



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 11:42 AM EDT

PDB ID : 2ZBE / pdb_00002zbe
Title : Calcium pump crystal structure with bound BeF₃ in the absence of calcium and TG
Authors : Toyoshima, C.; Ogawa, H.; Norimatsu, Y.
Deposited on : 2007-10-20
Resolution : 3.80 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

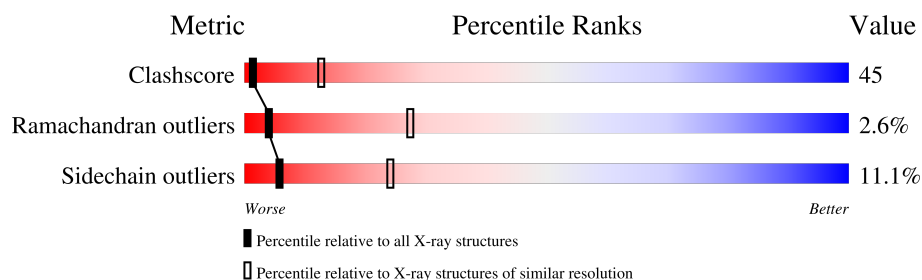
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	995	
1	B	995	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15358 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 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	995	Total	C	N	O	S	1	0	0
			7674	4878	1287	1452	57			
1	B	995	Total	C	N	O	S	1	0	0
			7674	4878	1287	1452	57			

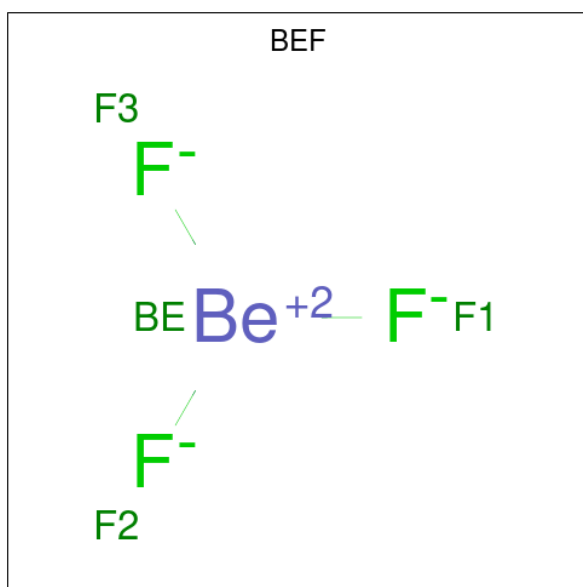
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	994	GLY	-	SEE REMARK 999	UNP P04191
B	994	GLY	-	SEE REMARK 999	UNP P04191

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF₃).



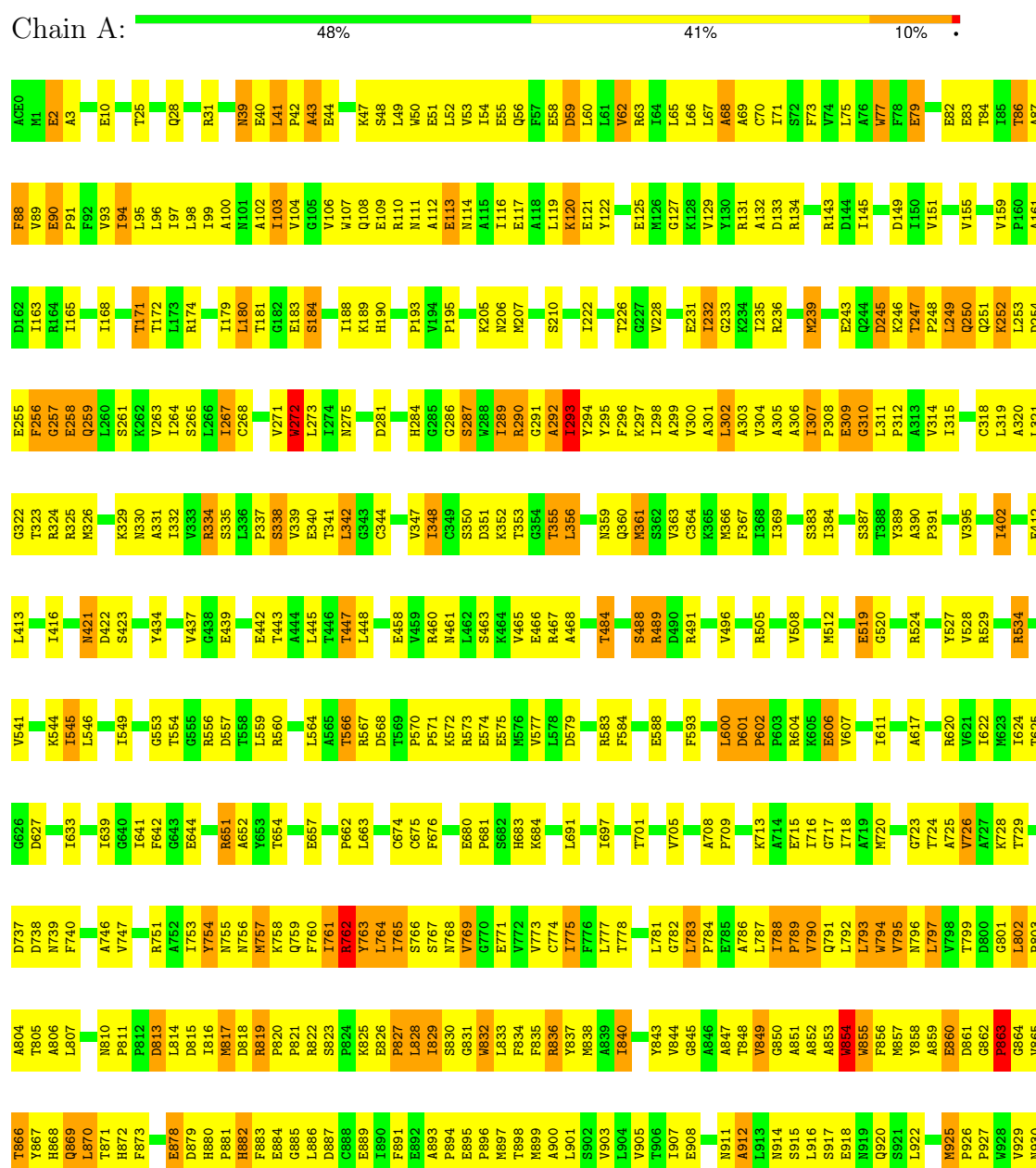
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Be	F	0	0
			4	1	3		
3	B	1	Total	Be	F	0	0
			4	1	3		

3 Residue-property plots

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

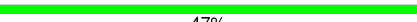
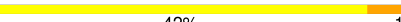
Note EDS was not executed.

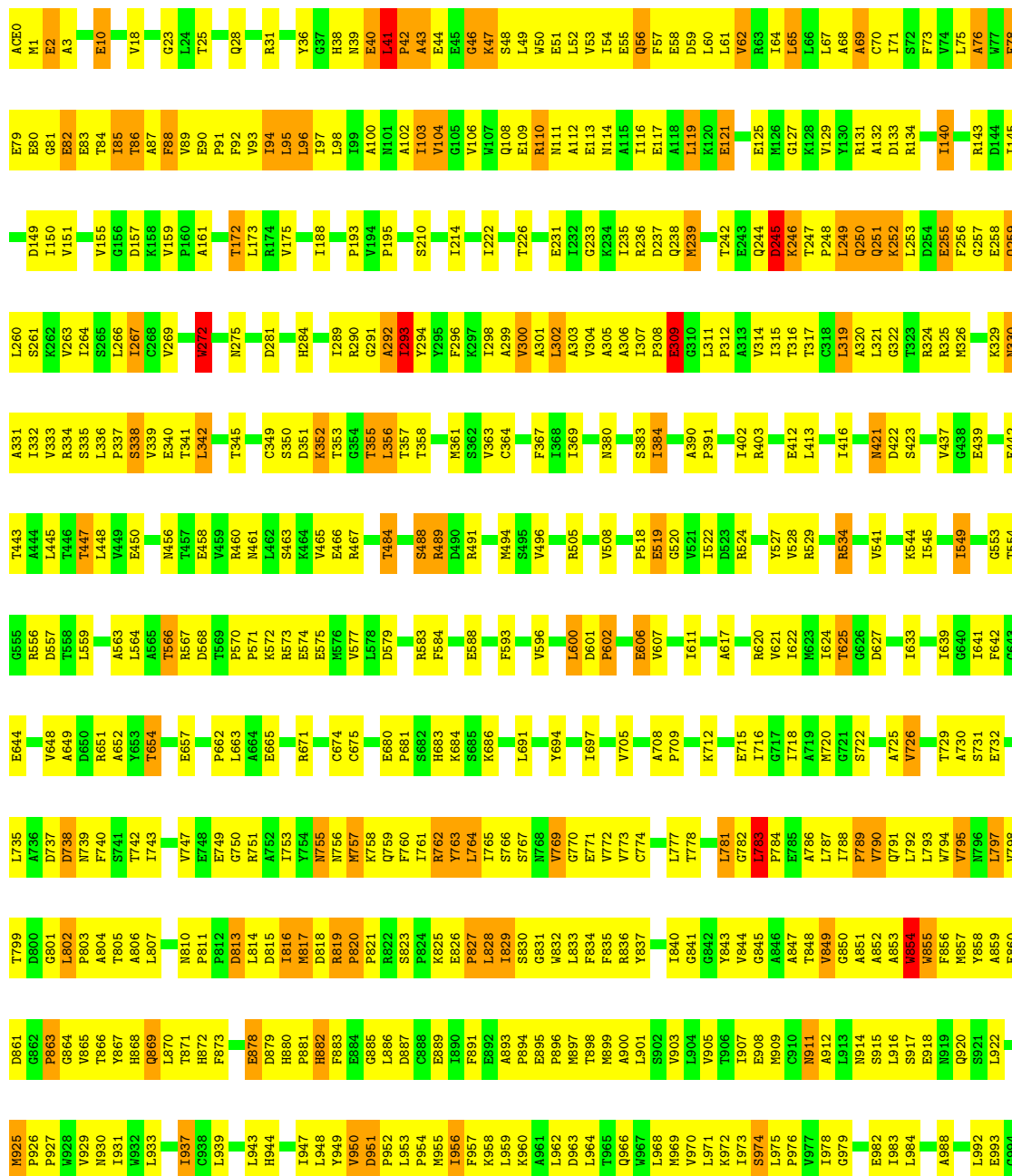
- Molecule 1: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1





• Molecule 1: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1

Chain B:  47%  42%  10%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	133.87Å 91.59Å 248.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 3.80	Depositor
% Data completeness (in resolution range)	90.3 (12.00-3.80)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.293 , 0.327	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	15358	wwPDB-VP
Average B, all atoms (Å ²)	163.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BEF, MG, ACE

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	0.89	12/7813 (0.2%)	1.15	32/10594 (0.3%)
1	B	0.94	7/7813 (0.1%)	1.16	29/10594 (0.3%)
All	All	0.91	19/15626 (0.1%)	1.16	61/21188 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	245	ASP	C-N	8.01	1.44	1.33
1	A	863	PRO	C-N	-7.40	1.22	1.33
1	A	956	ILE	C-N	6.79	1.43	1.33
1	B	494	MET	SD-CE	6.11	1.94	1.79
1	A	866	THR	C-N	-5.65	1.27	1.33
1	B	854	TRP	NE1-CE2	-5.54	1.31	1.37
1	B	272	TRP	NE1-CE2	-5.53	1.31	1.37
1	A	864	GLY	C-N	-5.53	1.27	1.33
1	A	854	TRP	NE1-CE2	-5.51	1.31	1.37
1	B	855	TRP	NE1-CE2	-5.49	1.31	1.37
1	A	955	MET	C-N	-5.44	1.28	1.34
1	A	832	TRP	NE1-CE2	-5.40	1.31	1.37
1	A	794	TRP	NE1-CE2	-5.38	1.31	1.37
1	A	272	TRP	NE1-CE2	-5.30	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	855	TRP	NE1-CE2	-5.28	1.31	1.37
1	B	602	PRO	CA-CB	-5.22	1.49	1.54
1	A	958	LYS	N-CA	5.20	1.52	1.46
1	A	77	TRP	NE1-CE2	-5.14	1.31	1.37
1	B	781	LEU	CA-C	5.07	1.57	1.52

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	602	PRO	N-CA-C	9.57	120.82	110.58
1	B	309	GLU	O-C-N	-7.11	113.14	122.59
1	B	76	ALA	N-CA-C	-7.09	103.56	111.71
1	A	869	GLN	N-CA-C	-7.02	104.72	113.28
1	B	601	ASP	CA-C-N	6.91	124.64	119.66
1	B	601	ASP	C-N-CA	6.91	124.64	119.66
1	A	281	ASP	CA-C-N	6.91	128.47	119.84
1	A	281	ASP	C-N-CA	6.91	128.47	119.84
1	A	254	ASP	N-CA-C	-6.67	104.09	111.36
1	B	41	LEU	CA-C-N	6.62	128.12	119.84
1	B	41	LEU	C-N-CA	6.62	128.12	119.84
1	B	869	GLN	N-CA-C	-6.57	105.26	113.28
1	B	820	PRO	N-CA-C	6.54	116.75	110.47
1	B	819	ARG	CA-C-N	6.50	124.41	119.66
1	B	819	ARG	C-N-CA	6.50	124.41	119.66
1	A	184	SER	N-CA-C	6.48	118.89	111.11
1	B	289	ILE	N-CA-C	-6.28	107.74	113.71
1	B	159	VAL	CA-C-N	6.16	125.72	119.19
1	B	159	VAL	C-N-CA	6.16	125.72	119.19
1	A	159	VAL	CA-C-N	6.12	125.68	119.19
1	A	159	VAL	C-N-CA	6.12	125.68	119.19
1	A	820	PRO	N-CA-C	6.06	116.29	110.47
1	B	275	ASN	O-C-N	-6.05	115.61	122.08
1	A	819	ARG	CA-C-N	5.99	124.03	119.66
1	A	819	ARG	C-N-CA	5.99	124.03	119.66
1	B	864	GLY	O-C-N	5.98	130.47	122.70
1	B	69	ALA	O-C-N	-5.76	114.92	122.59
1	B	732	GLU	N-CA-C	-5.72	106.14	113.23
1	A	602	PRO	N-CA-C	5.70	117.66	110.70
1	A	62	VAL	N-CA-C	-5.55	104.96	110.62
1	A	822	ARG	NE-CZ-NH2	5.51	124.16	119.20
1	B	2	GLU	N-CA-C	-5.46	103.32	110.53
1	A	163	ILE	N-CA-C	5.44	117.23	108.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	602	PRO	CB-CA-C	-5.43	104.30	110.92
1	B	834	PHE	N-CA-C	-5.36	105.36	111.14
1	A	2	GLU	N-CA-C	-5.34	103.48	110.53
1	B	549	ILE	N-CA-C	-5.34	105.33	110.72
1	B	654	THR	N-CA-C	-5.31	102.90	110.59
1	B	625	THR	N-CA-C	5.28	117.70	109.52
1	A	651	ARG	NE-CZ-NH2	5.25	123.92	119.20
1	A	762	ARG	NE-CZ-NH2	5.24	123.92	119.20
1	B	607	VAL	N-CA-C	5.24	116.01	110.72
1	A	442	GLU	N-CA-C	-5.20	106.62	113.12
1	B	40	GLU	O-C-N	5.17	129.47	122.59
1	B	266	LEU	N-CA-C	-5.15	105.66	111.28
1	B	738	ASP	N-CA-C	-5.14	106.09	112.47
1	A	290	ARG	NE-CZ-NH2	5.14	123.82	119.20
1	A	974	SER	N-CA-C	5.12	117.85	111.24
1	A	560	ARG	NE-CZ-NH2	5.11	123.80	119.20
1	B	974	SER	N-CA-C	5.10	117.82	111.24
1	A	39	ASN	CA-C-N	-5.10	111.80	121.54
1	A	39	ASN	C-N-CA	-5.10	111.80	121.54
1	A	836	ARG	NE-CZ-NH2	5.09	123.79	119.20
1	A	864	GLY	O-C-N	5.09	129.32	122.70
1	A	751	ARG	NE-CZ-NH2	5.08	123.78	119.20
1	A	120	LYS	O-C-N	-5.08	116.84	122.07
1	A	912	ALA	N-CA-C	-5.07	105.84	111.36
1	B	442	GLU	N-CA-C	-5.05	106.80	113.12
1	A	761	ILE	N-CA-C	-5.02	106.26	111.58
1	A	257	GLY	N-CA-C	-5.01	107.57	113.99
1	A	870	LEU	N-CA-C	-5.01	107.30	113.41

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	310	GLY	Mainchain
1	A	68	ALA	Mainchain
1	B	284	HIS	Mainchain
1	B	380	ASN	Mainchain

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	7674	0	7765	672	0
1	B	7674	0	7765	710	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	4	0	0	1	0
3	B	4	0	0	0	0
All	All	15358	0	15530	1382	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 45.

All (1382) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:757:MET:CE	1:A:761:ILE:HD11	1.60	1.30
1:B:762:ARG:HE	1:B:833:LEU:HD21	1.02	1.18
1:B:802:LEU:HD13	1:B:939:LEU:CD2	1.74	1.17
1:A:247:THR:OG1	1:A:250:GLN:HB3	1.45	1.17
1:A:802:LEU:HD13	1:A:939:LEU:CD2	1.76	1.15
1:B:802:LEU:HD13	1:B:939:LEU:HD23	1.23	1.15
1:B:735:LEU:HD11	1:B:743:ILE:HD11	1.23	1.12
1:A:762:ARG:HE	1:A:833:LEU:HD21	1.00	1.12
1:A:758:LYS:HA	1:A:761:ILE:HD12	1.32	1.11
1:A:802:LEU:HD13	1:A:939:LEU:HD23	1.25	1.09
1:A:898:THR:HA	1:A:959:LEU:HD22	1.33	1.09
1:A:248:PRO:HG2	1:A:341:THR:CG2	1.83	1.09
1:A:248:PRO:HG2	1:A:341:THR:HG21	1.27	1.08
1:A:757:MET:HE2	1:A:761:ILE:CD1	1.83	1.08
1:A:758:LYS:HB2	1:A:828:LEU:HD11	1.30	1.08
1:A:803:PRO:O	1:A:806:ALA:HB3	1.52	1.08
1:A:823:SER:HB3	1:A:826:GLU:HB2	1.35	1.07
1:B:549:ILE:HD11	1:B:596:VAL:HG21	1.37	1.07
1:B:803:PRO:O	1:B:806:ALA:HB3	1.55	1.06
1:B:823:SER:HB3	1:B:826:GLU:HB2	1.37	1.06
1:B:758:LYS:HB2	1:B:828:LEU:HD11	1.33	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:ARG:NE	1:A:833:LEU:HD21	1.69	1.05
1:B:898:THR:HA	1:B:959:LEU:HD22	1.33	1.05
1:A:899:MET:HE3	1:A:970:VAL:HG23	1.37	1.05
1:A:899:MET:HE1	1:A:966:GLN:O	1.56	1.05
1:B:855:TRP:HA	1:B:859:ALA:CB	1.87	1.05
1:A:855:TRP:HA	1:A:859:ALA:HB2	1.06	1.04
1:B:267:ILE:HG12	1:B:302:LEU:HD22	1.40	1.04
1:B:735:LEU:CD1	1:B:743:ILE:HD11	1.88	1.04
1:B:762:ARG:NE	1:B:833:LEU:HD21	1.70	1.04
1:B:899:MET:HE1	1:B:966:GLN:O	1.56	1.04
1:B:899:MET:HE3	1:B:970:VAL:HG23	1.36	1.03
1:A:341:THR:HG22	1:A:716:ILE:HD11	1.38	1.02
1:A:855:TRP:HA	1:A:859:ALA:CB	1.88	1.02
1:B:855:TRP:HA	1:B:859:ALA:HB2	1.05	1.02
1:B:342:LEU:HG	1:B:716:ILE:HG21	1.44	0.99
1:A:760:PHE:HB3	1:A:807:LEU:HD12	1.44	0.99
1:B:857:MET:HE1	1:B:867:TYR:HA	1.42	0.99
1:B:783:LEU:H	1:B:783:LEU:HD12	1.27	0.98
1:B:311:LEU:HD11	1:B:761:ILE:CD1	1.92	0.98
1:A:849:VAL:O	1:A:853:ALA:HB3	1.63	0.97
1:B:786:ALA:O	1:B:787:LEU:HG	1.65	0.96
1:A:120:LYS:HE2	1:A:728:LYS:NZ	1.80	0.96
1:B:963:ASP:HB3	1:B:966:GLN:HG3	1.48	0.96
1:A:963:ASP:HB3	1:A:966:GLN:HG3	1.48	0.95
1:B:617:ALA:O	1:B:821:PRO:HD3	1.66	0.95
1:B:311:LEU:HB3	1:B:312:PRO:HD3	1.46	0.95
1:B:49:LEU:HD13	1:B:110:ARG:HE	1.30	0.95
1:B:573:ARG:H	1:B:573:ARG:HD2	1.32	0.95
1:B:261:SER:HA	1:B:264:ILE:HD12	1.49	0.95
1:B:760:PHE:HB3	1:B:807:LEU:HD12	1.48	0.95
1:A:866:THR:H	1:A:869:GLN:HE21	1.12	0.94
1:A:622:ILE:HD12	1:A:674:CYS:HA	1.46	0.94
1:A:786:ALA:O	1:A:787:LEU:HG	1.67	0.94
1:B:866:THR:H	1:B:869:GLN:HE21	1.14	0.93
1:A:248:PRO:CG	1:A:341:THR:HG21	1.97	0.93
1:A:857:MET:HE1	1:A:867:TYR:HA	1.51	0.93
1:B:909:MET:SD	1:B:937:ILE:HD12	2.09	0.93
1:B:315:ILE:HD11	1:B:757:MET:HE3	1.49	0.92
1:A:783:LEU:HD12	1:A:783:LEU:H	1.32	0.92
1:B:383:SER:C	1:B:384:ILE:HD12	1.94	0.92
1:B:311:LEU:HD11	1:B:761:ILE:HD12	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:ARG:HE	1:A:833:LEU:CD2	1.82	0.91
1:A:788:ILE:HB	1:A:789:PRO:HD2	1.52	0.91
1:A:573:ARG:H	1:A:573:ARG:HD2	1.36	0.91
1:B:762:ARG:HE	1:B:833:LEU:CD2	1.83	0.90
1:A:59:ASP:OD2	1:A:62:VAL:HG23	1.72	0.90
1:A:849:VAL:O	1:A:853:ALA:CB	2.20	0.90
1:B:50:TRP:CD1	1:B:54:ILE:HD11	2.07	0.90
1:B:49:LEU:CD1	1:B:110:ARG:HE	1.84	0.89
1:B:844:VAL:HG22	1:B:907:ILE:HG21	1.52	0.89
1:A:762:ARG:HB3	1:A:837:TYR:CZ	2.07	0.89
1:B:762:ARG:HB3	1:B:837:TYR:CZ	2.07	0.89
1:B:80:GLU:HG2	1:B:82:GLU:HG2	1.52	0.89
1:A:395:VAL:HG12	1:A:402:ILE:HD11	1.55	0.89
1:B:622:ILE:HD12	1:B:674:CYS:HA	1.52	0.89
1:B:756:ASN:O	1:B:759:GLN:HB2	1.72	0.88
1:A:757:MET:HG2	1:A:760:PHE:CZ	2.08	0.88
1:A:777:LEU:O	1:A:781:LEU:HB3	1.73	0.88
1:A:899:MET:SD	1:A:962:LEU:HD13	2.13	0.88
1:A:757:MET:HE2	1:A:761:ILE:HD11	0.88	0.87
1:B:69:ALA:O	1:B:73:PHE:HB2	1.74	0.87
1:B:245:ASP:O	1:B:246:LYS:HG2	1.74	0.87
1:A:519:GLU:CD	1:A:519:GLU:H	1.83	0.87
1:B:57:PHE:CZ	1:B:102:ALA:HB2	2.10	0.86
1:B:899:MET:SD	1:B:962:LEU:HD13	2.16	0.86
1:A:248:PRO:CG	1:A:341:THR:CG2	2.54	0.86
1:B:855:TRP:CA	1:B:859:ALA:HB2	2.00	0.86
1:A:899:MET:CE	1:A:970:VAL:HG23	2.06	0.86
1:A:556:ARG:HG2	1:A:644:GLU:HG3	1.56	0.86
1:A:765:ILE:HD13	1:A:765:ILE:O	1.76	0.86
1:A:844:VAL:HG22	1:A:907:ILE:HG21	1.56	0.86
1:A:895:GLU:HG3	1:A:960:LYS:HD3	1.56	0.86
1:B:898:THR:CA	1:B:959:LEU:HD22	2.06	0.85
1:B:518:PRO:O	1:B:522:ILE:HD13	1.75	0.85
1:A:898:THR:CA	1:A:959:LEU:HD22	2.06	0.85
1:B:757:MET:HG2	1:B:760:PHE:CZ	2.12	0.84
1:A:39:ASN:OD1	1:A:226:THR:HB	1.75	0.84
1:A:120:LYS:HE2	1:A:728:LYS:HZ2	1.42	0.84
1:A:747:VAL:HG12	1:A:817:MET:HE1	1.58	0.84
1:B:899:MET:HE3	1:B:970:VAL:CG2	2.06	0.84
1:B:895:GLU:HG3	1:B:960:LYS:HD3	1.57	0.84
1:A:567:ARG:HH11	1:A:570:PRO:HA	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:787:LEU:HD11	1:B:900:ALA:HB1	1.59	0.84
1:A:843:TYR:OH	1:A:976:PRO:HG2	1.78	0.84
1:A:865:VAL:HG13	1:A:869:GLN:HG3	1.59	0.84
1:B:342:LEU:HD11	1:B:718:ILE:HD11	1.60	0.84
1:A:950:VAL:HG12	1:A:952:PRO:HD2	1.58	0.84
1:B:816:ILE:HA	1:B:819:ARG:HH21	1.39	0.84
1:B:899:MET:CE	1:B:970:VAL:HG23	2.07	0.84
1:A:833:LEU:HA	1:A:836:ARG:HB2	1.60	0.84
1:A:52:LEU:HD12	1:A:106:VAL:HG13	1.60	0.83
1:B:857:MET:HB2	1:B:858:TYR:CD1	2.13	0.83
1:B:421:ASN:ND2	1:B:423:SER:H	1.77	0.83
1:B:567:ARG:HH11	1:B:570:PRO:HA	1.43	0.83
1:A:899:MET:HE3	1:A:970:VAL:CG2	2.07	0.83
1:B:740:PHE:O	1:B:743:ILE:HD13	1.79	0.83
1:B:843:TYR:OH	1:B:976:PRO:HG2	1.78	0.83
1:A:857:MET:HB2	1:A:858:TYR:CD1	2.14	0.83
1:A:95:LEU:O	1:A:99:ILE:HD12	1.77	0.83
1:A:421:ASN:ND2	1:A:423:SER:H	1.77	0.83
1:A:245:ASP:O	1:A:246:LYS:HG3	1.77	0.83
1:B:157:ASP:HB2	1:B:214:ILE:HD13	1.61	0.83
1:B:833:LEU:HA	1:B:836:ARG:HB2	1.61	0.82
1:A:541:VAL:O	1:A:545:ILE:HD13	1.79	0.82
1:B:777:LEU:O	1:B:781:LEU:HB3	1.79	0.82
1:A:802:LEU:CD1	1:A:939:LEU:HG	2.10	0.82
1:B:788:ILE:HB	1:B:789:PRO:HD2	1.58	0.82
1:B:802:LEU:CD1	1:B:939:LEU:HG	2.09	0.82
1:A:878:GLU:HG3	1:A:879:ASP:H	1.45	0.81
1:A:773:VAL:O	1:A:777:LEU:HG	1.80	0.81
1:B:248:PRO:HG2	1:B:341:THR:CG2	2.11	0.81
1:B:519:GLU:H	1:B:519:GLU:CD	1.84	0.81
1:B:773:VAL:O	1:B:777:LEU:HG	1.81	0.81
1:B:849:VAL:O	1:B:853:ALA:HB3	1.80	0.81
1:A:758:LYS:CB	1:A:828:LEU:HD11	2.10	0.81
1:B:245:ASP:O	1:B:246:LYS:CG	2.29	0.81
1:A:865:VAL:HG13	1:A:869:GLN:CG	2.11	0.80
1:B:245:ASP:C	1:B:246:LYS:HG3	2.05	0.80
1:B:363:VAL:HG11	1:B:448:LEU:HD22	1.64	0.79
1:B:802:LEU:HD13	1:B:939:LEU:CG	2.12	0.79
1:B:878:GLU:HG3	1:B:879:ASP:H	1.45	0.79
1:A:50:TRP:CD1	1:A:54:ILE:HD11	2.17	0.79
1:A:802:LEU:HD13	1:A:939:LEU:CG	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:SER:OG	1:A:356:LEU:HD13	1.82	0.79
1:B:311:LEU:HD11	1:B:761:ILE:HD13	1.64	0.79
1:B:899:MET:HA	1:B:962:LEU:HD11	1.64	0.79
1:A:832:TRP:O	1:A:836:ARG:HG3	1.83	0.79
1:B:898:THR:OG1	1:B:959:LEU:HB3	1.83	0.79
1:A:898:THR:OG1	1:A:959:LEU:HB3	1.83	0.79
1:A:855:TRP:CA	1:A:859:ALA:HB2	2.01	0.78
1:B:787:LEU:HD21	1:B:901:LEU:N	1.97	0.78
1:B:484:THR:HB	1:B:496:VAL:HG12	1.64	0.78
1:A:484:THR:HB	1:A:496:VAL:HG12	1.64	0.78
1:A:899:MET:HA	1:A:962:LEU:HD11	1.64	0.78
1:B:248:PRO:HG2	1:B:341:THR:HG23	1.64	0.78
1:B:315:ILE:CD1	1:B:757:MET:HE3	2.14	0.78
1:A:771:GLU:O	1:A:775:ILE:HD13	1.83	0.78
1:A:852:ALA:HB1	1:A:896:PRO:O	1.84	0.78
1:A:488:SER:HB3	1:A:491:ARG:HH21	1.49	0.78
1:A:787:LEU:HD11	1:A:900:ALA:HB1	1.66	0.77
1:B:39:ASN:OD1	1:B:226:THR:HB	1.83	0.77
1:B:245:ASP:C	1:B:246:LYS:CG	2.57	0.77
1:B:926:PRO:O	1:B:929:VAL:HG23	1.85	0.77
1:B:23:GLY:HA2	1:B:150:ILE:HD13	1.65	0.77
1:B:140:ILE:HD13	1:B:140:ILE:H	1.50	0.77
1:B:786:ALA:O	1:B:897:MET:HA	1.84	0.77
1:A:851:ALA:HB2	1:A:973:ILE:HG13	1.67	0.77
1:B:832:TRP:O	1:B:836:ARG:HG3	1.84	0.77
1:A:249:LEU:HD11	1:A:253:LEU:HD21	1.64	0.76
1:B:852:ALA:HB1	1:B:896:PRO:O	1.86	0.76
1:B:855:TRP:O	1:B:859:ALA:HB3	1.85	0.76
1:A:421:ASN:HD22	1:A:423:SER:H	1.33	0.76
1:A:112:ALA:O	1:A:116:ILE:HG12	1.85	0.76
1:A:807:LEU:O	1:A:810:ASN:HB2	1.84	0.76
1:A:95:LEU:HA	1:A:98:LEU:HD12	1.66	0.75
1:A:99:ILE:O	1:A:103:ILE:HG22	1.86	0.75
1:A:787:LEU:HD21	1:A:901:LEU:N	2.01	0.75
1:A:866:THR:H	1:A:869:GLN:NE2	1.85	0.75
1:A:903:VAL:HG22	1:A:970:VAL:HG13	1.68	0.75
1:B:747:VAL:HG12	1:B:817:MET:HE1	1.68	0.75
1:B:851:ALA:HB2	1:B:973:ILE:HG13	1.68	0.75
1:B:54:ILE:O	1:B:58:GLU:HG3	1.87	0.74
1:B:807:LEU:O	1:B:810:ASN:HB2	1.86	0.74
1:A:326:MET:HB3	1:A:331:ALA:HB3	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:708:ALA:HB3	1:A:709:PRO:HD3	1.68	0.74
1:B:488:SER:HB3	1:B:491:ARG:HH21	1.51	0.74
1:A:42:PRO:O	1:A:43:ALA:C	2.31	0.74
1:B:75:LEU:HD11	1:B:300:VAL:HB	1.68	0.74
1:A:914:ASN:ND2	1:A:922:LEU:HD11	2.03	0.74
1:A:65:LEU:HD13	1:A:307:ILE:HG21	1.70	0.74
1:B:950:VAL:HG12	1:B:952:PRO:HD2	1.70	0.74
1:A:786:ALA:O	1:A:897:MET:HA	1.88	0.74
1:B:308:PRO:HG3	1:B:765:ILE:HG22	1.70	0.74
1:B:573:ARG:H	1:B:573:ARG:CD	2.01	0.74
1:B:421:ASN:HD22	1:B:423:SER:H	1.33	0.73
1:B:40:GLU:OE1	1:B:143:ARG:HB2	1.88	0.73
1:A:171:THR:HG22	1:A:172:THR:HG23	1.71	0.73
1:A:852:ALA:HA	1:A:899:MET:CG	2.19	0.73
1:B:758:LYS:CB	1:B:828:LEU:HD11	2.15	0.73
1:B:788:ILE:HG13	1:B:791:GLN:HB2	1.70	0.73
1:A:102:ALA:O	1:A:106:VAL:HG23	1.89	0.73
1:B:749:GLU:O	1:B:753:ILE:HD13	1.89	0.73
1:B:914:ASN:ND2	1:B:922:LEU:HD11	2.02	0.73
1:B:611:ILE:HD12	1:B:621:VAL:HG11	1.70	0.72
1:A:100:ALA:O	1:A:104:VAL:HG23	1.89	0.72
1:A:866:THR:N	1:A:869:GLN:HE21	1.85	0.72
1:B:899:MET:CE	1:B:966:GLN:O	2.36	0.72
1:B:903:VAL:HG22	1:B:970:VAL:HG13	1.71	0.72
1:A:51:GLU:HA	1:A:54:ILE:HD12	1.70	0.72
1:A:364:CYS:O	1:A:384:ILE:N	2.21	0.72
1:A:817:MET:C	1:A:819:ARG:H	1.97	0.72
1:B:817:MET:C	1:B:819:ARG:H	1.97	0.72
1:B:866:THR:H	1:B:869:GLN:NE2	1.86	0.72
1:B:76:ALA:HB1	1:B:88:PHE:HA	1.72	0.71
1:B:852:ALA:HA	1:B:899:MET:CG	2.19	0.71
1:B:311:LEU:CB	1:B:312:PRO:HD3	2.21	0.71
1:A:790:VAL:HG12	1:A:790:VAL:O	1.89	0.71
1:A:855:TRP:O	1:A:859:ALA:HB3	1.89	0.71
1:A:926:PRO:O	1:A:929:VAL:HG23	1.89	0.71
1:B:57:PHE:CZ	1:B:102:ALA:CB	2.73	0.71
1:B:802:LEU:N	1:B:803:PRO:HD2	2.06	0.71
1:B:326:MET:HB3	1:B:331:ALA:HB3	1.71	0.71
1:B:51:GLU:HA	1:B:54:ILE:HD12	1.70	0.71
1:B:611:ILE:HD12	1:B:621:VAL:HG21	1.72	0.71
1:B:349:CYS:HB3	1:B:624:ILE:CD1	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:PHE:O	1:A:91:PRO:HD2	1.92	0.70
1:A:112:ALA:HB1	1:A:334:ARG:HG2	1.74	0.70
1:B:790:VAL:HG12	1:B:790:VAL:O	1.92	0.70
1:A:573:ARG:H	1:A:573:ARG:CD	2.05	0.70
1:B:127:GLY:O	1:B:140:ILE:HD13	1.90	0.70
1:B:899:MET:HE1	1:B:966:GLN:C	2.17	0.70
1:A:40:GLU:OE1	1:A:143:ARG:HB2	1.91	0.70
1:A:757:MET:CE	1:A:761:ILE:CD1	2.54	0.70
1:B:844:VAL:CG2	1:B:907:ILE:HG21	2.21	0.70
1:A:817:MET:O	1:A:819:ARG:N	2.24	0.70
1:B:829:ILE:HD12	1:B:829:ILE:H	1.56	0.70
1:B:866:THR:N	1:B:869:GLN:HE21	1.88	0.70
1:A:181:THR:HB	1:A:183:GLU:HG3	1.74	0.69
1:B:311:LEU:HB3	1:B:312:PRO:CD	2.20	0.69
1:B:349:CYS:HB3	1:B:624:ILE:HD13	1.74	0.69
1:B:355:THR:HG23	1:B:720:MET:HG2	1.74	0.69
1:A:792:LEU:HA	1:A:795:VAL:CG2	2.23	0.69
1:A:802:LEU:CD1	1:A:939:LEU:CG	2.70	0.69
1:B:129:VAL:HG22	1:B:140:ILE:HD12	1.72	0.69
1:B:342:LEU:CG	1:B:716:ILE:HG21	2.21	0.69
1:B:817:MET:O	1:B:819:ARG:N	2.24	0.69
1:B:852:ALA:HA	1:B:899:MET:HB3	1.75	0.69
1:A:784:PRO:CD	1:A:870:LEU:HD11	2.22	0.69
1:A:788:ILE:HB	1:A:789:PRO:CD	2.22	0.69
1:B:802:LEU:CD1	1:B:939:LEU:CG	2.69	0.69
1:B:895:GLU:CG	1:B:960:LYS:HD3	2.22	0.69
1:A:75:LEU:HD12	1:A:300:VAL:HB	1.74	0.69
1:A:828:LEU:HG	1:A:829:ILE:HG13	1.75	0.69
1:B:157:ASP:O	1:B:214:ILE:HD12	1.93	0.69
1:B:762:ARG:NH2	1:B:918:GLU:HG3	2.08	0.69
1:B:61:LEU:CD1	1:B:311:LEU:HD23	2.23	0.69
1:B:412:GLU:OE1	1:B:529:ARG:HD2	1.93	0.69
1:B:757:MET:O	1:B:761:ILE:HG12	1.92	0.69
1:B:853:ALA:O	1:B:856:PHE:HB2	1.93	0.69
1:A:844:VAL:CG2	1:A:907:ILE:HG21	2.22	0.68
1:A:600:LEU:HD13	1:A:600:LEU:C	2.19	0.68
1:B:299:ALA:HA	1:B:302:LEU:HD11	1.73	0.68
1:B:56:GLN:HG3	1:B:106:VAL:HG23	1.75	0.68
1:A:944:HIS:O	1:A:947:ILE:HG22	1.93	0.68
1:B:802:LEU:CD1	1:B:939:LEU:CD2	2.65	0.68
1:A:489:ARG:CD	1:A:489:ARG:H	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:895:GLU:CG	1:A:960:LYS:HD3	2.23	0.68
1:A:931:ILE:HD12	1:A:931:ILE:H	1.59	0.68
1:B:308:PRO:CG	1:B:765:ILE:HG22	2.23	0.68
1:B:792:LEU:HA	1:B:795:VAL:CG2	2.23	0.68
1:B:129:VAL:HG11	1:B:145:ILE:HD12	1.76	0.68
1:A:111:ASN:O	1:A:114:ASN:HB2	1.92	0.68
1:B:49:LEU:CD1	1:B:110:ARG:HG3	2.23	0.68
1:B:67:LEU:O	1:B:71:ILE:HG12	1.94	0.68
1:B:849:VAL:O	1:B:853:ALA:CB	2.41	0.68
1:A:311:LEU:HG	1:A:315:ILE:HD13	1.75	0.68
1:A:963:ASP:H	1:A:966:GLN:HE21	1.42	0.68
1:B:61:LEU:HD11	1:B:311:LEU:HD23	1.74	0.68
1:B:767:SER:O	1:B:771:GLU:HG3	1.93	0.68
1:B:898:THR:OG1	1:B:959:LEU:CB	2.42	0.68
1:A:412:GLU:OE1	1:A:529:ARG:HD2	1.93	0.68
1:A:899:MET:SD	1:A:962:LEU:CD1	2.82	0.68
1:A:802:LEU:N	1:A:803:PRO:HD2	2.09	0.67
1:A:899:MET:HE1	1:A:966:GLN:C	2.19	0.67
1:A:600:LEU:HD13	1:A:600:LEU:O	1.94	0.67
1:B:489:ARG:CD	1:B:489:ARG:H	2.07	0.67
1:B:931:ILE:HD12	1:B:931:ILE:H	1.59	0.67
1:A:69:ALA:O	1:A:73:PHE:HB2	1.94	0.67
1:A:769:VAL:O	1:A:773:VAL:HG23	1.95	0.67
1:A:762:ARG:NH2	1:A:918:GLU:HG3	2.10	0.67
1:A:767:SER:O	1:A:771:GLU:HG3	1.93	0.67
1:B:42:PRO:O	1:B:43:ALA:C	2.38	0.67
1:B:784:PRO:CD	1:B:870:LEU:HD11	2.24	0.67
1:A:261:SER:O	1:A:264:ILE:HG12	1.93	0.67
1:A:829:ILE:HD12	1:A:829:ILE:H	1.59	0.67
1:A:120:LYS:NZ	1:A:723:GLY:O	2.24	0.67
1:B:786:ALA:HB2	1:B:849:VAL:HG13	1.77	0.67
1:A:65:LEU:HG	1:A:94:ILE:HD11	1.77	0.66
1:A:786:ALA:HB2	1:A:849:VAL:HG13	1.77	0.66
1:A:788:ILE:CD1	1:A:791:GLN:HB2	2.24	0.66
1:A:898:THR:OG1	1:A:959:LEU:CB	2.43	0.66
1:A:899:MET:CE	1:A:966:GLN:O	2.38	0.66
1:B:172:THR:HG23	1:B:489:ARG:HD2	1.77	0.66
1:B:252:LYS:HA	1:B:252:LYS:HE3	1.77	0.66
1:A:950:VAL:O	1:A:954:PRO:HD2	1.94	0.66
1:B:651:ARG:HG3	1:B:651:ARG:HH11	1.59	0.66
1:A:308:PRO:HB2	1:A:764:LEU:HD23	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:ARG:HH11	1:A:334:ARG:HB3	1.60	0.66
1:A:606:GLU:H	1:A:606:GLU:CD	2.04	0.66
1:A:774:CYS:SG	1:A:786:ALA:HB3	2.35	0.66
1:A:622:ILE:CD1	1:A:674:CYS:HA	2.23	0.66
1:A:247:THR:HG23	1:A:250:GLN:HG2	1.78	0.66
1:A:567:ARG:NH1	1:A:571:PRO:HD3	2.10	0.66
1:B:863:PRO:HB2	1:B:865:VAL:HG23	1.76	0.66
1:A:639:ILE:HD11	1:A:641:ILE:HD12	1.77	0.66
1:B:86:THR:HA	1:B:89:VAL:HG23	1.77	0.66
1:B:944:HIS:O	1:B:947:ILE:HG22	1.96	0.66
1:B:893:ALA:HB1	1:B:895:GLU:OE1	1.95	0.66
1:B:897:MET:CE	1:B:958:LYS:HB3	2.25	0.66
1:A:121:GLU:CD	1:A:121:GLU:O	2.39	0.65
1:B:963:ASP:H	1:B:966:GLN:HE21	1.44	0.65
1:A:54:ILE:O	1:A:58:GLU:HG3	1.96	0.65
1:A:651:ARG:HH11	1:A:651:ARG:HG3	1.61	0.65
1:A:680:GLU:HB3	1:A:681:PRO:HD2	1.77	0.65
1:A:852:ALA:HA	1:A:899:MET:HB3	1.78	0.65
1:B:781:LEU:C	1:B:781:LEU:HD23	2.21	0.65
1:B:314:VAL:HG11	1:B:804:ALA:HB1	1.76	0.65
1:A:762:ARG:HH22	1:A:918:GLU:HA	1.61	0.65
1:B:567:ARG:NH1	1:B:571:PRO:HD3	2.12	0.65
1:B:247:THR:HG21	1:B:337:PRO:HB2	1.79	0.65
1:B:611:ILE:CD1	1:B:621:VAL:HG11	2.25	0.65
1:A:25:THR:HA	1:A:132:ALA:HB3	1.77	0.65
1:A:784:PRO:HD2	1:A:870:LEU:HD11	1.77	0.65
1:B:899:MET:SD	1:B:962:LEU:CD1	2.84	0.65
1:A:232:ILE:HD13	1:A:232:ILE:O	1.97	0.65
1:A:803:PRO:O	1:A:806:ALA:CB	2.40	0.65
1:A:239:MET:HE2	1:A:708:ALA:HB1	1.78	0.65
1:A:259:GLN:O	1:A:263:VAL:HG23	1.96	0.65
1:B:421:ASN:HD22	1:B:421:ASN:C	2.05	0.65
1:A:760:PHE:CB	1:A:807:LEU:HD12	2.25	0.64
1:A:786:ALA:C	1:A:787:LEU:HG	2.21	0.64
1:A:914:ASN:C	1:A:916:LEU:H	2.05	0.64
1:B:786:ALA:C	1:B:787:LEU:HG	2.21	0.64
1:B:832:TRP:CZ3	1:B:835:PHE:CD2	2.85	0.64
1:A:97:ILE:O	1:A:100:ALA:HB3	1.98	0.64
1:A:113:GLU:O	1:A:117:GLU:HG2	1.97	0.64
1:A:326:MET:C	1:A:331:ALA:HB3	2.22	0.64
1:B:252:LYS:HA	1:B:252:LYS:CE	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:VAL:HA	1:A:303:ALA:HB3	1.80	0.64
1:A:600:LEU:O	1:A:602:PRO:HD3	1.97	0.64
1:B:55:GLU:HA	1:B:58:GLU:OE1	1.97	0.64
1:B:897:MET:HE1	1:B:958:LYS:HB3	1.80	0.64
1:A:795:VAL:HG22	1:A:901:LEU:HD11	1.80	0.64
1:A:857:MET:HB2	1:A:858:TYR:CE1	2.32	0.64
1:A:286:GLY:CA	1:A:290:ARG:HB3	2.27	0.64
1:A:342:LEU:HG	1:A:716:ILE:HG21	1.78	0.64
1:A:853:ALA:O	1:A:856:PHE:HB2	1.97	0.64
1:B:303:ALA:O	1:B:306:ALA:HB3	1.98	0.64
1:A:300:VAL:HA	1:A:303:ALA:CB	2.28	0.64
1:B:322:GLY:CA	1:B:325:ARG:HH21	2.11	0.64
1:B:857:MET:HB2	1:B:858:TYR:CE1	2.32	0.64
1:A:893:ALA:HB1	1:A:895:GLU:OE1	1.96	0.64
1:B:214:ILE:HD12	1:B:214:ILE:H	1.62	0.64
1:B:329:LYS:O	1:B:330:ASN:HB2	1.97	0.63
1:B:567:ARG:NH1	1:B:570:PRO:HA	2.13	0.63
1:B:715:GLU:O	1:B:716:ILE:HD13	1.97	0.63
1:B:778:THR:HB	1:B:783:LEU:O	1.98	0.63
1:A:311:LEU:HG	1:A:315:ILE:CD1	2.28	0.63
1:A:322:GLY:N	1:A:325:ARG:HH21	1.97	0.63
1:B:298:ILE:HD12	1:B:299:ALA:N	2.14	0.63
1:A:783:LEU:HA	1:A:870:LEU:HG	1.81	0.63
1:A:832:TRP:CZ3	1:A:835:PHE:CD2	2.86	0.63
1:B:49:LEU:HD13	1:B:110:ARG:NE	2.10	0.63
1:B:298:ILE:O	1:B:302:LEU:HG	1.98	0.63
1:B:781:LEU:HD23	1:B:782:GLY:N	2.13	0.63
1:B:803:PRO:O	1:B:806:ALA:CB	2.42	0.63
1:A:577:VAL:HG11	1:A:583:ARG:NH1	2.14	0.63
1:A:784:PRO:CD	1:A:870:LEU:CD1	2.76	0.63
1:B:49:LEU:HD11	1:B:110:ARG:HG3	1.80	0.63
1:B:384:ILE:HD12	1:B:384:ILE:N	2.13	0.63
1:B:335:SER:HB3	1:B:338:SER:OG	1.98	0.63
1:B:774:CYS:SG	1:B:786:ALA:HB3	2.38	0.63
1:B:917:SER:OG	1:B:920:GLN:HB2	1.98	0.63
1:A:55:GLU:HA	1:A:58:GLU:OE1	1.99	0.63
1:B:49:LEU:CD1	1:B:110:ARG:NE	2.60	0.63
1:B:129:VAL:HG22	1:B:140:ILE:CD1	2.28	0.63
1:B:788:ILE:HB	1:B:789:PRO:CD	2.29	0.63
1:A:120:LYS:HE2	1:A:728:LYS:HZ1	1.62	0.62
1:A:801:GLY:C	1:A:803:PRO:HD2	2.24	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:ASP:O	1:B:214:ILE:CD1	2.46	0.62
1:A:369:ILE:HD12	1:A:369:ILE:H	1.64	0.62
1:A:395:VAL:O	1:A:402:ILE:HD13	1.99	0.62
1:B:75:LEU:CD1	1:B:300:VAL:HB	2.29	0.62
1:B:795:VAL:HG22	1:B:901:LEU:HD11	1.80	0.62
1:A:620:ARG:NH2	1:A:622:ILE:HD11	2.13	0.62
1:B:577:VAL:HG11	1:B:583:ARG:NH1	2.14	0.62
1:B:622:ILE:CD1	1:B:674:CYS:HA	2.28	0.62
1:B:150:ILE:N	1:B:150:ILE:HD12	2.14	0.62
1:B:242:THR:O	1:B:712:LYS:HE2	1.99	0.62
1:A:2:GLU:O	1:A:3:ALA:HB3	2.00	0.62
1:A:188:ILE:HD12	1:A:188:ILE:N	2.15	0.62
1:A:897:MET:CE	1:A:958:LYS:HB3	2.30	0.62
1:A:527:TYR:HB3	1:A:534:ARG:HG3	1.82	0.62
1:A:866:THR:HG23	1:A:869:GLN:NE2	2.15	0.62
1:B:364:CYS:C	1:B:384:ILE:HD13	2.25	0.62
1:B:600:LEU:C	1:B:600:LEU:HD13	2.25	0.62
1:B:828:LEU:HG	1:B:829:ILE:HG13	1.80	0.62
1:B:969:MET:O	1:B:973:ILE:HG12	1.99	0.62
1:A:897:MET:HE1	1:A:958:LYS:HE3	1.81	0.62
1:B:784:PRO:HD3	1:B:870:LEU:CD1	2.30	0.62
1:A:121:GLU:O	1:A:121:GLU:OE2	2.16	0.61
1:A:897:MET:HE1	1:A:958:LYS:HB3	1.81	0.61
1:B:319:LEU:HD21	1:B:337:PRO:HA	1.81	0.61
1:B:783:LEU:H	1:B:783:LEU:CD1	2.07	0.61
1:B:914:ASN:C	1:B:916:LEU:H	2.06	0.61
1:A:248:PRO:CG	1:A:341:THR:HG23	2.30	0.61
1:A:917:SER:OG	1:A:920:GLN:HB2	1.99	0.61
1:B:606:GLU:CD	1:B:606:GLU:H	2.07	0.61
1:B:762:ARG:HH22	1:B:918:GLU:HA	1.63	0.61
1:B:952:PRO:O	1:B:956:ILE:HG12	2.00	0.61
1:A:795:VAL:O	1:A:799:THR:HB	2.01	0.61
1:B:83:GLU:O	1:B:87:ALA:HB2	2.00	0.61
1:B:769:VAL:O	1:B:773:VAL:HG23	2.00	0.61
1:B:897:MET:HE1	1:B:958:LYS:HE3	1.80	0.61
1:A:792:LEU:HA	1:A:795:VAL:HG23	1.82	0.61
1:A:969:MET:O	1:A:973:ILE:HG12	2.00	0.61
1:B:527:TYR:HB3	1:B:534:ARG:HG3	1.83	0.61
1:B:907:ILE:HD11	1:B:974:SER:HA	1.81	0.61
1:A:795:VAL:CG2	1:A:901:LEU:HD11	2.30	0.61
1:B:59:ASP:HB3	1:B:62:VAL:HG23	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:518:PRO:O	1:B:522:ILE:CD1	2.46	0.61
1:B:639:ILE:HD11	1:B:641:ILE:HD12	1.82	0.61
1:A:67:LEU:O	1:A:71:ILE:HG13	2.01	0.61
1:A:572:LYS:HD2	1:A:572:LYS:N	2.16	0.61
1:A:907:ILE:HD11	1:A:974:SER:HA	1.82	0.61
1:A:275:ASN:HA	1:A:295:TYR:OH	2.00	0.61
1:B:311:LEU:CD1	1:B:761:ILE:CD1	2.74	0.61
1:A:412:GLU:OE2	1:A:566:THR:HG21	2.01	0.61
1:A:775:ILE:CD1	1:A:775:ILE:N	2.63	0.61
1:A:802:LEU:CD1	1:A:939:LEU:CD2	2.67	0.61
1:B:2:GLU:O	1:B:3:ALA:HB3	2.01	0.61
1:A:802:LEU:N	1:A:803:PRO:CD	2.64	0.61
1:A:520:GLY:O	1:A:524:ARG:HG3	2.00	0.60
1:A:528:VAL:HG21	1:A:541:VAL:HG11	1.82	0.60
1:A:759:GLN:HA	1:A:762:ARG:HD2	1.83	0.60
1:B:792:LEU:HA	1:B:795:VAL:HG23	1.83	0.60
1:A:315:ILE:O	1:A:319:LEU:HB2	2.01	0.60
1:A:825:LYS:O	1:A:826:GLU:C	2.43	0.60
1:B:813:ASP:OD2	1:B:813:ASP:N	2.29	0.60
1:B:825:LYS:O	1:B:826:GLU:C	2.42	0.60
1:B:867:TYR:O	1:B:871:THR:HG23	2.01	0.60
1:A:755:ASN:O	1:A:759:GLN:HG2	2.01	0.60
1:A:784:PRO:HD3	1:A:870:LEU:CD1	2.32	0.60
1:A:781:LEU:HD23	1:A:781:LEU:C	2.26	0.60
1:B:351:ASP:HB3	1:B:355:THR:OG1	2.01	0.60
1:B:572:LYS:N	1:B:572:LYS:HD2	2.16	0.60
1:A:310:GLY:O	1:A:314:VAL:HG23	2.02	0.60
1:B:749:GLU:HG3	1:B:753:ILE:HD13	1.81	0.60
1:B:968:LEU:O	1:B:972:LYS:HG2	2.01	0.60
1:A:421:ASN:HD22	1:A:421:ASN:C	2.07	0.60
1:A:617:ALA:O	1:A:821:PRO:HD3	2.01	0.60
1:A:778:THR:HB	1:A:783:LEU:O	2.01	0.60
1:B:795:VAL:CG2	1:B:901:LEU:HD11	2.30	0.60
1:A:781:LEU:HD23	1:A:782:GLY:N	2.17	0.60
1:B:95:LEU:HD23	1:B:96:LEU:N	2.16	0.60
1:B:802:LEU:N	1:B:803:PRO:CD	2.63	0.60
1:B:784:PRO:HD2	1:B:870:LEU:HD11	1.81	0.60
1:A:119:LEU:O	1:A:122:TYR:HB3	2.02	0.60
1:A:567:ARG:NH1	1:A:570:PRO:HA	2.13	0.60
1:B:319:LEU:HD23	1:B:336:LEU:HB3	1.84	0.60
1:A:489:ARG:H	1:A:489:ARG:NE	1.99	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:577:VAL:HG11	1:B:583:ARG:HH11	1.67	0.59
1:B:760:PHE:CB	1:B:807:LEU:HD12	2.29	0.59
1:A:600:LEU:C	1:A:600:LEU:CD1	2.75	0.59
1:A:894:PRO:HB2	1:A:959:LEU:C	2.26	0.59
1:B:852:ALA:HA	1:B:899:MET:CB	2.32	0.59
1:B:865:VAL:HG13	1:B:869:GLN:HG3	1.83	0.59
1:A:94:ILE:O	1:A:98:LEU:HG	2.02	0.59
1:A:271:VAL:HG12	1:A:275:ASN:HD21	1.67	0.59
1:A:577:VAL:HG11	1:A:583:ARG:HH11	1.67	0.59
1:B:489:ARG:H	1:B:489:ARG:NE	2.00	0.59
1:A:303:ALA:O	1:A:306:ALA:HB3	2.03	0.59
1:B:57:PHE:CE1	1:B:102:ALA:HB2	2.36	0.59
1:B:855:TRP:CA	1:B:859:ALA:CB	2.73	0.59
1:B:248:PRO:O	1:B:249:LEU:C	2.43	0.59
1:B:826:GLU:HG2	1:B:827:PRO:HD2	1.85	0.59
1:A:95:LEU:HA	1:A:98:LEU:CD1	2.32	0.59
1:B:708:ALA:HB3	1:B:709:PRO:HD3	1.85	0.59
1:B:759:GLN:HA	1:B:762:ARG:HD2	1.84	0.59
1:B:784:PRO:CD	1:B:870:LEU:CD1	2.80	0.59
1:A:188:ILE:HD12	1:A:188:ILE:H	1.67	0.59
1:A:247:THR:HG23	1:A:250:GLN:CG	2.31	0.59
1:A:762:ARG:HB3	1:A:837:TYR:CE2	2.38	0.59
1:A:869:GLN:OE1	1:A:883:PHE:HB3	2.02	0.59
1:B:214:ILE:HD12	1:B:214:ILE:N	2.17	0.59
1:B:317:THR:O	1:B:321:LEU:HG	2.03	0.59
1:B:369:ILE:HD12	1:B:369:ILE:H	1.66	0.59
1:A:334:ARG:HH11	1:A:334:ARG:CB	2.16	0.59
1:A:369:ILE:HD13	1:A:529:ARG:O	2.03	0.59
1:A:826:GLU:HG2	1:A:827:PRO:HD2	1.85	0.59
1:B:18:VAL:HG21	1:B:150:ILE:HD11	1.85	0.59
1:A:334:ARG:HB3	1:A:334:ARG:NH1	2.18	0.58
1:A:369:ILE:HG12	1:A:528:VAL:CG1	2.33	0.58
1:B:322:GLY:HA2	1:B:325:ARG:HH21	1.68	0.58
1:B:950:VAL:O	1:B:954:PRO:HD2	2.02	0.58
1:A:311:LEU:O	1:A:315:ILE:HD13	2.03	0.58
1:A:413:LEU:HG	1:A:564:LEU:HD12	1.85	0.58
1:A:65:LEU:O	1:A:68:ALA:HB3	2.04	0.58
1:A:789:PRO:C	1:A:791:GLN:H	2.11	0.58
1:B:89:VAL:O	1:B:93:VAL:HG23	2.04	0.58
1:B:319:LEU:HD23	1:B:336:LEU:C	2.28	0.58
1:B:421:ASN:HD22	1:B:422:ASP:N	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:LEU:HD11	1:A:233:GLY:HA2	1.85	0.58
1:A:120:LYS:CE	1:A:728:LYS:NZ	2.63	0.58
1:B:53:VAL:HG22	1:B:106:VAL:HG21	1.85	0.58
1:B:869:GLN:OE1	1:B:883:PHE:HB3	2.03	0.58
1:A:90:GLU:HG3	1:A:91:PRO:N	2.18	0.58
1:A:247:THR:HG1	1:A:250:GLN:HB3	1.63	0.58
1:A:968:LEU:O	1:A:972:LYS:HG2	2.03	0.58
1:A:355:THR:HG23	1:A:720:MET:HG2	1.85	0.58
1:A:814:LEU:H	1:A:814:LEU:HD23	1.68	0.58
1:A:863:PRO:HB2	1:A:865:VAL:HG23	1.84	0.58
1:B:121:GLU:O	1:B:121:GLU:HG2	2.02	0.58
1:B:556:ARG:HG2	1:B:644:GLU:HG3	1.85	0.58
1:A:421:ASN:HD22	1:A:422:ASP:N	2.02	0.58
1:A:725:ALA:O	1:A:729:THR:HG23	2.04	0.58
1:A:963:ASP:N	1:A:966:GLN:HE21	2.01	0.58
1:A:964:LEU:O	1:A:968:LEU:HG	2.03	0.58
1:B:113:GLU:O	1:B:117:GLU:HG2	2.03	0.58
1:B:364:CYS:O	1:B:384:ILE:HD13	2.03	0.58
1:B:865:VAL:HG13	1:B:869:GLN:CG	2.33	0.58
1:B:964:LEU:O	1:B:968:LEU:HG	2.03	0.58
1:A:184:SER:HB3	1:A:627:ASP:OD2	2.04	0.58
1:A:308:PRO:HG3	1:A:765:ILE:HG12	1.84	0.58
1:A:783:LEU:HD12	1:A:783:LEU:N	2.12	0.58
1:B:340:GLU:HG2	1:B:750:GLY:O	2.04	0.58
1:B:663:LEU:H	1:B:663:LEU:CD1	2.17	0.58
1:B:783:LEU:HA	1:B:870:LEU:HG	1.86	0.58
1:B:833:LEU:HD12	1:B:836:ARG:HD3	1.86	0.58
1:A:39:ASN:O	1:A:40:GLU:HB3	2.02	0.57
1:B:783:LEU:HD12	1:B:783:LEU:N	2.09	0.57
1:A:338:SER:HA	1:A:341:THR:HB	1.86	0.57
1:A:952:PRO:O	1:A:956:ILE:HG12	2.04	0.57
1:B:342:LEU:HG	1:B:716:ILE:CG2	2.29	0.57
1:A:788:ILE:HD12	1:A:791:GLN:HB2	1.86	0.57
1:A:852:ALA:HA	1:A:899:MET:HG2	1.86	0.57
1:B:898:THR:OG1	1:B:959:LEU:CA	2.52	0.57
1:A:715:GLU:HB3	1:A:716:ILE:HD12	1.86	0.57
1:A:847:ALA:HB1	1:A:903:VAL:HG11	1.85	0.57
1:A:39:ASN:O	1:A:143:ARG:HA	2.05	0.57
1:B:894:PRO:HB2	1:B:959:LEU:C	2.29	0.57
1:A:760:PHE:O	1:A:764:LEU:HB2	2.05	0.57
1:B:91:PRO:O	1:B:94:ILE:HG22	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:789:PRO:C	1:B:791:GLN:H	2.13	0.57
1:B:795:VAL:O	1:B:799:THR:HB	2.04	0.57
1:A:341:THR:CG2	1:A:716:ILE:HD11	2.24	0.57
1:A:833:LEU:HD12	1:A:836:ARG:HD3	1.87	0.57
1:B:96:LEU:C	1:B:96:LEU:HD23	2.30	0.57
1:B:413:LEU:HG	1:B:564:LEU:HD12	1.86	0.57
1:A:898:THR:HA	1:A:959:LEU:CD2	2.22	0.57
1:B:112:ALA:C	1:B:116:ILE:HD12	2.30	0.57
1:B:528:VAL:HG21	1:B:541:VAL:HG11	1.85	0.57
1:A:867:TYR:O	1:A:871:THR:HG23	2.04	0.56
1:B:384:ILE:N	1:B:384:ILE:CD1	2.67	0.56
1:B:412:GLU:OE2	1:B:566:THR:HG21	2.04	0.56
1:B:898:THR:HA	1:B:959:LEU:CD2	2.23	0.56
1:B:964:LEU:C	1:B:964:LEU:HD23	2.30	0.56
1:A:315:ILE:CD1	1:A:760:PHE:HE1	2.18	0.56
1:A:782:GLY:HA3	1:A:871:THR:HB	1.88	0.56
1:B:520:GLY:O	1:B:524:ARG:HG3	2.04	0.56
1:A:756:ASN:O	1:A:759:GLN:HB2	2.05	0.56
1:A:802:LEU:HD11	1:A:939:LEU:HG	1.87	0.56
1:A:865:VAL:HG12	1:A:866:THR:O	2.05	0.56
1:B:749:GLU:HG3	1:B:753:ILE:CD1	2.34	0.56
1:B:762:ARG:HB3	1:B:837:TYR:CE2	2.40	0.56
1:A:311:LEU:CD2	1:A:761:ILE:HG23	2.36	0.56
1:B:311:LEU:O	1:B:315:ILE:HG12	2.06	0.56
1:B:620:ARG:NH2	1:B:622:ILE:HD11	2.19	0.56
1:A:402:ILE:HD13	1:A:402:ILE:H	1.70	0.56
1:A:423:SER:HB3	1:A:437:VAL:O	2.05	0.56
1:B:792:LEU:C	1:B:795:VAL:HG23	2.31	0.56
1:B:847:ALA:HB1	1:B:903:VAL:HG11	1.86	0.56
1:A:44:GLU:N	1:A:44:GLU:CD	2.64	0.56
1:B:41:LEU:HD11	1:B:233:GLY:HA2	1.87	0.56
1:B:369:ILE:HD13	1:B:529:ARG:O	2.05	0.56
1:B:423:SER:HB3	1:B:437:VAL:O	2.04	0.56
1:B:633:ILE:HD11	1:B:652:ALA:CB	2.36	0.56
1:B:866:THR:HG23	1:B:869:GLN:NE2	2.20	0.56
1:A:10:GLU:CD	1:A:10:GLU:H	2.12	0.56
1:A:360:GLN:HB3	1:A:389:TYR:CE2	2.40	0.56
1:A:364:CYS:HA	1:A:384:ILE:HB	1.87	0.56
1:A:840:ILE:CD1	1:A:840:ILE:N	2.69	0.56
1:A:852:ALA:HA	1:A:899:MET:CB	2.34	0.56
1:B:463:SER:OG	1:B:465:VAL:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:651:ARG:HG3	1:B:651:ARG:NH1	2.21	0.56
1:B:801:GLY:C	1:B:803:PRO:HD2	2.31	0.56
1:B:814:LEU:HD23	1:B:814:LEU:H	1.70	0.56
1:A:355:THR:HG21	1:A:701:THR:HG22	1.88	0.56
1:A:792:LEU:C	1:A:795:VAL:HG23	2.31	0.56
1:A:963:ASP:OD2	1:A:964:LEU:N	2.38	0.56
1:A:964:LEU:C	1:A:964:LEU:HD23	2.31	0.56
1:B:44:GLU:CD	1:B:44:GLU:N	2.63	0.56
1:B:157:ASP:CB	1:B:214:ILE:HD13	2.35	0.56
1:B:239:MET:CE	1:B:708:ALA:HB1	2.36	0.56
1:A:318:CYS:O	1:A:321:LEU:HB2	2.06	0.56
1:B:267:ILE:HD13	1:B:302:LEU:HD13	1.88	0.56
1:B:342:LEU:HD11	1:B:718:ILE:CD1	2.35	0.56
1:B:792:LEU:HA	1:B:795:VAL:HG21	1.88	0.56
1:B:832:TRP:CZ3	1:B:835:PHE:HD2	2.23	0.56
1:B:963:ASP:N	1:B:966:GLN:HE21	2.03	0.56
1:A:771:GLU:HG2	1:A:792:LEU:HD13	1.88	0.55
1:A:309:GLU:OE2	1:A:796:ASN:HB2	2.06	0.55
1:A:914:ASN:C	1:A:916:LEU:N	2.64	0.55
1:B:816:ILE:HA	1:B:819:ARG:NH2	2.16	0.55
1:A:355:THR:CG2	1:A:701:THR:HG22	2.36	0.55
1:A:759:GLN:HE22	1:A:762:ARG:HH11	1.54	0.55
1:B:121:GLU:O	1:B:121:GLU:CG	2.54	0.55
1:B:848:THR:O	1:B:852:ALA:HB3	2.06	0.55
1:A:795:VAL:HA	1:A:799:THR:OG1	2.07	0.55
1:A:832:TRP:CZ3	1:A:835:PHE:HD2	2.24	0.55
1:B:311:LEU:CD1	1:B:761:ILE:HD12	2.30	0.55
1:B:705:VAL:HG22	1:B:726:VAL:HG21	1.89	0.55
1:B:852:ALA:HA	1:B:899:MET:HG2	1.89	0.55
1:A:249:LEU:O	1:A:252:LYS:HB2	2.06	0.55
1:A:879:ASP:OD1	1:A:882:HIS:HB2	2.07	0.55
1:B:237:ASP:O	1:B:238:GLN:C	2.48	0.55
1:B:557:ASP:HB3	1:B:559:LEU:HG	1.89	0.55
1:A:329:LYS:O	1:A:330:ASN:HB2	2.07	0.55
1:A:757:MET:HG2	1:A:760:PHE:HZ	1.65	0.55
1:A:792:LEU:HA	1:A:795:VAL:HG21	1.87	0.55
1:A:899:MET:SD	1:A:962:LEU:HD22	2.46	0.55
1:B:662:PRO:HG2	1:B:665:GLU:HG2	1.87	0.55
1:B:771:GLU:HG2	1:B:792:LEU:HD13	1.89	0.55
1:A:747:VAL:CG1	1:A:817:MET:HE1	2.31	0.55
1:A:866:THR:HG23	1:A:869:GLN:HE21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:ASN:O	1:B:143:ARG:HA	2.07	0.55
1:B:600:LEU:C	1:B:600:LEU:CD1	2.80	0.55
1:B:762:ARG:HH22	1:B:918:GLU:HG3	1.72	0.55
1:A:463:SER:OG	1:A:465:VAL:HG22	2.06	0.55
1:A:41:LEU:HB3	1:A:44:GLU:OE2	2.07	0.54
1:A:460:ARG:CZ	1:A:461:ASN:HD21	2.21	0.54
1:A:848:THR:O	1:A:852:ALA:HB3	2.07	0.54
1:B:782:GLY:C	1:B:871:THR:HA	2.32	0.54
1:A:757:MET:O	1:A:761:ILE:HG13	2.07	0.54
1:B:248:PRO:HA	1:B:251:GLN:HB2	1.88	0.54
1:B:333:VAL:HG11	1:B:339:VAL:HG22	1.89	0.54
1:B:899:MET:SD	1:B:962:LEU:HD22	2.47	0.54
1:A:120:LYS:HE3	1:A:728:LYS:HE3	1.89	0.54
1:A:350:SER:HG	1:A:356:LEU:HD13	1.70	0.54
1:A:355:THR:HG23	1:A:720:MET:CG	2.36	0.54
1:B:747:VAL:CG1	1:B:817:MET:HE1	2.37	0.54
1:B:879:ASP:OD1	1:B:882:HIS:HB2	2.07	0.54
1:B:340:GLU:HA	1:B:750:GLY:HA2	1.88	0.54
1:B:757:MET:HE3	1:B:761:ILE:HD11	1.89	0.54
1:A:792:LEU:CA	1:A:795:VAL:HG23	2.38	0.54
1:B:759:GLN:HE22	1:B:762:ARG:HH11	1.55	0.54
1:A:898:THR:OG1	1:A:959:LEU:CA	2.55	0.54
1:B:722:SER:OG	1:B:738:ASP:OD2	2.20	0.54
1:A:315:ILE:CD1	1:A:760:PHE:CE1	2.91	0.54
1:A:315:ILE:HD11	1:A:760:PHE:HE1	1.71	0.54
1:A:366:MET:HE2	1:A:384:ILE:HD11	1.88	0.54
1:A:782:GLY:O	1:A:783:LEU:O	2.26	0.54
1:A:914:ASN:HD22	1:A:922:LEU:HD11	1.73	0.54
1:B:338:SER:HA	1:B:341:THR:HB	1.90	0.54
1:B:369:ILE:HG12	1:B:528:VAL:CG1	2.38	0.54
1:B:402:ILE:HD12	1:B:403:ARG:C	2.32	0.54
1:B:518:PRO:C	1:B:522:ILE:HD13	2.33	0.54
1:B:787:LEU:CD1	1:B:900:ALA:HB1	2.34	0.54
1:B:815:ASP:O	1:B:819:ARG:NE	2.41	0.54
1:B:912:ALA:HB1	1:B:933:LEU:HD11	1.90	0.54
1:A:165:ILE:HG21	1:A:168:ILE:HD11	1.89	0.54
1:B:755:ASN:O	1:B:759:GLN:HG2	2.07	0.54
1:A:782:GLY:C	1:A:871:THR:HA	2.32	0.54
1:B:112:ALA:O	1:B:116:ILE:HD12	2.07	0.54
1:A:180:LEU:HD12	1:A:180:LEU:O	2.08	0.54
1:B:140:ILE:HD13	1:B:140:ILE:N	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:LEU:HA	1:A:549:ILE:HD12	1.90	0.53
1:A:762:ARG:NH2	1:A:833:LEU:CD1	2.71	0.53
1:A:817:MET:C	1:A:819:ARG:N	2.66	0.53
1:A:840:ILE:HD13	1:A:840:ILE:H	1.74	0.53
1:B:116:ILE:HD11	1:B:334:ARG:HG2	1.90	0.53
1:B:749:GLU:C	1:B:751:ARG:H	2.16	0.53
1:B:979:GLY:O	1:B:983:ILE:HG12	2.08	0.53
1:A:326:MET:HB3	1:A:331:ALA:CB	2.37	0.53
1:B:761:ILE:O	1:B:765:ILE:HG12	2.08	0.53
1:B:795:VAL:HA	1:B:799:THR:OG1	2.08	0.53
1:B:914:ASN:C	1:B:916:LEU:N	2.65	0.53
1:B:914:ASN:HD22	1:B:922:LEU:HD11	1.70	0.53
1:A:189:LYS:HE3	1:A:207:MET:O	2.09	0.53
1:A:979:GLY:O	1:A:983:ILE:HG12	2.08	0.53
1:B:460:ARG:CZ	1:B:461:ASN:HD21	2.21	0.53
1:B:792:LEU:CA	1:B:795:VAL:HG23	2.39	0.53
1:A:86:THR:O	1:A:89:VAL:HB	2.08	0.53
1:A:129:VAL:HG12	1:A:151:VAL:HG22	1.90	0.53
1:A:161:ALA:HA	1:A:210:SER:HB2	1.91	0.53
1:A:249:LEU:HB2	1:A:340:GLU:OE1	2.08	0.53
1:A:395:VAL:CG1	1:A:402:ILE:HD11	2.35	0.53
1:B:519:GLU:CD	1:B:519:GLU:N	2.63	0.53
1:A:715:GLU:C	1:A:716:ILE:HD12	2.32	0.53
1:B:62:VAL:CG1	1:B:98:LEU:HD22	2.39	0.53
1:B:847:ALA:HA	1:B:973:ILE:HG21	1.90	0.53
1:A:66:LEU:HD13	1:A:98:LEU:HD13	1.91	0.53
1:A:847:ALA:HA	1:A:973:ILE:CG2	2.38	0.53
1:B:65:LEU:HB3	1:B:98:LEU:HD21	1.91	0.53
1:B:129:VAL:HG12	1:B:151:VAL:HG22	1.90	0.53
1:A:718:ILE:HD12	1:A:718:ILE:N	2.23	0.53
1:A:762:ARG:NH2	1:A:833:LEU:HD11	2.24	0.53
1:B:771:GLU:OE2	1:B:792:LEU:HD13	2.07	0.53
1:A:249:LEU:O	1:A:252:LYS:N	2.39	0.53
1:B:963:ASP:OD2	1:B:964:LEU:N	2.41	0.53
1:A:305:ALA:C	1:A:768:ASN:HD22	2.17	0.53
1:A:306:ALA:O	1:A:308:PRO:HD3	2.08	0.53
1:B:46:GLY:O	1:B:47:LYS:C	2.52	0.53
1:B:161:ALA:HA	1:B:210:SER:HB2	1.91	0.53
1:B:762:ARG:NH2	1:B:833:LEU:CD1	2.71	0.53
1:A:315:ILE:HD12	1:A:760:PHE:CE1	2.44	0.53
1:A:847:ALA:HA	1:A:973:ILE:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:735:LEU:HD11	1:B:743:ILE:CD1	2.17	0.53
1:B:725:ALA:O	1:B:729:THR:HG23	2.09	0.52
1:A:116:ILE:HG13	1:A:334:ARG:HD2	1.91	0.52
1:A:286:GLY:HA2	1:A:290:ARG:HB3	1.90	0.52
1:A:413:LEU:C	1:A:413:LEU:HD23	2.35	0.52
1:A:782:GLY:CA	1:A:871:THR:HA	2.39	0.52
1:B:23:GLY:HA2	1:B:150:ILE:CD1	2.39	0.52
1:B:248:PRO:HD2	1:B:341:THR:HG21	1.91	0.52
1:A:633:ILE:HD11	1:A:652:ALA:CB	2.39	0.52
1:B:326:MET:HE3	1:B:331:ALA:CB	2.40	0.52
1:A:311:LEU:HD21	1:A:761:ILE:HG23	1.90	0.52
1:A:326:MET:HE2	1:A:746:ALA:HB2	1.90	0.52
1:B:633:ILE:HD11	1:B:652:ALA:HB1	1.91	0.52
1:B:662:PRO:HG2	1:B:665:GLU:CG	2.40	0.52
1:B:743:ILE:N	1:B:743:ILE:HD12	2.25	0.52
1:B:847:ALA:HA	1:B:973:ILE:CG2	2.39	0.52
1:B:856:PHE:CZ	1:B:896:PRO:HG3	2.45	0.52
1:A:754:TYR:O	1:A:757:MET:N	2.37	0.52
1:A:978:ILE:O	1:A:982:GLU:HB2	2.09	0.52
1:B:545:ILE:O	1:B:549:ILE:HG12	2.09	0.52
1:B:969:MET:HE2	1:B:973:ILE:HG12	1.91	0.52
1:B:56:GLN:HG3	1:B:106:VAL:CG2	2.39	0.52
1:B:865:VAL:HG12	1:B:866:THR:O	2.08	0.52
1:A:75:LEU:CD1	1:A:300:VAL:HB	2.38	0.52
1:B:600:LEU:HD13	1:B:600:LEU:O	2.09	0.52
1:A:42:PRO:HD3	1:A:228:VAL:HG12	1.92	0.52
1:A:116:ILE:CD1	1:A:332:ILE:HG21	2.40	0.52
1:A:248:PRO:CB	1:A:341:THR:HG23	2.40	0.52
1:B:291:GLY:O	1:B:292:ALA:HB2	2.09	0.52
1:A:51:GLU:O	1:A:54:ILE:HB	2.10	0.52
1:A:189:LYS:HD2	1:A:205:LYS:O	2.10	0.52
1:A:489:ARG:H	1:A:489:ARG:HD3	1.75	0.52
1:A:611:ILE:CD1	1:A:639:ILE:HD12	2.40	0.52
1:A:651:ARG:HG3	1:A:651:ARG:NH1	2.23	0.52
1:A:859:ALA:O	1:A:861:ASP:N	2.43	0.52
1:A:895:GLU:CD	1:A:895:GLU:H	2.17	0.52
1:A:969:MET:HE2	1:A:973:ILE:HG12	1.91	0.52
1:B:94:ILE:HD13	1:B:98:LEU:HG	1.92	0.52
1:B:847:ALA:HB1	1:B:903:VAL:CG1	2.39	0.52
1:B:988:ALA:HA	1:B:992:LEU:HB2	1.91	0.52
1:A:912:ALA:HB1	1:A:933:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:LEU:HD12	1:B:249:LEU:O	2.10	0.52
1:A:369:ILE:HD12	1:A:369:ILE:N	2.25	0.51
1:A:680:GLU:O	1:A:683:HIS:HB2	2.10	0.51
1:A:737:ASP:O	1:A:738:ASP:HB2	2.10	0.51
1:B:48:SER:OG	1:B:51:GLU:HG2	2.09	0.51
1:B:111:ASN:O	1:B:114:ASN:HB2	2.10	0.51
1:B:329:LYS:O	1:B:330:ASN:CB	2.59	0.51
1:B:458:GLU:OE2	1:B:460:ARG:HG2	2.10	0.51
1:B:735:LEU:HD13	1:B:743:ILE:HD11	1.86	0.51
1:B:249:LEU:HG	1:B:250:GLN:N	2.25	0.51
1:B:782:GLY:HA3	1:B:871:THR:HB	1.92	0.51
1:A:367:PHE:C	1:A:367:PHE:CD2	2.88	0.51
1:A:383:SER:O	1:A:384:ILE:HD13	2.10	0.51
1:A:611:ILE:HD11	1:A:639:ILE:HD12	1.92	0.51
1:B:10:GLU:H	1:B:10:GLU:CD	2.13	0.51
1:B:341:THR:HB	1:B:716:ILE:HD11	1.91	0.51
1:B:413:LEU:C	1:B:413:LEU:HD23	2.35	0.51
1:B:762:ARG:NH2	1:B:833:LEU:HD11	2.25	0.51
1:A:94:ILE:HG23	1:A:95:LEU:N	2.26	0.51
1:B:311:LEU:CD1	1:B:761:ILE:HD13	2.35	0.51
1:A:66:LEU:O	1:A:69:ALA:HB3	2.11	0.51
1:A:94:ILE:HG23	1:A:95:LEU:H	1.76	0.51
1:B:663:LEU:CD1	1:B:663:LEU:N	2.74	0.51
1:B:866:THR:HG23	1:B:869:GLN:HE21	1.76	0.51
1:A:60:LEU:HD23	1:A:257:GLY:HA3	1.93	0.51
1:A:60:LEU:N	1:A:63:ARG:HH21	2.09	0.51
1:B:463:SER:OG	1:B:466:GLU:HG3	2.10	0.51
1:A:463:SER:OG	1:A:466:GLU:HG3	2.11	0.51
1:A:600:LEU:HD12	1:A:600:LEU:N	2.26	0.51
1:A:633:ILE:HD11	1:A:652:ALA:HB1	1.93	0.51
1:A:810:ASN:OD1	1:A:930:ASN:ND2	2.43	0.51
1:B:367:PHE:C	1:B:367:PHE:CD2	2.88	0.51
1:B:369:ILE:HD11	1:B:593:PHE:CD1	2.46	0.51
1:B:878:GLU:C	1:B:880:HIS:H	2.19	0.51
1:A:600:LEU:O	1:A:600:LEU:CD1	2.58	0.51
1:B:355:THR:HG23	1:B:720:MET:CG	2.40	0.51
1:B:810:ASN:OD1	1:B:930:ASN:ND2	2.44	0.51
1:A:65:LEU:HG	1:A:94:ILE:CD1	2.40	0.51
1:A:855:TRP:CA	1:A:859:ALA:CB	2.74	0.51
1:A:91:PRO:HA	1:A:94:ILE:HG22	1.91	0.50
1:B:41:LEU:HB3	1:B:44:GLU:OE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:765:ILE:O	1:B:766:SER:C	2.53	0.50
1:A:93:VAL:O	1:A:97:ILE:HG12	2.12	0.50
1:A:222:ILE:HG23	1:A:222:ILE:O	2.11	0.50
1:A:907:ILE:HD11	1:A:974:SER:CA	2.41	0.50
1:A:988:ALA:HA	1:A:992:LEU:HB2	1.92	0.50
1:B:235:ILE:HG21	1:B:705:VAL:HG12	1.93	0.50
1:B:249:LEU:C	1:B:249:LEU:HD12	2.36	0.50
1:B:749:GLU:OE2	1:B:753:ILE:HD11	2.10	0.50
1:A:104:VAL:O	1:A:107:TRP:HB3	2.12	0.50
1:A:813:ASP:OD2	1:A:813:ASP:N	2.33	0.50
1:B:238:GLN:O	1:B:242:THR:HG23	2.10	0.50
1:B:369:ILE:HD12	1:B:369:ILE:N	2.26	0.50
1:B:783:LEU:HG	1:B:870:LEU:HD23	1.94	0.50
1:B:845:GLY:C	1:B:847:ALA:H	2.18	0.50
1:B:939:LEU:O	1:B:943:LEU:HG	2.12	0.50
1:A:116:ILE:HD11	1:A:332:ILE:HG21	1.92	0.50
1:A:291:GLY:O	1:A:292:ALA:HB2	2.11	0.50
1:A:762:ARG:HH22	1:A:918:GLU:CA	2.25	0.50
1:A:963:ASP:H	1:A:966:GLN:NE2	2.08	0.50
1:B:172:THR:CG2	1:B:489:ARG:HD2	2.41	0.50
1:B:802:LEU:HD11	1:B:939:LEU:HG	1.89	0.50
1:B:855:TRP:HD1	1:B:966:GLN:OE1	1.94	0.50
1:A:252:LYS:HE2	1:A:252:LYS:HA	1.94	0.50
1:B:60:LEU:CD2	1:B:257:GLY:HA3	2.42	0.50
1:B:103:ILE:HG23	1:B:104:VAL:N	2.27	0.50
1:B:222:ILE:O	1:B:222:ILE:HG23	2.10	0.50
1:A:307:ILE:O	1:A:309:GLU:N	2.45	0.50
1:A:771:GLU:OE2	1:A:792:LEU:HD13	2.12	0.50
1:B:116:ILE:HG13	1:B:332:ILE:HG21	1.93	0.50
1:B:320:ALA:O	1:B:324:ARG:HG2	2.12	0.50
1:A:82:GLU:HG3	1:A:83:GLU:N	2.26	0.50
1:B:338:SER:HB2	1:B:716:ILE:HD12	1.94	0.50
1:B:897:MET:HE3	1:B:958:LYS:HB3	1.94	0.50
1:B:947:ILE:HD11	1:B:957:PHE:CZ	2.46	0.50
1:A:489:ARG:CD	1:A:489:ARG:N	2.75	0.50
1:B:236:ARG:O	1:B:239:MET:HB3	2.11	0.50
1:B:350:SER:OG	1:B:356:LEU:HD13	2.12	0.50
1:B:352:LYS:HE2	1:B:627:ASP:HB3	1.93	0.50
1:B:893:ALA:O	1:B:896:PRO:HD2	2.12	0.50
1:A:338:SER:O	1:A:339:VAL:C	2.55	0.50
1:B:334:ARG:HD3	1:B:731:SER:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:505:ARG:HB3	1:B:508:VAL:CG2	2.42	0.50
1:A:762:ARG:HH22	1:A:918:GLU:HG3	1.77	0.49
1:A:311:LEU:HB3	1:A:312:PRO:HD3	1.95	0.49
1:A:505:ARG:HB3	1:A:508:VAL:CG2	2.42	0.49
1:A:624:ILE:CG2	1:A:684:LYS:HG2	2.42	0.49
1:A:765:ILE:O	1:A:766:SER:C	2.55	0.49
1:A:775:ILE:HD13	1:A:775:ILE:H	1.77	0.49
1:B:465:VAL:HG23	1:B:466:GLU:N	2.27	0.49
1:B:757:MET:HG2	1:B:760:PHE:HZ	1.71	0.49
1:A:127:GLY:HA3	1:A:145:ILE:HD11	1.94	0.49
1:A:261:SER:O	1:A:264:ILE:HB	2.11	0.49
1:A:326:MET:O	1:A:331:ALA:HB3	2.12	0.49
1:B:743:ILE:HD12	1:B:743:ILE:H	1.77	0.49
1:B:787:LEU:HD23	1:B:791:GLN:OE1	2.12	0.49
1:B:907:ILE:HD11	1:B:974:SER:CA	2.40	0.49
1:A:369:ILE:HD11	1:A:593:PHE:CD1	2.47	0.49
1:A:947:ILE:HD11	1:A:957:PHE:CZ	2.46	0.49
1:B:25:THR:HA	1:B:132:ALA:HB3	1.94	0.49
1:B:306:ALA:O	1:B:308:PRO:HD3	2.12	0.49
1:B:340:GLU:HA	1:B:750:GLY:CA	2.42	0.49
1:B:352:LYS:HE2	1:B:627:ASP:CB	2.42	0.49
1:A:239:MET:HE1	1:A:726:VAL:HG12	1.95	0.49
1:A:320:ALA:O	1:A:324:ARG:HG2	2.11	0.49
1:A:342:LEU:HD22	1:A:747:VAL:CG2	2.42	0.49
1:A:458:GLU:OE2	1:A:460:ARG:HG2	2.12	0.49
1:A:784:PRO:HD3	1:A:870:LEU:HD12	1.94	0.49
1:B:383:SER:CA	1:B:384:ILE:HD12	2.42	0.49
1:B:737:ASP:C	1:B:739:ASN:N	2.69	0.49
1:B:895:GLU:CD	1:B:895:GLU:H	2.20	0.49
1:B:978:ILE:O	1:B:982:GLU:HB2	2.12	0.49
1:A:108:GLN:HA	1:A:108:GLN:NE2	2.26	0.49
1:A:939:LEU:O	1:A:943:LEU:HG	2.12	0.49
1:A:957:PHE:O	1:A:959:LEU:HG	2.13	0.49
1:B:633:ILE:HD12	1:B:642:PHE:CE1	2.47	0.49
1:B:654:THR:OG1	1:B:657:GLU:HG3	2.12	0.49
1:B:953:LEU:HB2	1:B:954:PRO:HD3	1.95	0.49
1:A:765:ILE:HD13	1:A:765:ILE:C	2.38	0.49
1:A:847:ALA:HB1	1:A:903:VAL:CG1	2.42	0.49
1:B:244:GLN:O	1:B:246:LYS:N	2.45	0.49
1:B:489:ARG:H	1:B:489:ARG:HD3	1.75	0.49
1:A:832:TRP:NE1	1:A:988:ALA:HB2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:ILE:HD11	1:B:145:ILE:HD11	1.95	0.49
1:B:782:GLY:CA	1:B:871:THR:HA	2.43	0.49
1:B:786:ALA:C	1:B:897:MET:HG2	2.37	0.49
1:B:267:ILE:HG21	1:B:302:LEU:CD1	2.42	0.49
1:B:794:TRP:CD1	1:B:794:TRP:C	2.90	0.49
1:B:795:VAL:HA	1:B:799:THR:CB	2.43	0.49
1:A:179:ILE:HG22	1:A:179:ILE:O	2.13	0.49
1:A:856:PHE:CZ	1:A:896:PRO:HG3	2.48	0.49
1:B:55:GLU:O	1:B:58:GLU:HB2	2.13	0.49
1:B:333:VAL:HG12	1:B:335:SER:O	2.13	0.49
1:A:179:ILE:HG23	1:A:724:THR:CG2	2.43	0.48
1:A:320:ALA:O	1:A:323:THR:HB	2.13	0.48
1:A:519:GLU:CD	1:A:519:GLU:N	2.63	0.48
1:A:705:VAL:HG22	1:A:726:VAL:HG21	1.94	0.48
1:A:787:LEU:CD1	1:A:900:ALA:HB1	2.40	0.48
1:A:855:TRP:HD1	1:A:966:GLN:OE1	1.96	0.48
1:B:622:ILE:O	1:B:624:ILE:HD12	2.13	0.48
1:B:762:ARG:HH22	1:B:918:GLU:CA	2.26	0.48
1:B:763:TYR:CE1	1:B:912:ALA:HB2	2.48	0.48
1:A:48:SER:OG	1:A:51:GLU:HG2	2.12	0.48
1:A:758:LYS:O	1:A:762:ARG:HG3	2.13	0.48
1:A:878:GLU:C	1:A:880:HIS:H	2.20	0.48
1:B:358:THR:OG1	1:B:602:PRO:HG2	2.13	0.48
1:B:758:LYS:O	1:B:762:ARG:HG3	2.14	0.48
1:B:759:GLN:O	1:B:760:PHE:C	2.55	0.48
1:A:79:GLU:HG2	1:A:84:THR:HB	1.94	0.48
1:A:708:ALA:HB3	1:A:709:PRO:CD	2.39	0.48
1:A:48:SER:H	1:A:51:GLU:HG2	1.79	0.48
1:A:697:ILE:HD12	1:A:697:ILE:N	2.29	0.48
1:A:795:VAL:HA	1:A:799:THR:CB	2.43	0.48
1:B:855:TRP:HZ3	1:B:856:PHE:CE2	2.32	0.48
1:A:314:VAL:HG11	1:A:804:ALA:HB1	1.96	0.48
1:A:833:LEU:CA	1:A:836:ARG:HB2	2.39	0.48
1:A:931:ILE:HD12	1:A:931:ILE:N	2.28	0.48
1:B:611:ILE:CD1	1:B:621:VAL:HG21	2.41	0.48
1:B:969:MET:HE3	1:B:969:MET:HA	1.95	0.48
1:A:235:ILE:HG21	1:A:705:VAL:HG12	1.94	0.48
1:A:878:GLU:HG3	1:A:879:ASP:N	2.23	0.48
1:B:48:SER:H	1:B:51:GLU:HG2	1.79	0.48
1:B:363:VAL:CG1	1:B:448:LEU:HD13	2.44	0.48
1:B:799:THR:HG21	1:B:905:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:832:TRP:NE1	1:B:988:ALA:HB2	2.28	0.48
1:B:267:ILE:HG21	1:B:302:LEU:HD13	1.94	0.48
1:B:804:ALA:O	1:B:805:THR:C	2.56	0.48
1:A:42:PRO:O	1:A:43:ALA:O	2.31	0.48
1:A:794:TRP:CD1	1:A:794:TRP:C	2.91	0.48
1:A:833:LEU:HD11	1:A:837:TYR:HE1	1.79	0.48
1:A:947:ILE:HD11	1:A:957:PHE:CE2	2.49	0.48
1:B:255:GLU:C	1:B:257:GLY:H	2.22	0.48
1:B:787:LEU:HD11	1:B:900:ALA:CB	2.37	0.48
1:B:813:ASP:HB2	1:B:815:ASP:OD1	2.14	0.48
1:A:359:ASN:O	1:A:359:ASN:ND2	2.46	0.48
1:A:787:LEU:HD23	1:A:791:GLN:OE1	2.13	0.48
1:B:489:ARG:CD	1:B:489:ARG:N	2.75	0.48
1:B:663:LEU:N	1:B:663:LEU:HD12	2.29	0.48
1:B:762:ARG:HH22	1:B:918:GLU:CB	2.27	0.48
1:A:387:SER:HB2	1:A:602:PRO:HB2	1.96	0.47
1:A:855:TRP:O	1:A:862:GLY:HA3	2.14	0.47
1:B:84:THR:HA	1:B:87:ALA:HB3	1.95	0.47
1:B:756:ASN:O	1:B:759:GLN:CB	2.55	0.47
1:B:784:PRO:HD3	1:B:870:LEU:HD12	1.94	0.47
1:B:852:ALA:O	1:B:855:TRP:HB3	2.14	0.47
1:B:899:MET:O	1:B:903:VAL:HG23	2.14	0.47
1:A:247:THR:CG2	1:A:250:GLN:HB3	2.44	0.47
1:A:763:TYR:CE1	1:A:912:ALA:HB2	2.49	0.47
1:A:786:ALA:C	1:A:897:MET:HG2	2.38	0.47
1:B:150:ILE:N	1:B:150:ILE:CD1	2.78	0.47
1:B:880:HIS:HB3	1:B:881:PRO:HD3	1.95	0.47
1:A:356:LEU:CD1	1:A:740:PHE:CE1	2.97	0.47
1:A:840:ILE:N	1:A:840:ILE:HD13	2.29	0.47
1:B:48:SER:H	1:B:51:GLU:CG	2.27	0.47
1:B:633:ILE:HD12	1:B:642:PHE:HE1	1.79	0.47
1:B:783:LEU:HG	1:B:870:LEU:CD2	2.43	0.47
1:B:848:THR:O	1:B:852:ALA:CB	2.62	0.47
1:B:854:TRP:CE3	1:B:855:TRP:N	2.82	0.47
1:B:947:ILE:HD11	1:B:957:PHE:CE2	2.49	0.47
1:A:73:PHE:O	1:A:77:TRP:HB2	2.15	0.47
1:A:845:GLY:C	1:A:847:ALA:H	2.20	0.47
1:B:51:GLU:O	1:B:54:ILE:HB	2.14	0.47
1:A:84:THR:HA	1:A:87:ALA:HB3	1.97	0.47
1:A:247:THR:CB	1:A:250:GLN:HB3	2.38	0.47
1:A:813:ASP:HB2	1:A:815:ASP:OD1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:893:ALA:O	1:A:896:PRO:HD2	2.14	0.47
1:B:782:GLY:O	1:B:783:LEU:O	2.33	0.47
1:B:894:PRO:HB3	1:B:958:LYS:C	2.39	0.47
1:B:897:MET:HE3	1:B:958:LYS:O	2.13	0.47
1:B:917:SER:CB	1:B:920:GLN:HB2	2.44	0.47
1:A:340:GLU:OE2	1:A:344:CYS:SG	2.69	0.47
1:B:639:ILE:HD11	1:B:641:ILE:CD1	2.43	0.47
1:B:931:ILE:HD12	1:B:931:ILE:N	2.27	0.47
1:A:236:ARG:HD3	1:A:236:ARG:C	2.39	0.47
1:A:545:ILE:N	1:A:545:ILE:CD1	2.77	0.47
1:B:735:LEU:HD22	1:B:742:THR:HB	1.97	0.47
1:B:880:HIS:N	1:B:881:PRO:HD2	2.30	0.47
1:B:898:THR:OG1	1:B:959:LEU:HA	2.15	0.47
1:A:112:ALA:O	1:A:113:GLU:C	2.58	0.47
1:A:782:GLY:CA	1:A:871:THR:HB	2.45	0.47
1:A:971:LEU:O	1:A:975:LEU:HD23	2.14	0.47
1:B:18:VAL:CG2	1:B:150:ILE:HD11	2.45	0.47
1:B:787:LEU:HD21	1:B:901:LEU:CA	2.44	0.47
1:A:465:VAL:HG23	1:A:466:GLU:N	2.29	0.47
1:A:762:ARG:HH22	1:A:918:GLU:CB	2.28	0.47
1:A:783:LEU:H	1:A:783:LEU:CD1	2.12	0.47
1:A:897:MET:HE3	1:A:958:LYS:O	2.14	0.47
1:A:969:MET:HA	1:A:969:MET:HE3	1.97	0.47
1:B:258:GLU:O	1:B:259:GLN:C	2.57	0.47
1:B:402:ILE:HD12	1:B:402:ILE:C	2.40	0.47
1:B:71:ILE:HD13	1:B:71:ILE:N	2.29	0.47
1:B:173:LEU:O	1:B:188:ILE:HA	2.15	0.47
1:A:86:THR:HA	1:A:89:VAL:HG23	1.97	0.46
1:A:606:GLU:CD	1:A:606:GLU:N	2.71	0.46
1:A:899:MET:O	1:A:903:VAL:HG23	2.16	0.46
1:B:60:LEU:O	1:B:64:ILE:HG12	2.15	0.46
1:B:858:TYR:CD1	1:B:858:TYR:N	2.83	0.46
1:B:957:PHE:O	1:B:959:LEU:HG	2.15	0.46
1:A:232:ILE:HD13	1:A:232:ILE:C	2.40	0.46
1:A:787:LEU:HD21	1:A:901:LEU:CA	2.45	0.46
1:B:82:GLU:C	1:B:83:GLU:HG3	2.40	0.46
1:B:308:PRO:HB2	1:B:764:LEU:HD23	1.96	0.46
1:B:338:SER:O	1:B:339:VAL:C	2.57	0.46
1:B:553:GLY:O	1:B:554:THR:HG23	2.15	0.46
1:B:840:ILE:HD13	1:B:911:ASN:HD21	1.80	0.46
1:B:878:GLU:HG3	1:B:879:ASP:N	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:895:GLU:HB2	1:B:896:PRO:HD3	1.96	0.46
1:A:654:THR:OG1	1:A:657:GLU:HG3	2.16	0.46
1:B:155:VAL:HG13	1:B:155:VAL:O	2.15	0.46
1:B:322:GLY:HA2	1:B:325:ARG:HE	1.78	0.46
1:B:749:GLU:C	1:B:751:ARG:N	2.74	0.46
1:A:715:GLU:CB	1:A:716:ILE:HD12	2.44	0.46
1:A:855:TRP:HZ3	1:A:856:PHE:CE2	2.33	0.46
1:B:315:ILE:HD13	1:B:760:PHE:CE1	2.50	0.46
1:B:522:ILE:HD12	1:B:522:ILE:N	2.31	0.46
1:B:549:ILE:CD1	1:B:596:VAL:HG21	2.25	0.46
1:A:48:SER:H	1:A:51:GLU:CG	2.28	0.46
1:A:261:SER:O	1:A:264:ILE:CG1	2.62	0.46
1:A:759:GLN:HE22	1:A:762:ARG:NH1	2.13	0.46
1:A:783:LEU:HG	1:A:870:LEU:CD2	2.46	0.46
1:B:757:MET:HA	1:B:760:PHE:CE2	2.51	0.46
1:A:762:ARG:HB3	1:A:837:TYR:CE1	2.49	0.46
1:B:311:LEU:CB	1:B:312:PRO:CD	2.88	0.46
1:B:751:ARG:O	1:B:755:ASN:OD1	2.34	0.46
1:B:859:ALA:O	1:B:861:ASP:N	2.48	0.46
1:A:103:ILE:HD13	1:A:103:ILE:C	2.41	0.46
1:A:326:MET:HE3	1:A:331:ALA:HB2	1.96	0.46
1:A:361:MET:HE1	1:A:601:ASP:N	2.31	0.46
1:A:604:ARG:NE	1:A:720:MET:HE2	2.31	0.46
1:A:633:ILE:HD12	1:A:642:PHE:CE1	2.50	0.46
1:A:716:ILE:HD12	1:A:716:ILE:N	2.30	0.46
1:A:868:HIS:O	1:A:872:HIS:ND1	2.46	0.46
1:B:39:ASN:O	1:B:40:GLU:HB3	2.15	0.46
1:B:108:GLN:HA	1:B:108:GLN:HE21	1.80	0.46
1:B:633:ILE:CD1	1:B:642:PHE:HE1	2.27	0.46
1:B:737:ASP:OD2	1:B:739:ASN:HB2	2.16	0.46
1:A:917:SER:CB	1:A:920:GLN:HB2	2.46	0.46
1:B:249:LEU:HB2	1:B:340:GLU:OE1	2.16	0.46
1:A:443:THR:O	1:A:447:THR:HG23	2.16	0.46
1:A:716:ILE:HG22	1:A:718:ILE:HD11	1.98	0.46
1:A:854:TRP:CE3	1:A:855:TRP:N	2.84	0.46
1:B:0:ACE:H3	1:B:36:TYR:CE2	2.51	0.46
1:B:86:THR:HA	1:B:89:VAL:CG2	2.44	0.46
1:A:53:VAL:HG22	1:A:106:VAL:HG21	1.97	0.46
1:A:75:LEU:CD2	1:A:297:LYS:HA	2.46	0.46
1:A:96:LEU:C	1:A:96:LEU:HD23	2.41	0.46
1:A:299:ALA:HA	1:A:302:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:858:TYR:CD1	1:A:858:TYR:N	2.83	0.46
1:B:309:GLU:CD	1:B:309:GLU:H	2.23	0.46
1:B:606:GLU:CD	1:B:606:GLU:N	2.72	0.46
1:B:782:GLY:CA	1:B:871:THR:HB	2.46	0.46
1:A:790:VAL:O	1:A:790:VAL:CG1	2.61	0.45
1:A:947:ILE:HD11	1:A:957:PHE:CE1	2.52	0.45
1:B:491:ARG:HD2	1:B:588:GLU:OE2	2.15	0.45
1:B:788:ILE:HD11	1:B:958:LYS:HB2	1.98	0.45
1:B:827:PRO:HB2	1:B:828:LEU:H	1.50	0.45
1:A:304:VAL:CG1	1:A:793:LEU:HD21	2.45	0.45
1:A:832:TRP:HZ2	1:A:984:LEU:O	1.99	0.45
1:B:757:MET:HA	1:B:760:PHE:CZ	2.51	0.45
1:B:762:ARG:HB3	1:B:837:TYR:CE1	2.50	0.45
1:B:823:SER:HB3	1:B:826:GLU:CB	2.27	0.45
1:B:868:HIS:O	1:B:872:HIS:ND1	2.47	0.45
1:A:652:ALA:HA	1:A:675:CYS:O	2.16	0.45
1:A:852:ALA:O	1:A:855:TRP:HB3	2.16	0.45
1:A:880:HIS:HB3	1:A:881:PRO:HD3	1.97	0.45
1:B:259:GLN:HE21	1:B:259:GLN:HB3	1.58	0.45
1:B:898:THR:OG1	1:B:960:LYS:N	2.45	0.45
1:A:91:PRO:HA	1:A:94:ILE:CG2	2.46	0.45
1:B:97:ILE:O	1:B:100:ALA:HB3	2.17	0.45
1:B:882:HIS:HB3	1:B:883:PHE:CD1	2.52	0.45
1:A:79:GLU:CG	1:A:84:THR:HB	2.47	0.45
1:B:62:VAL:HG12	1:B:98:LEU:HD22	1.99	0.45
1:B:239:MET:HE3	1:B:708:ALA:HB1	1.98	0.45
1:B:304:VAL:C	1:B:306:ALA:H	2.25	0.45
1:A:261:SER:HA	1:A:264:ILE:HG12	1.97	0.45
1:B:299:ALA:O	1:B:302:LEU:HD12	2.17	0.45
1:B:349:CYS:HB3	1:B:624:ILE:HD11	1.95	0.45
1:B:740:PHE:C	1:B:743:ILE:HD13	2.40	0.45
1:A:335:SER:OG	1:A:337:PRO:HD2	2.17	0.45
1:A:757:MET:HA	1:A:760:PHE:CZ	2.52	0.45
1:B:108:GLN:HA	1:B:108:GLN:NE2	2.32	0.45
1:B:767:SER:O	1:B:771:GLU:CG	2.63	0.45
1:B:947:ILE:HD11	1:B:957:PHE:CE1	2.51	0.45
1:A:639:ILE:HD11	1:A:641:ILE:CD1	2.47	0.45
1:A:854:TRP:HH2	1:A:966:GLN:HG2	1.81	0.45
1:A:898:THR:CA	1:A:959:LEU:CD2	2.88	0.45
1:B:236:ARG:C	1:B:236:ARG:HD3	2.41	0.45
1:B:311:LEU:HD11	1:B:761:ILE:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:342:LEU:O	1:B:747:VAL:HG22	2.17	0.45
1:B:833:LEU:CA	1:B:836:ARG:HB2	2.41	0.45
1:B:971:LEU:O	1:B:975:LEU:HD23	2.16	0.45
1:A:39:ASN:O	1:A:40:GLU:CB	2.62	0.45
1:A:86:THR:HG22	1:A:89:VAL:HG21	1.99	0.45
1:A:190:HIS:O	1:A:206:ASN:HA	2.17	0.45
1:A:757:MET:HA	1:A:760:PHE:CE2	2.51	0.45
1:A:849:VAL:O	1:A:853:ALA:HB2	2.12	0.45
1:A:983:ILE:O	1:A:987:ILE:HG12	2.16	0.45
1:B:352:LYS:HB2	1:B:625:THR:HB	1.99	0.45
1:B:810:ASN:HA	1:B:930:ASN:ND2	2.32	0.45
1:B:885:GLY:O	1:B:886:LEU:HG	2.17	0.45
1:A:633:ILE:CD1	1:A:642:PHE:HE1	2.29	0.45
1:A:799:THR:HG21	1:A:905:VAL:HG22	1.99	0.45
1:A:898:THR:OG1	1:A:960:LYS:N	2.47	0.45
1:A:914:ASN:HD21	1:A:922:LEU:HD11	1.80	0.45
1:A:975:LEU:H	1:A:975:LEU:CD2	2.30	0.45
1:B:112:ALA:O	1:B:113:GLU:C	2.58	0.45
1:A:633:ILE:HD12	1:A:642:PHE:HE1	1.82	0.44
1:A:663:LEU:H	1:A:663:LEU:CD1	2.30	0.44
1:A:804:ALA:O	1:A:805:THR:C	2.60	0.44
1:A:894:PRO:HB3	1:A:958:LYS:C	2.41	0.44
1:B:193:PRO:O	1:B:195:PRO:HD3	2.18	0.44
1:B:322:GLY:N	1:B:325:ARG:HH21	2.15	0.44
1:B:963:ASP:H	1:B:966:GLN:NE2	2.11	0.44
1:A:308:PRO:CB	1:A:764:LEU:HD23	2.46	0.44
1:A:782:GLY:HA3	1:A:871:THR:CB	2.46	0.44
1:B:671:ARG:HD3	1:B:694:TYR:CZ	2.52	0.44
1:B:794:TRP:CD1	1:B:794:TRP:O	2.70	0.44
1:A:48:SER:O	1:A:52:LEU:HG	2.18	0.44
1:A:256:PHE:C	1:A:258:GLU:N	2.75	0.44
1:A:553:GLY:O	1:A:554:THR:HG23	2.17	0.44
1:B:103:ILE:HD13	1:B:103:ILE:C	2.43	0.44
1:B:403:ARG:HH11	1:B:456:ASN:HD21	1.65	0.44
1:B:680:GLU:O	1:B:683:HIS:HB2	2.16	0.44
1:B:774:CYS:O	1:B:778:THR:HG23	2.17	0.44
1:A:271:VAL:O	1:A:273:LEU:N	2.50	0.44
1:A:491:ARG:HD2	1:A:588:GLU:OE2	2.17	0.44
1:A:248:PRO:HB2	1:A:341:THR:HG23	1.99	0.44
1:A:300:VAL:HA	1:A:303:ALA:HB2	2.00	0.44
1:A:557:ASP:HB3	1:A:559:LEU:HG	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:767:SER:O	1:A:771:GLU:CG	2.63	0.44
1:A:155:VAL:HG13	1:A:155:VAL:O	2.17	0.44
1:A:338:SER:HA	1:A:341:THR:CB	2.46	0.44
1:A:112:ALA:C	1:A:116:ILE:HG12	2.43	0.44
1:A:853:ALA:O	1:A:856:PHE:N	2.51	0.44
1:B:443:THR:O	1:B:447:THR:HG23	2.18	0.44
1:B:914:ASN:HD21	1:B:922:LEU:HD11	1.82	0.44
1:A:624:ILE:CD1	1:A:676:PHE:CD1	3.01	0.44
1:A:762:ARG:CZ	1:A:833:LEU:HD11	2.48	0.44
1:A:810:ASN:HA	1:A:930:ASN:ND2	2.33	0.44
1:B:85:ILE:HD13	1:B:85:ILE:O	2.17	0.44
1:B:663:LEU:H	1:B:663:LEU:HD13	1.82	0.44
1:B:833:LEU:HD11	1:B:837:TYR:HE1	1.83	0.44
1:B:336:LEU:O	1:B:339:VAL:HG23	2.18	0.44
1:A:307:ILE:HD13	1:A:307:ILE:N	2.33	0.43
1:B:737:ASP:C	1:B:739:ASN:H	2.26	0.43
1:A:895:GLU:N	1:A:896:PRO:HD2	2.33	0.43
1:B:755:ASN:HD21	1:B:816:ILE:HD11	1.82	0.43
1:A:44:GLU:CD	1:A:44:GLU:H	2.25	0.43
1:A:131:ARG:C	1:A:133:ASP:N	2.76	0.43
1:A:261:SER:O	1:A:264:ILE:CB	2.66	0.43
1:B:81:GLY:HA2	1:B:84:THR:HG22	2.00	0.43
1:B:239:MET:HE2	1:B:708:ALA:HB1	2.00	0.43
1:B:633:ILE:HD13	1:B:675:CYS:SG	2.59	0.43
1:B:873:PHE:HB2	1:B:891:PHE:CD2	2.53	0.43
1:B:982:GLU:OE1	1:B:982:GLU:HA	2.18	0.43
1:A:293:ILE:H	1:A:293:ILE:HG13	1.59	0.43
1:A:926:PRO:HA	1:A:927:PRO:HD3	1.95	0.43
1:B:524:ARG:HH21	1:B:588:GLU:HB2	1.83	0.43
1:B:975:LEU:CD2	1:B:975:LEU:H	2.31	0.43
1:A:102:ALA:O	1:A:106:VAL:CG2	2.64	0.43
1:A:342:LEU:O	1:A:747:VAL:HG22	2.18	0.43
1:A:762:ARG:HH21	1:A:833:LEU:HD13	1.83	0.43
1:A:895:GLU:HB2	1:A:896:PRO:HD3	2.00	0.43
1:B:802:LEU:H	1:B:802:LEU:HG	1.49	0.43
1:B:907:ILE:CD1	1:B:974:SER:HB3	2.49	0.43
1:A:873:PHE:HB2	1:A:891:PHE:CD2	2.53	0.43
1:B:70:CYS:O	1:B:73:PHE:HB3	2.18	0.43
1:B:617:ALA:O	1:B:820:PRO:HA	2.19	0.43
1:B:624:ILE:CG2	1:B:684:LYS:HG2	2.49	0.43
1:B:759:GLN:HE22	1:B:762:ARG:NH1	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:ALA:O	1:A:303:ALA:HB2	2.18	0.43
1:A:625:THR:HA	3:A:998:BEF:F1	2.08	0.43
1:B:38:HIS:HD2	1:B:143:ARG:NH1	2.17	0.43
1:B:49:LEU:HD12	1:B:110:ARG:HG3	1.98	0.43
1:B:522:ILE:HD11	1:B:563:ALA:CB	2.48	0.43
1:B:825:LYS:HE2	1:B:825:LYS:HA	2.00	0.43
1:A:267:ILE:HD12	1:A:302:LEU:HD22	2.00	0.43
1:A:680:GLU:HB3	1:A:681:PRO:CD	2.48	0.43
1:A:898:THR:OG1	1:A:959:LEU:HA	2.18	0.43
1:B:48:SER:O	1:B:52:LEU:HG	2.19	0.43
1:B:239:MET:HE2	1:B:730:ALA:HB2	2.00	0.43
1:B:367:PHE:HE2	1:B:545:ILE:HD12	1.83	0.43
1:A:55:GLU:O	1:A:58:GLU:HB2	2.19	0.43
1:A:624:ILE:HD13	1:A:676:PHE:HD1	1.84	0.43
1:A:783:LEU:HG	1:A:870:LEU:HD23	1.99	0.43
1:A:811:PRO:HG3	1:A:929:VAL:O	2.18	0.43
1:A:975:LEU:N	1:A:976:PRO:HD2	2.34	0.43
1:B:895:GLU:N	1:B:896:PRO:HD2	2.33	0.43
1:A:103:ILE:HG23	1:A:104:VAL:H	1.83	0.43
1:A:347:VAL:HG12	1:A:348:ILE:N	2.34	0.43
1:A:524:ARG:HH21	1:A:588:GLU:HB2	1.84	0.43
1:A:759:GLN:C	1:A:761:ILE:N	2.77	0.43
1:A:852:ALA:CA	1:A:899:MET:HB3	2.48	0.43
1:B:111:ASN:O	1:B:112:ALA:C	2.61	0.43
1:B:214:ILE:H	1:B:214:ILE:CD1	2.31	0.43
1:B:845:GLY:C	1:B:847:ALA:N	2.77	0.43
1:A:825:LYS:HE2	1:A:825:LYS:HA	2.00	0.42
1:B:119:LEU:HD12	1:B:119:LEU:HA	1.75	0.42
1:B:172:THR:CG2	1:B:489:ARG:CD	2.96	0.42
1:B:300:VAL:O	1:B:301:ALA:C	2.61	0.42
1:B:342:LEU:HA	1:B:716:ILE:HG13	2.00	0.42
1:A:774:CYS:O	1:A:778:THR:HG23	2.19	0.42
1:A:925:MET:HE2	1:A:929:VAL:HG11	2.01	0.42
1:A:982:GLU:HA	1:A:982:GLU:OE1	2.19	0.42
1:B:94:ILE:HD13	1:B:94:ILE:C	2.44	0.42
1:B:255:GLU:C	1:B:257:GLY:N	2.74	0.42
1:B:763:TYR:HE1	1:B:908:GLU:O	2.02	0.42
1:B:798:VAL:O	1:B:799:THR:C	2.62	0.42
1:B:811:PRO:HG3	1:B:929:VAL:O	2.18	0.42
1:A:314:VAL:CG1	1:A:804:ALA:HB1	2.49	0.42
1:A:887:ASP:C	1:A:889:GLU:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:PHE:HE2	1:B:293:ILE:HG23	1.83	0.42
1:B:100:ALA:O	1:B:103:ILE:HG22	2.19	0.42
1:B:851:ALA:HB3	1:B:903:VAL:HG21	2.00	0.42
1:A:823:SER:HB3	1:A:826:GLU:CB	2.26	0.42
1:A:848:THR:O	1:A:852:ALA:CB	2.68	0.42
1:B:28:GLN:HG2	1:B:31:ARG:HH22	1.85	0.42
1:B:62:VAL:HG13	1:B:98:LEU:HD22	2.00	0.42
1:A:342:LEU:HD22	1:A:747:VAL:HG22	2.00	0.42
1:A:884:GLU:H	1:A:884:GLU:HG2	1.63	0.42
1:B:60:LEU:HD23	1:B:257:GLY:CA	2.50	0.42
1:B:315:ILE:HD11	1:B:761:ILE:HD11	2.00	0.42
1:B:315:ILE:HD13	1:B:760:PHE:HE1	1.85	0.42
1:B:391:PRO:HB3	1:B:450:GLU:HB3	2.01	0.42
1:B:832:TRP:HZ2	1:B:984:LEU:O	2.03	0.42
1:B:851:ALA:C	1:B:854:TRP:HB3	2.45	0.42
1:B:887:ASP:C	1:B:889:GLU:H	2.27	0.42
1:A:28:GLN:HG2	1:A:31:ARG:HH22	1.85	0.42
1:A:624:ILE:HD13	1:A:676:PHE:HB2	2.01	0.42
1:A:880:HIS:N	1:A:881:PRO:HD2	2.34	0.42
1:A:882:HIS:HB3	1:A:883:PHE:CD1	2.54	0.42
1:A:975:LEU:N	1:A:975:LEU:HD22	2.35	0.42
1:B:260:LEU:O	1:B:263:VAL:HB	2.19	0.42
1:B:662:PRO:O	1:B:663:LEU:C	2.62	0.42
1:A:103:ILE:HG23	1:A:104:VAL:N	2.35	0.42
1:A:914:ASN:O	1:A:916:LEU:N	2.53	0.42
1:B:753:ILE:O	1:B:757:MET:HB2	2.19	0.42
1:A:120:LYS:CE	1:A:723:GLY:O	2.68	0.42
1:A:286:GLY:HA3	1:A:290:ARG:HB3	1.99	0.42
1:A:387:SER:O	1:A:602:PRO:HG2	2.20	0.42
1:A:577:VAL:HG12	1:A:579:ASP:OD2	2.20	0.42
1:A:827:PRO:HB2	1:A:828:LEU:H	1.49	0.42
1:A:834:PHE:O	1:A:838:MET:HB2	2.20	0.42
1:A:845:GLY:C	1:A:847:ALA:N	2.78	0.42
1:B:231:GLU:O	1:B:235:ILE:HG12	2.18	0.42
1:B:311:LEU:HD21	1:B:761:ILE:HD12	2.01	0.42
1:B:314:VAL:CG1	1:B:804:ALA:HB1	2.45	0.42
1:B:680:GLU:HB3	1:B:681:PRO:CD	2.49	0.42
1:B:795:VAL:HA	1:B:799:THR:HB	2.02	0.42
1:B:817:MET:C	1:B:819:ARG:N	2.66	0.42
1:B:948:LEU:C	1:B:949:TYR:HD1	2.28	0.42
1:B:950:VAL:O	1:B:954:PRO:CD	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:962:LEU:HB3	1:B:966:GLN:HB2	2.01	0.42
1:A:899:MET:SD	1:A:962:LEU:CD2	3.08	0.42
1:B:235:ILE:HD11	1:B:681:PRO:HG2	2.02	0.42
1:B:577:VAL:HG12	1:B:579:ASP:OD2	2.19	0.42
1:B:851:ALA:O	1:B:854:TRP:HB3	2.19	0.42
1:A:174:ARG:NH2	1:A:188:ILE:HD11	2.35	0.42
1:A:181:THR:CB	1:A:183:GLU:HG3	2.48	0.42
1:A:193:PRO:O	1:A:195:PRO:HD3	2.20	0.42
1:A:265:SER:O	1:A:268:CYS:HB2	2.20	0.42
1:A:624:ILE:HG22	1:A:684:LYS:HG2	2.00	0.42
1:B:2:GLU:O	1:B:3:ALA:CB	2.66	0.42
1:B:59:ASP:OD2	1:B:62:VAL:HG23	2.19	0.42
1:B:421:ASN:ND2	1:B:421:ASN:C	2.75	0.42
1:B:600:LEU:N	1:B:600:LEU:HD12	2.35	0.42
1:A:624:ILE:HD13	1:A:676:PHE:CD1	2.55	0.41
1:A:962:LEU:HB3	1:A:966:GLN:HB2	2.02	0.41
1:B:290:ARG:HE	1:B:291:GLY:N	2.18	0.41
1:B:315:ILE:CD1	1:B:757:MET:CE	2.93	0.41
1:B:606:GLU:HG3	1:B:739:ASN:OD1	2.20	0.41
1:B:751:ARG:NH1	1:B:819:ARG:O	2.52	0.41
1:B:770:GLY:HA2	1:B:841:GLY:O	2.20	0.41
1:A:2:GLU:O	1:A:3:ALA:CB	2.65	0.41
1:A:271:VAL:O	1:A:272:TRP:C	2.63	0.41
1:A:759:GLN:C	1:A:761:ILE:H	2.27	0.41
1:B:336:LEU:O	1:B:339:VAL:CG2	2.68	0.41
1:B:529:ARG:HH22	1:B:568:ASP:CG	2.28	0.41
1:B:549:ILE:CD1	1:B:596:VAL:HG11	2.50	0.41
1:B:975:LEU:N	1:B:976:PRO:HD2	2.35	0.41
1:A:112:ALA:O	1:A:114:ASN:N	2.53	0.41
1:A:290:ARG:HG3	1:A:291:GLY:N	2.34	0.41
1:A:311:LEU:HD11	1:A:761:ILE:HG12	2.02	0.41
1:A:868:HIS:NE2	1:A:883:PHE:HZ	2.18	0.41
1:A:901:LEU:O	1:A:905:VAL:HG23	2.20	0.41
1:A:931:ILE:H	1:A:931:ILE:CD1	2.31	0.41
1:B:1:MET:O	1:B:1:MET:HG2	2.20	0.41
1:B:60:LEU:HD21	1:B:257:GLY:HA3	2.03	0.41
1:B:336:LEU:HB2	1:B:337:PRO:HD3	2.02	0.41
1:B:584:PHE:N	1:B:584:PHE:CD2	2.86	0.41
1:A:231:GLU:O	1:A:235:ILE:HG12	2.20	0.41
1:A:311:LEU:HD22	1:A:761:ILE:HG23	2.02	0.41
1:A:351:ASP:CG	1:A:352:LYS:N	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:TYR:HE2	1:A:468:ALA:HB2	1.85	0.41
1:A:969:MET:HE2	1:A:973:ILE:CD1	2.50	0.41
1:B:762:ARG:CZ	1:B:833:LEU:HD11	2.51	0.41
1:B:784:PRO:HG2	1:B:856:PHE:CE1	2.54	0.41
1:B:854:TRP:HH2	1:B:966:GLN:HG2	1.84	0.41
1:B:895:GLU:OE2	1:B:960:LYS:HD2	2.21	0.41
1:B:925:MET:HE2	1:B:929:VAL:HG11	2.01	0.41
1:A:90:GLU:OE1	1:A:793:LEU:HD11	2.21	0.41
1:A:287:SER:C	1:A:289:ILE:H	2.29	0.41
1:A:529:ARG:HH22	1:A:568:ASP:CG	2.29	0.41
1:A:762:ARG:NH2	1:A:833:LEU:HD13	2.36	0.41
1:A:762:ARG:O	1:A:765:ILE:HG22	2.20	0.41
1:A:763:TYR:HE1	1:A:908:GLU:O	2.03	0.41
1:A:804:ALA:C	1:A:806:ALA:N	2.75	0.41
1:A:897:MET:CE	1:A:958:LYS:HE3	2.50	0.41
1:B:42:PRO:O	1:B:43:ALA:O	2.37	0.41
1:B:556:ARG:NE	1:B:644:GLU:CG	2.83	0.41
1:B:762:ARG:HH21	1:B:833:LEU:HD13	1.85	0.41
1:A:70:CYS:O	1:A:73:PHE:HB3	2.21	0.41
1:A:584:PHE:N	1:A:584:PHE:CD2	2.87	0.41
1:A:697:ILE:HD12	1:A:697:ILE:H	1.85	0.41
1:A:859:ALA:O	1:A:860:GLU:C	2.63	0.41
1:A:897:MET:HE3	1:A:958:LYS:HB3	2.01	0.41
1:B:686:LYS:HE3	1:B:686:LYS:HB2	1.90	0.41
1:B:804:ALA:O	1:B:807:LEU:N	2.52	0.41
1:B:868:HIS:NE2	1:B:883:PHE:HZ	2.18	0.41
1:B:975:LEU:N	1:B:975:LEU:HD22	2.36	0.41
1:A:180:LEU:HD12	1:A:180:LEU:C	2.46	0.41
1:A:305:ALA:O	1:A:768:ASN:HA	2.20	0.41
1:A:851:ALA:HB3	1:A:903:VAL:HG21	2.01	0.41
1:A:895:GLU:OE2	1:A:960:LYS:CD	2.69	0.41
1:A:325:ARG:NH2	1:A:753:ILE:HD11	2.36	0.41
1:A:663:LEU:CD1	1:A:663:LEU:N	2.83	0.41
1:A:775:ILE:HD13	1:A:775:ILE:N	2.31	0.41
1:A:794:TRP:CD1	1:A:794:TRP:O	2.73	0.41
1:B:116:ILE:CD1	1:B:334:ARG:HG2	2.51	0.41
1:B:390:ALA:HA	1:B:391:PRO:HD3	1.82	0.41
1:B:781:LEU:C	1:B:781:LEU:CD2	2.89	0.41
1:B:794:TRP:CD1	1:B:799:THR:HG1	2.38	0.41
1:B:926:PRO:HA	1:B:927:PRO:HD3	1.95	0.41
1:B:964:LEU:O	1:B:964:LEU:HD23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:512:MET:HB2	1:A:567:ARG:HB3	2.03	0.41
1:A:797:LEU:HD23	1:A:797:LEU:HA	1.64	0.41
1:A:848:THR:C	1:A:850:GLY:N	2.78	0.41
1:A:885:GLY:O	1:A:886:LEU:HG	2.21	0.41
1:A:907:ILE:CD1	1:A:974:SER:HB3	2.51	0.41
1:B:338:SER:HA	1:B:341:THR:CB	2.50	0.41
1:B:624:ILE:HG22	1:B:684:LYS:HG2	2.03	0.41
1:B:652:ALA:HA	1:B:675:CYS:O	2.20	0.41
1:B:740:PHE:HA	1:B:743:ILE:HD13	2.01	0.41
1:B:853:ALA:O	1:B:856:PHE:N	2.54	0.41
1:B:880:HIS:N	1:B:881:PRO:CD	2.83	0.41
1:B:947:ILE:HD11	1:B:957:PHE:CD2	2.56	0.41
1:A:390:ALA:HA	1:A:391:PRO:HD3	1.83	0.41
1:A:416:ILE:HD11	1:A:566:THR:HG22	2.03	0.41
1:A:717:GLY:C	1:A:718:ILE:HD12	2.46	0.41
1:B:261:SER:O	1:B:264:ILE:HB	2.20	0.41
1:B:290:ARG:HE	1:B:291:GLY:CA	2.34	0.41
1:B:305:ALA:HB3	1:B:772:VAL:HG22	2.03	0.41
1:B:369:ILE:HD11	1:B:593:PHE:HD1	1.85	0.41
1:B:895:GLU:OE2	1:B:960:LYS:CD	2.68	0.41
1:A:300:VAL:O	1:A:301:ALA:C	2.64	0.40
1:A:606:GLU:HG3	1:A:739:ASN:OD1	2.22	0.40
1:A:895:GLU:OE2	1:A:960:LYS:HD2	2.21	0.40
1:B:315:ILE:HG22	1:B:316:THR:N	2.36	0.40
1:B:345:THR:HG23	1:B:697:ILE:O	2.21	0.40
1:B:352:LYS:HG2	1:B:353:THR:N	2.35	0.40
1:B:369:ILE:HG12	1:B:528:VAL:HG11	2.03	0.40
1:B:648:VAL:O	1:B:649:ALA:C	2.64	0.40
1:B:897:MET:CE	1:B:958:LYS:HE3	2.47	0.40
1:A:363:VAL:HG11	1:A:448:LEU:HD22	2.03	0.40
1:B:68:ALA:O	1:B:69:ALA:C	2.64	0.40
1:B:269:VAL:O	1:B:272:TRP:HE3	2.05	0.40
1:B:556:ARG:NE	1:B:644:GLU:HG2	2.37	0.40
1:B:740:PHE:O	1:B:743:ILE:CD1	2.60	0.40
1:B:848:THR:C	1:B:850:GLY:N	2.78	0.40
1:B:131:ARG:C	1:B:133:ASP:N	2.77	0.40
1:B:357:THR:HB	1:B:602:PRO:O	2.21	0.40
1:B:914:ASN:O	1:B:916:LEU:N	2.55	0.40
1:A:75:LEU:HD11	1:A:300:VAL:HG23	2.04	0.40
1:A:604:ARG:HB2	1:A:607:VAL:HG23	2.03	0.40
1:A:795:VAL:HA	1:A:799:THR:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:947:ILE:HD11	1:A:957:PHE:CD2	2.57	0.40
1:B:253:LEU:C	1:B:255:GLU:N	2.79	0.40
1:B:762:ARG:NH2	1:B:833:LEU:HD13	2.36	0.40
1:B:797:LEU:HA	1:B:797:LEU:HD23	1.62	0.40
1:B:898:THR:HG21	1:B:960:LYS:O	2.22	0.40
1:A:662:PRO:O	1:A:663:LEU:C	2.64	0.40
1:B:103:ILE:CG2	1:B:104:VAL:N	2.84	0.40
1:B:416:ILE:HD11	1:B:566:THR:HG22	2.03	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	993/995 (100%)	883 (89%)	84 (8%)	26 (3%)	4	27
1	B	993/995 (100%)	876 (88%)	91 (9%)	26 (3%)	4	27
All	All	1986/1990 (100%)	1759 (89%)	175 (9%)	52 (3%)	4	27

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	LYS
1	A	245	ASP
1	A	292	ALA
1	A	783	LEU
1	A	818	ASP
1	A	827	PRO
1	A	828	LEU
1	B	47	LYS
1	B	245	ASP
1	B	292	ALA

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Mol	Chain	Res	Type
1	B	783	LEU
1	B	818	ASP
1	B	827	PRO
1	B	828	LEU
1	B	863	PRO
1	A	43	ALA
1	A	293	ILE
1	A	309	GLU
1	A	790	VAL
1	A	860	GLU
1	A	863	PRO
1	A	878	GLU
1	B	43	ALA
1	B	293	ILE
1	B	790	VAL
1	B	860	GLU
1	B	878	GLU
1	A	762	ARG
1	A	830	SER
1	B	309	GLU
1	B	330	ASN
1	B	762	ARG
1	B	830	SER
1	A	272	TRP
1	A	287	SER
1	A	754	TYR
1	A	915	SER
1	B	42	PRO
1	B	831	GLY
1	A	294	TYR
1	A	951	ASP
1	B	294	TYR
1	B	915	SER
1	A	831	GLY
1	B	352	LYS
1	B	951	ASP
1	A	789	PRO
1	A	601	ASP
1	B	46	GLY
1	B	789	PRO
1	A	950	VAL
1	B	950	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	840/840 (100%)	748 (89%)	92 (11%)	6	24
1	B	840/840 (100%)	745 (89%)	95 (11%)	5	23
All	All	1680/1680 (100%)	1493 (89%)	187 (11%)	6	24

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LEU
1	A	49	LEU
1	A	56	GLN
1	A	59	ASP
1	A	79	GLU
1	A	86	THR
1	A	88	PHE
1	A	90	GLU
1	A	94	ILE
1	A	103	ILE
1	A	109	GLU
1	A	110	ARG
1	A	113	GLU
1	A	125	GLU
1	A	134	ARG
1	A	149	ASP
1	A	171	THR
1	A	180	LEU
1	A	232	ILE
1	A	239	MET
1	A	243	GLU
1	A	247	THR
1	A	249	LEU
1	A	250	GLN
1	A	251	GLN
1	A	252	LYS
1	A	255	GLU

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Mol	Chain	Res	Type
1	A	256	PHE
1	A	258	GLU
1	A	259	GLN
1	A	267	ILE
1	A	284	HIS
1	A	289	ILE
1	A	293	ILE
1	A	296	PHE
1	A	298	ILE
1	A	302	LEU
1	A	307	ILE
1	A	334	ARG
1	A	338	SER
1	A	342	LEU
1	A	348	ILE
1	A	353	THR
1	A	355	THR
1	A	356	LEU
1	A	361	MET
1	A	402	ILE
1	A	421	ASN
1	A	439	GLU
1	A	445	LEU
1	A	447	THR
1	A	467	ARG
1	A	484	THR
1	A	488	SER
1	A	489	ARG
1	A	519	GLU
1	A	534	ARG
1	A	544	LYS
1	A	545	ILE
1	A	566	THR
1	A	574	GLU
1	A	575	GLU
1	A	600	LEU
1	A	606	GLU
1	A	691	LEU
1	A	713	LYS
1	A	726	VAL
1	A	757	MET
1	A	763	TYR

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Mol	Chain	Res	Type
1	A	764	LEU
1	A	765	ILE
1	A	769	VAL
1	A	775	ILE
1	A	788	ILE
1	A	793	LEU
1	A	795	VAL
1	A	797	LEU
1	A	802	LEU
1	A	813	ASP
1	A	816	ILE
1	A	817	MET
1	A	829	ILE
1	A	840	ILE
1	A	849	VAL
1	A	854	TRP
1	A	882	HIS
1	A	911	ASN
1	A	925	MET
1	A	951	ASP
1	A	955	MET
1	A	956	ILE
1	A	993	GLU
1	B	10	GLU
1	B	41	LEU
1	B	56	GLN
1	B	62	VAL
1	B	65	LEU
1	B	78	PHE
1	B	79	GLU
1	B	82	GLU
1	B	85	ILE
1	B	86	THR
1	B	88	PHE
1	B	90	GLU
1	B	92	PHE
1	B	94	ILE
1	B	95	LEU
1	B	96	LEU
1	B	103	ILE
1	B	104	VAL
1	B	109	GLU

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Mol	Chain	Res	Type
1	B	110	ARG
1	B	119	LEU
1	B	121	GLU
1	B	125	GLU
1	B	134	ARG
1	B	140	ILE
1	B	149	ASP
1	B	172	THR
1	B	175	VAL
1	B	239	MET
1	B	246	LYS
1	B	249	LEU
1	B	250	GLN
1	B	251	GLN
1	B	252	LYS
1	B	255	GLU
1	B	256	PHE
1	B	259	GLN
1	B	267	ILE
1	B	272	TRP
1	B	281	ASP
1	B	293	ILE
1	B	296	PHE
1	B	300	VAL
1	B	302	LEU
1	B	307	ILE
1	B	309	GLU
1	B	319	LEU
1	B	338	SER
1	B	342	LEU
1	B	355	THR
1	B	356	LEU
1	B	361	MET
1	B	384	ILE
1	B	421	ASN
1	B	439	GLU
1	B	445	LEU
1	B	447	THR
1	B	467	ARG
1	B	484	THR
1	B	488	SER
1	B	489	ARG

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Mol	Chain	Res	Type
1	B	519	GLU
1	B	534	ARG
1	B	544	LYS
1	B	566	THR
1	B	574	GLU
1	B	575	GLU
1	B	600	LEU
1	B	606	GLU
1	B	691	LEU
1	B	726	VAL
1	B	755	ASN
1	B	757	MET
1	B	763	TYR
1	B	764	LEU
1	B	769	VAL
1	B	783	LEU
1	B	793	LEU
1	B	795	VAL
1	B	797	LEU
1	B	802	LEU
1	B	813	ASP
1	B	816	ILE
1	B	817	MET
1	B	829	ILE
1	B	849	VAL
1	B	854	TRP
1	B	882	HIS
1	B	911	ASN
1	B	925	MET
1	B	937	ILE
1	B	951	ASP
1	B	955	MET
1	B	956	ILE
1	B	993	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	56	GLN
1	A	108	GLN
1	A	111	ASN

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Mol	Chain	Res	Type
1	A	114	ASN
1	A	177	GLN
1	A	251	GLN
1	A	275	ASN
1	A	359	ASN
1	A	421	ASN
1	A	461	ASN
1	A	510	ASN
1	A	759	GLN
1	A	869	GLN
1	A	875	GLN
1	A	911	ASN
1	A	914	ASN
1	A	919	ASN
1	A	966	GLN
1	B	5	HIS
1	B	38	HIS
1	B	108	GLN
1	B	111	ASN
1	B	114	ASN
1	B	250	GLN
1	B	251	GLN
1	B	259	GLN
1	B	278	HIS
1	B	330	ASN
1	B	359	ASN
1	B	421	ASN
1	B	456	ASN
1	B	461	ASN
1	B	510	ASN
1	B	759	GLN
1	B	869	GLN
1	B	875	GLN
1	B	911	ASN
1	B	914	ASN
1	B	919	ASN
1	B	966	GLN

5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	BEF	B	1098	1	0,3,3	-	-	-		
3	BEF	A	998	1	0,3,3	-	-	-		

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	998	BEF	1	0

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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.