:LYS:CD	1:A:635:ILE:HG21	2.50	0.41
1:B:467:ARG:O	1:B:467:ARG:HD2	2.20	0.41
1:A:218:LYS:O	1:A:219:ALA:HB2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:58:GLU:OE1	1:A:309:GLU:OE2	2.39	0.41
1:A:262:LYS:O	1:A:263:VAL:C	2.58	0.41
1:B:2:GLU:CG	1:B:3:ALA:N	2.83	0.41
1:A:866:THR:HG22	1:A:886:LEU:HD22	2.02	0.41
1:B:735:LEU:HD13	1:B:739:ASN:O	2.19	0.41
1:B:939:LEU:O	1:B:939:LEU:HG	2.20	0.41
1:B:832:TRP:CZ2	1:B:988:ALA:HB2	2.55	0.41
1:A:253:LEU:O	1:A:256:PHE:HB3	2.21	0.41
1:A:755:ASN:HD21	1:A:819:ARG:HH12	1.68	0.41
1:B:563:ALA:HA	1:B:596:VAL:HG22	2.02	0.41
1:A:72:SER:HA	1:A:293:ILE:HD12	2.02	0.41
1:A:161:ALA:CA	1:A:210:SER:HB2	2.46	0.41
1:A:964:LEU:O	1:A:968:LEU:HB2	2.20	0.41
1:A:501:ALA:O	1:A:502:LYS:HB2	2.21	0.41
1:B:759:GLN:C	1:B:761:ILE:H	2.24	0.41
1:A:840:ILE:O	1:A:843:TYR:N	2.50	0.41
1:B:782:GLY:O	1:B:783:LEU:O	2.38	0.41
1:A:125:GLU:OE1	1:A:158:LYS:HG2	2.20	0.41
1:B:342:LEU:HG	1:B:747:VAL:HA	2.02	0.41
1:A:862:GLY:HA2	1:A:863:PRO:HD3	1.80	0.41
1:B:772:VAL:O	1:B:773:VAL:C	2.58	0.41
1:B:795:VAL:HG22	1:B:901:LEU:HD13	2.03	0.41
1:B:323:THR:HA	1:B:326:MET:HE3	2.03	0.41
1:B:352:LYS:CD	1:B:635:ILE:HD13	2.51	0.41
1:A:81:GLY:CA	1:A:82:GLU:OE1	2.69	0.41
1:A:1:MET:HE1	1:A:7:LYS:CD	2.51	0.41
1:A:654:THR:O	1:A:655:GLY:C	2.58	0.41
1:B:791:GLN:O	1:B:794:TRP:HB3	2.21	0.41
1:A:906:THR:HG22	1:A:974:SER:OG	2.20	0.41
1:B:335:SER:C	1:B:337:PRO:HD2	2.40	0.41
1:B:357:THR:C	1:B:604:ARG:HG3	2.41	0.41
1:A:140:ILE:CG1	1:A:141:LYS:N	2.84	0.41
1:A:611:ILE:HD13	1:A:641:ILE:HG13	2.02	0.41
1:B:737:ASP:O	1:B:738:ASP:CB	2.68	0.41
1:A:89:VAL:HA	1:A:92:PHE:HD2	1.86	0.41
1:B:527:TYR:O	1:B:592:THR:HA	2.21	0.41
1:A:717:GLY:C	1:A:731:SER:HB2	2.42	0.41
1:A:366:MET:CB	1:A:597:VAL:HG12	2.51	0.41
1:A:768:ASN:C	1:A:770:GLY:N	2.72	0.41
1:A:979:GLY:O	1:A:983:ILE:HG13	2.21	0.41
1:A:565:ALA:HB2	1:A:593:PHE:HA	2.02	0.41
1:A:620:ARG:NH2	1:A:670:CYS:O	2.53	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:359:ASN:HA	1:B:601:ASP:CG	2.41	0.41
1:B:678:ARG:NH1	1:B:678:ARG:CG	2.83	0.41
1:A:689:GLU:HB2	1:A:713:LYS:NZ	2.34	0.41
1:B:246:LYS:HA	1:B:251:GLN:CG	2.51	0.41
1:B:527:TYR:HA	1:B:536:PRO:HA	2.03	0.41
1:B:930:ASN:C	1:B:930:ASN:OD1	2.60	0.41
1:A:658:PHE:CA	1:A:661:LEU:HD12	2.35	0.40
1:A:764:LEU:C	1:A:768:ASN:HD22	2.25	0.40
1:B:108:GLN:OE1	1:B:310:GLY:HA2	2.21	0.40
1:B:326:MET:HB3	1:B:331:ALA:HB3	2.02	0.40
1:A:125:GLU:HB3	1:A:142:ALA:CB	2.43	0.40
1:A:988:ALA:HB2	1:A:992:LEU:HD12	2.03	0.40
1:B:671:ARG:HB3	1:B:694:TYR:CD2	2.55	0.40
1:A:520:GLY:O	1:A:524:ARG:HG3	2.21	0.40
1:B:421:ASN:OD1	1:B:422:ASP:N	2.55	0.40
1:A:316:THR:HG22	1:A:316:THR:O	2.20	0.40
1:B:770:GLY:HA2	1:B:841:GLY:O	2.21	0.40
1:B:679:VAL:HG13	1:B:683:HIS:CG	2.56	0.40
1:B:604:ARG:HB3	1:B:604:ARG:HE	1.72	0.40
1:A:635:ILE:HG13	1:A:635:ILE:H	1.60	0.40
1:A:108:GLN:OE1	1:A:310:GLY:HA2	2.21	0.40
1:B:895:GLU:CD	1:B:895:GLU:N	2.74	0.40
1:B:14:ALA:C	1:B:16:PHE:N	2.75	0.40
1:B:946:LEU:O	1:B:946:LEU:HD23	2.20	0.40
1:B:140:ILE:CG1	1:B:141:LYS:N	2.85	0.40
1:A:32:HIS:O	1:A:36:TYR:HD2	2.03	0.40
1:A:550:LYS:O	1:A:554:THR:HG23	2.21	0.40
1:B:667:ARG:HA	1:B:690:TYR:CD1	2.57	0.40
1:B:338:SER:C	1:B:340:GLU:N	2.74	0.40
1:B:906:THR:CG2	1:B:974:SER:HB2	2.50	0.40
1:A:807:LEU:HD22	1:A:810:ASN:HD21	1.85	0.40
1:A:823:SER:O	1:A:825:LYS:N	2.55	0.40
1:B:662:PRO:CD	1:B:665:GLU:HB2	2.47	0.40
1:B:541:VAL:O	1:B:543:GLU:N	2.55	0.40
1:A:54:ILE:HA	1:A:57:PHE:CB	2.52	0.40
1:A:541:VAL:O	1:A:544:LYS:N	2.55	0.40
1:B:855:TRP:CE2	1:B:895:GLU:HB2	2.56	0.40
1:A:22:THR:HG22	1:A:135:LYS:HZ2	1.86	0.40
1:A:301:ALA:O	1:A:302:LEU:C	2.59	0.40
1:B:519:GLU:O	1:B:520:GLY:C	2.59	0.40
1:A:421:ASN:OD1	1:A:422:ASP:N	2.54	0.40
1:B:962:LEU:HD23	1:B:966:GLN:HB3	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:24:LEU:O	1:A:132:ALA:N	2.53	0.40
1:A:751:ARG:HB2	1:A:816:ILE:HD11	2.02	0.40
1:A:841:GLY:HA2	1:A:844:VAL:HG22	2.03	0.40
1:A:843:TYR:CD2	1:A:844:VAL:N	2.90	0.40
1:A:319:LEU:HA	1:A:319:LEU:HD12	1.79	0.40
1:A:969:MET:O	1:A:970:VAL:C	2.60	0.40
1:A:541:VAL:C	1:A:543:GLU:N	2.75	0.40
1:A:942:SER:C	1:A:944:HIS:N	2.74	0.40
1:A:588:GLU:O	1:A:591:LEU:HD11	2.21	0.40
1:B:781:LEU:HA	1:B:781:LEU:HD23	1.82	0.40
1:B:44:GLU:CD	1:B:44:GLU:O	2.59	0.40
1:B:371:LYS:O	1:B:377:CYS:HB2	2.22	0.40
1:A:600:LEU:HD23	1:A:600:LEU:C	2.40	0.40
1:B:792:LEU:O	1:B:795:VAL:N	2.55	0.40
1:B:106:VAL:HA	1:B:109:GLU:HB2	2.03	0.40
1:A:926:PRO:HB2	1:A:928:TRP:CE2	2.56	0.40
1:B:459:VAL:O	1:B:462:LEU:N	2.48	0.40
1:A:81:GLY:HA2	1:A:82:GLU:OE1	2.22	0.40
1:B:654:THR:O	1:B:655:GLY:C	2.59	0.40
1:B:877:THR:HA	1:B:888:CYS:SG	2.61	0.40
1:B:583:ARG:HG3	1:B:583:ARG:HH11	1.86	0.40

There are no symmetry-related clashes.

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	992/994 (100%)	785 (79%)	152 (15%)	55 (6%)	3	16
1	B	992/994 (100%)	774 (78%)	160 (16%)	58 (6%)	3	15
All	All	1984/1988 (100%)	1559 (79%)	312 (16%)	113 (6%)	3	16

All (113) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	ILE
1	A	205	LYS
1	A	283	VAL
1	A	518	PRO
1	A	519	GLU
1	A	801	GLY
1	A	860	GLU
1	A	868	HIS
1	A	880	HIS
1	A	881	PRO
1	B	85	ILE
1	B	205	LYS
1	B	241	ALA
1	B	283	VAL
1	B	518	PRO
1	B	519	GLU
1	B	789	PRO
1	B	813	ASP
1	B	827	PRO
1	B	865	VAL
1	A	82	GLU
1	A	127	GLY
1	A	265	SER
1	A	316	THR
1	A	342	LEU
1	A	531	GLY
1	A	555	GLY
1	A	627	ASP
1	A	781	LEU
1	A	782	GLY
1	A	807	LEU
1	A	987	ILE
1	B	15	TYR
1	B	82	GLU
1	B	243	GLU
1	B	265	SER
1	B	316	THR
1	B	531	GLY
1	B	555	GLY
1	B	604	ARG
1	B	627	ASP
1	B	673	ALA
1	B	766	SER

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Mol	Chain	Res	Type
1	B	797	LEU
1	B	866	THR
1	B	904	LEU
1	B	987	ILE
1	A	15	TYR
1	A	24	LEU
1	A	72	SER
1	A	133	ASP
1	A	307	ILE
1	A	534	ARG
1	A	575	GLU
1	A	604	ARG
1	A	673	ALA
1	A	703	ASP
1	A	904	LEU
1	B	24	LEU
1	B	72	SER
1	B	133	ASP
1	B	342	LEU
1	B	534	ARG
1	B	575	GLU
1	B	703	ASP
1	B	796	ASN
1	A	303	ALA
1	A	372	VAL
1	A	460	ARG
1	A	533	THR
1	A	743	ILE
1	A	796	ASN
1	B	303	ALA
1	B	372	VAL
1	B	533	THR
1	B	743	ILE
1	B	783	LEU
1	A	42	PRO
1	A	282	PRO
1	A	789	PRO
1	A	802	LEU
1	A	961	ALA
1	B	48	SER
1	B	123	GLU
1	B	282	PRO

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Mol	Chain	Res	Type
1	B	953	LEU
1	A	272	TRP
1	A	281	ASP
1	A	289	ILE
1	A	951	ASP
1	A	953	LEU
1	A	954	PRO
1	B	53	VAL
1	B	281	ASP
1	B	289	ILE
1	B	307	ILE
1	B	460	ARG
1	B	747	VAL
1	B	951	ASP
1	B	954	PRO
1	B	961	ALA
1	A	849	VAL
1	B	304	VAL
1	A	765	ILE
1	B	391	PRO
1	B	896	PRO
1	A	277	GLY
1	A	308	PRO
1	A	530	VAL
1	B	277	GLY
1	B	530	VAL
1	B	905	VAL
1	B	308	PRO

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	840/840 (100%)	782 (93%)	58 (7%)	22	62
1	B	840/840 (100%)	786 (94%)	54 (6%)	25	66
All	All	1680/1680 (100%)	1568 (93%)	112 (7%)	23	64

All (112) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	GLU
1	A	60	LEU
1	A	64	ILE
1	A	67	LEU
1	A	82	GLU
1	A	111	ASN
1	A	122	TYR
1	A	133	ASP
1	A	155	VAL
1	A	187	VAL
1	A	214	ILE
1	A	225	THR
1	A	249	LEU
1	A	353	THR
1	A	357	THR
1	A	358	THR
1	A	372	VAL
1	A	441	THR
1	A	445	LEU
1	A	457	THR
1	A	464	LYS
1	A	467	ARG
1	A	472	ASN
1	A	473	SER
1	A	484	THR
1	A	486	GLU
1	A	534	ARG
1	A	562	LEU
1	A	566	THR
1	A	573	ARG
1	A	600	LEU
1	A	613	LEU
1	A	627	ASP
1	A	647	GLU
1	A	696	GLU
1	A	698	THR
1	A	703	ASP
1	A	706	ASN
1	A	724	THR
1	A	737	ASP
1	A	756	ASN
1	A	774	CYS

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Mol	Chain	Res	Type
1	A	776	PHE
1	A	789	PRO
1	A	813	ASP
1	A	818	ASP
1	A	824	PRO
1	A	832	TRP
1	A	836	ARG
1	A	854	TRP
1	A	895	GLU
1	A	904	LEU
1	A	906	THR
1	A	941	MET
1	A	949	TYR
1	A	965	THR
1	A	971	LEU
1	A	973	ILE
1	B	60	LEU
1	B	64	ILE
1	B	67	LEU
1	B	82	GLU
1	B	111	ASN
1	B	133	ASP
1	B	155	VAL
1	B	187	VAL
1	B	214	ILE
1	B	225	THR
1	B	276	ILE
1	B	353	THR
1	B	357	THR
1	B	358	THR
1	B	372	VAL
1	B	441	THR
1	B	445	LEU
1	B	457	THR
1	B	464	LYS
1	B	467	ARG
1	B	472	ASN
1	B	473	SER
1	B	484	THR
1	B	486	GLU
1	B	534	ARG
1	B	566	THR

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Mol	Chain	Res	Type
1	B	573	ARG
1	B	600	LEU
1	B	613	LEU
1	B	627	ASP
1	B	645	ASN
1	B	647	GLU
1	B	696	GLU
1	B	698	THR
1	B	703	ASP
1	B	706	ASN
1	B	724	THR
1	B	737	ASP
1	B	761	ILE
1	B	762	ARG
1	B	776	PHE
1	B	777	LEU
1	B	789	PRO
1	B	813	ASP
1	B	814	LEU
1	B	832	TRP
1	B	883	PHE
1	B	904	LEU
1	B	906	THR
1	B	941	MET
1	B	949	TYR
1	B	965	THR
1	B	971	LEU
1	B	973	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	111	ASN
1	A	114	ASN
1	A	138	GLN
1	A	284	HIS
1	A	359	ASN
1	A	360	GLN
1	A	472	ASN
1	A	477	GLN
1	A	510	ASN

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Mol	Chain	Res	Type
1	A	706	ASN
1	A	759	GLN
1	A	768	ASN
1	A	869	GLN
1	A	872	HIS
1	A	919	ASN
1	B	101	ASN
1	B	111	ASN
1	B	114	ASN
1	B	138	GLN
1	B	244	GLN
1	B	284	HIS
1	B	360	GLN
1	B	472	ASN
1	B	477	GLN
1	B	510	ASN
1	B	706	ASN
1	B	756	ASN
1	B	768	ASN
1	B	791	GLN
1	B	872	HIS
1	B	911	ASN
1	B	914	ASN
1	B	919	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 11 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	994/994 (100%)	-0.24	5 (0%)	88 36	24, 73, 138, 174	0
1	B	994/994 (100%)	-0.20	4 (0%)	90 41	24, 77, 138, 175	0
All	All	1988/1988 (100%)	-0.22	9 (0%)	88 36	24, 75, 138, 175	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	80	GLU	4.1
1	A	858	TYR	3.4
1	A	49	LEU	3.2
1	B	80	GLU	3.0
1	B	85	ILE	2.8
1	B	83	GLU	2.6
1	B	287	SER	2.2
1	A	46	GLY	2.2
1	A	288	TRP	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	K	B	997	1/1	0.26	3.84	69,69,69,69	0
2	CA	B	996	1/1	0.29	2.22	52,52,52,52	0
2	CA	B	995	1/1	0.25	0.95	70,70,70,70	0
2	CA	A	995	1/1	0.26	0.90	49,49,49,49	0
3	K	A	997	1/1	0.19	0.62	91,91,91,91	0
2	CA	A	996	1/1	0.23	0.56	39,39,39,39	0
2	CA	B	998	1/1	0.18	0.04	84,84,84,84	0
4	CL	A	1000	1/1	0.14	-0.47	56,56,56,56	0
2	CA	A	998	1/1	0.13	-0.72	64,64,64,64	0
4	CL	B	999	1/1	0.09	-2.35	40,40,40,40	0
2	CA	A	999	1/1	0.09	-4.29	83,83,83,83	0

6.5 Other polymers ⓘ

There are no such residues in this entry.