



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:14 AM UTC

PDB ID : 1KPL / pdb_00001kpl
Title : Crystal Structure of the ClC Chloride Channel from *S. typhimurium*
Authors : Dutzler, R.; Campbell, E.B.; Cadene, M.; Chait, B.T.; MacKinnon, R.
Deposited on : 2001-12-31
Resolution : 3.00 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

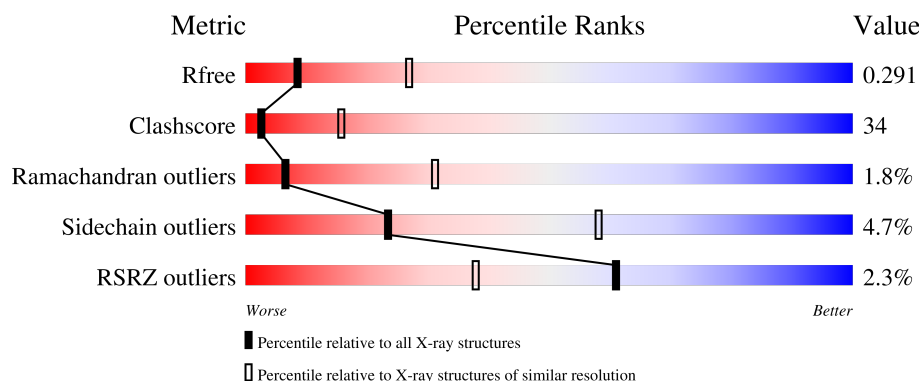
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	473	
1	B	473	
1	C	473	
1	D	473	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13216 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 putative ClC family, chlorine transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3193	2105	528	540	20			
1	B	451	Total	C	N	O	S	0	0	0
			3379	2217	574	568	20			
1	C	430	Total	C	N	O	S	0	0	0
			3193	2105	528	540	20			
1	D	451	Total	C	N	O	S	0	0	0
			3379	2217	574	568	20			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	LEU	MET	engineered mutation	UNP Q8ZRP8
A	264	VAL	CYS	engineered mutation	UNP Q8ZRP8
B	26	LEU	MET	engineered mutation	UNP Q8ZRP8
B	264	VAL	CYS	engineered mutation	UNP Q8ZRP8
C	26	LEU	MET	engineered mutation	UNP Q8ZRP8
C	264	VAL	CYS	engineered mutation	UNP Q8ZRP8
D	26	LEU	MET	engineered mutation	UNP Q8ZRP8
D	264	VAL	CYS	engineered mutation	UNP Q8ZRP8

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

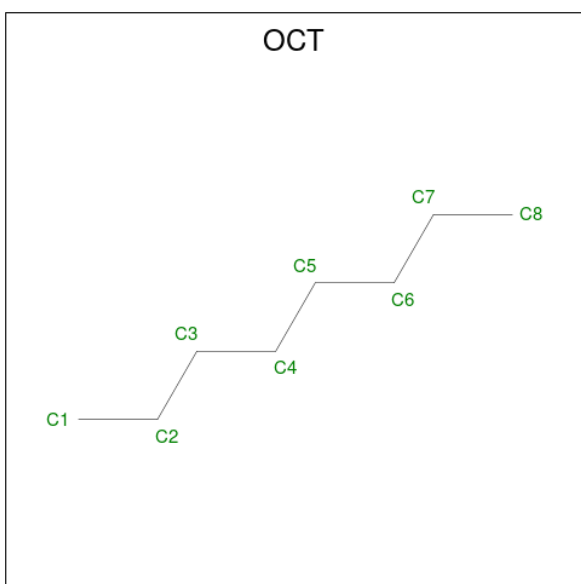
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	B	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



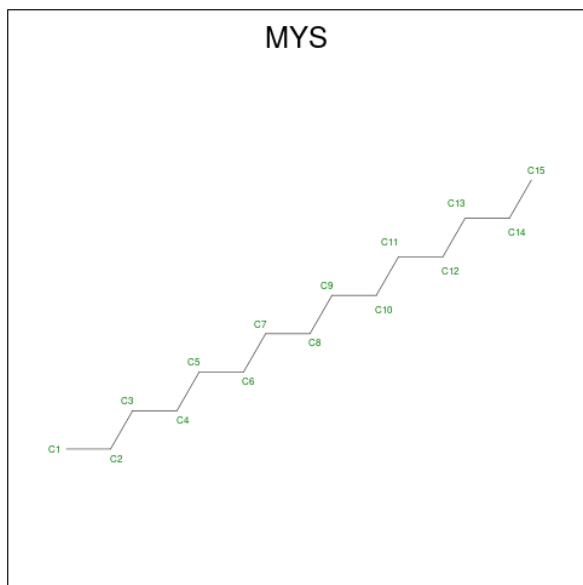
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is N-OCTANE (CCD ID: OCT) (formula: C₈H₁₈).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 8 8	0	0
4	C	1	Total C 8 8	0	0

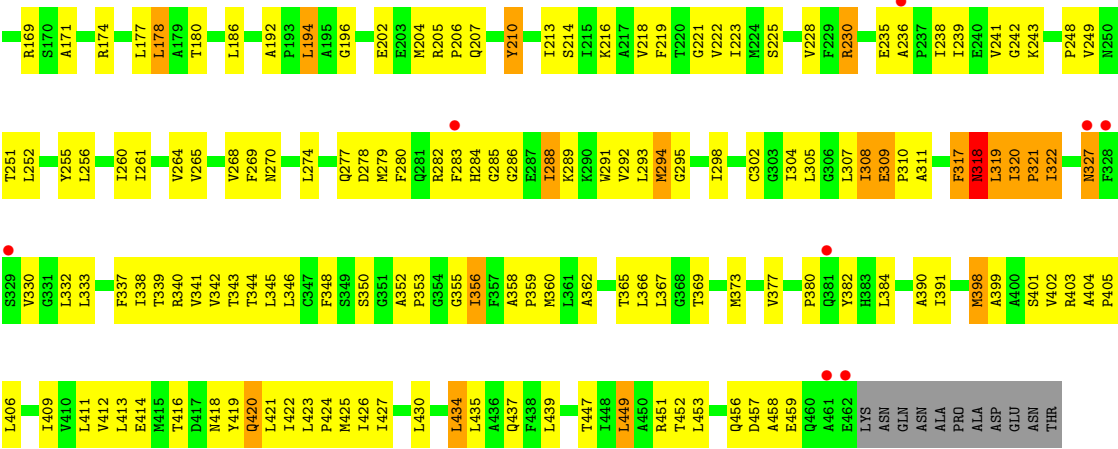
- Molecule 5 is PENTADECANE (CCD ID: MYS) (formula: $C_{15}H_{32}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C 15 15	0	0
5	D	1	Total C 15 15	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total O 1 1	0	0
6	D	1	Total O 1 1	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	185.72Å 90.16Å 80.75Å 90.00° 98.95° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.4 (20.00-3.00) 94.2 (20.00-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 3.00Å)	Xtriage
Refinement program	CNS 0.3	Depositor
R, R_{free}	0.254 , 0.289 0.257 , 0.291	Depositor DCC
R_{free} test set	4991 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	85.9	Xtriage
Anisotropy	0.524	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13216	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OCT, CL, SO4, MYS

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	0.52	0/3262	1.07	16/4432 (0.4%)
1	B	0.55	0/3448	1.09	19/4678 (0.4%)
1	C	0.52	0/3262	1.07	16/4432 (0.4%)
1	D	0.55	0/3448	1.09	19/4678 (0.4%)
All	All	0.54	0/13420	1.08	70/18220 (0.4%)

There are no bond length outliers.

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	210	TYR	N-CA-C	-11.27	92.41	110.32
1	B	210	TYR	N-CA-C	-11.26	92.42	110.32
1	D	320	ILE	N-CA-C	8.89	128.08	108.88
1	B	320	ILE	N-CA-C	8.88	128.06	108.88
1	C	309	GLU	CA-C-N	8.23	128.34	119.28
1	C	309	GLU	C-N-CA	8.23	128.34	119.28
1	A	309	GLU	CA-C-N	8.22	128.32	119.28
1	A	309	GLU	C-N-CA	8.22	128.32	119.28
1	D	101	ALA	CA-C-N	6.86	126.67	119.05
1	D	101	ALA	C-N-CA	6.86	126.67	119.05
1	B	101	ALA	CA-C-N	6.80	126.60	119.05
1	B	101	ALA	C-N-CA	6.80	126.60	119.05
1	A	205	ARG	CA-C-N	6.74	128.27	119.84
1	A	205	ARG	C-N-CA	6.74	128.27	119.84
1	C	205	ARG	CA-C-N	6.72	128.24	119.84
1	C	205	ARG	C-N-CA	6.72	128.24	119.84
1	D	236	ALA	CA-C-N	6.62	126.54	119.85
1	D	236	ALA	C-N-CA	6.62	126.54	119.85
1	B	236	ALA	CA-C-N	6.58	126.49	119.85
1	B	236	ALA	C-N-CA	6.58	126.49	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	404	ALA	CA-C-N	6.42	126.18	119.05
1	B	404	ALA	C-N-CA	6.42	126.18	119.05
1	D	404	ALA	CA-C-N	6.41	126.16	119.05
1	D	404	ALA	C-N-CA	6.41	126.16	119.05
1	B	327	ASN	N-CA-C	6.38	118.10	108.46
1	D	327	ASN	N-CA-C	6.38	118.10	108.46
1	A	320	ILE	N-CA-C	6.13	122.13	108.88
1	C	320	ILE	N-CA-C	6.13	122.13	108.88
1	B	390	ALA	N-CA-C	-6.09	104.33	110.97
1	D	390	ALA	N-CA-C	-6.08	104.35	110.97
1	D	30	LYS	N-CA-C	-6.03	98.26	108.26
1	B	30	LYS	N-CA-C	-6.02	98.27	108.26
1	B	243	LYS	N-CA-C	-5.99	96.61	107.75
1	D	243	LYS	N-CA-C	-5.99	96.61	107.75
1	A	204	MET	N-CA-C	5.97	117.48	110.97
1	C	204	MET	N-CA-C	5.96	117.47	110.97
1	A	396	ALA	N-CA-C	5.91	117.53	111.14
1	C	396	ALA	N-CA-C	5.89	117.50	111.14
1	D	100	PHE	N-CA-C	5.66	120.32	112.45
1	C	108	GLY	N-CA-C	-5.66	107.52	113.58
1	B	100	PHE	N-CA-C	5.64	120.28	112.45
1	A	108	GLY	N-CA-C	-5.63	107.56	113.58
1	A	209	ARG	N-CA-C	5.48	118.02	109.52
1	C	209	ARG	N-CA-C	5.47	118.01	109.52
1	A	84	ILE	N-CA-C	5.42	115.62	110.42
1	A	207	GLN	N-CA-C	5.41	117.60	111.11
1	D	309	GLU	CA-C-N	5.40	125.22	119.28
1	D	309	GLU	C-N-CA	5.40	125.22	119.28
1	C	84	ILE	N-CA-C	5.39	115.60	110.42
1	B	309	GLU	CA-C-N	5.39	125.21	119.28
1	B	309	GLU	C-N-CA	5.39	125.21	119.28
1	C	207	GLN	N-CA-C	5.39	117.57	111.11
1	D	356	ILE	N-CA-C	-5.34	107.77	112.90
1	B	356	ILE	N-CA-C	-5.33	107.79	112.90
1	D	252	LEU	N-CA-C	5.22	119.99	111.37
1	B	252	LEU	N-CA-C	5.21	119.97	111.37
1	C	169	ARG	N-CA-C	5.19	117.10	110.61
1	A	169	ARG	N-CA-C	5.18	117.09	110.61
1	C	205	ARG	N-CA-C	5.10	116.30	109.83
1	C	354	GLY	CA-C-N	-5.09	118.67	122.18
1	C	354	GLY	C-N-CA	-5.09	118.67	122.18
1	D	120	ARG	CA-C-N	5.09	125.07	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	120	ARG	C-N-CA	5.09	125.07	120.03
1	C	356	ILE	N-CA-C	-5.08	105.92	113.39
1	A	205	ARG	N-CA-C	5.07	116.27	109.83
1	A	356	ILE	N-CA-C	-5.06	105.95	113.39
1	A	354	GLY	CA-C-N	-5.06	118.69	122.18
1	A	354	GLY	C-N-CA	-5.06	118.69	122.18
1	B	120	ARG	CA-C-N	5.06	125.03	120.03
1	B	120	ARG	C-N-CA	5.06	125.03	120.03

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3193	0	3349	245	0
1	B	3379	0	3556	248	0
1	C	3193	0	3349	248	2
1	D	3379	0	3556	249	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	5	0	0	0	0
3	B	10	0	0	2	0
3	C	5	0	0	0	0
4	A	8	0	18	0	0
4	C	8	0	18	0	0
5	B	15	0	32	1	0
5	D	15	0	32	1	0
6	B	1	0	0	1	0
6	D	1	0	0	1	0
All	All	13216	0	13910	927	2

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 34.

All (927) 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:B:317:PHE:HA	1:B:321:PRO:HD2	1.33	1.11
1:A:230:ARG:HH11	1:A:230:ARG:HB3	1.18	1.07
1:D:317:PHE:HA	1:D:321:PRO:HD2	1.33	1.07
1:C:230:ARG:HB3	1:C:230:ARG:HH11	1.18	1.06
1:D:298:ILE:HD11	1:D:346:LEU:HB3	1.38	1.04
1:C:288:ILE:HD12	1:C:288:ILE:H	1.23	1.04
1:D:163:LEU:HD21	1:D:174:ARG:HA	1.34	1.03
1:B:163:LEU:HD21	1:B:174:ARG:HA	1.34	1.03
1:D:163:LEU:HD13	1:D:177:LEU:HD12	1.40	1.03
1:B:298:ILE:HD11	1:B:346:LEU:HB3	1.38	1.02
1:B:163:LEU:HD13	1:B:177:LEU:HD12	1.40	0.99
1:A:288:ILE:HD12	1:A:288:ILE:H	1.23	0.99
1:B:288:ILE:HD12	1:B:288:ILE:H	1.30	0.94
1:D:288:ILE:HD12	1:D:288:ILE:H	1.30	0.94
1:C:420:GLN:H	1:C:420:GLN:NE2	1.68	0.92
1:B:230:ARG:HH11	1:B:230:ARG:HB3	1.35	0.91
1:D:230:ARG:HH11	1:D:230:ARG:HB3	1.35	0.91
1:C:71:VAL:HG21	1:C:81:LEU:HD12	1.53	0.91
1:A:420:GLN:H	1:A:420:GLN:NE2	1.68	0.90
1:C:239:ILE:HG13	1:C:322:ILE:HD11	1.53	0.90
1:A:239:ILE:HG13	1:A:322:ILE:HD11	1.53	0.89
1:B:144:VAL:HG11	1:B:344:THR:HG22	1.53	0.89
1:B:37:PHE:HE2	1:D:13:ILE:HD11	1.38	0.89
1:A:71:VAL:HG21	1:A:81:LEU:HD12	1.53	0.88
1:D:144:VAL:HG11	1:D:344:THR:HG22	1.53	0.88
1:C:317:PHE:HA	1:C:321:PRO:HD3	1.56	0.88
1:A:317:PHE:HA	1:A:321:PRO:CD	2.03	0.87
1:C:317:PHE:HA	1:C:321:PRO:CD	2.04	0.86
1:A:317:PHE:HA	1:A:321:PRO:HD3	1.56	0.86
1:C:230:ARG:HB3	1:C:230:ARG:NH1	1.90	0.86
1:C:455:LYS:O	1:C:459:GLU:HG3	1.75	0.86
1:A:230:ARG:HB3	1:A:230:ARG:NH1	1.90	0.86
1:A:455:LYS:O	1:A:459:GLU:HG3	1.75	0.86
1:A:274:LEU:HD11	1:A:447:THR:HG21	1.59	0.85
1:B:169:ARG:HD2	1:C:210:TYR:O	1.78	0.84
1:C:373:MET:HE3	1:C:373:MET:HA	1.60	0.84
1:C:200:ILE:HD13	1:C:204:MET:HG3	1.60	0.83
1:C:274:LEU:HD11	1:C:447:THR:HG21	1.59	0.83
1:D:147:ARG:HB3	1:D:147:ARG:NH1	1.93	0.82
1:A:200:ILE:HD13	1:A:204:MET:HG3	1.60	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:LYS:HD2	1:C:56:ALA:N	1.94	0.82
1:B:147:ARG:HB3	1:B:147:ARG:NH1	1.93	0.82
1:A:55:LYS:HD2	1:A:56:ALA:N	1.94	0.82
1:A:373:MET:HE3	1:A:373:MET:HA	1.60	0.81
1:D:133:ILE:HA	1:D:136:MET:HE2	1.63	0.80
1:B:133:ILE:HA	1:B:136:MET:HE2	1.63	0.79
1:D:230:ARG:HB3	1:D:230:ARG:NH1	1.97	0.78
1:A:74:HIS:HD2	1:A:76:PHE:HB2	1.48	0.78
1:B:230:ARG:HB3	1:B:230:ARG:NH1	1.97	0.78
1:A:98:ARG:HD2	1:A:291:TRP:CE3	2.19	0.78
1:B:318:ASN:HD22	1:B:318:ASN:H	1.31	0.78
1:C:98:ARG:HD2	1:C:291:TRP:CE3	2.19	0.77
1:A:223:ILE:HD11	1:B:427:ILE:HG13	1.66	0.77
1:C:81:LEU:HD22	1:C:85:LEU:HD21	1.67	0.77
1:C:420:GLN:H	1:C:420:GLN:HE21	1.32	0.77
1:A:288:ILE:H	1:A:288:ILE:CD1	1.97	0.76
1:C:74:HIS:HD2	1:C:76:PHE:HB2	1.48	0.76
1:C:223:ILE:HD11	1:D:427:ILE:HG13	1.66	0.76
1:C:337:PHE:O	1:C:341:VAL:HG23	1.86	0.76
1:A:437:GLN:HG3	1:A:438:PHE:N	1.99	0.76
1:C:437:GLN:HG3	1:C:438:PHE:N	1.99	0.76
1:A:337:PHE:O	1:A:341:VAL:HG23	1.86	0.76
1:D:318:ASN:H	1:D:318:ASN:HD22	1.31	0.75
1:A:81:LEU:HD22	1:A:85:LEU:HD21	1.67	0.75
1:B:288:ILE:H	1:B:288:ILE:CD1	2.00	0.75
1:D:269:PHE:CE2	1:D:360:MET:HE2	2.21	0.75
1:B:269:PHE:CE2	1:B:360:MET:HE2	2.21	0.75
1:D:317:PHE:HA	1:D:321:PRO:CD	2.16	0.75
1:B:317:PHE:HA	1:B:321:PRO:CD	2.16	0.74
1:C:260:ILE:HG23	1:C:435:LEU:CD2	2.17	0.74
1:D:147:ARG:HB3	1:D:147:ARG:HH11	1.52	0.74
1:A:420:GLN:H	1:A:420:GLN:HE21	1.32	0.74
1:B:322:ILE:N	1:B:322:ILE:HD12	2.02	0.74
1:D:322:ILE:N	1:D:322:ILE:HD12	2.02	0.74
1:A:260:ILE:HG23	1:A:435:LEU:CD2	2.17	0.74
1:B:81:LEU:HA	1:B:84:ILE:CG2	2.18	0.74
1:D:81:LEU:HA	1:D:84:ILE:CG2	2.18	0.74
1:C:283:PHE:CD2	1:C:294:MET:HE3	2.23	0.73
1:C:288:ILE:H	1:C:288:ILE:CD1	1.97	0.73
1:A:74:HIS:CD2	1:A:76:PHE:HB2	2.24	0.73
1:A:283:PHE:CD2	1:A:294:MET:HE3	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:ARG:HB3	1:B:147:ARG:HH11	1.52	0.73
1:A:194:LEU:HG	1:B:422:ILE:HD11	1.71	0.73
1:B:80:PRO:O	1:B:84:ILE:HG22	1.89	0.72
1:C:74:HIS:CD2	1:C:76:PHE:HB2	2.24	0.72
1:B:37:PHE:CE2	1:D:13:ILE:HD11	2.22	0.72
1:C:239:ILE:CG1	1:C:322:ILE:HD11	2.20	0.72
1:D:288:ILE:H	1:D:288:ILE:CD1	2.00	0.72
1:B:138:THR:HG21	1:B:353:PRO:HD2	1.71	0.72
1:C:194:LEU:HG	1:D:422:ILE:HD11	1.71	0.72
1:A:239:ILE:CG1	1:A:322:ILE:HD11	2.20	0.71
1:D:163:LEU:CD2	1:D:174:ARG:HA	2.18	0.71
1:C:92:VAL:O	1:C:96:LEU:HD13	1.91	0.71
1:D:80:PRO:O	1:D:84:ILE:HG22	1.89	0.71
1:D:138:THR:HG21	1:D:353:PRO:HD2	1.71	0.71
1:A:288:ILE:HD12	1:A:288:ILE:N	2.03	0.71
1:B:17:ARG:HH11	1:B:17:ARG:HB3	1.55	0.71
1:D:288:ILE:HD12	1:D:288:ILE:N	2.05	0.71
1:A:92:VAL:O	1:A:96:LEU:HD13	1.91	0.70
1:A:419:TYR:OH	1:B:414:GLU:HG2	1.91	0.70
1:C:288:ILE:HD12	1:C:288:ILE:N	2.03	0.70
1:A:124:TRP:HZ3	1:A:164:ASP:OD2	1.74	0.70
1:C:409:ILE:HD13	1:C:426:ILE:HG12	1.74	0.70
1:B:81:LEU:HD22	1:B:85:LEU:HD21	1.73	0.70
1:D:81:LEU:HD22	1:D:85:LEU:HD21	1.73	0.70
1:C:419:TYR:OH	1:D:414:GLU:HG2	1.91	0.70
1:D:17:ARG:HH11	1:D:17:ARG:HB3	1.55	0.70
1:D:362:ALA:HA	1:D:365:THR:HG22	1.74	0.70
1:A:132:PHE:CE2	1:A:136:MET:HE2	2.27	0.70
1:B:169:ARG:HB2	1:C:209:ARG:CZ	2.22	0.70
1:B:362:ALA:HA	1:B:365:THR:HG22	1.74	0.69
1:C:132:PHE:CE2	1:C:136:MET:HE2	2.27	0.69
1:C:223:ILE:HD11	1:D:427:ILE:CG1	2.22	0.69
1:B:163:LEU:CD2	1:B:174:ARG:HA	2.18	0.69
1:C:124:TRP:HZ3	1:C:164:ASP:OD2	1.74	0.69
1:D:308:ILE:HD13	1:D:308:ILE:C	2.18	0.69
1:B:81:LEU:O	1:B:85:LEU:HD23	1.93	0.69
1:B:308:ILE:HD13	1:B:308:ILE:C	2.18	0.68
1:D:81:LEU:O	1:D:85:LEU:HD23	1.93	0.68
1:A:289:LYS:O	1:A:293:LEU:HG	1.93	0.68
1:A:71:VAL:CG2	1:A:81:LEU:HD12	2.22	0.68
1:A:409:ILE:HD13	1:A:426:ILE:HG12	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:VAL:CG2	1:C:81:LEU:HD12	2.22	0.68
1:C:239:ILE:HG13	1:C:322:ILE:CD1	2.24	0.68
1:A:223:ILE:HD11	1:B:427:ILE:CG1	2.22	0.68
1:D:147:ARG:HH11	1:D:147:ARG:CB	2.06	0.68
1:B:147:ARG:HH11	1:B:147:ARG:CB	2.06	0.68
1:B:288:ILE:HD12	1:B:288:ILE:N	2.05	0.68
1:D:97:VAL:HG21	1:D:353:PRO:HG3	1.76	0.68
1:A:207:GLN:O	1:B:205:ARG:NH2	2.27	0.67
1:B:144:VAL:CG1	1:B:344:THR:HG22	2.24	0.67
1:B:269:PHE:HE2	1:B:360:MET:HE2	1.60	0.67
1:B:280:PHE:CD2	1:B:294:MET:HE1	2.30	0.67
1:B:377:VAL:O	1:B:380:PRO:HD3	1.94	0.67
1:B:298:ILE:HD11	1:B:346:LEU:CB	2.21	0.67
1:B:168:MET:HG2	1:D:17:ARG:CD	2.24	0.67
1:C:336:ILE:O	1:C:340:ARG:HG3	1.95	0.67
1:D:148:GLU:OE2	1:D:355:GLY:HA3	1.95	0.67
1:D:377:VAL:O	1:D:380:PRO:HD3	1.95	0.67
1:C:289:LYS:O	1:C:293:LEU:HG	1.93	0.67
1:D:280:PHE:CD2	1:D:294:MET:HE1	2.30	0.67
1:B:97:VAL:HG21	1:B:353:PRO:HG3	1.76	0.66
1:B:298:ILE:CD1	1:B:346:LEU:HB3	2.22	0.66
1:D:144:VAL:CG1	1:D:344:THR:HG22	2.24	0.66
1:A:336:ILE:O	1:A:340:ARG:HG3	1.95	0.66
1:C:109:ILE:N	1:C:110:PRO:HD2	2.11	0.66
1:C:220:THR:O	1:C:223:ILE:HG22	1.95	0.66
1:D:298:ILE:CD1	1:D:346:LEU:HB3	2.22	0.66
1:D:318:ASN:HD22	1:D:318:ASN:N	1.91	0.66
1:D:269:PHE:HE2	1:D:360:MET:HE2	1.60	0.66
1:A:109:ILE:N	1:A:110:PRO:HD2	2.11	0.66
1:A:239:ILE:HG13	1:A:322:ILE:CD1	2.24	0.66
1:B:148:GLU:OE2	1:B:355:GLY:HA3	1.95	0.66
1:C:144:VAL:CG1	1:C:344:THR:HG22	2.26	0.66
1:A:240:GLU:H	1:A:322:ILE:HD11	1.61	0.65
1:A:423:LEU:HB2	1:A:424:PRO:HD3	1.78	0.65
1:B:79:TRP:N	1:B:80:PRO:HD2	2.11	0.65
1:D:362:ALA:O	1:D:365:THR:HG22	1.96	0.65
1:A:144:VAL:CG1	1:A:344:THR:HG22	2.26	0.65
1:B:398:MET:HG3	1:B:399:ALA:N	2.11	0.65
1:C:240:GLU:H	1:C:322:ILE:HD11	1.61	0.65
1:D:18:ARG:O	1:D:22:ILE:HG23	1.96	0.65
1:B:18:ARG:O	1:B:22:ILE:HG23	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:TYR:CZ	1:B:414:GLU:HG2	2.31	0.65
1:A:220:THR:O	1:A:223:ILE:HG22	1.95	0.65
1:A:298:ILE:HD11	1:A:346:LEU:HB3	1.77	0.65
1:B:318:ASN:HD22	1:B:318:ASN:N	1.91	0.65
1:C:207:GLN:O	1:D:205:ARG:NH2	2.27	0.65
1:C:298:ILE:HD11	1:C:346:LEU:HB3	1.77	0.65
1:C:419:TYR:CZ	1:D:414:GLU:HG2	2.31	0.65
1:C:423:LEU:HB2	1:C:424:PRO:HD3	1.78	0.65
1:D:79:TRP:N	1:D:80:PRO:HD2	2.11	0.65
1:D:298:ILE:HD11	1:D:346:LEU:CB	2.21	0.65
1:A:333:LEU:HD21	1:A:369:THR:HG22	1.79	0.65
1:B:398:MET:HE2	1:B:398:MET:O	1.97	0.65
1:B:362:ALA:O	1:B:365:THR:HG22	1.96	0.64
1:C:333:LEU:HD21	1:C:369:THR:HG22	1.79	0.64
1:A:260:ILE:HG23	1:A:435:LEU:HD22	1.79	0.64
1:A:332:LEU:HD13	1:A:332:LEU:C	2.22	0.64
1:B:280:PHE:CD1	1:B:350:SER:HA	2.33	0.64
1:C:202:GLU:OE2	1:C:405:PRO:HD2	1.97	0.64
1:D:398:MET:HG3	1:D:399:ALA:N	2.11	0.64
1:D:280:PHE:CD1	1:D:350:SER:HA	2.33	0.64
1:D:398:MET:O	1:D:398:MET:HE2	1.97	0.64
1:A:202:GLU:OE2	1:A:405:PRO:HD2	1.97	0.64
1:C:138:THR:HG21	1:C:353:PRO:HD2	1.80	0.64
1:C:332:LEU:HD13	1:C:332:LEU:C	2.22	0.64
1:B:168:MET:HG2	1:D:17:ARG:HD2	1.80	0.63
1:B:109:ILE:N	1:B:110:PRO:HD2	2.13	0.63
1:B:163:LEU:CD1	1:B:177:LEU:HD12	2.22	0.63
1:C:183:ALA:HB2	1:C:200:ILE:HG13	1.80	0.63
1:D:109:ILE:N	1:D:110:PRO:HD2	2.13	0.63
1:C:260:ILE:HG23	1:C:435:LEU:HD22	1.79	0.63
1:C:308:ILE:HG13	1:C:308:ILE:O	1.98	0.63
1:D:320:ILE:O	1:D:322:ILE:N	2.31	0.63
1:A:183:ALA:HB2	1:A:200:ILE:HG13	1.79	0.63
1:B:81:LEU:HA	1:B:84:ILE:HG22	1.80	0.63
1:D:81:LEU:HA	1:D:84:ILE:HG22	1.80	0.63
1:B:279:MET:O	1:B:282:ARG:HG2	1.99	0.63
1:B:304:ILE:O	1:B:308:ILE:HG22	1.99	0.63
1:B:320:ILE:O	1:B:322:ILE:N	2.31	0.62
1:D:304:ILE:O	1:D:308:ILE:HG22	1.99	0.62
1:A:308:ILE:O	1:A:308:ILE:HG13	1.98	0.62
1:B:449:LEU:HA	1:B:452:THR:HG22	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ARG:O	1:A:68:LEU:HB2	2.00	0.62
1:A:138:THR:HG21	1:A:353:PRO:HD2	1.80	0.62
1:B:295:GLY:O	1:B:298:ILE:HG22	2.00	0.62
1:C:64:ARG:O	1:C:68:LEU:HB2	2.00	0.62
1:D:449:LEU:HA	1:D:452:THR:HG22	1.81	0.62
1:B:47:GLY:HA3	1:B:228:VAL:HG21	1.82	0.62
1:D:47:GLY:HA3	1:D:228:VAL:HG21	1.82	0.61
1:D:295:GLY:O	1:D:298:ILE:HG22	2.00	0.61
1:A:124:TRP:CZ3	1:A:164:ASP:OD2	2.54	0.61
1:B:274:LEU:HD11	1:B:447:THR:HG21	1.83	0.61
1:D:279:MET:O	1:D:282:ARG:HG2	1.99	0.61
1:B:17:ARG:HB3	1:B:17:ARG:NH1	2.16	0.61
1:B:320:ILE:C	1:B:322:ILE:H	2.09	0.61
1:D:320:ILE:C	1:D:322:ILE:H	2.09	0.61
1:A:394:MET:HE1	1:A:415:MET:HE3	1.83	0.61
1:C:298:ILE:CD1	1:C:346:LEU:HB3	2.31	0.61
1:B:165:VAL:HG23	1:B:166:PHE:CD1	2.36	0.60
1:D:163:LEU:CD1	1:D:177:LEU:HD12	2.22	0.60
1:C:66:GLY:O	1:C:69:VAL:HG12	2.01	0.60
1:C:102:PRO:HD2	1:C:123:ARG:HH22	1.66	0.60
1:A:66:GLY:O	1:A:69:VAL:HG12	2.01	0.60
1:B:147:ARG:O	1:B:150:PRO:HG2	2.02	0.60
1:D:147:ARG:O	1:D:150:PRO:HG2	2.02	0.60
1:C:287:GLU:OE2	1:C:289:LYS:HD2	2.02	0.60
1:D:340:ARG:O	1:D:344:THR:HG23	2.01	0.60
1:A:298:ILE:CD1	1:A:346:LEU:HB3	2.31	0.60
1:B:340:ARG:O	1:B:344:THR:HG23	2.01	0.60
1:A:147:ARG:O	1:A:150:PRO:HD2	2.01	0.60
1:B:84:ILE:HG23	1:B:85:LEU:HD22	1.83	0.60
1:D:84:ILE:HG23	1:D:85:LEU:HD22	1.83	0.60
1:D:165:VAL:HG23	1:D:166:PHE:CD1	2.36	0.60
1:D:309:GLU:N	1:D:310:PRO:HD3	2.17	0.60
1:B:66:GLY:O	1:B:69:VAL:HG12	2.02	0.60
1:C:103:GLU:HG2	1:C:123:ARG:HH21	1.67	0.60
1:C:124:TRP:CZ3	1:C:164:ASP:OD2	2.54	0.60
1:D:17:ARG:HB3	1:D:17:ARG:NH1	2.16	0.60
1:D:66:GLY:O	1:D:69:VAL:HG12	2.02	0.60
1:D:308:ILE:O	1:D:309:GLU:HB3	2.02	0.60
1:A:287:GLU:OE2	1:A:289:LYS:HD2	2.02	0.59
1:A:403:ARG:HG3	1:A:443:PRO:HG3	1.84	0.59
1:C:381:GLN:OE1	1:C:381:GLN:N	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:PHE:HE2	1:C:136:MET:HE2	1.67	0.59
1:A:102:PRO:HD2	1:A:123:ARG:HH22	1.66	0.59
1:A:103:GLU:HG2	1:A:123:ARG:HH21	1.67	0.59
1:C:49:VAL:HG21	1:C:158:LEU:HD11	1.85	0.59
1:C:147:ARG:O	1:C:150:PRO:HD2	2.01	0.59
1:C:394:MET:HE1	1:C:415:MET:HE3	1.83	0.59
1:C:403:ARG:HG3	1:C:443:PRO:HG3	1.84	0.59
1:D:274:LEU:HD11	1:D:447:THR:HG21	1.83	0.59
1:D:420:GLN:H	1:D:420:GLN:HE21	1.48	0.59
1:D:241:VAL:HG12	1:D:242:GLY:H	1.67	0.59
1:C:88:LEU:HD12	1:C:91:MET:HE3	1.85	0.59
1:B:241:VAL:HG12	1:B:242:GLY:H	1.67	0.59
1:C:180:THR:HA	1:C:218:VAL:HG13	1.85	0.59
1:A:88:LEU:HD12	1:A:91:MET:HE3	1.85	0.58
1:A:132:PHE:HE2	1:A:136:MET:HE2	1.67	0.58
1:B:284:HIS:C	1:B:286:GLY:H	2.11	0.58
1:B:309:GLU:N	1:B:310:PRO:HD3	2.17	0.58
1:D:98:ARG:NE	1:D:98:ARG:HA	2.18	0.58
1:A:126:ARG:O	1:A:130:VAL:HG23	2.02	0.58
1:A:144:VAL:HG11	1:A:344:THR:HG22	1.85	0.58
1:B:308:ILE:O	1:B:309:GLU:HB3	2.02	0.58
1:B:420:GLN:H	1:B:420:GLN:HE21	1.48	0.58
1:A:240:GLU:N	1:A:322:ILE:HD11	2.17	0.58
1:C:126:ARG:O	1:C:130:VAL:HG23	2.02	0.58
1:D:339:THR:O	1:D:342:VAL:HG22	2.04	0.58
1:D:57:VAL:O	1:D:61:GLN:HG3	2.04	0.58
1:A:381:GLN:N	1:A:381:GLN:OE1	2.33	0.58
1:B:98:ARG:NE	1:B:98:ARG:HA	2.18	0.58
1:C:240:GLU:N	1:C:322:ILE:HD11	2.17	0.58
1:A:49:VAL:HG21	1:A:158:LEU:HD11	1.85	0.58
1:A:200:ILE:HD13	1:A:204:MET:CG	2.33	0.58
1:C:83:PHE:C	1:C:83:PHE:CD2	2.82	0.58
1:B:419:TYR:HE1	1:B:422:ILE:HD12	1.68	0.58
1:D:308:ILE:O	1:D:308:ILE:HG23	2.03	0.58
1:B:317:PHE:O	1:B:319:LEU:N	2.37	0.57
1:C:144:VAL:HG11	1:C:344:THR:HG22	1.85	0.57
1:C:420:GLN:NE2	1:C:420:GLN:N	2.48	0.57
1:A:200:ILE:CD1	1:A:204:MET:HG3	2.34	0.57
1:A:317:PHE:O	1:A:319:LEU:N	2.37	0.57
1:D:317:PHE:O	1:D:319:LEU:N	2.37	0.57
1:A:83:PHE:C	1:A:83:PHE:CD2	2.82	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:THR:O	1:B:342:VAL:HG22	2.03	0.57
1:D:419:TYR:HE1	1:D:422:ILE:HD12	1.68	0.57
1:A:180:THR:HA	1:A:218:VAL:HG13	1.85	0.57
1:D:288:ILE:O	1:D:292:VAL:HG23	2.05	0.57
1:A:115:ALA:CB	1:A:178:LEU:HD21	2.35	0.57
1:B:308:ILE:O	1:B:308:ILE:HG23	2.03	0.57
1:D:284:HIS:C	1:D:286:GLY:H	2.11	0.57
1:B:57:VAL:O	1:B:61:GLN:HG3	2.04	0.57
1:D:119:LEU:HD23	1:D:453:LEU:HD11	1.87	0.57
1:C:356:ILE:C	1:C:359:PRO:HD2	2.30	0.57
1:A:80:PRO:O	1:A:84:ILE:HG13	2.05	0.57
1:A:356:ILE:C	1:A:359:PRO:HD2	2.30	0.57
1:C:115:ALA:CB	1:C:178:LEU:HD21	2.35	0.57
1:C:317:PHE:O	1:C:319:LEU:N	2.37	0.57
1:C:456:GLN:NE2	1:D:18:ARG:HH21	2.03	0.57
1:D:192:ALA:HB1	1:D:414:GLU:OE2	2.05	0.57
1:D:412:VAL:HB	1:D:425:MET:HE3	1.87	0.57
1:D:356:ILE:C	1:D:359:PRO:HD2	2.30	0.57
1:A:123:ARG:O	1:A:127:VAL:HG23	2.05	0.56
1:C:123:ARG:O	1:C:127:VAL:HG23	2.05	0.56
1:A:147:ARG:C	1:A:150:PRO:HD2	2.30	0.56
1:B:289:LYS:O	1:B:293:LEU:HG	2.05	0.56
1:D:289:LYS:O	1:D:293:LEU:HG	2.05	0.56
1:B:409:ILE:HD13	1:B:426:ILE:HG12	1.88	0.56
1:C:200:ILE:HD13	1:C:204:MET:CG	2.33	0.56
1:C:200:ILE:CD1	1:C:204:MET:HG3	2.34	0.56
1:A:456:GLN:NE2	1:B:18:ARG:HH21	2.03	0.56
1:B:192:ALA:HB1	1:B:414:GLU:OE2	2.05	0.56
1:B:356:ILE:C	1:B:359:PRO:HD2	2.30	0.56
1:B:288:ILE:O	1:B:292:VAL:HG23	2.04	0.56
1:D:457:ASP:C	1:D:459:GLU:H	2.13	0.56
1:B:251:THR:HG22	1:B:255:TYR:HE1	1.71	0.56
1:B:305:LEU:HA	1:B:308:ILE:O	2.06	0.56
1:D:264:VAL:O	1:D:268:VAL:HG23	2.06	0.56
1:A:198:LEU:CD1	1:A:410:VAL:HG21	2.35	0.56
1:C:80:PRO:O	1:C:84:ILE:HG13	2.05	0.56
1:C:147:ARG:C	1:C:150:PRO:HD2	2.30	0.56
1:C:411:LEU:HD13	1:C:411:LEU:C	2.31	0.56
1:D:251:THR:HG22	1:D:255:TYR:HE1	1.71	0.56
1:D:420:GLN:H	1:D:420:GLN:NE2	2.04	0.56
1:D:256:LEU:O	1:D:260:ILE:HG13	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:LEU:HD13	1:A:411:LEU:C	2.31	0.56
1:B:416:THR:CG2	1:B:418:ASN:HD22	2.18	0.56
1:B:420:GLN:H	1:B:420:GLN:NE2	2.04	0.56
1:D:305:LEU:HA	1:D:308:ILE:O	2.06	0.56
1:C:198:LEU:CD1	1:C:410:VAL:HG21	2.36	0.55
1:B:264:VAL:O	1:B:268:VAL:HG23	2.06	0.55
1:C:270:ASN:HD21	1:C:401:SER:HA	1.71	0.55
1:B:119:LEU:HD23	1:B:453:LEU:HD11	1.87	0.55
1:D:416:THR:CG2	1:D:418:ASN:HD22	2.19	0.55
1:C:301:LEU:HD13	1:C:301:LEU:O	2.07	0.55
1:B:412:VAL:HB	1:B:425:MET:HE3	1.86	0.55
1:A:301:LEU:HD13	1:A:301:LEU:O	2.07	0.55
1:B:148:GLU:CD	1:B:148:GLU:H	2.15	0.55
1:A:156:GLY:O	1:A:178:LEU:HD12	2.07	0.55
1:B:341:VAL:O	1:B:345:LEU:HG	2.07	0.55
1:C:255:TYR:CE2	1:C:424:PRO:HB3	2.42	0.55
1:A:420:GLN:NE2	1:A:420:GLN:N	2.48	0.55
1:B:107:SER:HB3	6:B:507:HOH:O	2.07	0.55
1:B:457:ASP:C	1:B:459:GLU:H	2.13	0.55
1:A:433:THR:HG22	1:B:216:LYS:HE2	1.89	0.55
1:C:156:GLY:O	1:C:178:LEU:HD12	2.07	0.55
1:A:270:ASN:HD21	1:A:401:SER:HA	1.71	0.54
1:D:13:ILE:O	1:D:17:ARG:HG3	2.07	0.54
1:B:37:PHE:CE2	1:D:13:ILE:CD1	2.89	0.54
1:B:256:LEU:O	1:B:260:ILE:HG13	2.06	0.54
1:A:148:GLU:OE1	1:A:358:ALA:HB2	2.08	0.54
1:D:341:VAL:O	1:D:345:LEU:HG	2.07	0.54
1:D:148:GLU:CD	1:D:148:GLU:H	2.15	0.54
1:D:409:ILE:HD13	1:D:426:ILE:HG12	1.88	0.54
1:C:148:GLU:OE1	1:C:358:ALA:HB2	2.08	0.54
1:A:342:VAL:HG23	1:A:343:THR:N	2.23	0.54
1:B:13:ILE:O	1:B:17:ARG:HG3	2.07	0.54
1:D:107:SER:HB3	6:D:607:HOH:O	2.07	0.54
1:A:332:LEU:O	1:A:336:ILE:HG13	2.07	0.53
1:C:433:THR:HG22	1:D:216:LYS:HE2	1.89	0.53
1:A:255:TYR:CE2	1:A:424:PRO:HB3	2.42	0.53
1:D:307:LEU:HD12	1:D:308:ILE:N	2.23	0.53
1:A:115:ALA:HB3	1:A:178:LEU:HD21	1.89	0.53
1:B:21:GLN:NE2	1:B:25:LEU:HD13	2.24	0.53
1:C:311:ALA:O	1:C:340:ARG:HD2	2.09	0.53
1:C:332:LEU:O	1:C:336:ILE:HG13	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:420:GLN:HE21	1:C:420:GLN:N	2.04	0.53
1:B:194:LEU:HB2	1:B:414:GLU:OE1	2.09	0.53
1:B:307:LEU:HD12	1:B:308:ILE:N	2.23	0.53
1:C:55:LYS:HD2	1:C:55:LYS:C	2.34	0.53
1:A:251:THR:HG22	1:A:255:TYR:HE1	1.73	0.53
1:A:269:PHE:O	1:A:273:VAL:HG23	2.09	0.53
1:A:422:ILE:O	1:A:426:ILE:HG13	2.09	0.53
1:C:100:PHE:O	1:C:126:ARG:HD3	2.09	0.53
1:C:249:VAL:C	1:C:251:THR:H	2.17	0.53
1:B:403:ARG:NH1	1:B:437:GLN:HG3	2.23	0.53
1:B:419:TYR:CE1	1:B:422:ILE:HD12	2.44	0.53
1:C:251:THR:HG22	1:C:255:TYR:HE1	1.73	0.53
1:D:194:LEU:HB2	1:D:414:GLU:OE1	2.09	0.53
1:D:419:TYR:CE1	1:D:422:ILE:HD12	2.44	0.53
1:A:129:PRO:HG2	1:A:130:VAL:H	1.74	0.53
1:A:144:VAL:HG12	1:A:344:THR:HG22	1.91	0.53
1:A:311:ALA:O	1:A:340:ARG:HD2	2.09	0.53
1:B:117:GLU:O	1:B:119:LEU:HD13	2.09	0.53
1:C:342:VAL:HG23	1:C:343:THR:N	2.23	0.53
1:D:403:ARG:NH1	1:D:437:GLN:HG3	2.23	0.53
1:A:100:PHE:O	1:A:126:ARG:HD3	2.09	0.52
1:A:420:GLN:HE21	1:A:420:GLN:N	2.04	0.52
1:C:269:PHE:O	1:C:273:VAL:HG23	2.09	0.52
1:D:117:GLU:O	1:D:119:LEU:HD13	2.09	0.52
1:D:238:ILE:HG22	1:D:239:ILE:HG23	1.92	0.52
1:C:38:MET:HG3	1:C:168:MET:SD	2.50	0.52
1:D:309:GLU:H	1:D:310:PRO:HD3	1.74	0.52
1:D:430:LEU:HG	1:D:434:LEU:CD2	2.39	0.52
1:A:95:PHE:HD2	1:A:96:LEU:HD12	1.75	0.52
1:C:115:ALA:HB3	1:C:178:LEU:HD21	1.89	0.52
1:C:144:VAL:HG21	1:C:343:THR:CG2	2.39	0.52
1:D:21:GLN:NE2	1:D:25:LEU:HD13	2.24	0.52
1:A:38:MET:HG3	1:A:168:MET:SD	2.50	0.52
1:A:55:LYS:HD2	1:A:55:LYS:C	2.34	0.52
1:A:88:LEU:O	1:A:92:VAL:HG23	2.09	0.52
1:A:241:VAL:HG12	1:A:242:GLY:N	2.25	0.52
1:A:284:HIS:C	1:A:286:GLY:H	2.17	0.52
1:B:168:MET:HG2	1:D:17:ARG:HD3	1.90	0.52
1:A:144:VAL:HG21	1:A:343:THR:CG2	2.39	0.52
1:A:193:PRO:HG2	1:A:194:LEU:H	1.74	0.52
1:B:144:VAL:HG21	1:B:343:THR:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:MET:HE2	1:D:17:ARG:HG2	1.91	0.52
1:B:398:MET:CE	1:B:402:VAL:HB	2.39	0.52
1:C:193:PRO:HG2	1:C:194:LEU:H	1.74	0.52
1:C:422:ILE:O	1:C:426:ILE:HG13	2.09	0.52
1:D:256:LEU:HD22	5:D:601:MYS:H122	1.92	0.52
1:A:308:ILE:O	1:A:309:GLU:HB2	2.10	0.52
1:A:97:VAL:HG21	1:A:353:PRO:HG3	1.92	0.52
1:A:249:VAL:C	1:A:251:THR:H	2.17	0.52
1:C:88:LEU:O	1:C:92:VAL:HG23	2.09	0.52
1:C:98:ARG:HD2	1:C:291:TRP:CD2	2.44	0.52
1:A:35:ILE:HD12	1:A:173:ALA:HA	1.92	0.52
1:A:230:ARG:HH11	1:A:230:ARG:CB	2.07	0.52
1:A:329:SER:O	1:A:330:VAL:C	2.53	0.52
1:B:241:VAL:HG12	1:B:242:GLY:N	2.25	0.52
1:C:144:VAL:HG11	1:C:344:THR:CG2	2.40	0.52
1:C:241:VAL:HG12	1:C:242:GLY:N	2.24	0.52
1:A:307:LEU:CD1	1:A:308:ILE:HG23	2.40	0.52
1:B:204:MET:O	1:B:205:ARG:C	2.53	0.52
1:B:356:ILE:O	1:B:360:MET:HG3	2.10	0.52
1:B:456:GLN:HE21	1:B:456:GLN:HA	1.75	0.52
1:A:98:ARG:HD2	1:A:291:TRP:CD2	2.44	0.51
1:B:256:LEU:HD22	5:B:501:MYS:H122	1.92	0.51
1:D:398:MET:CE	1:D:402:VAL:HB	2.40	0.51
1:B:238:ILE:HG22	1:B:239:ILE:HG23	1.92	0.51
1:C:284:HIS:C	1:C:286:GLY:H	2.17	0.51
1:D:356:ILE:O	1:D:360:MET:HG3	2.10	0.51
1:D:456:GLN:HE21	1:D:456:GLN:HA	1.75	0.51
1:B:430:LEU:HG	1:B:434:LEU:CD2	2.39	0.51
1:C:91:MET:HG2	1:C:292:VAL:O	2.10	0.51
1:C:129:PRO:HG2	1:C:130:VAL:H	1.74	0.51
1:C:163:LEU:HD22	1:C:174:ARG:HA	1.92	0.51
1:C:240:GLU:H	1:C:322:ILE:CD1	2.23	0.51
1:A:144:VAL:HG11	1:A:344:THR:CG2	2.40	0.51
1:A:369:THR:O	1:A:373:MET:HB2	2.11	0.51
1:B:320:ILE:C	1:B:322:ILE:N	2.68	0.51
1:C:144:VAL:HG12	1:C:344:THR:HG22	1.90	0.51
1:D:449:LEU:O	1:D:452:THR:HG22	2.10	0.51
1:B:98:ARG:HD2	1:B:291:TRP:CD2	2.46	0.51
1:B:205:ARG:N	1:B:206:PRO:HD2	2.26	0.51
1:B:449:LEU:O	1:B:452:THR:HG22	2.10	0.51
1:D:320:ILE:C	1:D:322:ILE:N	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:ASP:O	1:B:459:GLU:N	2.44	0.51
1:C:307:LEU:CD1	1:C:308:ILE:HG23	2.40	0.51
1:D:241:VAL:HG12	1:D:242:GLY:N	2.25	0.51
1:A:163:LEU:HD22	1:A:174:ARG:HA	1.92	0.51
1:C:97:VAL:HG21	1:C:353:PRO:HG3	1.92	0.51
1:C:124:TRP:CD1	1:C:124:TRP:C	2.89	0.51
1:D:317:PHE:C	1:D:319:LEU:N	2.69	0.51
1:D:318:ASN:H	1:D:318:ASN:ND2	2.04	0.51
1:A:91:MET:HG2	1:A:292:VAL:O	2.10	0.51
1:C:308:ILE:O	1:C:309:GLU:HB2	2.10	0.51
1:C:369:THR:O	1:C:373:MET:HB2	2.11	0.51
1:D:457:ASP:O	1:D:459:GLU:N	2.44	0.51
1:A:240:GLU:H	1:A:322:ILE:CD1	2.23	0.51
1:B:317:PHE:C	1:B:319:LEU:N	2.69	0.51
1:D:98:ARG:HD2	1:D:291:TRP:CD2	2.46	0.51
1:D:144:VAL:HG21	1:D:343:THR:HG22	1.92	0.50
1:A:109:ILE:HG23	1:A:204:MET:SD	2.52	0.50
1:C:163:LEU:HD12	1:C:168:MET:HB2	1.93	0.50
1:C:329:SER:O	1:C:330:VAL:C	2.53	0.50
1:A:433:THR:CG2	1:B:216:LYS:HE2	2.41	0.50
1:B:309:GLU:H	1:B:310:PRO:HD3	1.74	0.50
1:C:95:PHE:HD2	1:C:96:LEU:HD12	1.75	0.50
1:A:163:LEU:HD12	1:A:168:MET:HB2	1.93	0.50
1:C:240:GLU:C	1:C:322:ILE:HD12	2.36	0.50
1:A:304:ILE:HG22	1:A:308:ILE:HD11	1.94	0.50
1:B:318:ASN:H	1:B:318:ASN:ND2	2.04	0.50
1:A:124:TRP:CD1	1:A:124:TRP:C	2.89	0.50
1:C:255:TYR:CD2	1:C:424:PRO:HB3	2.47	0.50
1:A:133:ILE:HA	1:A:136:MET:HE3	1.94	0.50
1:B:284:HIS:O	1:B:286:GLY:N	2.44	0.50
1:C:294:MET:O	1:C:298:ILE:HG22	2.12	0.50
1:D:251:THR:HG22	1:D:255:TYR:CE1	2.47	0.50
1:B:270:ASN:HD21	1:B:401:SER:HA	1.76	0.50
1:C:304:ILE:HG22	1:C:308:ILE:HD11	1.94	0.50
1:C:433:THR:CG2	1:D:216:LYS:HE2	2.41	0.50
1:D:449:LEU:HA	1:D:452:THR:CG2	2.42	0.50
1:A:294:MET:O	1:A:298:ILE:HG22	2.12	0.49
1:C:144:VAL:HG21	1:C:343:THR:HG21	1.94	0.49
1:B:24:ARG:HG2	1:B:24:ARG:HH11	1.77	0.49
1:D:270:ASN:HD21	1:D:401:SER:HA	1.77	0.49
1:A:165:VAL:HG23	1:A:166:PHE:CD1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:GLU:C	1:A:322:ILE:HD12	2.36	0.49
1:A:255:TYR:CD2	1:A:424:PRO:HB3	2.47	0.49
1:C:165:VAL:HG23	1:C:166:PHE:CD1	2.47	0.49
1:C:426:ILE:HG22	1:D:223:ILE:HD12	1.94	0.49
1:A:245:SER:HB3	1:A:385:GLU:OE2	2.12	0.49
1:C:35:ILE:HD12	1:C:173:ALA:HA	1.92	0.49
1:D:282:ARG:HG3	1:D:283:PHE:N	2.28	0.49
1:D:292:VAL:O	1:D:292:VAL:HG12	2.13	0.49
1:D:348:PHE:CD2	1:D:356:ILE:HD12	2.47	0.49
1:A:333:LEU:HD21	1:A:369:THR:CG2	2.41	0.49
1:C:109:ILE:HG23	1:C:204:MET:SD	2.52	0.49
1:D:14:VAL:O	1:D:18:ARG:HG3	2.13	0.49
1:D:205:ARG:N	1:D:206:PRO:HD2	2.26	0.49
1:B:28:ARG:O	1:B:29:ASP:C	2.55	0.49
1:B:124:TRP:HA	1:B:157:ASN:HD22	1.77	0.49
1:B:348:PHE:CD2	1:B:356:ILE:HD12	2.47	0.49
1:C:245:SER:HB3	1:C:385:GLU:OE2	2.12	0.49
1:D:28:ARG:O	1:D:29:ASP:C	2.55	0.49
1:D:147:ARG:NH1	1:D:147:ARG:CB	2.68	0.49
1:B:251:THR:HG22	1:B:255:TYR:CE1	2.47	0.49
1:D:204:MET:O	1:D:205:ARG:C	2.53	0.49
1:A:449:LEU:HD22	1:A:453:LEU:HG	1.95	0.49
1:B:13:ILE:HD12	1:B:13:ILE:N	2.28	0.49
1:D:24:ARG:HH11	1:D:24:ARG:HG2	1.77	0.49
1:B:14:VAL:O	1:B:18:ARG:HG3	2.13	0.49
1:B:218:VAL:O	1:B:222:VAL:HG23	2.13	0.49
1:B:317:PHE:C	1:B:319:LEU:H	2.21	0.49
1:C:133:ILE:HA	1:C:136:MET:HE3	1.94	0.49
1:C:449:LEU:HD22	1:C:453:LEU:HG	1.95	0.49
1:D:308:ILE:C	1:D:308:ILE:CD1	2.85	0.49
1:B:308:ILE:C	1:B:308:ILE:CD1	2.85	0.48
1:B:282:ARG:HG3	1:B:283:PHE:N	2.28	0.48
1:B:416:THR:HG23	1:B:418:ASN:HD22	1.78	0.48
1:C:101:ALA:HB2	1:C:126:ARG:HG3	1.95	0.48
1:C:402:VAL:O	1:C:403:ARG:HB2	2.13	0.48
1:B:449:LEU:HA	1:B:452:THR:CG2	2.42	0.48
1:D:124:TRP:HA	1:D:157:ASN:HD22	1.78	0.48
1:D:317:PHE:C	1:D:319:LEU:H	2.21	0.48
1:D:457:ASP:C	1:D:459:GLU:N	2.69	0.48
1:A:144:VAL:HG21	1:A:343:THR:HG21	1.94	0.48
1:A:402:VAL:O	1:A:403:ARG:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:ILE:HD11	1:B:346:LEU:HD13	1.95	0.48
1:C:333:LEU:HD21	1:C:369:THR:CG2	2.41	0.48
1:C:237:PRO:HG2	1:C:240:GLU:HG2	1.96	0.48
1:A:427:ILE:CG1	1:B:223:ILE:HD11	2.44	0.48
1:B:292:VAL:HG12	1:B:292:VAL:O	2.13	0.48
1:D:13:ILE:N	1:D:13:ILE:HD12	2.28	0.48
1:D:449:LEU:CA	1:D:452:THR:HG22	2.43	0.48
1:B:457:ASP:C	1:B:459:GLU:N	2.69	0.48
1:C:54:GLU:HG2	1:C:147:ARG:HD2	1.96	0.48
1:A:373:MET:HA	1:A:373:MET:CE	2.39	0.48
1:B:78:LEU:C	1:B:80:PRO:HD2	2.39	0.48
1:C:427:ILE:CG1	1:D:223:ILE:HD11	2.44	0.48
1:D:218:VAL:O	1:D:222:VAL:HG23	2.13	0.48
1:A:81:LEU:HD22	1:A:85:LEU:CD2	2.41	0.48
1:A:426:ILE:HG22	1:B:223:ILE:HD12	1.94	0.48
1:D:78:LEU:C	1:D:80:PRO:HD2	2.39	0.48
1:A:437:GLN:CG	1:A:438:PHE:N	2.76	0.47
1:A:161:MET:O	1:A:162:VAL:C	2.56	0.47
1:C:230:ARG:HH11	1:C:230:ARG:CB	2.07	0.47
1:D:284:HIS:O	1:D:286:GLY:N	2.44	0.47
1:D:416:THR:HG23	1:D:418:ASN:HD22	1.78	0.47
1:A:248:PRO:O	1:A:251:THR:HB	2.14	0.47
1:D:412:VAL:HB	1:D:425:MET:CE	2.44	0.47
1:A:70:GLN:C	1:A:72:ALA:H	2.22	0.47
1:A:200:ILE:HA	1:A:204:MET:HB2	1.97	0.47
1:B:449:LEU:CA	1:B:452:THR:HG22	2.43	0.47
1:D:298:ILE:HD11	1:D:346:LEU:HD13	1.95	0.47
1:C:373:MET:HA	1:C:373:MET:CE	2.39	0.47
1:C:435:LEU:O	1:C:439:LEU:HB2	2.15	0.47
1:A:94:TYR:OH	1:A:143:MET:HE1	2.14	0.47
1:A:101:ALA:HB2	1:A:126:ARG:HG3	1.95	0.47
1:A:132:PHE:CD2	1:A:136:MET:HE2	2.50	0.47
1:B:412:VAL:HB	1:B:425:MET:CE	2.44	0.47
1:C:423:LEU:O	1:C:424:PRO:C	2.58	0.47
1:D:282:ARG:CG	1:D:283:PHE:N	2.77	0.47
1:A:435:LEU:O	1:A:439:LEU:HB2	2.15	0.47
1:B:282:ARG:CG	1:B:283:PHE:N	2.77	0.47
1:D:399:ALA:O	1:D:403:ARG:HA	2.15	0.47
1:B:322:ILE:HD12	1:B:322:ILE:H	1.78	0.47
1:C:94:TYR:OH	1:C:143:MET:HE1	2.14	0.47
1:C:248:PRO:O	1:C:251:THR:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:284:HIS:C	1:C:286:GLY:N	2.72	0.47
1:D:81:LEU:C	1:D:85:LEU:HD23	2.40	0.47
1:A:398:MET:SD	1:A:398:MET:C	2.98	0.47
1:C:70:GLN:C	1:C:72:ALA:H	2.22	0.47
1:A:54:GLU:HG2	1:A:147:ARG:HD2	1.96	0.46
1:C:161:MET:O	1:C:162:VAL:C	2.56	0.46
1:C:409:ILE:CD1	1:C:426:ILE:HA	2.45	0.46
1:A:210:TYR:HE1	1:D:171:ALA:HA	1.80	0.46
1:A:246:ASP:OD1	1:A:247:ALA:N	2.48	0.46
1:A:409:ILE:CD1	1:A:426:ILE:HA	2.45	0.46
1:B:81:LEU:C	1:B:85:LEU:HD23	2.40	0.46
1:B:362:ALA:CA	1:B:365:THR:HG22	2.43	0.46
1:D:61:GLN:HG2	1:D:140:GLY:HA2	1.97	0.46
1:A:456:GLN:HE21	1:B:18:ARG:HH21	1.63	0.46
1:B:399:ALA:O	1:B:403:ARG:HA	2.15	0.46
1:C:94:TYR:CZ	1:C:352:ALA:HB2	2.51	0.46
1:C:132:PHE:CD2	1:C:136:MET:HE2	2.50	0.46
1:C:200:ILE:HA	1:C:204:MET:HB2	1.97	0.46
1:D:38:MET:HE3	1:D:162:VAL:CG1	2.45	0.46
1:A:94:TYR:CZ	1:A:352:ALA:HB2	2.51	0.46
1:A:237:PRO:HG2	1:A:240:GLU:HG2	1.96	0.46
1:B:61:GLN:HG2	1:B:140:GLY:HA2	1.97	0.46
1:B:338:ILE:O	1:B:342:VAL:HG13	2.16	0.46
1:C:327:ASN:O	1:C:328:PHE:CD1	2.69	0.46
1:D:163:LEU:HD21	1:D:174:ARG:CA	2.26	0.46
1:A:456:GLN:HE21	1:B:18:ARG:NH2	2.14	0.46
1:B:274:LEU:O	1:B:277:GLN:HB3	2.16	0.46
1:C:398:MET:SD	1:C:398:MET:C	2.98	0.46
1:D:21:GLN:HE21	1:D:25:LEU:HD13	1.81	0.46
1:D:322:ILE:HD12	1:D:322:ILE:H	1.78	0.46
1:A:122:VAL:CG1	1:A:157:ASN:OD1	2.64	0.46
1:A:124:TRP:CD1	1:A:125:TRP:N	2.84	0.46
1:A:132:PHE:CD2	1:A:132:PHE:C	2.94	0.46
1:C:122:VAL:CG1	1:C:157:ASN:OD1	2.64	0.46
1:C:246:ASP:OD1	1:C:247:ALA:N	2.48	0.46
1:D:362:ALA:CA	1:D:365:THR:HG22	2.43	0.46
1:A:423:LEU:O	1:A:424:PRO:C	2.58	0.46
1:C:124:TRP:CD1	1:C:125:TRP:N	2.84	0.46
1:B:38:MET:HE3	1:B:162:VAL:CG1	2.45	0.46
1:B:322:ILE:N	1:B:322:ILE:CD1	2.71	0.46
1:C:160:ARG:O	1:C:163:LEU:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:261:ILE:O	1:D:265:VAL:HG23	2.16	0.46
1:D:274:LEU:O	1:D:277:GLN:HB3	2.16	0.46
1:A:160:ARG:O	1:A:163:LEU:HB3	2.16	0.46
1:A:253:TRP:O	1:A:256:LEU:HB3	2.15	0.46
1:B:261:ILE:O	1:B:265:VAL:HG23	2.16	0.46
1:C:197:ILE:HD11	1:D:406:LEU:HD13	1.98	0.46
1:D:230:ARG:HH11	1:D:230:ARG:CB	2.19	0.46
1:A:284:HIS:C	1:A:286:GLY:N	2.72	0.45
1:B:143:MET:HA	1:B:302:CYS:SG	2.56	0.45
1:C:309:GLU:N	1:C:310:PRO:HD3	2.32	0.45
1:D:109:ILE:N	1:D:110:PRO:CD	2.80	0.45
1:A:90:ALA:O	1:A:94:TYR:HD1	2.00	0.45
1:A:206:PRO:CB	1:A:209:ARG:HD3	2.46	0.45
1:A:235:GLU:O	1:A:236:ALA:C	2.59	0.45
1:B:124:TRP:CZ3	1:B:161:MET:HG3	2.51	0.45
1:B:255:TYR:CE2	1:B:424:PRO:HB3	2.51	0.45
1:B:269:PHE:HE2	1:B:360:MET:CE	2.29	0.45
1:C:206:PRO:CB	1:C:209:ARG:HD3	2.46	0.45
1:C:456:GLN:HE21	1:D:18:ARG:HH21	1.63	0.45
1:D:124:TRP:CZ3	1:D:161:MET:HG3	2.52	0.45
1:A:88:LEU:HD12	1:A:91:MET:CE	2.45	0.45
1:A:308:ILE:O	1:A:309:GLU:CB	2.64	0.45
1:C:88:LEU:HD12	1:C:91:MET:CE	2.45	0.45
1:C:253:TRP:O	1:C:256:LEU:HB3	2.15	0.45
1:C:308:ILE:O	1:C:309:GLU:CB	2.64	0.45
1:C:403:ARG:NH2	1:C:437:GLN:HA	2.32	0.45
1:D:449:LEU:C	1:D:452:THR:HG22	2.42	0.45
1:A:197:ILE:HD11	1:B:406:LEU:HD13	1.98	0.45
1:B:398:MET:HE2	1:B:402:VAL:HB	1.97	0.45
1:C:304:ILE:O	1:C:308:ILE:HG12	2.16	0.45
1:C:456:GLN:HE21	1:D:18:ARG:NH2	2.14	0.45
1:A:403:ARG:NH2	1:A:437:GLN:HA	2.32	0.45
1:B:21:GLN:HE21	1:B:25:LEU:HD13	1.81	0.45
1:C:81:LEU:HD22	1:C:85:LEU:CD2	2.41	0.45
1:C:109:ILE:N	1:C:110:PRO:CD	2.80	0.45
1:A:304:ILE:O	1:A:308:ILE:HG12	2.16	0.45
1:A:309:GLU:N	1:A:310:PRO:HD3	2.32	0.45
1:A:327:ASN:O	1:A:328:PHE:CD1	2.69	0.45
1:B:163:LEU:HD21	1:B:174:ARG:CA	2.26	0.45
1:B:165:VAL:CG2	1:B:166:PHE:CD1	3.00	0.45
1:C:132:PHE:CD2	1:C:132:PHE:C	2.94	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:LEU:HB2	1:D:129:PRO:HD3	1.99	0.45
1:D:338:ILE:O	1:D:342:VAL:HG13	2.16	0.45
1:A:427:ILE:HG12	1:B:223:ILE:HD11	1.99	0.45
1:B:123:ARG:CZ	1:B:126:ARG:HD2	2.46	0.45
1:C:67:ALA:HA	1:C:70:GLN:NE2	2.32	0.45
1:C:205:ARG:NH2	1:D:205:ARG:HD2	2.31	0.45
1:C:427:ILE:HG12	1:D:223:ILE:HD11	1.99	0.45
1:D:255:TYR:CE2	1:D:424:PRO:HB3	2.51	0.45
1:D:398:MET:HE2	1:D:402:VAL:HB	1.97	0.45
1:A:205:ARG:NH2	1:B:205:ARG:HD2	2.31	0.45
1:C:103:GLU:CG	1:C:123:ARG:HH21	2.29	0.45
1:A:67:ALA:HA	1:A:70:GLN:NE2	2.32	0.45
1:A:404:ALA:HB1	1:A:407:THR:HB	1.99	0.45
1:C:230:ARG:HH12	1:D:249:VAL:CG2	2.30	0.45
1:A:126:ARG:O	1:A:129:PRO:HG2	2.17	0.45
1:C:235:GLU:O	1:C:236:ALA:C	2.59	0.45
1:D:143:MET:HA	1:D:302:CYS:SG	2.56	0.45
1:D:148:GLU:O	1:D:149:GLY:C	2.60	0.45
1:D:165:VAL:CG2	1:D:166:PHE:CD1	3.00	0.45
1:A:103:GLU:CG	1:A:123:ARG:HH21	2.29	0.44
1:A:109:ILE:N	1:A:110:PRO:CD	2.80	0.44
1:A:230:ARG:HH12	1:B:249:VAL:CG2	2.30	0.44
1:A:298:ILE:HD11	1:A:346:LEU:CB	2.46	0.44
1:B:449:LEU:C	1:B:452:THR:HG22	2.42	0.44
1:C:260:ILE:HG23	1:C:435:LEU:HD21	1.97	0.44
1:D:32:PRO:HG2	1:D:35:ILE:HD12	1.99	0.44
1:D:138:THR:HG21	1:D:353:PRO:CD	2.45	0.44
1:D:405:PRO:O	1:D:409:ILE:HG13	2.17	0.44
1:B:32:PRO:HG2	1:B:35:ILE:HD12	1.99	0.44
1:D:94:TYR:CZ	1:D:352:ALA:HB2	2.53	0.44
1:D:123:ARG:CZ	1:D:126:ARG:HD2	2.46	0.44
1:D:274:LEU:HD22	1:D:451:ARG:CZ	2.47	0.44
1:A:329:SER:HB3	1:A:332:LEU:HB3	1.99	0.44
1:B:405:PRO:O	1:B:409:ILE:HG13	2.17	0.44
1:C:90:ALA:O	1:C:94:TYR:HD1	2.00	0.44
1:C:126:ARG:O	1:C:129:PRO:HG2	2.17	0.44
1:C:437:GLN:CG	1:C:438:PHE:N	2.76	0.44
1:A:155:GLY:O	1:A:181:GLY:HA3	2.18	0.44
1:B:168:MET:CG	1:D:17:ARG:HD3	2.47	0.44
1:B:274:LEU:HD22	1:B:451:ARG:CZ	2.47	0.44
1:B:309:GLU:O	1:B:309:GLU:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:LEU:CD1	1:C:168:MET:HB2	2.48	0.44
1:D:402:VAL:O	1:D:403:ARG:HB3	2.17	0.44
1:A:330:VAL:O	1:A:334:LEU:HB2	2.18	0.44
1:B:84:ILE:HG23	1:B:85:LEU:H	1.83	0.44
1:B:109:ILE:N	1:B:110:PRO:CD	2.80	0.44
1:A:113:GLU:O	1:A:117:GLU:HG3	2.18	0.44
1:A:295:GLY:HA2	1:A:298:ILE:HG22	2.00	0.44
1:C:165:VAL:HG23	1:C:166:PHE:HD1	1.83	0.44
1:B:94:TYR:CZ	1:B:352:ALA:HB2	2.53	0.44
1:B:248:PRO:HG2	1:B:251:THR:OG1	2.18	0.44
1:C:404:ALA:HB1	1:C:407:THR:HB	1.99	0.44
1:D:362:ALA:HA	1:D:365:THR:CG2	2.46	0.44
1:A:223:ILE:HD11	1:B:427:ILE:HG12	2.00	0.44
1:B:402:VAL:O	1:B:403:ARG:HB3	2.18	0.44
1:C:113:GLU:O	1:C:117:GLU:HG3	2.18	0.44
1:D:278:ASP:O	1:D:279:MET:C	2.61	0.44
1:B:25:LEU:HA	1:B:25:LEU:HD12	1.82	0.43
1:C:240:GLU:O	1:C:322:ILE:HD12	2.18	0.43
1:D:25:LEU:C	1:D:27:GLN:H	2.26	0.43
1:D:248:PRO:HG2	1:D:251:THR:OG1	2.18	0.43
1:D:309:GLU:O	1:D:309:GLU:HG3	2.18	0.43
1:A:309:GLU:H	1:A:310:PRO:HD3	1.83	0.43
1:B:330:VAL:HG22	1:B:373:MET:CB	2.48	0.43
1:C:81:LEU:O	1:C:82:ALA:C	2.60	0.43
1:C:329:SER:HB3	1:C:332:LEU:HB3	1.99	0.43
1:C:330:VAL:O	1:C:334:LEU:HB2	2.18	0.43
1:C:340:ARG:HE	1:C:340:ARG:HB3	1.64	0.43
1:D:362:ALA:C	1:D:365:THR:HG22	2.43	0.43
1:D:435:LEU:HD11	1:D:439:LEU:HD22	2.00	0.43
1:A:317:PHE:C	1:A:319:LEU:N	2.76	0.43
1:B:79:TRP:N	1:B:79:TRP:HE3	2.17	0.43
1:B:135:GLY:O	1:B:139:LEU:HB2	2.18	0.43
1:B:148:GLU:O	1:B:149:GLY:C	2.60	0.43
1:C:35:ILE:HD11	1:C:173:ALA:HB2	2.00	0.43
1:D:330:VAL:HG22	1:D:373:MET:CB	2.48	0.43
1:B:128:LEU:HB2	1:B:129:PRO:HD3	1.99	0.43
1:C:295:GLY:HA2	1:C:298:ILE:HG22	2.00	0.43
1:D:135:GLY:O	1:D:139:LEU:HB2	2.18	0.43
1:A:240:GLU:O	1:A:322:ILE:HD12	2.18	0.43
1:A:363:LEU:HB2	1:A:397:LEU:HD23	2.00	0.43
1:C:155:GLY:O	1:C:181:GLY:HA3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:ARG:NH1	1:D:249:VAL:HG22	2.34	0.43
1:D:456:GLN:HE21	1:D:456:GLN:CA	2.31	0.43
1:A:79:TRP:HB2	1:A:80:PRO:HD3	2.01	0.43
1:A:163:LEU:CD1	1:A:168:MET:HB2	2.48	0.43
1:A:356:ILE:O	1:A:360:MET:HG3	2.19	0.43
1:B:25:LEU:C	1:B:27:GLN:H	2.26	0.43
1:B:362:ALA:C	1:B:365:THR:HG22	2.43	0.43
1:B:435:LEU:HD11	1:B:439:LEU:HD22	1.99	0.43
1:D:32:PRO:CG	1:D:35:ILE:HD12	2.49	0.43
1:D:79:TRP:N	1:D:79:TRP:HE3	2.17	0.43
1:D:202:GLU:CD	1:D:406:LEU:HB3	2.44	0.43
1:A:230:ARG:NH1	1:B:249:VAL:HG22	2.34	0.43
1:C:161:MET:O	1:C:164:ASP:N	2.51	0.43
1:C:356:ILE:O	1:C:360:MET:HG3	2.19	0.43
1:D:25:LEU:HD12	1:D:25:LEU:HA	1.82	0.43
1:B:337:PHE:O	1:B:341:VAL:HG23	2.19	0.43
1:C:91:MET:HG3	1:C:296:GLY:CA	2.49	0.43
1:D:84:ILE:HG23	1:D:85:LEU:H	1.82	0.43
1:D:358:ALA:N	1:D:359:PRO:CD	2.82	0.43
1:D:382:TYR:HB2	1:D:384:LEU:HG	2.00	0.43
1:D:456:GLN:HA	1:D:456:GLN:NE2	2.33	0.43
1:C:132:PHE:C	1:C:132:PHE:HD2	2.27	0.43
1:A:132:PHE:C	1:A:132:PHE:HD2	2.27	0.43
1:A:317:PHE:HA	1:A:321:PRO:HD2	1.96	0.43
1:B:79:TRP:N	1:B:80:PRO:CD	2.81	0.43
1:B:358:ALA:N	1:B:359:PRO:CD	2.82	0.43
1:B:456:GLN:HA	1:B:456:GLN:NE2	2.34	0.43
1:D:423:LEU:HA	1:D:423:LEU:HD23	1.82	0.43
1:A:165:VAL:HG23	1:A:166:PHE:HD1	1.82	0.42
1:A:81:LEU:O	1:A:82:ALA:C	2.60	0.42
1:A:264:VAL:O	1:A:268:VAL:HG23	2.19	0.42
1:A:288:ILE:O	1:A:289:LYS:C	2.61	0.42
1:B:382:TYR:HB2	1:B:384:LEU:HG	2.00	0.42
1:C:288:ILE:O	1:C:289:LYS:C	2.61	0.42
1:D:180:THR:CG2	1:D:221:GLY:HA3	2.49	0.42
1:C:223:ILE:HD11	1:D:427:ILE:HG12	2.00	0.42
1:C:358:ALA:HB3	1:C:359:PRO:HD3	2.01	0.42
1:D:421:LEU:O	1:D:424:PRO:HD2	2.20	0.42
1:B:69:VAL:HG22	1:B:69:VAL:O	2.19	0.42
1:C:79:TRP:HB2	1:C:80:PRO:HD3	2.01	0.42
1:C:205:ARG:HA	1:C:206:PRO:HD3	1.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:363:LEU:HB2	1:C:397:LEU:HD23	2.00	0.42
1:B:32:PRO:CG	1:B:35:ILE:HD12	2.49	0.42
1:C:298:ILE:HD11	1:C:346:LEU:CB	2.46	0.42
1:D:115:ALA:CB	1:D:178:LEU:HD11	2.50	0.42
1:B:186:LEU:HD23	1:B:196:GLY:HA2	2.01	0.42
1:B:225:SER:O	1:B:228:VAL:HG22	2.20	0.42
1:C:81:LEU:O	1:C:85:LEU:HD23	2.19	0.42
1:C:294:MET:O	1:C:297:ALA:HB3	2.20	0.42
1:C:382:TYR:O	1:C:383:HIS:HB2	2.20	0.42
1:D:69:VAL:HG22	1:D:69:VAL:O	2.19	0.42
1:D:79:TRP:N	1:D:80:PRO:CD	2.81	0.42
1:D:269:PHE:HE2	1:D:360:MET:CE	2.29	0.42
1:A:91:MET:HG3	1:A:296:GLY:CA	2.49	0.42
1:A:327:ASN:O	1:A:328:PHE:HD1	2.03	0.42
1:B:17:ARG:NH1	3:B:505:SO4:O2	2.53	0.42
1:B:202:GLU:CD	1:B:406:LEU:HB3	2.44	0.42
1:B:278:ASP:O	1:B:279:MET:C	2.61	0.42
3:B:605:SO4:O2	1:D:17:ARG:NH1	2.53	0.42
1:C:31:THR:O	1:C:35:ILE:HG12	2.20	0.42
1:C:218:VAL:O	1:C:222:VAL:HG23	2.20	0.42
1:A:81:LEU:O	1:A:85:LEU:HD23	2.19	0.42
1:B:115:ALA:CB	1:B:178:LEU:HD11	2.50	0.42
1:B:213:ILE:HG22	1:B:214:SER:N	2.35	0.42
1:B:398:MET:HE3	1:B:398:MET:HB2	1.87	0.42
1:C:47:GLY:O	1:C:51:VAL:HG23	2.20	0.42
1:C:211:ASN:O	1:C:212:LEU:HB2	2.20	0.42
1:C:317:PHE:C	1:C:319:LEU:N	2.76	0.42
1:C:400:ALA:HB2	1:C:432:ALA:HB1	2.02	0.42
1:D:144:VAL:CG2	1:D:343:THR:HG22	2.49	0.42
1:D:337:PHE:O	1:D:341:VAL:HG23	2.19	0.42
1:A:246:ASP:OD2	1:B:235:GLU:OE1	2.37	0.42
1:A:382:TYR:O	1:A:383:HIS:HB2	2.20	0.42
1:A:456:GLN:NE2	1:B:18:ARG:NH2	2.68	0.42
1:B:32:PRO:HB2	1:D:20:ASP:CG	2.45	0.42
1:B:333:LEU:HD11	1:B:369:THR:HG22	2.02	0.42
1:B:435:LEU:CD1	1:B:439:LEU:HD22	2.50	0.42
1:A:35:ILE:HD11	1:A:173:ALA:HB2	2.00	0.42
1:A:394:MET:HE1	1:A:415:MET:CE	2.49	0.42
1:A:458:ALA:O	1:A:459:GLU:C	2.63	0.42
1:B:115:ALA:HB1	1:B:178:LEU:HD11	2.02	0.42
1:B:284:HIS:C	1:B:286:GLY:N	2.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:398:MET:HE1	1:C:408:GLY:CA	2.50	0.42
1:C:398:MET:HE3	1:C:398:MET:HB3	1.75	0.42
1:C:403:ARG:C	1:C:405:PRO:HD3	2.45	0.42
1:D:115:ALA:HA	1:D:120:ARG:O	2.20	0.42
1:D:435:LEU:CD1	1:D:439:LEU:HD22	2.50	0.42
1:A:115:ALA:HB1	1:A:178:LEU:HD21	2.02	0.41
1:A:340:ARG:HE	1:A:340:ARG:HB3	1.64	0.41
1:A:398:MET:HE1	1:A:408:GLY:CA	2.50	0.41
1:B:88:LEU:HD23	1:B:91:MET:CE	2.50	0.41
1:B:180:THR:CG2	1:B:221:GLY:HA3	2.49	0.41
1:C:208:PHE:HD1	1:C:209:ARG:HG3	1.85	0.41
1:D:81:LEU:HD22	1:D:85:LEU:CD2	2.46	0.41
1:D:213:ILE:HG22	1:D:214:SER:N	2.35	0.41
1:D:333:LEU:HD11	1:D:369:THR:HG22	2.02	0.41
1:B:421:LEU:C	1:B:424:PRO:HD2	2.45	0.41
1:C:192:ALA:HB1	1:C:414:GLU:OE2	2.20	0.41
1:C:309:GLU:H	1:C:310:PRO:HD3	1.84	0.41
1:D:186:LEU:HD23	1:D:196:GLY:HA2	2.01	0.41
1:A:205:ARG:HA	1:A:206:PRO:HD3	1.73	0.41
1:A:403:ARG:C	1:A:405:PRO:HD3	2.45	0.41
1:B:171:ALA:HA	1:C:210:TYR:HE1	1.85	0.41
1:C:264:VAL:O	1:C:268:VAL:HG23	2.19	0.41
1:C:327:ASN:O	1:C:328:PHE:HD1	2.03	0.41
1:D:104:ALA:HB2	1:D:127:VAL:HG13	2.02	0.41
1:D:284:HIS:C	1:D:286:GLY:N	2.76	0.41
1:D:421:LEU:C	1:D:424:PRO:HD2	2.45	0.41
1:A:400:ALA:HB2	1:A:432:ALA:HB1	2.02	0.41
1:B:138:THR:HG21	1:B:353:PRO:CD	2.45	0.41
1:B:391:ILE:CD1	1:B:391:ILE:N	2.83	0.41
1:C:117:GLU:HG2	1:C:206:PRO:CG	2.51	0.41
1:D:391:ILE:N	1:D:391:ILE:HD12	2.35	0.41
1:A:249:VAL:C	1:A:251:THR:N	2.79	0.41
1:A:449:LEU:CD2	1:A:453:LEU:HG	2.51	0.41
1:C:97:VAL:CG2	1:C:353:PRO:HG3	2.51	0.41
1:C:194:LEU:HG	1:D:422:ILE:CD1	2.45	0.41
1:A:178:LEU:HD12	1:A:178:LEU:HA	1.94	0.41
1:A:208:PHE:HD1	1:A:209:ARG:HG3	1.85	0.41
1:B:421:LEU:O	1:B:424:PRO:HD2	2.20	0.41
1:C:239:ILE:C	1:C:240:GLU:HG3	2.46	0.41
1:C:332:LEU:C	1:C:332:LEU:CD1	2.93	0.41
1:C:456:GLN:NE2	1:D:18:ARG:NH2	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:458:ALA:O	1:C:459:GLU:C	2.63	0.41
1:A:117:GLU:HG2	1:A:206:PRO:CG	2.51	0.41
1:A:161:MET:O	1:A:164:ASP:N	2.51	0.41
1:A:294:MET:O	1:A:297:ALA:HB3	2.20	0.41
1:A:398:MET:HB3	1:A:398:MET:HE3	1.75	0.41
1:A:434:LEU:CD2	1:B:36:LEU:HD21	2.51	0.41
1:B:32:PRO:CB	1:D:20:ASP:OD1	2.69	0.41
1:B:168:MET:HE2	1:D:17:ARG:CG	2.51	0.41
1:B:283:PHE:CD2	1:B:294:MET:HE3	2.56	0.41
1:D:115:ALA:HB1	1:D:178:LEU:HD11	2.02	0.41
1:D:144:VAL:HG21	1:D:343:THR:CG2	2.51	0.41
1:A:210:TYR:O	1:D:169:ARG:HD2	2.21	0.41
1:B:367:LEU:HD13	1:B:367:LEU:O	2.20	0.41
1:B:391:ILE:N	1:B:391:ILE:HD12	2.36	0.41
1:C:115:ALA:HB1	1:C:178:LEU:HD21	2.02	0.41
1:D:391:ILE:N	1:D:391:ILE:CD1	2.83	0.41
1:A:47:GLY:O	1:A:51:VAL:HG23	2.20	0.41
1:A:192:ALA:HB1	1:A:414:GLU:OE2	2.20	0.41
1:A:211:ASN:O	1:A:212:LEU:HB2	2.20	0.41
1:A:403:ARG:HH22	1:A:437:GLN:HA	1.86	0.41
1:B:63:MET:HE3	1:B:63:MET:HB3	1.91	0.41
1:B:88:LEU:HA	1:B:91:MET:HE3	2.03	0.41
1:B:144:VAL:HG21	1:B:343:THR:CG2	2.51	0.41
1:B:144:VAL:CG2	1:B:343:THR:HG22	2.49	0.41
1:B:289:LYS:HD3	1:B:289:LYS:HA	1.83	0.41
1:B:308:ILE:O	1:B:309:GLU:CB	2.69	0.41
1:B:311:ALA:O	1:B:340:ARG:HD2	2.21	0.41
1:B:398:MET:HE2	1:B:398:MET:C	2.46	0.41
1:C:379:PHE:C	1:C:381:GLN:OE1	2.64	0.41
1:C:421:LEU:C	1:C:424:PRO:HD2	2.46	0.41
1:C:434:LEU:CD2	1:D:36:LEU:HD21	2.51	0.41
1:C:449:LEU:CD2	1:C:453:LEU:HG	2.51	0.41
1:D:88:LEU:HD23	1:D:91:MET:CE	2.50	0.41
1:A:218:VAL:O	1:A:222:VAL:HG23	2.20	0.41
1:A:281:GLN:O	1:A:285:GLY:N	2.54	0.41
1:B:115:ALA:HA	1:B:120:ARG:O	2.20	0.41
1:B:365:THR:HG23	1:B:366:LEU:N	2.36	0.41
1:C:246:ASP:OD2	1:D:235:GLU:OE1	2.37	0.41
1:D:131:LYS:HE2	1:D:153:GLN:HE21	1.86	0.41
1:A:321:PRO:HA	1:A:365:THR:HG21	2.03	0.40
1:A:358:ALA:HB3	1:A:359:PRO:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:LEU:HD11	1:A:415:MET:HE2	2.04	0.40
1:B:382:TYR:HB3	1:B:384:LEU:HD21	2.03	0.40
1:C:366:LEU:HD23	1:C:366:LEU:HA	1.89	0.40
1:C:66:GLY:C	1:C:69:VAL:HG12	2.46	0.40
1:D:207:GLN:O	1:D:210:TYR:O	2.39	0.40
1:D:225:SER:O	1:D:228:VAL:HG22	2.20	0.40
1:A:31:THR:O	1:A:35:ILE:HG12	2.20	0.40
1:C:411:LEU:HD11	1:C:415:MET:HE2	2.04	0.40
1:D:365:THR:HG23	1:D:366:LEU:N	2.36	0.40
1:D:398:MET:HE2	1:D:398:MET:C	2.46	0.40
1:A:97:VAL:CG2	1:A:353:PRO:HG3	2.51	0.40
1:A:128:LEU:N	1:A:129:PRO:HD2	2.37	0.40
1:A:276:THR:O	1:A:280:PHE:HD1	2.05	0.40
1:A:379:PHE:C	1:A:381:GLN:OE1	2.64	0.40
1:C:83:PHE:C	1:C:83:PHE:HD2	2.28	0.40
1:C:398:MET:HE1	1:C:408:GLY:HA3	2.03	0.40
1:D:311:ALA:O	1:D:340:ARG:HD2	2.21	0.40
1:A:59:TRP:O	1:A:60:VAL:C	2.64	0.40
1:A:194:LEU:HG	1:B:422:ILE:CD1	2.45	0.40
1:B:362:ALA:HA	1:B:365:THR:CG2	2.46	0.40
1:C:148:GLU:O	1:C:149:GLY:C	2.64	0.40
1:C:223:ILE:HD12	1:D:426:ILE:HG22	2.03	0.40
1:C:249:VAL:C	1:C:251:THR:N	2.79	0.40
1:C:399:ALA:O	1:C:403:ARG:HA	2.21	0.40
1:D:289:LYS:HA	1:D:289:LYS:HD3	1.82	0.40
1:D:367:LEU:HD13	1:D:367:LEU:O	2.20	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:PHE:CA	1:D:327:ASN:ND2[2_545]	1.75	0.45
1:C:328:PHE:CD1	1:D:327:ASN:ND2[2_545]	1.87	0.33

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	428/473 (90%)	371 (87%)	48 (11%)	9 (2%)	5	27
1	B	449/473 (95%)	400 (89%)	42 (9%)	7 (2%)	7	34
1	C	428/473 (90%)	371 (87%)	48 (11%)	9 (2%)	5	27
1	D	449/473 (95%)	400 (89%)	42 (9%)	7 (2%)	7	34
All	All	1754/1892 (93%)	1542 (88%)	180 (10%)	32 (2%)	6	31

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	ASN
1	C	318	ASN
1	B	29	ASP
1	B	318	ASN
1	B	458	ALA
1	D	29	ASP
1	D	318	ASN
1	D	458	ALA
1	A	250	ASN
1	A	319	LEU
1	A	357	PHE
1	A	456	GLN
1	B	321	PRO
1	C	250	ASN
1	C	319	LEU
1	C	357	PHE
1	C	456	GLN
1	D	321	PRO
1	A	107	SER
1	A	238	ILE
1	C	107	SER
1	C	238	ILE
1	B	64	ARG
1	D	64	ARG
1	B	319	LEU
1	D	319	LEU
1	B	285	GLY
1	D	285	GLY

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Mol	Chain	Res	Type
1	A	71	VAL
1	A	330	VAL
1	C	71	VAL
1	C	330	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	322/361 (89%)	311 (97%)	11 (3%)	32	66
1	B	341/361 (94%)	321 (94%)	20 (6%)	18	50
1	C	322/361 (89%)	311 (97%)	11 (3%)	32	66
1	D	341/361 (94%)	321 (94%)	20 (6%)	18	50
All	All	1326/1444 (92%)	1264 (95%)	62 (5%)	23	58

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	TRP
1	A	121	PRO
1	A	216	LYS
1	A	230	ARG
1	A	239	ILE
1	A	288	ILE
1	A	328	PHE
1	A	332	LEU
1	A	420	GLN
1	A	424	PRO
1	A	449	LEU
1	B	25	LEU
1	B	79	TRP
1	B	84	ILE
1	B	178	LEU
1	B	194	LEU
1	B	219	PHE

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Mol	Chain	Res	Type
1	B	230	ARG
1	B	288	ILE
1	B	294	MET
1	B	308	ILE
1	B	317	PHE
1	B	318	ASN
1	B	322	ILE
1	B	332	LEU
1	B	398	MET
1	B	411	LEU
1	B	413	LEU
1	B	420	GLN
1	B	434	LEU
1	B	449	LEU
1	C	79	TRP
1	C	121	PRO
1	C	216	LYS
1	C	230	ARG
1	C	239	ILE
1	C	288	ILE
1	C	328	PHE
1	C	332	LEU
1	C	420	GLN
1	C	424	PRO
1	C	449	LEU
1	D	25	LEU
1	D	79	TRP
1	D	84	ILE
1	D	178	LEU
1	D	194	LEU
1	D	219	PHE
1	D	230	ARG
1	D	288	ILE
1	D	294	MET
1	D	308	ILE
1	D	317	PHE
1	D	318	ASN
1	D	322	ILE
1	D	332	LEU
1	D	398	MET
1	D	411	LEU
1	D	413	LEU

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Mol	Chain	Res	Type
1	D	420	GLN
1	D	434	LEU
1	D	449	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	62	ASN
1	A	70	GLN
1	A	207	GLN
1	A	211	ASN
1	A	250	ASN
1	A	277	GLN
1	A	281	GLN
1	A	318	ASN
1	A	420	GLN
1	B	21	GLN
1	B	27	GLN
1	B	61	GLN
1	B	62	ASN
1	B	74	HIS
1	B	153	GLN
1	B	157	ASN
1	B	175	HIS
1	B	207	GLN
1	B	233	ASN
1	B	281	GLN
1	B	318	ASN
1	B	418	ASN
1	B	420	GLN
1	B	456	GLN
1	C	61	GLN
1	C	62	ASN
1	C	70	GLN
1	C	207	GLN
1	C	211	ASN
1	C	250	ASN
1	C	277	GLN
1	C	281	GLN
1	C	318	ASN
1	C	420	GLN

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Mol	Chain	Res	Type
1	D	21	GLN
1	D	27	GLN
1	D	61	GLN
1	D	62	ASN
1	D	74	HIS
1	D	153	GLN
1	D	157	ASN
1	D	175	HIS
1	D	207	GLN
1	D	233	ASN
1	D	281	GLN
1	D	318	ASN
1	D	418	ASN
1	D	420	GLN
1	D	456	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	SO4	B	605	-	4,4,4	0.31	0	6,6,6	0.27	0
3	SO4	C	606	-	4,4,4	0.30	0	6,6,6	0.15	0
4	OCT	C	602	-	7,7,7	0.55	0	6,6,6	0.50	0
5	MYS	B	501	-	14,14,14	0.47	0	13,13,13	0.61	0
4	OCT	A	502	-	7,7,7	0.55	0	6,6,6	0.50	0
3	SO4	B	505	-	4,4,4	0.30	0	6,6,6	0.27	0
3	SO4	A	506	-	4,4,4	0.30	0	6,6,6	0.15	0
5	MYS	D	601	-	14,14,14	0.47	0	13,13,13	0.61	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	OCT	C	602	-	-	1/5/5/5	-
5	MYS	B	501	-	-	3/12/12/12	-
5	MYS	D	601	-	-	3/12/12/12	-
4	OCT	A	502	-	-	1/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	MYS	C2-C3-C4-C5
5	D	601	MYS	C2-C3-C4-C5
5	D	601	MYS	C1-C2-C3-C4
5	B	501	MYS	C1-C2-C3-C4
5	B	501	MYS	C7-C8-C9-C10
5	D	601	MYS	C7-C8-C9-C10
4	A	502	OCT	C5-C6-C7-C8
4	C	602	OCT	C5-C6-C7-C8

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	605	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	501	MYS	1	0
3	B	505	SO4	1	0
5	D	601	MYS	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	430/473 (90%)	0.05	10 (2%) 61 38	49, 74, 114, 155	0
1	B	451/473 (95%)	0.18	9 (1%) 65 41	49, 74, 118, 154	0
1	C	430/473 (90%)	0.12	12 (2%) 55 32	49, 74, 114, 155	0
1	D	451/473 (95%)	0.11	9 (1%) 65 41	49, 74, 118, 154	0
All	All	1762/1892 (93%)	0.11	40 (2%) 61 38	49, 74, 117, 155	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	347	CYS	4.5
1	D	461	ALA	4.3
1	C	331	GLY	4.3
1	A	144	VAL	4.2
1	B	461	ALA	4.1
1	D	329	SER	3.7
1	B	321	PRO	3.4
1	C	246	ASP	3.1
1	C	103	GLU	3.1
1	C	319	LEU	3.0
1	D	12	GLN	3.0
1	B	315	GLY	2.9
1	C	321	PRO	2.9
1	B	328	PHE	2.9
1	D	328	PHE	2.8
1	C	386	ALA	2.8
1	A	103	GLU	2.8
1	B	245	SER	2.7
1	B	317	PHE	2.7
1	D	381	GLN	2.6
1	B	104	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	319	LEU	2.6
1	A	326	GLY	2.6
1	C	330	VAL	2.5
1	C	104	ALA	2.5
1	C	317	PHE	2.5
1	D	462	GLU	2.5
1	D	283	PHE	2.4
1	B	301	LEU	2.3
1	A	143	MET	2.3
1	C	117	GLU	2.2
1	A	111	GLU	2.2
1	A	457	ASP	2.2
1	A	328	PHE	2.2
1	A	333	LEU	2.2
1	D	236	ALA	2.1
1	D	327	ASN	2.1
1	A	117	GLU	2.1
1	C	283	PHE	2.1
1	A	236	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	OCT	C	602	8/8	0.47	0.34	43,53,71,79	0
4	OCT	A	502	8/8	0.50	0.32	43,53,71,79	0
5	MYS	D	601	15/15	0.76	0.20	55,75,88,92	0
5	MYS	B	501	15/15	0.77	0.18	55,75,88,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	B	605	5/5	0.79	0.14	72,87,93,99	0
3	SO4	B	505	5/5	0.87	0.15	72,87,93,99	0
2	CL	C	603	1/1	0.89	0.14	100,100,100,100	0
2	CL	B	504	1/1	0.90	0.12	81,81,81,81	0
2	CL	D	604	1/1	0.92	0.12	81,81,81,81	0
2	CL	A	503	1/1	0.95	0.13	100,100,100,100	0
3	SO4	C	606	5/5	0.96	0.06	59,62,66,70	0
3	SO4	A	506	5/5	0.98	0.04	59,62,66,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.