



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 01:58 AM UTC

PDB ID : 3S24 / pdb_00003s24
Title : Crystal structure of human mRNA guanylyltransferase
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Deposited on : 2011-05-16
Resolution : 3.01 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

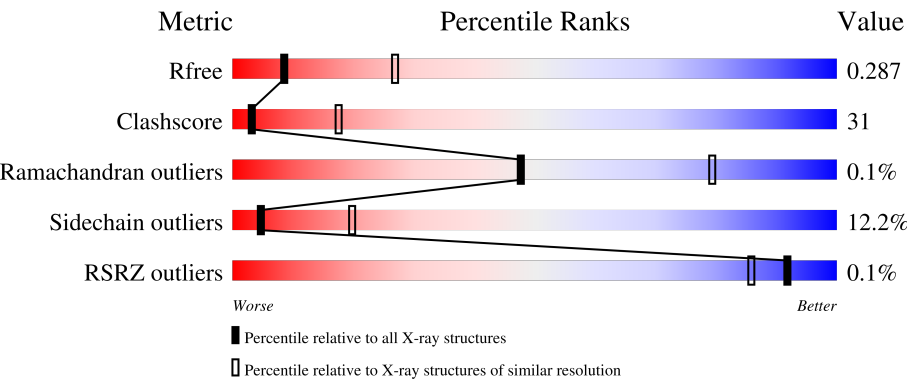
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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.



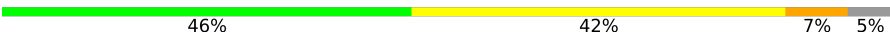
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	347	46%38%11%• 5%
1	B	347	38%43%10%9%
1	C	347	41%43%7%10%
1	D	347	48%40%6%5%
1	E	347	46%42%6%5%

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Mol	Chain	Length	Quality of chain
1	F	347	
1	G	347	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	5	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18387 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 mRNA-capping enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2646	1688	457	481	20			
1	B	316	Total	C	N	O	S	0	0	0
			2561	1637	440	465	19			
1	C	314	Total	C	N	O	S	0	0	0
			2547	1628	438	462	19			
1	D	328	Total	C	N	O	S	0	0	0
			2646	1688	457	481	20			
1	E	329	Total	C	N	O	S	0	0	0
			2649	1689	456	483	21			
1	G	329	Total	C	N	O	S	0	0	0
			2651	1691	458	482	20			
1	F	333	Total	C	N	O	S	0	0	0
			2662	1698	460	484	20			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	568	LEU	-	expression tag	UNP O60942
A	569	GLU	-	expression tag	UNP O60942
A	570	HIS	-	expression tag	UNP O60942
A	571	HIS	-	expression tag	UNP O60942
A	572	HIS	-	expression tag	UNP O60942
A	573	HIS	-	expression tag	UNP O60942
A	574	HIS	-	expression tag	UNP O60942
A	575	HIS	-	expression tag	UNP O60942
B	568	LEU	-	expression tag	UNP O60942
B	569	GLU	-	expression tag	UNP O60942
B	570	HIS	-	expression tag	UNP O60942
B	571	HIS	-	expression tag	UNP O60942
B	572	HIS	-	expression tag	UNP O60942
B	573	HIS	-	expression tag	UNP O60942
B	574	HIS	-	expression tag	UNP O60942

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Chain	Residue	Modelled	Actual	Comment	Reference
B	575	HIS	-	expression tag	UNP O60942
C	568	LEU	-	expression tag	UNP O60942
C	569	GLU	-	expression tag	UNP O60942
C	570	HIS	-	expression tag	UNP O60942
C	571	HIS	-	expression tag	UNP O60942
C	572	HIS	-	expression tag	UNP O60942
C	573	HIS	-	expression tag	UNP O60942
C	574	HIS	-	expression tag	UNP O60942
C	575	HIS	-	expression tag	UNP O60942
D	568	LEU	-	expression tag	UNP O60942
D	569	GLU	-	expression tag	UNP O60942
D	570	HIS	-	expression tag	UNP O60942
D	571	HIS	-	expression tag	UNP O60942
D	572	HIS	-	expression tag	UNP O60942
D	573	HIS	-	expression tag	UNP O60942
D	574	HIS	-	expression tag	UNP O60942
D	575	HIS	-	expression tag	UNP O60942
E	568	LEU	-	expression tag	UNP O60942
E	569	GLU	-	expression tag	UNP O60942
E	570	HIS	-	expression tag	UNP O60942
E	571	HIS	-	expression tag	UNP O60942
E	572	HIS	-	expression tag	UNP O60942
E	573	HIS	-	expression tag	UNP O60942
E	574	HIS	-	expression tag	UNP O60942
E	575	HIS	-	expression tag	UNP O60942
G	568	LEU	-	expression tag	UNP O60942
G	569	GLU	-	expression tag	UNP O60942
G	570	HIS	-	expression tag	UNP O60942
G	571	HIS	-	expression tag	UNP O60942
G	572	HIS	-	expression tag	UNP O60942
G	573	HIS	-	expression tag	UNP O60942
G	574	HIS	-	expression tag	UNP O60942
G	575	HIS	-	expression tag	UNP O60942
F	568	LEU	-	expression tag	UNP O60942
F	569	GLU	-	expression tag	UNP O60942
F	570	HIS	-	expression tag	UNP O60942
F	571	HIS	-	expression tag	UNP O60942
F	572	HIS	-	expression tag	UNP O60942
F	573	HIS	-	expression tag	UNP O60942
F	574	HIS	-	expression tag	UNP O60942
F	575	HIS	-	expression tag	UNP O60942

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

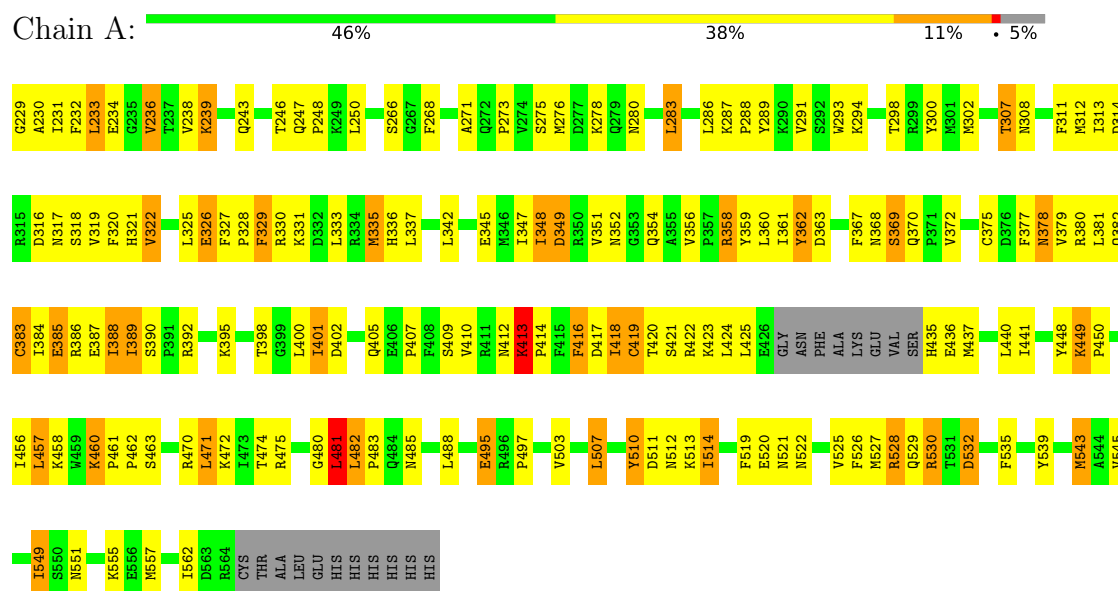


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

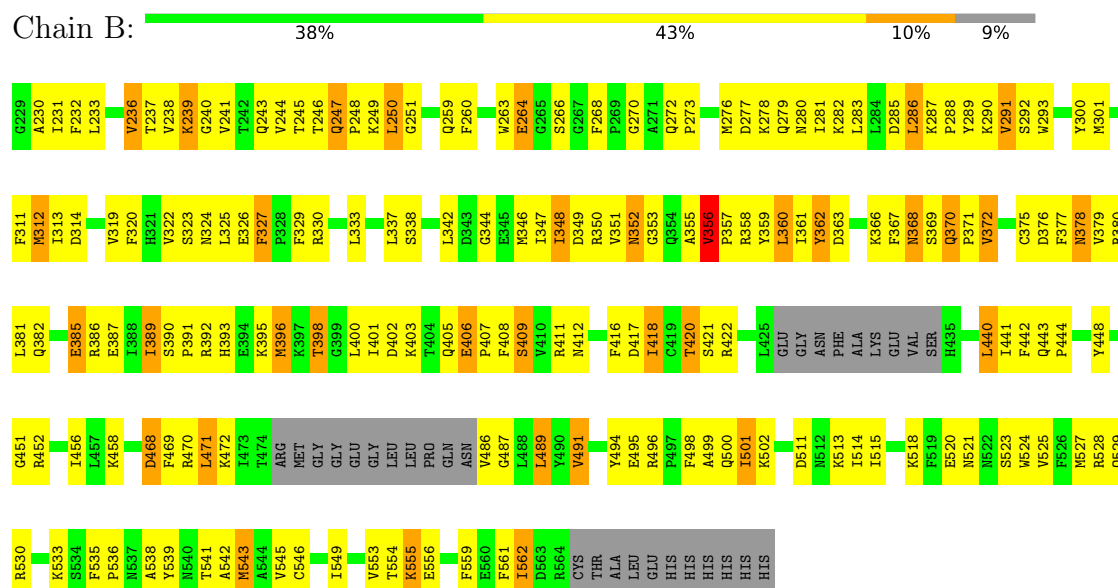
3 Residue-property plots

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

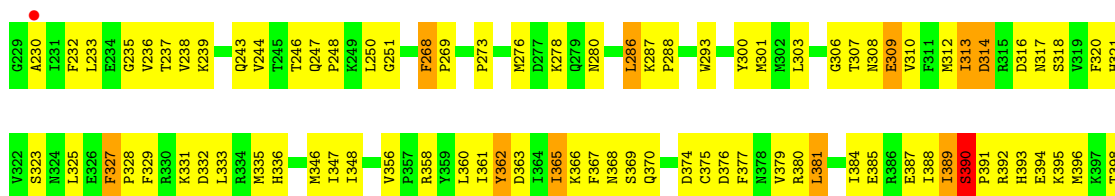
• Molecule 1: mRNA-capping enzyme

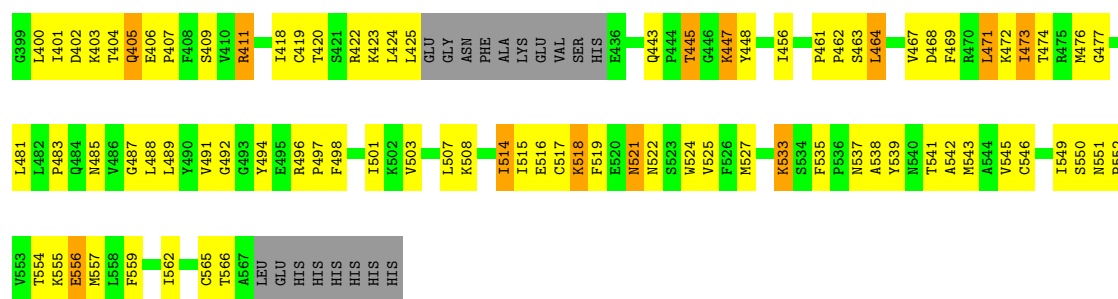


• Molecule 1: mRNA-capping enzyme



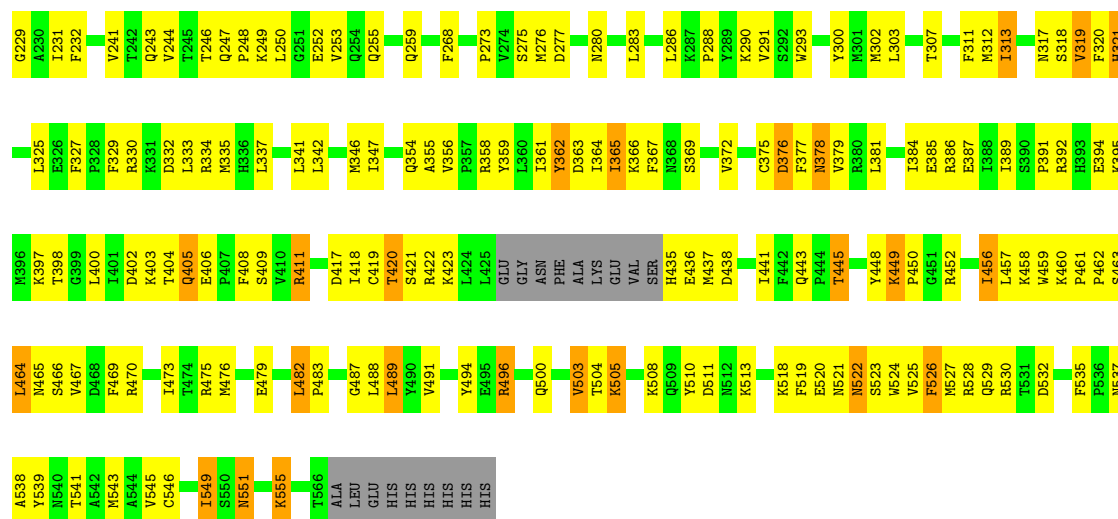
Chain C: 41% 43% 7% 10%





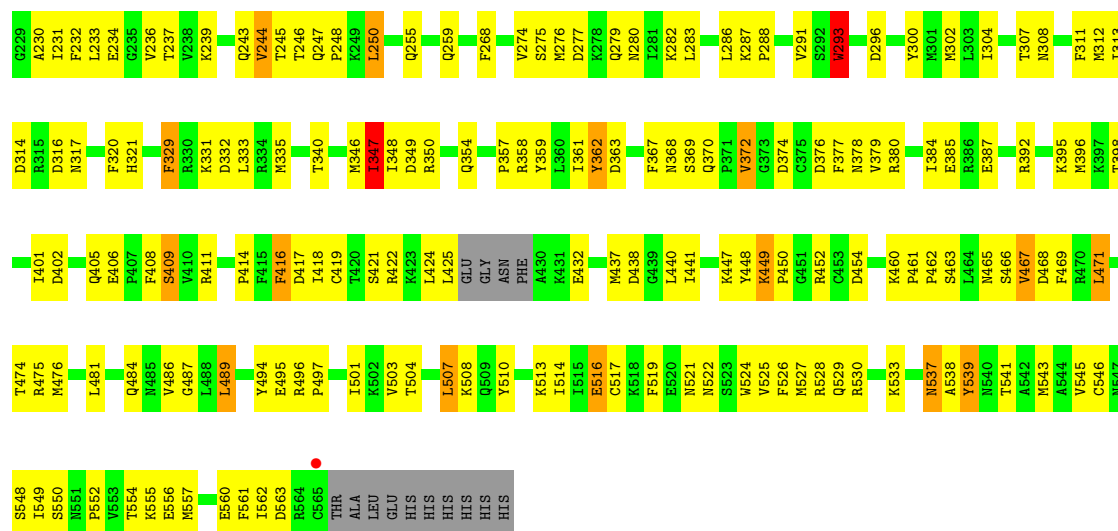
• Molecule 1: mRNA-capping enzyme

Chain G: 46% 42% 7% 5%



• Molecule 1: mRNA-capping enzyme

Chain F: 47% 44%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.12Å 104.66Å 149.57Å 90.00° 94.95° 90.00°	Depositor
Resolution (Å)	35.43 – 3.01 35.43 – 3.01	Depositor EDS
% Data completeness (in resolution range)	95.1 (35.43-3.01) 95.0 (35.43-3.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.258 , 0.296 0.246 , 0.287	Depositor DCC
R_{free} test set	2724 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	94.6	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	18387	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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: SO4

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	0.70	0/2704	1.11	13/3643 (0.4%)
1	B	0.62	0/2617	1.07	16/3525 (0.5%)
1	C	0.68	0/2603	1.11	13/3505 (0.4%)
1	D	0.64	0/2704	1.05	9/3643 (0.2%)
1	E	0.69	0/2706	1.10	11/3646 (0.3%)
1	F	0.69	0/2719	1.13	11/3665 (0.3%)
1	G	0.62	0/2709	1.07	20/3650 (0.5%)
All	All	0.66	0/18762	1.09	93/25277 (0.4%)

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

There are no bond length outliers.

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	406	GLU	CA-C-N	12.09	133.11	119.32
1	C	406	GLU	C-N-CA	12.09	133.11	119.32
1	F	449	LYS	CA-C-N	11.27	131.03	120.21
1	F	449	LYS	C-N-CA	11.27	131.03	120.21
1	F	268	PHE	CA-C-N	8.60	128.25	119.56
1	F	268	PHE	C-N-CA	8.60	128.25	119.56
1	B	268	PHE	CA-C-N	8.49	128.14	119.56
1	B	268	PHE	C-N-CA	8.49	128.14	119.56
1	G	268	PHE	CA-C-N	8.35	128.04	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	268	PHE	C-N-CA	8.35	128.04	119.19
1	D	449	LYS	CA-C-N	8.26	128.41	120.31
1	D	449	LYS	C-N-CA	8.26	128.41	120.31
1	C	268	PHE	CA-C-N	8.23	128.18	119.05
1	C	268	PHE	C-N-CA	8.23	128.18	119.05
1	A	268	PHE	CA-C-N	8.21	127.85	119.56
1	A	268	PHE	C-N-CA	8.21	127.85	119.56
1	A	449	LYS	CA-C-N	7.98	128.13	120.31
1	A	449	LYS	C-N-CA	7.98	128.13	120.31
1	G	449	LYS	CA-C-N	7.72	127.88	120.31
1	G	449	LYS	C-N-CA	7.72	127.88	120.31
1	F	293	TRP	N-CA-C	7.70	121.77	108.76
1	G	356	VAL	CB-CA-C	-7.57	102.79	110.13
1	G	406	GLU	CA-C-N	7.46	128.12	119.47
1	G	406	GLU	C-N-CA	7.46	128.12	119.47
1	F	362	TYR	CB-CA-C	7.44	122.60	109.65
1	D	268	PHE	CA-C-N	7.43	127.07	119.19
1	D	268	PHE	C-N-CA	7.43	127.07	119.19
1	E	365	ILE	N-CA-C	7.34	117.94	110.82
1	A	362	TYR	CB-CA-C	7.33	122.41	109.65
1	C	362	TYR	CB-CA-C	7.21	121.67	109.55
1	A	481	LEU	N-CA-C	7.15	118.97	111.03
1	E	310	VAL	N-CA-C	6.99	118.03	109.30
1	C	389	ILE	N-CA-C	6.94	117.03	110.30
1	D	270	GLY	N-CA-C	6.69	119.63	111.93
1	A	413	LYS	CA-C-N	6.68	126.91	119.90
1	A	413	LYS	C-N-CA	6.68	126.91	119.90
1	G	551	ASN	CA-C-N	6.66	126.64	119.78
1	G	551	ASN	C-N-CA	6.66	126.64	119.78
1	E	268	PHE	CA-C-N	6.54	126.25	119.64
1	E	268	PHE	C-N-CA	6.54	126.25	119.64
1	G	482	LEU	CA-C-N	6.53	126.16	119.56
1	G	482	LEU	C-N-CA	6.53	126.16	119.56
1	C	324	ASN	N-CA-C	6.52	120.94	112.92
1	G	456	ILE	CB-CA-C	-6.39	103.22	110.96
1	E	390	SER	CA-C-N	6.34	125.56	118.97
1	E	390	SER	C-N-CA	6.34	125.56	118.97
1	D	362	TYR	CB-CA-C	6.31	120.62	109.65
1	B	362	TYR	CB-CA-C	6.25	120.52	109.65
1	G	537	ASN	N-CA-C	6.22	117.90	110.19
1	B	247	GLN	CA-C-N	6.18	125.59	118.85
1	B	247	GLN	C-N-CA	6.18	125.59	118.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	362	TYR	CB-CA-C	6.14	120.34	110.09
1	G	356	VAL	CA-C-N	-6.11	113.39	119.99
1	G	356	VAL	C-N-CA	-6.11	113.39	119.99
1	E	508	LYS	N-CA-C	5.95	117.44	111.07
1	F	372	VAL	CB-CA-C	-5.95	103.36	112.05
1	B	356	VAL	N-CA-C	5.83	113.32	107.55
1	C	399	GLY	N-CA-C	-5.73	108.26	115.08
1	C	499	ALA	N-CA-C	5.72	116.92	108.86
1	E	521	ASN	N-CA-C	5.64	119.16	112.72
1	G	505	LYS	N-CA-C	5.64	117.90	111.02
1	B	495	GLU	N-CA-C	5.61	118.16	111.71
1	B	362	TYR	CA-CB-CG	5.56	123.90	113.90
1	D	298	THR	CB-CA-C	5.55	119.87	109.71
1	F	481	LEU	N-CA-C	5.51	119.70	113.15
1	A	238	VAL	N-CA-C	5.50	115.90	107.77
1	B	270	GLY	N-CA-C	5.49	118.24	111.93
1	E	327	PHE	CA-C-N	5.47	125.40	119.76
1	E	327	PHE	C-N-CA	5.47	125.40	119.76
1	A	495	GLU	N-CA-C	5.46	117.03	111.14
1	B	406	GLU	CA-C-N	5.46	125.80	119.47
1	B	406	GLU	C-N-CA	5.46	125.80	119.47
1	B	562	ILE	N-CA-C	5.43	116.92	111.00
1	B	327	PHE	CA-C-N	5.43	125.60	119.90
1	B	327	PHE	C-N-CA	5.43	125.60	119.90
1	C	456	ILE	CB-CA-C	-5.43	104.39	110.96
1	E	362	TYR	CB-CA-C	5.42	119.08	109.65
1	D	365	ILE	N-CA-C	5.42	116.91	111.00
1	F	362	TYR	CA-CB-CG	5.32	123.48	113.90
1	C	443	GLN	CA-C-N	5.28	125.49	120.31
1	C	443	GLN	C-N-CA	5.28	125.49	120.31
1	G	365	ILE	N-CA-C	5.25	117.14	111.58
1	A	551	ASN	CA-C-N	5.23	125.44	120.31
1	A	551	ASN	C-N-CA	5.23	125.44	120.31
1	F	347	ILE	N-CA-C	5.20	115.46	107.77
1	F	296	ASP	N-CA-C	-5.17	101.98	109.59
1	G	523	SER	N-CA-C	5.12	117.50	108.75
1	C	374	ASP	N-CA-C	-5.09	107.07	113.28
1	B	272	GLN	CA-C-N	5.08	125.53	120.14
1	B	272	GLN	C-N-CA	5.08	125.53	120.14
1	D	527	MET	N-CA-C	5.07	119.50	112.45
1	A	352	ASN	N-CA-C	5.06	117.69	110.24
1	G	362	TYR	CA-CB-CG	5.03	122.96	113.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	351	VAL	Peptide
1	A	480	GLY	Peptide

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	2646	0	2650	166	0
1	B	2561	0	2567	170	0
1	C	2547	0	2551	153	0
1	D	2646	0	2650	156	0
1	E	2649	0	2658	188	0
1	F	2662	0	2654	165	0
1	G	2651	0	2652	169	0
2	A	20	0	0	3	0
2	B	5	0	0	0	0
All	All	18387	0	18382	1138	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 31.

All (1138) 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:246:THR:HG22	1:B:248:PRO:HD2	1.22	1.13
1:D:239:LYS:H	1:D:239:LYS:HD3	1.17	1.08
1:C:462:PRO:HD2	1:C:555:LYS:HE3	1.37	1.06
1:A:230:ALA:HA	1:A:243:GLN:HE22	1.21	1.05
1:A:335:MET:HE3	1:A:336:HIS:H	1.21	1.04
1:F:537:ASN:H	1:F:537:ASN:ND2	1.53	1.03
1:A:236:VAL:CG2	1:A:348:ILE:HD11	1.89	1.02
1:E:473:ILE:HD12	1:E:503:VAL:HG21	1.42	1.01
1:G:555:LYS:H	1:G:555:LYS:HD2	1.26	1.00
1:F:496:ARG:HB2	1:F:497:PRO:HD2	1.44	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:ARG:HG3	1:C:409:SER:HB3	1.44	0.99
1:D:398:THR:HG22	1:D:400:LEU:HD13	1.47	0.97
1:F:537:ASN:HD22	1:F:537:ASN:N	1.53	0.96
1:G:541:THR:O	1:G:545:VAL:HG23	1.67	0.94
1:E:496:ARG:HB3	1:E:497:PRO:HD2	1.49	0.94
1:A:236:VAL:HG22	1:A:348:ILE:HD11	1.49	0.93
1:A:233:LEU:HG	1:A:236:VAL:HG21	1.51	0.92
1:A:233:LEU:HG	1:A:236:VAL:CG2	1.99	0.91
1:G:504:THR:HG22	1:G:505:LYS:H	1.35	0.91
1:G:419:CYS:HA	1:G:422:ARG:HH21	1.37	0.88
1:B:546:CYS:HA	1:B:549:ILE:HG12	1.54	0.88
1:E:233:LEU:HD21	1:E:348:ILE:HD11	1.55	0.87
1:G:358:ARG:HH11	1:G:411:ARG:HE	1.23	0.87
1:C:315:ARG:HE	1:C:533:LYS:NZ	1.73	0.86
1:E:293:TRP:HD1	1:E:424:LEU:HD21	1.40	0.86
1:E:420:THR:HG23	1:E:423:LYS:HE2	1.55	0.86
1:B:358:ARG:NH1	1:B:411:ARG:HH21	1.76	0.84
1:G:504:THR:HG22	1:G:505:LYS:HG2	1.59	0.84
1:D:300:TYR:CE2	1:D:314:ASP:HB3	2.12	0.84
1:B:396:MET:CE	1:B:403:LYS:HB2	2.08	0.84
1:D:278:LYS:HG3	1:D:557:MET:HE1	1.60	0.83
1:A:233:LEU:HB3	1:A:236:VAL:HG23	1.58	0.83
1:C:335:MET:HE2	1:C:335:MET:HA	1.61	0.83
1:G:555:LYS:HD2	1:G:555:LYS:N	1.91	0.83
1:C:489:LEU:HD12	1:C:499:ALA:HB3	1.59	0.83
1:F:467:VAL:CG2	1:F:469:PHE:CE1	2.62	0.83
1:E:246:THR:HG22	1:E:248:PRO:HD2	1.58	0.82
1:G:358:ARG:NH1	1:G:411:ARG:HE	1.77	0.82
1:B:396:MET:HE1	1:B:403:LYS:HB2	1.61	0.82
1:F:489:LEU:HD21	1:F:501:ILE:HG22	1.61	0.82
1:B:501:ILE:HD12	1:B:502:LYS:H	1.45	0.81
1:E:309:GLU:HA	1:E:309:GLU:OE1	1.81	0.81
1:G:346:MET:HE1	1:G:359:TYR:HB2	1.63	0.81
1:A:276:MET:HA	1:A:280:ASN:HD22	1.44	0.81
1:A:327:PHE:CD1	1:A:392:ARG:HD2	2.15	0.81
1:E:314:ASP:HB3	1:E:316:ASP:H	1.44	0.80
1:A:522:ASN:C	1:E:286:LEU:HD21	2.06	0.80
1:A:230:ALA:HA	1:A:243:GLN:NE2	1.93	0.80
1:C:246:THR:HG22	1:C:248:PRO:HD2	1.63	0.80
1:G:543:MET:HA	1:G:543:MET:HE3	1.63	0.80
1:F:402:ASP:HB3	1:F:405:GLN:HG2	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ALA:CA	1:A:243:GLN:HE22	1.94	0.79
1:E:398:THR:OG1	1:E:400:LEU:HD13	1.82	0.79
1:B:273:PRO:HG2	1:B:458:LYS:HE3	1.65	0.78
1:C:350:ARG:NH2	1:C:353:GLY:HA2	1.97	0.78
1:A:372:VAL:HG12	1:A:380:ARG:HG2	1.65	0.78
1:B:501:ILE:HD13	1:B:524:TRP:O	1.83	0.78
1:D:358:ARG:HG3	1:D:409:SER:HB3	1.65	0.78
1:B:232:PHE:HB2	1:B:320:PHE:CE2	2.19	0.78
1:A:286:LEU:HD13	1:D:519:PHE:HE1	1.49	0.78
1:F:422:ARG:HH11	1:F:563:ASP:HA	1.48	0.78
1:G:435:HIS:CD2	1:G:436:GLU:H	2.00	0.77
1:C:560:GLU:HA	1:C:563:ASP:HB2	1.65	0.77
1:E:514:ILE:HD12	1:E:533:LYS:HB3	1.67	0.77
1:A:302:MET:HE3	1:A:359:TYR:CE2	2.20	0.77
1:B:246:THR:CG2	1:B:248:PRO:HD2	2.12	0.77
1:F:246:THR:HG22	1:F:248:PRO:HD2	1.65	0.76
1:C:294:LYS:HZ3	1:C:460:LYS:NZ	1.82	0.76
1:B:501:ILE:HD12	1:B:502:LYS:N	2.00	0.76
1:C:284:LEU:HD13	1:C:418:ILE:HD11	1.67	0.76
1:E:554:THR:OG1	1:E:557:MET:HB2	1.86	0.76
1:F:230:ALA:HB3	1:F:243:GLN:OE1	1.86	0.76
1:E:545:VAL:HG12	1:E:549:ILE:HD11	1.66	0.75
1:A:522:ASN:O	1:E:286:LEU:HD21	1.85	0.75
1:B:541:THR:O	1:B:545:VAL:HG23	1.86	0.75
1:A:539:TYR:OH	1:E:445:THR:HG21	1.86	0.75
1:D:392:ARG:O	1:D:396:MET:HG3	1.85	0.75
1:D:554:THR:HB	1:D:557:MET:H	1.51	0.75
1:D:329:PHE:CD1	1:D:335:MET:HE2	2.22	0.74
1:F:276:MET:HA	1:F:280:ASN:HD22	1.52	0.74
1:B:236:VAL:CG1	1:B:348:ILE:HD11	2.17	0.74
1:F:291:VAL:HG11	1:F:421:SER:HB3	1.69	0.74
1:A:335:MET:HE3	1:A:336:HIS:N	1.98	0.74
1:A:236:VAL:HG21	1:A:348:ILE:HD11	1.70	0.74
1:C:315:ARG:HE	1:C:533:LYS:HZ1	1.31	0.74
1:F:501:ILE:HD13	1:F:524:TRP:O	1.87	0.74
1:D:395:LYS:HB3	1:D:401:ILE:HG13	1.71	0.73
1:F:530:ARG:HH11	1:F:533:LYS:HD3	1.52	0.73
1:G:376:ASP:OD2	1:G:445:THR:HG22	1.88	0.73
1:C:276:MET:HA	1:C:280:ASN:HD22	1.53	0.73
1:G:273:PRO:HB3	1:G:456:ILE:CG2	2.18	0.72
1:A:420:THR:HG23	1:A:423:LYS:HD2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:377:PHE:CE2	1:G:443:GLN:HG2	2.25	0.72
1:B:539:TYR:CE2	1:B:543:MET:HG3	2.25	0.72
1:C:294:LYS:HZ3	1:C:460:LYS:HZ1	1.37	0.72
1:C:329:PHE:HD2	1:C:331:LYS:H	1.34	0.72
1:D:398:THR:CG2	1:D:400:LEU:HD13	2.19	0.72
1:A:481:LEU:HD23	1:A:482:LEU:HD23	1.71	0.72
1:B:346:MET:SD	1:B:359:TYR:HB2	2.29	0.72
1:A:347:ILE:HD13	1:A:360:LEU:HD11	1.71	0.71
1:E:514:ILE:HD11	1:E:535:PHE:O	1.90	0.71
1:A:358:ARG:HG3	1:A:409:SER:HB3	1.73	0.71
1:E:332:ASP:OD2	1:E:335:MET:HG3	1.90	0.71
1:A:398:THR:HG22	1:A:400:LEU:HD13	1.72	0.71
1:D:239:LYS:H	1:D:239:LYS:CD	1.95	0.71
1:D:377:PHE:HD1	1:D:380:ARG:HH21	1.39	0.71
1:B:358:ARG:HG3	1:B:409:SER:HB3	1.71	0.71
1:B:285:ASP:HB3	1:C:500:GLN:HB2	1.73	0.70
1:D:380:ARG:HH12	1:D:448:TYR:N	1.89	0.70
1:E:519:PHE:HE1	1:G:286:LEU:CD2	2.03	0.70
1:B:283:LEU:HA	1:B:286:LEU:HG	1.73	0.70
1:A:377:PHE:HD1	1:A:380:ARG:HH21	1.37	0.70
1:B:393:HIS:HA	1:B:396:MET:HB2	1.73	0.70
1:A:289:TYR:HB3	1:A:418:ILE:HD11	1.73	0.70
1:D:239:LYS:HD3	1:D:239:LYS:N	2.01	0.70
1:D:543:MET:HE3	1:D:543:MET:HA	1.73	0.70
1:A:247:GLN:N	1:A:248:PRO:HD2	2.07	0.70
1:E:420:THR:HG23	1:E:423:LYS:CE	2.20	0.70
1:G:475:ARG:HD3	1:G:483:PRO:O	1.92	0.70
1:F:421:SER:HA	1:F:424:LEU:HD12	1.74	0.70
1:F:554:THR:H	1:F:557:MET:HE3	1.55	0.70
1:B:489:LEU:HD21	1:B:501:ILE:HG22	1.74	0.69
1:B:367:PHE:CZ	1:B:387:GLU:HB3	2.28	0.69
1:G:460:LYS:HG2	1:G:464:LEU:HD22	1.74	0.69
1:F:422:ARG:NH1	1:F:563:ASP:HA	2.06	0.69
1:C:299:ARG:HH21	1:C:343:ASP:CG	1.99	0.69
1:C:377:PHE:HD1	1:C:380:ARG:HH21	1.38	0.69
1:A:530:ARG:HG2	1:A:530:ARG:HH11	1.57	0.69
1:D:505:LYS:HA	1:D:508:LYS:HE3	1.75	0.69
1:C:273:PRO:HB3	1:C:456:ILE:HG22	1.75	0.69
1:G:283:LEU:HD23	1:G:286:LEU:HD22	1.75	0.69
1:E:276:MET:HA	1:E:280:ASN:HD22	1.57	0.68
1:F:467:VAL:HG21	1:F:469:PHE:CE1	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:255:GLN:O	1:D:259:GLN:HG2	1.93	0.68
1:E:496:ARG:HB3	1:E:497:PRO:CD	2.22	0.68
1:F:387:GLU:OE1	1:F:387:GLU:HA	1.94	0.68
1:D:469:PHE:CB	1:D:489:LEU:HB3	2.23	0.68
1:A:422:ARG:HB3	1:A:562:ILE:HG21	1.76	0.68
1:F:246:THR:C	1:F:248:PRO:HD2	2.19	0.68
1:F:468:ASP:OD1	1:F:516:GLU:HB2	1.94	0.68
1:D:351:VAL:HG12	1:D:354:GLN:HB2	1.76	0.68
1:G:312:MET:HE1	1:G:346:MET:CE	2.24	0.68
1:D:494:TYR:CD1	1:D:539:TYR:CE1	2.82	0.68
1:G:347:ILE:HD12	1:G:435:HIS:HB2	1.76	0.68
1:C:299:ARG:NH2	1:C:343:ASP:OD1	2.23	0.67
1:E:395:LYS:HB3	1:E:401:ILE:HG13	1.76	0.67
1:F:293:TRP:HB3	1:F:440:LEU:HD23	1.75	0.67
1:G:435:HIS:CG	1:G:436:GLU:H	2.09	0.67
1:G:460:LYS:HG2	1:G:464:LEU:CD2	2.23	0.67
1:D:278:LYS:CG	1:D:557:MET:HE1	2.24	0.67
1:G:277:ASP:H	1:G:280:ASN:HB2	1.58	0.67
1:B:286:LEU:HD11	1:C:522:ASN:C	2.20	0.67
1:A:367:PHE:CE1	1:A:387:GLU:HB3	2.30	0.67
1:B:538:ALA:HB3	1:B:541:THR:OG1	1.94	0.66
1:C:283:LEU:HD23	1:C:286:LEU:HD12	1.75	0.66
1:E:522:ASN:C	1:G:286:LEU:HD21	2.21	0.66
1:A:342:LEU:HD13	1:A:361:ILE:HG21	1.77	0.66
1:E:392:ARG:O	1:E:396:MET:HG3	1.95	0.66
1:E:541:THR:O	1:E:545:VAL:HG23	1.95	0.66
1:A:349:ASP:OD2	1:A:358:ARG:NH1	2.29	0.66
1:D:471:LEU:HD12	1:D:472:LYS:N	2.11	0.66
1:E:422:ARG:NH1	1:E:566:THR:HG21	2.10	0.66
1:G:398:THR:O	1:G:400:LEU:HD12	1.95	0.66
1:B:358:ARG:HG3	1:B:409:SER:CB	2.25	0.66
1:D:494:TYR:CD1	1:D:539:TYR:CD1	2.84	0.66
1:E:329:PHE:CE2	1:E:331:LYS:HB2	2.31	0.66
1:E:471:LEU:HB2	1:E:515:ILE:HD13	1.78	0.66
1:A:335:MET:CE	1:A:336:HIS:H	2.05	0.66
1:B:230:ALA:HB1	1:B:243:GLN:OE1	1.95	0.66
1:B:236:VAL:HG22	1:B:237:THR:H	1.61	0.66
1:A:545:VAL:O	1:A:549:ILE:HG23	1.95	0.66
1:B:489:LEU:HD21	1:B:501:ILE:CG2	2.26	0.65
1:B:350:ARG:HH21	1:B:353:GLY:HA2	1.60	0.65
1:B:396:MET:HG2	1:B:401:ILE:CG2	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:494:TYR:HE2	1:D:496:ARG:HB2	1.60	0.65
1:E:278:LYS:HG2	1:E:557:MET:HE1	1.76	0.65
1:A:422:ARG:HB3	1:A:562:ILE:CG2	2.27	0.65
1:A:520:GLU:HG3	1:A:521:ASN:ND2	2.11	0.65
1:D:376:ASP:OD2	1:D:445:THR:HG22	1.97	0.65
1:G:403:LYS:HZ3	1:G:411:ARG:HH22	1.43	0.65
1:F:467:VAL:HG12	1:F:545:VAL:HG21	1.78	0.65
1:D:504:THR:HG22	1:D:507:LEU:HB2	1.79	0.65
1:B:358:ARG:HH11	1:B:411:ARG:HH21	1.45	0.65
1:C:376:ASP:OD2	1:C:445:THR:HG22	1.97	0.65
1:E:327:PHE:CD1	1:E:392:ARG:HD2	2.32	0.65
1:B:291:VAL:HG21	1:B:440:LEU:HD13	1.79	0.65
1:C:491:VAL:HG21	1:C:539:TYR:HA	1.79	0.65
1:C:503:VAL:HG12	1:C:508:LYS:HE3	1.77	0.65
1:D:469:PHE:CG	1:D:489:LEU:HB3	2.31	0.65
1:E:494:TYR:CD1	1:E:539:TYR:CE1	2.84	0.65
1:A:368:ASN:O	1:A:369:SER:HB2	1.97	0.64
1:A:471:LEU:HD12	1:A:472:LYS:N	2.12	0.64
1:G:511:ASP:C	1:G:513:LYS:H	2.05	0.64
1:F:312:MET:HE1	1:F:346:MET:HE1	1.79	0.64
1:A:232:PHE:HB2	1:A:320:PHE:CE2	2.31	0.64
1:B:327:PHE:CD1	1:B:392:ARG:HD2	2.32	0.64
1:E:293:TRP:CD1	1:E:424:LEU:HD21	2.29	0.64
1:E:420:THR:HG22	1:E:420:THR:O	1.98	0.64
1:G:403:LYS:NZ	1:G:411:ARG:NH2	2.45	0.64
1:F:541:THR:O	1:F:545:VAL:HG23	1.96	0.64
1:G:519:PHE:HB2	1:G:524:TRP:CZ3	2.33	0.64
1:F:467:VAL:CG2	1:F:469:PHE:CZ	2.80	0.64
1:A:294:LYS:HE3	1:A:345:GLU:OE1	1.98	0.63
1:B:232:PHE:CD1	1:B:241:VAL:HG11	2.33	0.63
1:A:519:PHE:CD2	1:A:549:ILE:HD12	2.33	0.63
1:C:313:ILE:N	1:C:313:ILE:HD12	2.12	0.63
1:D:351:VAL:CG1	1:D:354:GLN:HB2	2.28	0.63
1:G:538:ALA:HB3	1:G:541:THR:OG1	1.96	0.63
1:F:358:ARG:CG	1:F:409:SER:HB3	2.28	0.63
1:B:358:ARG:HD3	1:B:411:ARG:HE	1.64	0.63
1:E:278:LYS:HE3	1:E:552:PRO:O	1.98	0.63
1:G:332:ASP:HB3	1:G:335:MET:HE3	1.81	0.63
1:F:332:ASP:HB3	1:F:335:MET:HE3	1.80	0.63
1:C:335:MET:HA	1:C:335:MET:CE	2.29	0.63
1:C:501:ILE:HD13	1:C:524:TRP:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:THR:HG22	1:A:248:PRO:HD2	1.81	0.63
1:D:441:ILE:HD12	1:D:458:LYS:HB3	1.79	0.63
1:E:463:SER:HB2	1:E:464:LEU:HD23	1.81	0.63
1:F:233:LEU:HD22	1:F:346:MET:HG3	1.79	0.63
1:D:358:ARG:HD3	1:D:411:ARG:HD2	1.80	0.63
1:A:424:LEU:HD13	1:A:440:LEU:HD21	1.79	0.63
1:D:329:PHE:HD1	1:D:335:MET:HE2	1.62	0.63
1:C:380:ARG:HH12	1:C:448:TYR:N	1.97	0.62
1:B:347:ILE:HD13	1:B:360:LEU:HD21	1.80	0.62
1:C:286:LEU:HD11	1:F:522:ASN:O	1.99	0.62
1:C:555:LYS:HB2	1:C:556:GLU:OE1	1.98	0.62
1:E:393:HIS:HA	1:E:396:MET:HE2	1.81	0.62
1:D:378:ASN:O	1:D:382:GLN:HG3	1.99	0.62
1:B:527:MET:HG3	1:B:528:ARG:H	1.65	0.62
1:E:425:LEU:HD11	1:E:559:PHE:HE1	1.64	0.62
1:A:380:ARG:HH12	1:A:448:TYR:N	1.97	0.62
1:E:358:ARG:HH11	1:E:411:ARG:CZ	2.13	0.62
1:G:333:LEU:HD11	1:G:394:GLU:HG2	1.81	0.62
1:G:526:PHE:C	1:G:526:PHE:CD2	2.78	0.62
1:G:510:TYR:HD2	1:G:529:GLN:CD	2.08	0.62
1:B:539:TYR:C	1:B:539:TYR:CD2	2.77	0.62
1:C:236:VAL:CG1	1:C:237:THR:N	2.63	0.62
1:C:554:THR:OG1	1:C:557:MET:HB2	1.99	0.62
1:G:555:LYS:H	1:G:555:LYS:CD	2.08	0.62
1:F:469:PHE:CD2	1:F:489:LEU:HB3	2.34	0.62
1:B:333:LEU:HB3	1:B:395:LYS:HE3	1.81	0.61
1:C:498:PHE:HD2	1:C:498:PHE:O	1.83	0.61
1:A:289:TYR:CB	1:A:418:ILE:HD11	2.29	0.61
1:A:300:TYR:CE2	1:A:314:ASP:HB3	2.35	0.61
1:E:312:MET:C	1:E:313:ILE:HD12	2.25	0.61
1:E:377:PHE:HD1	1:E:380:ARG:HH21	1.48	0.61
1:G:273:PRO:HB3	1:G:456:ILE:HG21	1.81	0.61
1:F:467:VAL:HG23	1:F:469:PHE:CE1	2.35	0.61
1:F:466:SER:HB2	1:F:517:CYS:O	2.00	0.61
1:D:293:TRP:HD1	1:D:424:LEU:HD11	1.64	0.61
1:E:489:LEU:CD2	1:E:515:ILE:HD11	2.31	0.61
1:E:522:ASN:HA	1:G:286:LEU:HD21	1.82	0.61
1:D:469:PHE:CD2	1:D:489:LEU:HD13	2.35	0.61
1:G:435:HIS:CG	1:G:436:GLU:N	2.65	0.61
1:G:520:GLU:HG3	1:G:525:VAL:HG11	1.82	0.61
1:A:514:ILE:HG22	1:A:530:ARG:HB3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:421:SER:O	1:F:424:LEU:HB2	2.00	0.61
1:A:419:CYS:O	1:A:422:ARG:HG2	2.00	0.61
1:D:246:THR:HG22	1:D:248:PRO:HD2	1.82	0.61
1:D:363:ASP:OD1	1:D:448:TYR:HD1	1.84	0.61
1:E:464:LEU:HD23	1:E:464:LEU:N	2.16	0.61
1:G:341:LEU:HD23	1:G:365:ILE:HB	1.83	0.61
1:A:416:PHE:HE1	1:A:424:LEU:HD11	1.66	0.60
1:C:246:THR:CG2	1:C:248:PRO:HD2	2.31	0.60
1:A:475:ARG:HA	1:A:485:ASN:CB	2.31	0.60
1:F:530:ARG:NH1	1:F:533:LYS:HD3	2.14	0.60
1:A:280:ASN:HB3	1:A:457:LEU:CD1	2.30	0.60
1:C:348:ILE:HG23	1:C:355:ALA:HB1	1.82	0.60
1:G:246:THR:HG22	1:G:248:PRO:CD	2.31	0.60
1:E:247:GLN:OE1	1:E:247:GLN:HA	2.01	0.60
1:F:287:LYS:HB2	1:F:288:PRO:CD	2.30	0.60
1:F:487:GLY:H	1:F:503:VAL:HG23	1.67	0.60
1:C:376:ASP:HB3	1:C:379:VAL:HG23	1.81	0.60
1:D:329:PHE:HD2	1:D:330:ARG:N	2.00	0.60
1:A:229:GLY:N	1:A:318:SER:HG	1.99	0.60
1:A:293:TRP:HB3	1:A:437:MET:SD	2.41	0.60
1:E:329:PHE:HE2	1:E:331:LYS:HB2	1.64	0.60
1:E:361:ILE:HG22	1:E:384:ILE:HD13	1.83	0.60
1:E:363:ASP:OD1	1:E:448:TYR:HD1	1.84	0.60
1:D:470:ARG:HH21	1:D:536:PRO:HD3	1.65	0.60
1:E:358:ARG:HD3	1:E:411:ARG:CD	2.31	0.60
1:F:419:CYS:HB3	1:F:422:ARG:HH21	1.67	0.60
1:E:519:PHE:HE1	1:G:286:LEU:HD21	1.64	0.60
1:G:334:ARG:HD3	1:F:432:GLU:CB	2.31	0.60
1:G:420:THR:HG23	1:G:423:LYS:HD2	1.84	0.60
1:B:469:PHE:CG	1:B:489:LEU:HB3	2.37	0.59
1:F:494:TYR:CD2	1:F:539:TYR:CE1	2.90	0.59
1:A:271:ALA:HB2	1:A:449:LYS:O	2.01	0.59
1:A:417:ASP:HB3	1:D:496:ARG:NH1	2.18	0.59
1:D:236:VAL:HG21	1:D:355:ALA:HB1	1.84	0.59
1:A:342:LEU:HD13	1:A:361:ILE:CG2	2.33	0.59
1:G:291:VAL:HG11	1:G:421:SER:HB3	1.83	0.59
1:B:290:LYS:HA	1:B:417:ASP:HA	1.84	0.59
1:D:494:TYR:CE2	1:D:496:ARG:HB2	2.38	0.59
1:F:329:PHE:HD2	1:F:331:LYS:H	1.49	0.59
1:A:435:HIS:CG	1:A:436:GLU:N	2.70	0.59
1:C:232:PHE:HZ	1:C:312:MET:HE2	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:435:HIS:CD2	1:G:436:GLU:N	2.70	0.59
1:F:363:ASP:OD1	1:F:448:TYR:HD1	1.86	0.59
1:B:491:VAL:HG22	1:B:498:PHE:HB2	1.84	0.59
1:A:293:TRP:O	1:A:293:TRP:CE3	2.56	0.58
1:F:246:THR:HG22	1:F:248:PRO:CD	2.32	0.58
1:A:316:ASP:O	1:A:317:ASN:HB2	2.03	0.58
1:D:477:GLY:HA2	1:D:483:PRO:HB3	1.85	0.58
1:E:313:ILE:HD12	1:E:313:ILE:N	2.18	0.58
1:G:504:THR:O	1:G:508:LYS:HG3	2.04	0.58
1:G:246:THR:HG22	1:G:248:PRO:HD2	1.84	0.58
1:G:543:MET:HE3	1:G:543:MET:CA	2.33	0.58
1:A:280:ASN:HB3	1:A:457:LEU:HD11	1.84	0.58
1:B:417:ASP:OD2	1:B:420:THR:HG22	2.03	0.58
1:D:293:TRP:HE3	1:D:293:TRP:O	1.86	0.58
1:D:276:MET:HA	1:D:280:ASN:HD22	1.69	0.58
1:E:518:LYS:HG2	1:E:519:PHE:H	1.67	0.58
1:G:528:ARG:HH11	1:G:528:ARG:HG2	1.68	0.58
1:A:511:ASP:O	1:A:512:ASN:HB2	2.04	0.58
1:E:268:PHE:CD1	1:E:269:PRO:HD2	2.38	0.58
1:G:400:LEU:HD12	1:G:400:LEU:N	2.18	0.58
1:F:526:PHE:HZ	1:F:529:GLN:HB2	1.69	0.58
1:C:273:PRO:HB3	1:C:456:ILE:CG2	2.34	0.58
1:D:293:TRP:HD1	1:D:424:LEU:CD1	2.16	0.58
1:A:280:ASN:O	1:A:283:LEU:HB2	2.03	0.57
1:G:494:TYR:CD2	1:G:539:TYR:CD1	2.92	0.57
1:C:489:LEU:C	1:C:490:TYR:CD2	2.82	0.57
1:D:232:PHE:HB2	1:D:320:PHE:CE2	2.39	0.57
1:D:268:PHE:CE1	1:D:301:MET:HG3	2.40	0.57
1:D:471:LEU:HD12	1:D:472:LYS:H	1.69	0.57
1:E:316:ASP:O	1:E:317:ASN:HB2	2.05	0.57
1:C:232:PHE:CZ	1:C:312:MET:HE2	2.40	0.57
1:E:306:GLY:CA	1:E:309:GLU:HB2	2.35	0.57
1:G:526:PHE:C	1:G:526:PHE:HD2	2.13	0.57
1:F:280:ASN:O	1:F:283:LEU:HD12	2.05	0.57
1:B:372:VAL:HG12	1:B:380:ARG:HG2	1.85	0.57
1:G:470:ARG:HH22	1:G:535:PHE:HD1	1.52	0.57
1:G:513:LYS:HB3	1:G:529:GLN:NE2	2.19	0.57
1:B:396:MET:HG2	1:B:401:ILE:HG22	1.87	0.57
1:B:469:PHE:CB	1:B:489:LEU:HB3	2.33	0.57
1:C:546:CYS:HA	1:C:549:ILE:HG12	1.86	0.57
1:D:330:ARG:NH2	1:D:331:LYS:HE2	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:351:VAL:O	1:D:351:VAL:HG13	2.04	0.57
1:E:236:VAL:HG12	1:E:237:THR:O	2.04	0.57
1:E:374:ASP:HA	1:E:447:LYS:HB3	1.87	0.57
1:G:325:LEU:HD11	1:G:408:PHE:CE1	2.39	0.57
1:F:462:PRO:HA	1:F:465:ASN:OD1	2.04	0.57
1:C:236:VAL:HG12	1:C:237:THR:N	2.18	0.57
1:F:513:LYS:HD2	1:F:529:GLN:HE22	1.69	0.57
1:D:489:LEU:N	1:D:489:LEU:HD23	2.19	0.57
1:D:539:TYR:C	1:D:539:TYR:CD2	2.82	0.57
1:D:269:PRO:HG2	1:D:301:MET:CE	2.34	0.57
1:E:247:GLN:N	1:E:248:PRO:HD2	2.20	0.57
1:A:239:LYS:NZ	1:A:239:LYS:HB3	2.20	0.57
1:A:291:VAL:HG11	1:A:421:SER:CB	2.35	0.57
1:E:273:PRO:HB3	1:E:456:ILE:HG22	1.87	0.57
1:E:314:ASP:HB3	1:E:316:ASP:N	2.18	0.56
1:B:300:TYR:CE2	1:B:314:ASP:HB3	2.40	0.56
1:D:329:PHE:HD2	1:D:329:PHE:C	2.13	0.56
1:D:470:ARG:HB2	1:D:536:PRO:HG3	1.88	0.56
1:E:246:THR:HG22	1:E:248:PRO:CD	2.31	0.56
1:G:293:TRP:HB2	1:G:437:MET:HB3	1.87	0.56
1:A:471:LEU:HD12	1:A:471:LEU:C	2.31	0.56
1:B:520:GLU:O	1:B:521:ASN:C	2.47	0.56
1:G:461:PRO:HD2	1:G:464:LEU:HD22	1.86	0.56
1:C:293:TRP:HD1	1:C:424:LEU:HD21	1.69	0.56
1:D:313:ILE:HD12	1:D:313:ILE:N	2.20	0.56
1:F:475:ARG:HG3	1:F:484:GLN:O	2.05	0.56
1:D:236:VAL:CG2	1:D:355:ALA:HB1	2.35	0.56
1:E:246:THR:CG2	1:E:248:PRO:HD2	2.32	0.56
1:B:377:PHE:HD1	1:B:380:ARG:HH21	1.54	0.56
1:C:316:ASP:O	1:C:317:ASN:CB	2.53	0.56
1:D:506:GLU:O	1:D:509:GLN:HG2	2.06	0.56
1:G:467:VAL:HG11	1:G:469:PHE:CZ	2.40	0.56
1:D:293:TRP:CD1	1:D:424:LEU:HD11	2.41	0.56
1:G:342:LEU:HD23	1:G:364:ILE:HG13	1.88	0.56
1:B:385:GLU:HG2	1:B:412:ASN:ND2	2.20	0.56
1:G:459:TRP:CZ2	1:G:461:PRO:HA	2.40	0.56
1:B:232:PHE:HZ	1:B:312:MET:CE	2.19	0.56
1:G:253:VAL:HG13	1:G:303:LEU:HD23	1.88	0.56
1:A:402:ASP:OD2	1:A:405:GLN:HG2	2.06	0.55
1:C:392:ARG:NH2	1:C:406:GLU:OE2	2.40	0.55
1:C:469:PHE:CB	1:C:489:LEU:HB3	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:492:GLY:O	1:E:539:TYR:N	2.39	0.55
1:G:386:ARG:O	1:G:391:PRO:HD3	2.06	0.55
1:G:403:LYS:HZ3	1:G:411:ARG:NH2	2.03	0.55
1:B:276:MET:HA	1:B:280:ASN:HD22	1.71	0.55
1:C:300:TYR:CE2	1:C:314:ASP:HB3	2.41	0.55
1:C:541:THR:O	1:C:545:VAL:HG23	2.06	0.55
1:G:276:MET:HA	1:G:280:ASN:HD22	1.71	0.55
1:B:232:PHE:HZ	1:B:312:MET:HE2	1.70	0.55
1:E:467:VAL:HG23	1:E:545:VAL:HG11	1.87	0.55
1:B:520:GLU:HG3	1:B:525:VAL:CG1	2.36	0.55
1:G:361:ILE:HG22	1:G:384:ILE:HD13	1.89	0.55
1:F:333:LEU:O	1:F:395:LYS:HE3	2.06	0.55
1:E:517:CYS:HA	1:E:525:VAL:O	2.06	0.55
1:G:247:GLN:HB3	1:G:248:PRO:CD	2.36	0.55
1:F:543:MET:HE3	1:F:543:MET:HA	1.89	0.55
1:A:316:ASP:O	1:A:317:ASN:CB	2.54	0.55
1:A:543:MET:HE3	1:A:543:MET:HA	1.89	0.55
1:D:549:ILE:O	1:D:552:PRO:HD3	2.06	0.55
1:D:555:LYS:O	1:D:559:PHE:HB2	2.06	0.55
1:D:380:ARG:NH1	1:D:448:TYR:N	2.55	0.55
1:E:467:VAL:HG22	1:E:545:VAL:HG21	1.88	0.55
1:E:519:PHE:HE1	1:G:286:LEU:HD23	1.70	0.55
1:F:300:TYR:CE2	1:F:314:ASP:HB3	2.42	0.55
1:F:376:ASP:HB3	1:F:379:VAL:HG23	1.88	0.55
1:F:539:TYR:C	1:F:539:TYR:CD2	2.84	0.55
1:C:365:ILE:N	1:C:365:ILE:HD12	2.22	0.55
1:E:367:PHE:O	1:E:370:GLN:HB2	2.06	0.55
1:G:300:TYR:HA	1:G:313:ILE:O	2.07	0.55
1:G:358:ARG:NH1	1:G:411:ARG:NE	2.53	0.55
1:E:522:ASN:CA	1:G:286:LEU:HD21	2.37	0.55
1:B:260:PHE:CG	1:B:366:LYS:HD2	2.42	0.54
1:C:368:ASN:O	1:C:369:SER:HB2	2.07	0.54
1:A:511:ASP:C	1:A:513:LYS:H	2.16	0.54
1:B:238:VAL:HG21	1:B:407:PRO:O	2.07	0.54
1:B:260:PHE:CD2	1:B:366:LYS:HD2	2.41	0.54
1:D:356:VAL:HG12	1:D:356:VAL:O	2.05	0.54
1:G:229:GLY:HA2	1:G:243:GLN:HE22	1.71	0.54
1:F:312:MET:HE3	1:F:346:MET:HE3	1.89	0.54
1:B:347:ILE:HD13	1:B:360:LEU:CD2	2.37	0.54
1:E:235:GLY:O	1:E:236:VAL:HG23	2.07	0.54
1:G:518:LYS:HE2	1:G:527:MET:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:380:ARG:HH12	1:E:448:TYR:N	2.05	0.54
1:B:280:ASN:O	1:B:283:LEU:HD12	2.08	0.54
1:D:329:PHE:C	1:D:329:PHE:CD2	2.85	0.54
1:G:487:GLY:H	1:G:503:VAL:CG2	2.20	0.54
1:F:474:THR:HG22	1:F:476:MET:HG2	1.89	0.54
1:B:418:ILE:HA	1:B:421:SER:OG	2.08	0.54
1:F:358:ARG:HD3	1:F:411:ARG:HD2	1.90	0.54
1:C:315:ARG:NE	1:C:533:LYS:HZ1	2.02	0.54
1:C:517:CYS:HB3	1:C:525:VAL:O	2.08	0.54
1:E:424:LEU:O	1:E:425:LEU:HG	2.07	0.54
1:G:504:THR:HG22	1:G:505:LYS:N	2.15	0.54
1:A:327:PHE:HD1	1:A:392:ARG:HD2	1.71	0.54
1:B:389:ILE:HD11	1:B:411:ARG:HA	1.90	0.54
1:D:505:LYS:HG3	1:D:506:GLU:N	2.23	0.54
1:D:539:TYR:CE2	1:D:543:MET:HG2	2.43	0.54
1:E:375:CYS:HB3	1:E:379:VAL:HG11	1.90	0.54
1:E:476:MET:O	1:E:483:PRO:HB3	2.08	0.54
1:A:475:ARG:HA	1:A:485:ASN:HB3	1.88	0.54
1:E:389:ILE:HG22	1:E:390:SER:N	2.21	0.53
1:G:488:LEU:HD22	1:G:500:GLN:HG2	1.89	0.53
1:F:313:ILE:HD12	1:F:313:ILE:N	2.22	0.53
1:A:233:LEU:CG	1:A:236:VAL:CG2	2.81	0.53
1:A:363:ASP:OD1	1:A:448:TYR:HD1	1.92	0.53
1:C:435:HIS:CD2	1:C:436:GLU:H	2.27	0.53
1:E:233:LEU:HD23	1:E:233:LEU:C	2.33	0.53
1:E:360:LEU:HA	1:E:411:ARG:O	2.08	0.53
1:G:247:GLN:HB3	1:G:248:PRO:HD3	1.90	0.53
1:F:277:ASP:H	1:F:280:ASN:HB2	1.72	0.53
1:F:496:ARG:HB2	1:F:497:PRO:CD	2.28	0.53
1:C:278:LYS:HE2	1:C:551:ASN:HD21	1.74	0.53
1:E:307:THR:HG23	1:E:336:HIS:CE1	2.43	0.53
1:E:494:TYR:HD2	1:E:496:ARG:O	1.91	0.53
1:F:417:ASP:CG	1:F:418:ILE:H	2.16	0.53
1:B:518:LYS:O	1:B:525:VAL:HG12	2.07	0.53
1:B:530:ARG:HG2	1:B:533:LYS:HD2	1.89	0.53
1:F:358:ARG:HG2	1:F:409:SER:HB3	1.90	0.53
1:F:291:VAL:HG13	1:F:416:PHE:CD1	2.43	0.53
1:E:469:PHE:CG	1:E:489:LEU:HB3	2.43	0.53
1:D:269:PRO:HG2	1:D:301:MET:HE1	1.89	0.53
1:D:293:TRP:O	1:D:293:TRP:CE3	2.61	0.53
1:G:367:PHE:CE1	1:G:387:GLU:HB3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:469:PHE:CD2	1:F:489:LEU:HD13	2.44	0.53
1:A:246:THR:HG22	1:A:248:PRO:HG2	1.91	0.53
1:D:424:LEU:HD21	1:D:440:LEU:HD21	1.90	0.53
1:E:300:TYR:HA	1:E:313:ILE:O	2.08	0.53
1:F:538:ALA:HB3	1:F:541:THR:OG1	2.09	0.53
1:A:348:ILE:HG22	1:A:348:ILE:O	2.08	0.53
1:C:376:ASP:OD2	1:C:445:THR:CG2	2.56	0.53
1:F:291:VAL:HG13	1:F:416:PHE:CE1	2.44	0.53
1:F:358:ARG:HG3	1:F:409:SER:HB3	1.90	0.53
1:B:470:ARG:HD3	1:B:514:ILE:HD11	1.91	0.53
1:D:418:ILE:O	1:D:421:SER:OG	2.26	0.53
1:E:566:THR:HG22	1:E:566:THR:O	2.08	0.53
1:F:230:ALA:CB	1:F:243:GLN:CD	2.82	0.53
1:F:468:ASP:O	1:F:537:ASN:ND2	2.42	0.53
1:C:264:GLU:OE1	1:F:282:LYS:HE2	2.09	0.52
1:D:293:TRP:HA	1:D:440:LEU:HD23	1.89	0.52
1:D:347:ILE:HG13	1:D:347:ILE:O	2.08	0.52
1:A:514:ILE:CG2	1:A:530:ARG:HB3	2.40	0.52
1:B:273:PRO:CG	1:B:458:LYS:HE3	2.38	0.52
1:C:278:LYS:HD2	1:C:557:MET:HE1	1.90	0.52
1:F:418:ILE:O	1:F:421:SER:OG	2.26	0.52
1:E:538:ALA:HB3	1:E:541:THR:OG1	2.10	0.52
1:A:460:LYS:HG3	1:A:461:PRO:HD2	1.92	0.52
1:B:367:PHE:CE1	1:B:387:GLU:HB3	2.44	0.52
1:C:380:ARG:NH1	1:C:448:TYR:N	2.57	0.52
1:D:327:PHE:CD1	1:D:392:ARG:HD2	2.45	0.52
1:D:469:PHE:HB3	1:D:489:LEU:HB3	1.91	0.52
1:G:312:MET:CE	1:G:346:MET:HE3	2.39	0.52
1:D:329:PHE:CD1	1:D:335:MET:CE	2.92	0.52
1:E:233:LEU:HD21	1:E:348:ILE:CD1	2.35	0.52
1:A:333:LEU:HD22	1:A:395:LYS:HD2	1.91	0.52
1:C:363:ASP:OD1	1:C:448:TYR:HD1	1.92	0.52
1:G:510:TYR:HB3	1:G:529:GLN:NE2	2.25	0.52
1:C:358:ARG:HD3	1:C:411:ARG:HD2	1.91	0.52
1:C:539:TYR:O	1:C:542:ALA:HB3	2.09	0.52
1:E:494:TYR:HB2	1:E:539:TYR:HD1	1.73	0.52
1:F:346:MET:HE2	1:F:359:TYR:HD1	1.75	0.52
1:C:329:PHE:CE2	1:C:331:LYS:HB2	2.45	0.52
1:C:496:ARG:HB3	1:C:497:PRO:HD2	1.92	0.52
1:D:233:LEU:HD12	1:D:346:MET:HB3	1.92	0.52
1:B:363:ASP:OD1	1:B:448:TYR:HD1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:395:LYS:HB3	1:B:401:ILE:HG13	1.92	0.52
1:B:418:ILE:O	1:B:421:SER:OG	2.28	0.52
1:E:388:ILE:O	1:E:388:ILE:HG22	2.09	0.52
1:F:546:CYS:O	1:F:549:ILE:HG12	2.09	0.52
1:B:422:ARG:HB3	1:B:562:ILE:CG2	2.40	0.52
1:G:354:GLN:HG3	1:G:355:ALA:H	1.75	0.52
1:E:356:VAL:CG1	1:E:358:ARG:HH21	2.23	0.51
1:C:499:ALA:HB1	1:C:524:TRP:CD1	2.45	0.51
1:G:232:PHE:CG	1:G:241:VAL:HG11	2.46	0.51
1:B:236:VAL:HG11	1:B:348:ILE:HD11	1.93	0.51
1:C:342:LEU:HD13	1:C:361:ILE:HD13	1.92	0.51
1:F:510:TYR:O	1:F:513:LYS:HB2	2.09	0.51
1:A:526:PHE:C	1:A:526:PHE:CD2	2.88	0.51
1:B:358:ARG:HD3	1:B:411:ARG:NE	2.26	0.51
1:G:386:ARG:HH11	1:G:386:ARG:HB2	1.76	0.51
1:F:245:THR:HG22	1:F:245:THR:O	2.11	0.51
1:A:294:LYS:NZ	2:A:5:SO4:O1	2.39	0.51
1:C:293:TRP:HB3	1:C:437:MET:SD	2.50	0.51
1:C:294:LYS:NZ	1:C:460:LYS:NZ	2.58	0.51
1:C:467:VAL:CG2	1:C:545:VAL:HG11	2.40	0.51
1:E:268:PHE:CE1	1:E:301:MET:HG3	2.46	0.51
1:B:396:MET:HG2	1:B:401:ILE:HG21	1.92	0.51
1:C:387:GLU:OE1	1:C:387:GLU:HA	2.10	0.51
1:F:469:PHE:CB	1:F:489:LEU:HB3	2.41	0.51
1:B:396:MET:SD	1:B:403:LYS:HD3	2.51	0.51
1:D:251:GLY:O	1:D:255:GLN:HB2	2.11	0.51
1:D:529:GLN:HG2	1:D:530:ARG:N	2.25	0.51
1:G:346:MET:HE2	1:G:359:TYR:HD1	1.75	0.51
1:F:350:ARG:HA	1:F:354:GLN:O	2.11	0.51
1:B:535:PHE:CD1	1:B:536:PRO:HD2	2.46	0.51
1:G:545:VAL:O	1:G:549:ILE:HG23	2.10	0.51
1:F:312:MET:C	1:F:313:ILE:HD12	2.36	0.51
1:A:519:PHE:HE1	1:E:286:LEU:HD23	1.75	0.51
1:B:356:VAL:HG12	1:B:356:VAL:O	2.09	0.51
1:B:385:GLU:HG2	1:B:412:ASN:HD21	1.76	0.51
1:B:471:LEU:HD12	1:B:472:LYS:N	2.26	0.51
1:D:232:PHE:HB2	1:D:320:PHE:CD2	2.46	0.51
1:E:230:ALA:HA	1:E:243:GLN:OE1	2.11	0.51
1:E:268:PHE:CZ	1:E:301:MET:HG3	2.46	0.51
1:G:462:PRO:HD2	1:G:555:LYS:NZ	2.25	0.51
1:B:368:ASN:O	1:B:369:SER:HB2	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:477:GLY:HA2	1:D:483:PRO:CB	2.41	0.51
1:E:239:LYS:O	1:E:407:PRO:HB3	2.10	0.51
1:G:246:THR:CG2	1:G:248:PRO:HD2	2.40	0.51
1:B:288:PRO:HD3	1:C:498:PHE:CE2	2.46	0.50
1:B:357:PRO:HB2	1:B:408:PHE:HB3	1.91	0.50
1:C:245:THR:O	1:C:245:THR:HG22	2.11	0.50
1:D:390:SER:O	1:D:394:GLU:HG2	2.11	0.50
1:E:542:ALA:O	1:E:545:VAL:HB	2.11	0.50
1:G:520:GLU:O	1:G:521:ASN:C	2.54	0.50
1:A:287:LYS:HB2	1:A:288:PRO:CD	2.41	0.50
1:B:402:ASP:HB3	1:B:405:GLN:HG2	1.94	0.50
1:C:461:PRO:HD2	1:C:464:LEU:HD13	1.93	0.50
1:E:556:GLU:H	1:E:556:GLU:CD	2.18	0.50
1:A:313:ILE:HD12	1:A:313:ILE:N	2.27	0.50
1:B:398:THR:HG22	1:B:400:LEU:H	1.76	0.50
1:C:325:LEU:HD11	1:C:408:PHE:HE1	1.75	0.50
1:C:467:VAL:HB	1:C:469:PHE:CE2	2.47	0.50
1:C:498:PHE:HD2	1:C:498:PHE:C	2.18	0.50
1:F:244:VAL:O	1:F:250:LEU:HD13	2.11	0.50
1:C:283:LEU:HA	1:C:286:LEU:HG	1.92	0.50
1:C:315:ARG:HE	1:C:533:LYS:HZ3	1.58	0.50
1:G:479:GLU:H	1:G:479:GLU:CD	2.19	0.50
1:F:282:LYS:O	1:F:286:LEU:HD13	2.11	0.50
1:F:438:ASP:O	1:F:460:LYS:HG3	2.11	0.50
1:A:435:HIS:CG	1:A:436:GLU:H	2.29	0.50
1:A:539:TYR:CE2	1:A:543:MET:HG3	2.45	0.50
1:B:380:ARG:HH12	1:B:448:TYR:N	2.09	0.50
1:D:312:MET:C	1:D:313:ILE:HD12	2.36	0.50
1:D:467:VAL:HG11	1:D:469:PHE:CE1	2.46	0.50
1:E:481:LEU:O	1:E:483:PRO:HD3	2.12	0.50
1:G:232:PHE:CZ	1:G:312:MET:HE2	2.46	0.50
1:G:488:LEU:CD2	1:G:500:GLN:HG2	2.42	0.50
1:F:422:ARG:HD3	1:F:563:ASP:OD1	2.11	0.50
1:B:246:THR:HG22	1:B:248:PRO:CD	2.16	0.50
1:C:469:PHE:HB3	1:C:489:LEU:HB3	1.92	0.50
1:C:503:VAL:CG1	1:C:508:LYS:HE3	2.41	0.50
1:D:396:MET:HG2	1:D:401:ILE:HB	1.93	0.50
1:D:422:ARG:HD3	1:D:563:ASP:OD1	2.11	0.50
1:D:554:THR:H	1:D:557:MET:HB3	1.77	0.50
1:E:293:TRP:O	1:E:293:TRP:CE3	2.65	0.50
1:E:419:CYS:HB3	1:E:566:THR:HG23	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:330:ARG:NH1	1:G:386:ARG:NH2	2.60	0.50
1:E:396:MET:HG2	1:E:401:ILE:HB	1.94	0.50
1:E:468:ASP:HB2	1:E:537:ASN:OD1	2.12	0.50
1:E:533:LYS:HG2	1:E:535:PHE:O	2.11	0.50
1:G:375:CYS:HB3	1:G:379:VAL:HG11	1.93	0.50
1:A:380:ARG:NH1	1:A:448:TYR:N	2.60	0.50
1:B:232:PHE:CZ	1:B:312:MET:HE2	2.47	0.50
1:B:376:ASP:HB3	1:B:379:VAL:HG23	1.93	0.50
1:D:367:PHE:CE1	1:D:387:GLU:HB3	2.47	0.50
1:D:516:GLU:HG2	1:D:527:MET:HG3	1.93	0.50
1:F:332:ASP:CB	1:F:335:MET:HE3	2.42	0.50
1:F:561:PHE:CD2	1:F:561:PHE:C	2.89	0.50
1:B:486:VAL:HG23	1:B:486:VAL:O	2.12	0.49
1:F:275:SER:O	1:F:280:ASN:ND2	2.44	0.49
1:C:260:PHE:CG	1:C:366:LYS:HD2	2.47	0.49
1:F:247:GLN:N	1:F:248:PRO:HD2	2.27	0.49
1:E:325:LEU:HA	1:E:406:GLU:HG2	1.94	0.49
1:E:358:ARG:HD3	1:E:411:ARG:HD3	1.92	0.49
1:E:487:GLY:C	1:E:488:LEU:HD23	2.37	0.49
1:F:300:TYR:HA	1:F:313:ILE:O	2.11	0.49
1:C:248:PRO:O	1:C:252:GLU:HB2	2.11	0.49
1:C:489:LEU:C	1:C:490:TYR:HD2	2.20	0.49
1:E:232:PHE:CD1	1:E:238:VAL:HG21	2.47	0.49
1:G:543:MET:HA	1:G:543:MET:CE	2.32	0.49
1:B:543:MET:HA	1:B:543:MET:CE	2.42	0.49
1:D:513:LYS:HB3	1:D:529:GLN:HE21	1.78	0.49
1:E:358:ARG:HG3	1:E:409:SER:HB3	1.94	0.49
1:G:346:MET:HE2	1:G:359:TYR:CD1	2.47	0.49
1:G:358:ARG:HH11	1:G:411:ARG:NE	2.03	0.49
1:A:530:ARG:HG2	1:A:530:ARG:NH1	2.27	0.49
1:B:240:GLY:HA3	1:B:323:SER:HB2	1.95	0.49
1:C:425:LEU:HD13	1:C:559:PHE:CD1	2.47	0.49
1:C:498:PHE:C	1:C:498:PHE:CD2	2.89	0.49
1:G:418:ILE:HG22	1:G:418:ILE:O	2.11	0.49
1:A:401:ILE:O	1:A:401:ILE:HG22	2.13	0.49
1:A:293:TRP:CB	1:A:437:MET:SD	3.01	0.49
1:D:467:VAL:CG1	1:D:469:PHE:CE1	2.96	0.49
1:D:488:LEU:HB2	1:D:490:TYR:HE2	1.77	0.49
1:E:232:PHE:HB2	1:E:320:PHE:CE2	2.47	0.49
1:F:519:PHE:C	1:F:519:PHE:CD2	2.90	0.49
1:B:372:VAL:O	1:B:375:CYS:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:535:PHE:HD1	1:B:536:PRO:HD2	1.78	0.49
1:C:291:VAL:HG11	1:C:421:SER:HB2	1.95	0.49
1:F:236:VAL:HG23	1:F:348:ILE:HD13	1.94	0.49
1:D:467:VAL:HG23	1:D:545:VAL:HG11	1.95	0.48
1:G:403:LYS:NZ	1:G:411:ARG:HH22	2.06	0.48
1:F:358:ARG:HG3	1:F:409:SER:CB	2.43	0.48
1:A:307:THR:HG23	1:A:336:HIS:ND1	2.28	0.48
1:A:519:PHE:CD2	1:A:519:PHE:C	2.91	0.48
1:D:278:LYS:CD	1:D:557:MET:HE1	2.43	0.48
1:G:526:PHE:HD2	1:G:526:PHE:O	1.95	0.48
1:A:293:TRP:HA	1:A:440:LEU:HD23	1.95	0.48
1:C:311:PHE:C	1:C:312:MET:HG2	2.38	0.48
1:D:268:PHE:HE1	1:D:301:MET:HG3	1.78	0.48
1:E:236:VAL:HG12	1:E:237:THR:N	2.28	0.48
1:G:539:TYR:C	1:G:539:TYR:CD2	2.90	0.48
1:F:231:ILE:HG21	1:F:234:GLU:HG3	1.95	0.48
1:B:329:PHE:HD2	1:B:330:ARG:N	2.11	0.48
1:B:358:ARG:HH11	1:B:411:ARG:NH2	2.10	0.48
1:G:249:LYS:HD2	1:G:252:GLU:OE1	2.13	0.48
1:A:326:GLU:OE1	1:A:401:ILE:HD11	2.13	0.48
1:G:546:CYS:HA	1:G:549:ILE:HD13	1.95	0.48
1:F:550:SER:C	1:F:552:PRO:HD3	2.39	0.48
1:A:276:MET:HE2	1:A:457:LEU:HD12	1.96	0.48
1:E:235:GLY:O	1:E:236:VAL:CG2	2.62	0.48
1:G:327:PHE:CD1	1:G:392:ARG:HD2	2.48	0.48
1:A:247:GLN:N	1:A:248:PRO:CD	2.75	0.48
1:A:398:THR:HG22	1:A:398:THR:O	2.13	0.48
1:A:543:MET:HE3	1:A:543:MET:CA	2.43	0.48
1:B:291:VAL:CG2	1:B:292:SER:N	2.76	0.48
1:D:504:THR:HG22	1:D:507:LEU:HD13	1.94	0.48
1:E:377:PHE:O	1:E:381:LEU:HB2	2.14	0.48
1:E:473:ILE:HD11	1:E:485:ASN:OD1	2.13	0.48
1:F:471:LEU:C	1:F:471:LEU:HD12	2.39	0.48
1:C:232:PHE:CD1	1:C:241:VAL:HG11	2.48	0.48
1:E:306:GLY:C	1:E:309:GLU:HB2	2.39	0.48
1:G:403:LYS:HZ1	1:G:411:ARG:NH2	2.11	0.48
1:F:255:GLN:O	1:F:259:GLN:HG3	2.14	0.48
1:F:469:PHE:CG	1:F:489:LEU:HB3	2.49	0.48
1:A:273:PRO:HB2	1:A:458:LYS:HD3	1.95	0.48
1:A:529:GLN:HG2	1:A:530:ARG:N	2.27	0.48
1:B:542:ALA:O	1:B:545:VAL:HB	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:473:ILE:HD13	1:C:503:VAL:HG11	1.95	0.48
1:E:347:ILE:HG13	1:E:347:ILE:O	2.12	0.48
1:E:461:PRO:HG2	1:E:464:LEU:HG	1.96	0.48
1:E:519:PHE:CE1	1:G:286:LEU:HD23	2.47	0.48
1:B:247:GLN:N	1:B:248:PRO:CD	2.77	0.48
1:B:376:ASP:O	1:B:379:VAL:HB	2.14	0.48
1:F:468:ASP:H	1:F:537:ASN:HD21	1.60	0.48
1:A:363:ASP:C	1:A:384:ILE:HD11	2.39	0.47
1:B:380:ARG:NH1	1:B:448:TYR:N	2.62	0.47
1:F:467:VAL:HG22	1:F:469:PHE:CZ	2.49	0.47
1:A:418:ILE:HG22	1:A:562:ILE:HG13	1.95	0.47
1:C:556:GLU:H	1:C:556:GLU:CD	2.22	0.47
1:D:518:LYS:HB3	1:D:518:LYS:HE3	1.51	0.47
1:E:287:LYS:HB2	1:E:288:PRO:CD	2.45	0.47
1:E:422:ARG:HH21	1:E:423:LYS:NZ	2.12	0.47
1:B:233:LEU:HD12	1:B:233:LEU:HA	1.68	0.47
1:B:287:LYS:HB2	1:B:288:PRO:CD	2.44	0.47
1:F:346:MET:CE	1:F:359:TYR:HD1	2.27	0.47
1:F:537:ASN:H	1:F:537:ASN:HD22	0.71	0.47
1:A:422:ARG:CG	1:A:423:LYS:N	2.77	0.47
1:C:367:PHE:CE1	1:C:387:GLU:HB3	2.49	0.47
1:D:286:LEU:HD23	1:D:286:LEU:N	2.29	0.47
1:G:482:LEU:HA	1:G:483:PRO:HD2	1.82	0.47
1:D:271:ALA:HB2	1:D:449:LYS:O	2.15	0.47
1:D:519:PHE:CZ	1:D:522:ASN:HA	2.50	0.47
1:E:472:LYS:NZ	1:E:474:THR:HG21	2.29	0.47
1:F:232:PHE:HB2	1:F:320:PHE:CE2	2.50	0.47
1:F:489:LEU:HD21	1:F:501:ILE:CG2	2.40	0.47
1:B:239:LYS:HB2	1:B:239:LYS:NZ	2.30	0.47
1:B:260:PHE:HA	1:B:366:LYS:HE3	1.97	0.47
1:G:363:ASP:OD1	1:G:448:TYR:HD1	1.98	0.47
1:G:473:ILE:HD13	1:G:503:VAL:CG1	2.45	0.47
1:D:422:ARG:HA	1:D:559:PHE:HE2	1.79	0.47
1:D:422:ARG:HG3	1:D:559:PHE:CE2	2.50	0.47
1:D:471:LEU:CD2	1:D:507:LEU:HD23	2.44	0.47
1:E:424:LEU:O	1:E:425:LEU:CB	2.62	0.47
1:G:312:MET:HE1	1:G:346:MET:HE3	1.94	0.47
1:A:425:LEU:CD2	1:A:555:LYS:HE3	2.44	0.47
1:B:511:ASP:C	1:B:513:LYS:H	2.20	0.47
1:C:511:ASP:O	1:C:512:ASN:HB2	2.13	0.47
1:E:494:TYR:CD1	1:E:539:TYR:CD1	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:513:LYS:HB3	1:G:529:GLN:HE21	1.79	0.47
1:F:347:ILE:HD12	1:F:349:ASP:HB2	1.96	0.47
1:C:389:ILE:HG22	1:C:390:SER:N	2.30	0.47
1:C:467:VAL:HG23	1:C:545:VAL:HG11	1.97	0.47
1:E:546:CYS:HA	1:E:549:ILE:HD12	1.97	0.47
1:A:233:LEU:CB	1:A:236:VAL:HG23	2.37	0.47
1:B:358:ARG:HH12	1:B:411:ARG:HH21	1.60	0.47
1:C:294:LYS:NZ	1:C:458:LYS:HE3	2.30	0.47
1:C:491:VAL:HG11	1:C:542:ALA:HB2	1.97	0.47
1:D:470:ARG:NH2	1:D:536:PRO:HD3	2.30	0.47
1:E:420:THR:O	1:E:420:THR:CG2	2.61	0.47
1:A:322:VAL:HG12	1:A:407:PRO:HG2	1.96	0.46
1:B:236:VAL:HG12	1:B:348:ILE:HD11	1.93	0.46
1:E:358:ARG:HH11	1:E:411:ARG:NH1	2.12	0.46
1:E:381:LEU:HD12	1:E:381:LEU:HA	1.72	0.46
1:F:527:MET:HG3	1:F:528:ARG:N	2.30	0.46
1:B:232:PHE:CZ	1:B:312:MET:CE	2.98	0.46
1:C:329:PHE:HD2	1:C:331:LYS:N	2.07	0.46
1:C:511:ASP:C	1:C:513:LYS:H	2.24	0.46
1:B:468:ASP:N	1:B:468:ASP:OD1	2.48	0.46
1:C:491:VAL:CG2	1:C:539:TYR:HA	2.43	0.46
1:D:358:ARG:HD3	1:D:411:ARG:CD	2.44	0.46
1:E:278:LYS:HD2	1:E:551:ASN:OD1	2.14	0.46
1:E:309:GLU:OE1	1:E:309:GLU:CA	2.59	0.46
1:G:467:VAL:CG1	1:G:469:PHE:CZ	2.98	0.46
1:G:511:ASP:C	1:G:513:LYS:N	2.68	0.46
1:F:363:ASP:OD1	1:F:448:TYR:CD1	2.68	0.46
1:F:437:MET:O	1:F:437:MET:HG3	2.15	0.46
1:A:539:TYR:C	1:A:539:TYR:CD2	2.94	0.46
1:B:232:PHE:CE1	1:B:241:VAL:HG11	2.50	0.46
1:C:236:VAL:HB	1:C:348:ILE:HD11	1.97	0.46
1:D:234:GLU:OE2	1:D:234:GLU:HA	2.14	0.46
1:D:281:ILE:HD11	1:D:561:PHE:CB	2.45	0.46
1:D:438:ASP:O	1:D:460:LYS:HG2	2.16	0.46
1:E:521:ASN:O	1:E:522:ASN:HB2	2.15	0.46
1:F:560:GLU:HA	1:F:563:ASP:OD2	2.16	0.46
1:C:471:LEU:O	1:C:472:LYS:HG3	2.15	0.46
1:G:378:ASN:H	1:G:378:ASN:ND2	2.13	0.46
1:A:246:THR:HG22	1:A:248:PRO:CD	2.44	0.46
1:C:462:PRO:CD	1:C:555:LYS:HE3	2.28	0.46
1:D:248:PRO:O	1:D:252:GLU:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:511:ASP:OD1	1:D:512:ASN:ND2	2.48	0.46
1:F:293:TRP:CD1	1:F:293:TRP:N	2.83	0.46
1:A:294:LYS:HE2	2:A:5:SO4:O4	2.15	0.46
1:B:250:LEU:HD23	1:B:251:GLY:N	2.31	0.46
1:B:276:MET:HE2	1:B:281:ILE:HA	1.98	0.46
1:C:328:PRO:HD2	1:C:392:ARG:HG2	1.97	0.46
1:C:469:PHE:CG	1:C:489:LEU:HB3	2.50	0.46
1:D:539:TYR:CE2	1:D:543:MET:CG	2.99	0.46
1:G:400:LEU:HD12	1:G:400:LEU:H	1.81	0.46
1:A:519:PHE:CG	1:A:549:ILE:HD12	2.51	0.46
1:B:286:LEU:CD1	1:C:519:PHE:HE1	2.28	0.46
1:C:405:GLN:HA	1:C:405:GLN:OE1	2.15	0.46
1:C:471:LEU:HD22	1:C:515:ILE:HD13	1.97	0.46
1:G:494:TYR:CD2	1:G:539:TYR:CE1	3.04	0.46
1:A:246:THR:HG22	1:A:248:PRO:CG	2.46	0.46
1:A:449:LYS:HG2	1:A:450:PRO:HD2	1.98	0.46
1:B:236:VAL:HG13	1:B:237:THR:N	2.30	0.46
1:B:330:ARG:HB2	1:B:391:PRO:HG3	1.96	0.46
1:B:347:ILE:O	1:B:347:ILE:HG13	2.15	0.46
1:B:381:LEU:HA	1:B:381:LEU:HD23	1.72	0.46
1:B:386:ARG:HB2	1:B:386:ARG:NH1	2.31	0.46
1:F:367:PHE:O	1:F:370:GLN:HB2	2.16	0.46
1:F:529:GLN:HG3	1:F:530:ARG:N	2.30	0.46
1:F:533:LYS:HA	1:F:533:LYS:HD2	1.81	0.46
1:D:519:PHE:CD2	1:D:549:ILE:HD12	2.51	0.46
1:G:293:TRP:HE3	1:G:293:TRP:O	1.99	0.46
1:G:494:TYR:CE1	1:G:496:ARG:HG2	2.51	0.46
1:F:517:CYS:HB3	1:F:525:VAL:O	2.15	0.46
1:B:247:GLN:N	1:B:248:PRO:HD3	2.31	0.45
1:E:278:LYS:HB2	1:E:551:ASN:HD21	1.81	0.45
1:E:522:ASN:HA	1:G:286:LEU:CD2	2.46	0.45
1:G:397:LYS:O	1:F:414:PRO:HB2	2.16	0.45
1:G:510:TYR:HD2	1:G:529:GLN:OE1	2.00	0.45
1:A:328:PRO:HD2	1:A:392:ARG:HG2	1.99	0.45
1:D:329:PHE:CD2	1:D:330:ARG:N	2.83	0.45
1:E:363:ASP:OD1	1:E:448:TYR:CD1	2.68	0.45
1:A:527:MET:HG3	1:A:528:ARG:HG3	1.98	0.45
1:E:316:ASP:O	1:E:317:ASN:CB	2.61	0.45
1:E:477:GLY:HA2	1:E:483:PRO:HB3	1.99	0.45
1:G:321:HIS:ND1	1:G:321:HIS:C	2.74	0.45
1:F:233:LEU:HD21	1:F:348:ILE:HG13	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:VAL:HG12	1:B:407:PRO:HG2	1.99	0.45
1:C:307:THR:HG23	1:C:308:ASN:H	1.81	0.45
1:C:406:GLU:HB2	1:C:407:PRO:HD2	1.99	0.45
1:E:244:VAL:O	1:E:244:VAL:HG12	2.16	0.45
1:E:491:VAL:HG11	1:E:498:PHE:HD1	1.81	0.45
1:G:255:GLN:O	1:G:259:GLN:HG3	2.17	0.45
1:A:327:PHE:CE1	1:A:392:ARG:HD2	2.49	0.45
1:G:528:ARG:HG3	1:G:529:GLN:N	2.32	0.45
1:F:244:VAL:HG23	1:F:250:LEU:HB2	1.99	0.45
1:C:287:LYS:HB2	1:C:288:PRO:CD	2.47	0.45
1:D:398:THR:HG21	1:D:400:LEU:HD22	1.98	0.45
1:E:314:ASP:C	1:E:316:ASP:N	2.73	0.45
1:E:550:SER:O	1:E:552:PRO:HD3	2.16	0.45
1:B:300:TYR:HA	1:B:313:ILE:O	2.16	0.45
1:C:386:ARG:O	1:C:391:PRO:HD3	2.16	0.45
1:D:244:VAL:O	1:D:244:VAL:CG2	2.64	0.45
1:E:278:LYS:HG2	1:E:557:MET:CE	2.46	0.45
1:B:554:THR:C	1:B:556:GLU:N	2.74	0.45
1:C:527:MET:HG3	1:C:528:ARG:H	1.82	0.45
1:E:293:TRP:O	1:E:293:TRP:HE3	1.98	0.45
1:E:314:ASP:HB2	1:E:318:SER:HB2	1.99	0.45
1:G:243:GLN:HB2	1:G:320:PHE:CE2	2.51	0.45
1:F:357:PRO:HB2	1:F:408:PHE:HB3	1.98	0.45
1:A:233:LEU:HD12	1:A:234:GLU:N	2.32	0.45
1:B:291:VAL:HG22	1:B:292:SER:N	2.30	0.45
1:D:513:LYS:HG2	1:D:529:GLN:NE2	2.31	0.45
1:F:307:THR:HG23	1:F:308:ASN:N	2.32	0.45
1:A:375:CYS:HB3	1:A:379:VAL:HG11	1.98	0.45
1:A:460:LYS:HG3	1:A:461:PRO:CD	2.47	0.45
1:B:348:ILE:HD12	1:B:355:ALA:HB1	1.99	0.45
1:B:487:GLY:O	1:B:500:GLN:HA	2.17	0.45
1:D:549:ILE:HG13	1:D:550:SER:N	2.32	0.45
1:A:367:PHE:CZ	1:A:387:GLU:HB3	2.52	0.44
1:B:370:GLN:HA	1:B:371:PRO:HD3	1.60	0.44
1:C:278:LYS:HG3	1:C:551:ASN:HD21	1.82	0.44
1:D:329:PHE:HD2	1:D:331:LYS:H	1.65	0.44
1:E:392:ARG:HH21	1:E:406:GLU:CD	2.25	0.44
1:E:395:LYS:HB3	1:E:401:ILE:CG1	2.46	0.44
1:B:471:LEU:HD23	1:B:515:ILE:HD13	1.99	0.44
1:E:230:ALA:CA	1:E:243:GLN:OE1	2.65	0.44
1:E:329:PHE:HD2	1:E:331:LYS:H	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:368:ASN:O	1:E:369:SER:HB2	2.17	0.44
1:E:402:ASP:O	1:E:403:LYS:C	2.60	0.44
1:G:469:PHE:CB	1:G:489:LEU:HB3	2.47	0.44
1:F:422:ARG:HG3	1:F:562:ILE:CG2	2.47	0.44
1:G:273:PRO:HB3	1:G:456:ILE:HG22	1.96	0.44
1:G:311:PHE:HA	1:G:320:PHE:O	2.17	0.44
1:G:329:PHE:HD2	1:G:330:ARG:N	2.16	0.44
1:A:239:LYS:HB3	1:A:239:LYS:HZ3	1.82	0.44
1:A:325:LEU:HD23	1:A:325:LEU:HA	1.66	0.44
1:C:520:GLU:O	1:C:521:ASN:C	2.60	0.44
1:D:376:ASP:OD2	1:D:445:THR:CG2	2.65	0.44
1:E:244:VAL:HG12	1:E:250:LEU:HB2	1.99	0.44
1:E:347:ILE:CD1	1:E:360:LEU:HD11	2.47	0.44
1:E:365:ILE:N	1:E:365:ILE:HD12	2.32	0.44
1:A:311:PHE:HA	1:A:320:PHE:O	2.18	0.44
1:C:470:ARG:HD3	1:C:514:ILE:CD1	2.47	0.44
1:D:233:LEU:O	1:D:233:LEU:HD23	2.17	0.44
1:D:424:LEU:CD2	1:D:440:LEU:HD21	2.48	0.44
1:D:498:PHE:CE1	1:D:542:ALA:HB1	2.53	0.44
1:E:380:ARG:O	1:E:384:ILE:HG13	2.18	0.44
1:E:516:GLU:HG2	1:E:527:MET:HG3	1.99	0.44
1:F:494:TYR:CD2	1:F:539:TYR:CD1	3.05	0.44
1:A:329:PHE:HD2	1:A:331:LYS:H	1.66	0.44
1:A:461:PRO:HA	1:A:462:PRO:HD3	1.84	0.44
1:C:247:GLN:N	1:C:248:PRO:CD	2.81	0.44
1:G:290:LYS:HD3	1:G:417:ASP:HA	2.00	0.44
1:F:230:ALA:HB3	1:F:243:GLN:CD	2.40	0.44
1:C:367:PHE:CZ	1:C:387:GLU:HB3	2.52	0.44
1:E:230:ALA:HB2	1:E:243:GLN:OE1	2.17	0.44
1:G:402:ASP:C	1:G:404:THR:N	2.76	0.44
1:G:449:LYS:HG2	1:G:450:PRO:O	2.18	0.44
1:G:473:ILE:HD13	1:G:503:VAL:HG13	2.00	0.44
1:F:312:MET:CE	1:F:346:MET:CE	2.95	0.44
1:A:488:LEU:HD13	1:A:497:PRO:HG3	2.00	0.44
1:B:520:GLU:HG3	1:B:525:VAL:HG11	1.99	0.44
1:C:473:ILE:CD1	1:C:503:VAL:HG11	2.48	0.44
1:C:554:THR:OG1	1:C:557:MET:CB	2.66	0.44
1:D:392:ARG:NH2	1:D:406:GLU:OE1	2.50	0.44
1:D:541:THR:O	1:D:545:VAL:HG23	2.17	0.44
1:G:288:PRO:HB2	1:G:445:THR:OG1	2.18	0.44
1:F:293:TRP:HD1	1:F:293:TRP:H	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:TYR:HD2	1:B:442:PHE:HB3	1.83	0.44
1:C:332:ASP:O	1:C:332:ASP:CG	2.61	0.44
1:E:377:PHE:CZ	1:E:443:GLN:HG2	2.53	0.44
1:E:390:SER:N	1:E:391:PRO:CD	2.81	0.44
1:G:333:LEU:O	1:G:395:LYS:HE3	2.17	0.44
1:F:461:PRO:HA	1:F:462:PRO:HD3	1.83	0.44
1:A:342:LEU:CD1	1:A:361:ILE:HD13	2.48	0.43
1:A:378:ASN:O	1:A:382:GLN:HG3	2.17	0.43
1:B:277:ASP:HA	1:B:553:VAL:CG2	2.48	0.43
1:D:279:GLN:O	1:D:282:LYS:HB2	2.17	0.43
1:G:489:LEU:HD23	1:G:489:LEU:N	2.33	0.43
1:D:543:MET:HE3	1:D:543:MET:CA	2.46	0.43
1:E:269:PRO:HG2	1:E:301:MET:CE	2.48	0.43
1:E:462:PRO:HD2	1:E:555:LYS:HE2	1.99	0.43
1:F:422:ARG:HG3	1:F:562:ILE:HG21	1.99	0.43
1:A:389:ILE:HD12	1:A:389:ILE:HA	1.69	0.43
1:C:303:LEU:HD12	1:C:340:THR:O	2.19	0.43
1:C:327:PHE:CD1	1:C:392:ARG:HD2	2.53	0.43
1:C:372:VAL:O	1:C:375:CYS:HB2	2.18	0.43
1:E:501:ILE:CD1	1:E:524:TRP:O	2.66	0.43
1:F:312:MET:CE	1:F:346:MET:HE1	2.46	0.43
1:F:452:ARG:NH1	1:F:454:ASP:OD1	2.51	0.43
1:B:378:ASN:O	1:B:382:GLN:HG3	2.19	0.43
1:C:326:GLU:OE2	1:C:336:HIS:CE1	2.71	0.43
1:E:380:ARG:NH1	1:E:448:TYR:N	2.66	0.43
1:E:390:SER:O	1:E:394:GLU:HG3	2.18	0.43
1:G:459:TRP:CH2	1:G:461:PRO:HG3	2.54	0.43
1:F:537:ASN:ND2	1:F:537:ASN:N	2.29	0.43
1:F:556:GLU:O	1:F:560:GLU:HG2	2.18	0.43
1:A:294:LYS:CE	2:A:5:SO4:O4	2.67	0.43
1:A:470:ARG:NH2	1:A:535:PHE:HD1	2.16	0.43
1:B:249:LYS:HE3	1:B:311:PHE:CZ	2.53	0.43
1:B:291:VAL:CG1	1:B:421:SER:HB3	2.49	0.43
1:B:471:LEU:HD12	1:B:471:LEU:C	2.43	0.43
1:A:363:ASP:OD1	1:A:448:TYR:CD1	2.71	0.43
1:A:511:ASP:C	1:A:513:LYS:N	2.76	0.43
1:D:398:THR:CG2	1:D:398:THR:O	2.66	0.43
1:E:303:LEU:C	1:E:303:LEU:HD12	2.44	0.43
1:G:405:GLN:OE1	1:G:405:GLN:N	2.51	0.43
1:A:395:LYS:HB2	1:A:401:ILE:HD12	2.01	0.43
1:B:377:PHE:CE2	1:B:443:GLN:HG2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:VAL:HG23	1:C:348:ILE:HD13	2.00	0.43
1:C:443:GLN:HA	1:C:444:PRO:HD2	1.91	0.43
1:D:402:ASP:OD1	1:D:405:GLN:HG2	2.19	0.43
1:D:503:VAL:CG1	1:D:508:LYS:HG2	2.49	0.43
1:E:402:ASP:HB3	1:E:405:GLN:CG	2.49	0.43
1:A:329:PHE:C	1:A:329:PHE:CD2	2.97	0.43
1:B:288:PRO:HD3	1:C:498:PHE:CD2	2.54	0.43
1:B:351:VAL:HG22	1:B:352:ASN:OD1	2.18	0.43
1:C:439:GLY:O	1:C:440:LEU:HD23	2.18	0.43
1:G:302:MET:HE3	1:G:359:TYR:CE2	2.53	0.43
1:G:487:GLY:H	1:G:503:VAL:HG21	1.82	0.43
1:A:327:PHE:HB3	1:A:337:LEU:HD12	2.01	0.43
1:A:329:PHE:HD2	1:A:330:ARG:N	2.16	0.43
1:A:402:ASP:HB3	1:A:405:GLN:CG	2.49	0.43
1:A:413:LYS:HG2	1:A:414:PRO:HD2	2.01	0.43
1:A:416:PHE:CE1	1:A:424:LEU:HD11	2.49	0.43
1:A:449:LYS:HA	1:A:450:PRO:HD3	1.65	0.43
1:B:344:GLY:HA3	1:B:360:LEU:O	2.19	0.43
1:C:337:LEU:HD23	1:C:337:LEU:HA	1.69	0.43
1:E:247:GLN:N	1:E:248:PRO:CD	2.82	0.43
1:E:367:PHE:CZ	1:E:387:GLU:HB3	2.53	0.43
1:E:402:ASP:OD2	1:E:404:THR:HB	2.19	0.43
1:G:467:VAL:HG12	1:G:469:PHE:CE2	2.54	0.43
1:D:294:LYS:NZ	1:D:460:LYS:NZ	2.67	0.42
1:D:504:THR:HG23	1:D:506:GLU:HG3	2.00	0.42
1:G:518:LYS:O	1:G:525:VAL:HG22	2.19	0.42
1:A:293:TRP:O	1:A:293:TRP:HE3	2.00	0.42
1:B:273:PRO:HB3	1:B:456:ILE:CG2	2.49	0.42
1:B:358:ARG:HG3	1:B:409:SER:HB2	1.99	0.42
1:B:494:TYR:CD2	1:B:539:TYR:CD1	3.07	0.42
1:C:294:LYS:NZ	1:C:460:LYS:HZ2	2.16	0.42
1:C:539:TYR:C	1:C:539:TYR:CD2	2.96	0.42
1:D:546:CYS:HA	1:D:549:ILE:HG12	2.01	0.42
1:F:230:ALA:CB	1:F:243:GLN:OE1	2.62	0.42
1:F:417:ASP:CG	1:F:418:ILE:N	2.77	0.42
1:A:507:LEU:HD11	1:A:526:PHE:HB2	2.02	0.42
1:B:333:LEU:HB3	1:B:395:LYS:CE	2.49	0.42
1:B:555:LYS:O	1:B:559:PHE:HB2	2.20	0.42
1:C:264:GLU:HG3	1:F:282:LYS:NZ	2.33	0.42
1:C:470:ARG:HD3	1:C:514:ILE:HD11	2.01	0.42
1:E:269:PRO:HG2	1:E:301:MET:HE1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:302:MET:HE3	1:F:302:MET:HB2	1.88	0.42
1:F:387:GLU:OE1	1:F:387:GLU:CA	2.63	0.42
1:F:474:THR:CG2	1:F:476:MET:HG2	2.48	0.42
1:B:301:MET:O	1:B:313:ILE:HD12	2.20	0.42
1:B:337:LEU:HD23	1:B:337:LEU:HA	1.71	0.42
1:B:470:ARG:NH1	1:B:536:PRO:HD3	2.35	0.42
1:G:283:LEU:HD23	1:G:286:LEU:CD2	2.47	0.42
1:G:312:MET:C	1:G:313:ILE:HD13	2.44	0.42
1:G:366:LYS:HD2	1:G:369:SER:O	2.19	0.42
1:G:470:ARG:NH2	1:G:535:PHE:HD1	2.15	0.42
1:F:346:MET:HE2	1:F:346:MET:HB2	1.78	0.42
1:F:527:MET:HE2	1:F:528:ARG:HG2	2.01	0.42
1:B:325:LEU:HD11	1:B:408:PHE:CE1	2.53	0.42
1:C:286:LEU:CD1	1:F:522:ASN:O	2.67	0.42
1:C:385:GLU:HG2	1:C:412:ASN:ND2	2.35	0.42
1:D:231:ILE:HG21	1:D:234:GLU:HB2	2.01	0.42
1:D:494:TYR:CE1	1:D:539:TYR:CE1	3.07	0.42
1:G:275:SER:O	1:G:280:ASN:ND2	2.53	0.42
1:G:337:LEU:HA	1:G:337:LEU:HD23	1.78	0.42
1:G:367:PHE:CZ	1:G:387:GLU:HB3	2.55	0.42
1:F:422:ARG:CD	1:F:563:ASP:OD1	2.68	0.42
1:B:342:LEU:HD13	1:B:361:ILE:HD13	2.01	0.42
1:B:452:ARG:NH1	1:B:452:ARG:HG3	2.34	0.42
1:C:316:ASP:O	1:C:317:ASN:HB3	2.20	0.42
1:D:564:ARG:HE	1:D:564:ARG:HB2	1.53	0.42
1:G:402:ASP:C	1:G:404:THR:H	2.26	0.42
1:A:384:ILE:O	1:A:388:ILE:HB	2.19	0.42
1:B:398:THR:O	1:B:398:THR:CG2	2.67	0.42
1:D:470:ARG:CZ	1:D:514:ILE:HD11	2.50	0.42
1:E:328:PRO:HD2	1:E:392:ARG:HG2	2.01	0.42
1:E:335:MET:HE2	1:E:335:MET:HB3	1.85	0.42
1:E:474:THR:O	1:E:485:ASN:HB2	2.19	0.42
1:E:494:TYR:HB2	1:E:539:TYR:CD1	2.54	0.42
1:E:518:LYS:HG2	1:E:519:PHE:N	2.34	0.42
1:F:368:ASN:O	1:F:369:SER:HB2	2.19	0.42
1:A:273:PRO:HB3	1:A:456:ILE:HG22	2.02	0.42
1:D:502:LYS:HG2	1:D:503:VAL:N	2.34	0.42
1:D:511:ASP:OD1	1:D:512:ASN:N	2.52	0.42
1:F:466:SER:CB	1:F:517:CYS:O	2.64	0.42
1:F:543:MET:HE3	1:F:543:MET:CA	2.48	0.42
1:A:425:LEU:HD22	1:A:555:LYS:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:390:SER:HB3	1:D:391:PRO:HD3	2.01	0.42
1:E:233:LEU:HD12	1:E:346:MET:HB3	2.02	0.42
1:E:556:GLU:CD	1:E:556:GLU:N	2.78	0.42
1:G:325:LEU:HD23	1:G:325:LEU:HA	1.89	0.42
1:G:354:GLN:HG3	1:G:355:ALA:N	2.34	0.42
1:G:420:THR:HA	1:G:423:LYS:HE2	2.01	0.42
1:A:321:HIS:ND1	1:A:321:HIS:C	2.78	0.42
1:A:385:GLU:HG2	1:A:412:ASN:HD21	1.85	0.42
1:A:510:TYR:CD1	1:A:529:GLN:HB2	2.55	0.42
1:B:236:VAL:CG2	1:B:355:ALA:HB3	2.50	0.42
1:B:244:VAL:HG12	1:B:250:LEU:HB2	2.01	0.42
1:B:363:ASP:OD1	1:B:448:TYR:CD1	2.73	0.42
1:C:488:LEU:HB2	1:C:490:TYR:HE2	1.85	0.42
1:C:561:PHE:C	1:C:561:PHE:CD2	2.98	0.42
1:D:344:GLY:HA3	1:D:360:LEU:O	2.20	0.42
1:D:503:VAL:HG12	1:D:508:LYS:HE2	2.02	0.42
1:F:527:MET:HG3	1:F:528:ARG:H	1.85	0.42
1:A:495:GLU:CD	1:A:495:GLU:H	2.28	0.41
1:B:279:GLN:O	1:B:282:LYS:HB2	2.20	0.41
1:B:491:VAL:CG2	1:B:498:PHE:HB2	2.50	0.41
1:E:402:ASP:CG	1:E:404:THR:HB	2.44	0.41
1:F:419:CYS:O	1:F:422:ARG:HB2	2.20	0.41
1:F:507:LEU:HD23	1:F:507:LEU:N	2.35	0.41
1:A:530:ARG:NH1	1:A:530:ARG:CG	2.83	0.41
1:D:250:LEU:C	1:D:252:GLU:N	2.77	0.41
1:E:235:GLY:C	1:E:236:VAL:HG23	2.45	0.41
1:G:277:ASP:HB2	1:G:551:ASN:OD1	2.21	0.41
1:A:382:GLN:O	1:A:383:CYS:C	2.62	0.41
1:B:264:GLU:OE2	1:B:264:GLU:HA	2.20	0.41
1:C:282:LYS:HE2	1:C:282:LYS:HB3	1.89	0.41
1:D:440:LEU:HD23	1:D:440:LEU:HA	1.85	0.41
1:D:516:GLU:HG2	1:D:527:MET:CG	2.50	0.41
1:E:250:LEU:O	1:E:251:GLY:C	2.62	0.41
1:E:361:ILE:CG2	1:E:384:ILE:HD13	2.48	0.41
1:E:402:ASP:O	1:E:405:GLN:HG2	2.19	0.41
1:E:545:VAL:O	1:E:549:ILE:HG13	2.19	0.41
1:F:374:ASP:OD2	1:F:447:LYS:HE3	2.20	0.41
1:F:467:VAL:HG21	1:F:469:PHE:HE1	1.81	0.41
1:F:468:ASP:HB2	1:F:537:ASN:ND2	2.36	0.41
1:A:278:LYS:HG2	1:A:557:MET:HE1	2.03	0.41
1:A:286:LEU:HD13	1:D:519:PHE:CE1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:VAL:HG11	1:A:421:SER:HB2	2.01	0.41
1:A:422:ARG:HB3	1:A:562:ILE:HG22	2.01	0.41
1:D:488:LEU:HB2	1:D:490:TYR:CE2	2.55	0.41
1:E:377:PHE:CE2	1:E:381:LEU:HD22	2.56	0.41
1:B:259:GLN:O	1:F:521:ASN:ND2	2.53	0.41
1:B:325:LEU:HD13	1:B:327:PHE:CZ	2.56	0.41
1:B:443:GLN:HA	1:B:444:PRO:HD2	1.82	0.41
1:C:546:CYS:C	1:C:548:SER:H	2.27	0.41
1:D:484:GLN:HG2	1:D:485:ASN:N	2.35	0.41
1:E:321:HIS:HE1	1:E:323:SER:HA	1.86	0.41
1:E:521:ASN:O	1:E:522:ASN:CB	2.69	0.41
1:G:521:ASN:O	1:G:522:ASN:OD1	2.39	0.41
1:A:287:LYS:HA	1:D:498:PHE:O	2.20	0.41
1:A:370:GLN:O	1:A:372:VAL:N	2.53	0.41
1:A:410:VAL:O	1:A:410:VAL:HG12	2.18	0.41
1:B:291:VAL:CG2	1:B:440:LEU:HD13	2.48	0.41
1:C:312:MET:O	1:C:319:VAL:HA	2.20	0.41
1:C:546:CYS:C	1:C:548:SER:N	2.78	0.41
1:E:489:LEU:HD22	1:E:515:ILE:HD11	2.03	0.41
1:G:438:ASP:O	1:G:460:LYS:HG3	2.20	0.41
1:A:543:MET:HE2	1:A:543:MET:HB3	1.89	0.41
1:B:232:PHE:HB2	1:B:320:PHE:CZ	2.54	0.41
1:B:386:ARG:HB2	1:B:386:ARG:HH11	1.84	0.41
1:B:494:TYR:CZ	1:B:496:ARG:HB2	2.55	0.41
1:C:298:THR:HG23	1:C:315:ARG:HH22	1.84	0.41
1:G:467:VAL:CG1	1:G:469:PHE:CE2	3.03	0.41
1:F:311:PHE:HA	1:F:320:PHE:O	2.21	0.41
1:F:377:PHE:HD1	1:F:380:ARG:HH21	1.67	0.41
1:C:377:PHE:CE2	1:C:443:GLN:HG2	2.56	0.41
1:D:247:GLN:N	1:D:248:PRO:HD2	2.36	0.41
1:F:508:LYS:HE3	1:F:508:LYS:HB2	1.70	0.41
1:B:263:TRP:CH2	1:B:451:GLY:HA3	2.55	0.41
1:B:290:LYS:NZ	1:B:417:ASP:HB3	2.36	0.41
1:C:233:LEU:HD11	1:C:348:ILE:HG13	2.03	0.41
1:D:358:ARG:HE	1:D:358:ARG:HB2	1.66	0.41
1:E:325:LEU:HD12	1:E:406:GLU:OE2	2.21	0.41
1:G:276:MET:HG3	1:G:457:LEU:HD13	2.01	0.41
1:G:381:LEU:HD23	1:G:381:LEU:HA	1.91	0.41
1:G:520:GLU:CG	1:G:525:VAL:HG11	2.50	0.41
1:F:279:GLN:O	1:F:282:LYS:HB2	2.21	0.41
1:F:467:VAL:CG1	1:F:545:VAL:HG11	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:HIS:CD2	1:A:436:GLU:H	2.39	0.41
1:A:435:HIS:CE1	1:A:436:GLU:HB2	2.56	0.41
1:B:324:ASN:O	1:B:406:GLU:HG2	2.21	0.41
1:C:325:LEU:HD23	1:C:325:LEU:HA	1.92	0.41
1:D:328:PRO:HG3	1:D:395:LYS:HD2	2.02	0.41
1:D:364:ILE:HG23	1:D:364:ILE:O	2.21	0.41
1:D:498:PHE:CZ	1:D:542:ALA:HB1	2.55	0.41
1:E:358:ARG:HE	1:E:358:ARG:HB2	1.61	0.41
1:E:358:ARG:NH1	1:E:411:ARG:CZ	2.83	0.41
1:E:376:ASP:O	1:E:379:VAL:HB	2.20	0.41
1:E:461:PRO:HA	1:E:462:PRO:HD3	1.95	0.41
1:G:244:VAL:HB	1:G:319:VAL:HG22	2.03	0.41
1:F:274:VAL:HG21	1:F:454:ASP:HA	2.02	0.41
1:F:304:ILE:HB	1:F:340:THR:HB	2.03	0.41
1:F:514:ILE:HD12	1:F:514:ILE:N	2.36	0.41
1:B:499:ALA:HB1	1:B:524:TRP:CD1	2.56	0.40
1:C:498:PHE:CE1	1:C:542:ALA:HB1	2.56	0.40
1:E:333:LEU:O	1:E:395:LYS:HE3	2.20	0.40
1:E:503:VAL:HA	1:E:507:LEU:HD22	2.03	0.40
1:G:494:TYR:HD1	1:G:496:ARG:O	2.04	0.40
1:F:287:LYS:HB2	1:F:288:PRO:HD2	2.03	0.40
1:A:420:THR:O	1:A:420:THR:HG22	2.21	0.40
1:B:406:GLU:HA	1:B:407:PRO:HD3	1.86	0.40
1:C:304:ILE:HD13	1:C:327:PHE:CD2	2.56	0.40
1:C:406:GLU:HA	1:C:407:PRO:HD3	1.67	0.40
1:C:560:GLU:HA	1:C:563:ASP:CB	2.44	0.40
1:D:257:CYS:O	1:D:258:HIS:C	2.64	0.40
1:G:341:LEU:HD23	1:G:365:ILE:CB	2.50	0.40
1:F:329:PHE:CE2	1:F:331:LYS:CG	3.04	0.40
1:F:346:MET:CE	1:F:359:TYR:CD1	3.04	0.40
1:F:526:PHE:CZ	1:F:528:ARG:O	2.75	0.40
1:F:545:VAL:O	1:F:548:SER:HB2	2.22	0.40
1:A:312:MET:C	1:A:313:ILE:HD12	2.47	0.40
1:C:515:ILE:HB	1:C:526:PHE:HE1	1.86	0.40
1:C:555:LYS:H	1:C:555:LYS:HD2	1.87	0.40
1:G:494:TYR:CE2	1:G:539:TYR:CE1	3.09	0.40
1:F:449:LYS:HA	1:F:450:PRO:HD3	1.77	0.40
1:A:319:VAL:HG12	1:A:320:PHE:N	2.37	0.40
1:A:513:LYS:HE2	1:A:529:GLN:HE22	1.87	0.40
1:A:530:ARG:HG3	1:A:532:ASP:OD1	2.22	0.40
1:B:278:LYS:O	1:B:281:ILE:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:ASP:CG	1:B:405:GLN:HG2	2.47	0.40
1:D:368:ASN:O	1:D:369:SER:HB2	2.22	0.40
1:D:449:LYS:HA	1:D:450:PRO:HD2	1.86	0.40
1:G:505:LYS:H	1:G:505:LYS:HG2	1.59	0.40
1:G:510:TYR:CD2	1:G:529:GLN:CD	2.96	0.40
1:F:316:ASP:O	1:F:317:ASN:CB	2.69	0.40
1:F:361:ILE:HG22	1:F:384:ILE:HD13	2.02	0.40
1:F:392:ARG:NH2	1:F:406:GLU:OE1	2.55	0.40
1:A:482:LEU:HD22	1:A:483:PRO:HD2	2.02	0.40
1:B:285:ASP:OD1	1:B:561:PHE:HE2	2.05	0.40
1:B:289:TYR:O	1:B:418:ILE:HG13	2.21	0.40
1:C:402:ASP:OD2	1:C:405:GLN:HG2	2.22	0.40
1:C:564:ARG:HH11	1:F:486:VAL:HG21	1.86	0.40
1:E:367:PHE:O	1:E:368:ASN:HB2	2.21	0.40
1:E:489:LEU:HD11	1:E:501:ILE:HB	2.04	0.40
1:G:377:PHE:CD2	1:G:443:GLN:HG2	2.56	0.40
1:G:459:TRP:CD2	1:G:459:TRP:C	2.98	0.40
1:G:462:PRO:O	1:G:465:ASN:HB2	2.21	0.40
1:G:491:VAL:HG22	1:G:539:TYR:HA	2.03	0.40
1:F:243:GLN:HG2	1:F:244:VAL:N	2.37	0.40
1:F:396:MET:HG3	1:F:401:ILE:CG2	2.52	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	324/347 (93%)	313 (97%)	11 (3%)	0	100	100
1	B	310/347 (89%)	291 (94%)	18 (6%)	1 (0%)	36	68
1	C	308/347 (89%)	296 (96%)	11 (4%)	1 (0%)	36	68
1	D	324/347 (93%)	313 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	325/347 (94%)	308 (95%)	17 (5%)	0	100	100
1	F	329/347 (95%)	312 (95%)	17 (5%)	0	100	100
1	G	325/347 (94%)	307 (94%)	18 (6%)	0	100	100
All	All	2245/2429 (92%)	2140 (95%)	103 (5%)	2 (0%)	48	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	236	VAL
1	C	232	PHE

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	296/313 (95%)	243 (82%)	53 (18%)	2	9
1	B	288/313 (92%)	245 (85%)	43 (15%)	3	14
1	C	286/313 (91%)	257 (90%)	29 (10%)	7	27
1	D	296/313 (95%)	259 (88%)	37 (12%)	4	19
1	E	297/313 (95%)	271 (91%)	26 (9%)	9	33
1	F	294/313 (94%)	266 (90%)	28 (10%)	8	30
1	G	296/313 (95%)	261 (88%)	35 (12%)	5	21
All	All	2053/2191 (94%)	1802 (88%)	251 (12%)	5	20

All (251) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	231	ILE
1	A	233	LEU
1	A	236	VAL
1	A	239	LYS
1	A	250	LEU

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Mol	Chain	Res	Type
1	A	266	SER
1	A	275	SER
1	A	283	LEU
1	A	298	THR
1	A	307	THR
1	A	308	ASN
1	A	322	VAL
1	A	326	GLU
1	A	329	PHE
1	A	335	MET
1	A	348	ILE
1	A	349	ASP
1	A	354	GLN
1	A	356	VAL
1	A	358	ARG
1	A	362	TYR
1	A	369	SER
1	A	378	ASN
1	A	381	LEU
1	A	383	CYS
1	A	385	GLU
1	A	386	ARG
1	A	388	ILE
1	A	389	ILE
1	A	390	SER
1	A	401	ILE
1	A	413	LYS
1	A	416	PHE
1	A	418	ILE
1	A	419	CYS
1	A	441	ILE
1	A	457	LEU
1	A	460	LYS
1	A	463	SER
1	A	471	LEU
1	A	474	THR
1	A	481	LEU
1	A	482	LEU
1	A	503	VAL
1	A	507	LEU
1	A	510	TYR
1	A	514	ILE

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Mol	Chain	Res	Type
1	A	525	VAL
1	A	528	ARG
1	A	530	ARG
1	A	532	ASP
1	A	543	MET
1	A	549	ILE
1	B	231	ILE
1	B	239	LYS
1	B	245	THR
1	B	250	LEU
1	B	264	GLU
1	B	266	SER
1	B	286	LEU
1	B	291	VAL
1	B	293	TRP
1	B	312	MET
1	B	319	VAL
1	B	326	GLU
1	B	338	SER
1	B	348	ILE
1	B	349	ASP
1	B	352	ASN
1	B	356	VAL
1	B	360	LEU
1	B	362	TYR
1	B	368	ASN
1	B	370	GLN
1	B	372	VAL
1	B	378	ASN
1	B	385	GLU
1	B	389	ILE
1	B	390	SER
1	B	396	MET
1	B	398	THR
1	B	409	SER
1	B	416	PHE
1	B	418	ILE
1	B	420	THR
1	B	440	LEU
1	B	441	ILE
1	B	468	ASP
1	B	471	LEU

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Mol	Chain	Res	Type
1	B	489	LEU
1	B	491	VAL
1	B	501	ILE
1	B	523	SER
1	B	529	GLN
1	B	543	MET
1	B	555	LYS
1	C	233	LEU
1	C	237	THR
1	C	253	VAL
1	C	275	SER
1	C	298	THR
1	C	312	MET
1	C	313	ILE
1	C	319	VAL
1	C	323	SER
1	C	326	GLU
1	C	335	MET
1	C	336	HIS
1	C	347	ILE
1	C	362	TYR
1	C	368	ASN
1	C	378	ASN
1	C	390	SER
1	C	416	PHE
1	C	425	LEU
1	C	445	THR
1	C	449	LYS
1	C	457	LEU
1	C	458	LYS
1	C	488	LEU
1	C	505	LYS
1	C	529	GLN
1	C	537	ASN
1	C	541	THR
1	C	548	SER
1	D	239	LYS
1	D	242	THR
1	D	244	VAL
1	D	245	THR
1	D	313	ILE
1	D	316	ASP

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Mol	Chain	Res	Type
1	D	318	SER
1	D	329	PHE
1	D	337	LEU
1	D	351	VAL
1	D	362	TYR
1	D	376	ASP
1	D	379	VAL
1	D	381	LEU
1	D	385	GLU
1	D	389	ILE
1	D	409	SER
1	D	419	CYS
1	D	421	SER
1	D	437	MET
1	D	441	ILE
1	D	449	LYS
1	D	452	ARG
1	D	453	CYS
1	D	464	LEU
1	D	470	ARG
1	D	486	VAL
1	D	488	LEU
1	D	506	GLU
1	D	507	LEU
1	D	518	LYS
1	D	531	THR
1	D	548	SER
1	D	554	THR
1	D	558	LEU
1	D	559	PHE
1	D	564	ARG
1	E	286	LEU
1	E	308	ASN
1	E	309	GLU
1	E	313	ILE
1	E	314	ASP
1	E	362	TYR
1	E	366	LYS
1	E	381	LEU
1	E	385	GLU
1	E	389	ILE
1	E	390	SER

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Mol	Chain	Res	Type
1	E	405	GLN
1	E	411	ARG
1	E	418	ILE
1	E	445	THR
1	E	447	LYS
1	E	464	LEU
1	E	471	LEU
1	E	473	ILE
1	E	514	ILE
1	E	518	LYS
1	E	533	LYS
1	E	543	MET
1	E	556	GLU
1	E	562	ILE
1	E	565	CYS
1	G	231	ILE
1	G	250	LEU
1	G	307	THR
1	G	313	ILE
1	G	317	ASN
1	G	318	SER
1	G	319	VAL
1	G	321	HIS
1	G	362	TYR
1	G	372	VAL
1	G	376	ASP
1	G	378	ASN
1	G	385	GLU
1	G	389	ILE
1	G	405	GLN
1	G	409	SER
1	G	411	ARG
1	G	420	THR
1	G	441	ILE
1	G	445	THR
1	G	452	ARG
1	G	458	LYS
1	G	463	SER
1	G	464	LEU
1	G	466	SER
1	G	476	MET
1	G	489	LEU

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Mol	Chain	Res	Type
1	G	496	ARG
1	G	503	VAL
1	G	522	ASN
1	G	526	PHE
1	G	530	ARG
1	G	532	ASP
1	G	549	ILE
1	G	555	LYS
1	F	237	THR
1	F	239	LYS
1	F	244	VAL
1	F	250	LEU
1	F	293	TRP
1	F	321	HIS
1	F	329	PHE
1	F	347	ILE
1	F	362	TYR
1	F	372	VAL
1	F	378	ASN
1	F	385	GLU
1	F	398	THR
1	F	409	SER
1	F	416	PHE
1	F	425	LEU
1	F	441	ILE
1	F	463	SER
1	F	467	VAL
1	F	471	LEU
1	F	489	LEU
1	F	495	GLU
1	F	504	THR
1	F	507	LEU
1	F	516	GLU
1	F	537	ASN
1	F	539	TYR
1	F	555	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	243	GLN
1	A	280	ASN

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Mol	Chain	Res	Type
1	A	324	ASN
1	A	405	GLN
1	A	412	ASN
1	A	435	HIS
1	A	521	ASN
1	A	537	ASN
1	B	412	ASN
1	C	280	ASN
1	C	368	ASN
1	C	412	ASN
1	C	435	HIS
1	C	443	GLN
1	C	551	ASN
1	D	280	ASN
1	D	512	ASN
1	D	529	GLN
1	E	280	ASN
1	E	393	HIS
1	E	484	GLN
1	E	540	ASN
1	G	280	ASN
1	G	308	ASN
1	G	336	HIS
1	G	435	HIS
1	G	512	ASN
1	G	529	GLN
1	F	280	ASN
1	F	443	GLN
1	F	537	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

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	$\# Z > 2$
2	SO4	A	2	-	4,4,4	0.29	0	6,6,6	0.16	0
2	SO4	A	1	-	4,4,4	0.29	0	6,6,6	0.27	0
2	SO4	B	4	-	4,4,4	0.28	0	6,6,6	0.35	0
2	SO4	A	5	-	4,4,4	0.31	0	6,6,6	0.26	0
2	SO4	A	3	-	4,4,4	0.27	0	6,6,6	0.27	0

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 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5	SO4	3	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	328/347 (94%)	-0.41	0	100	100	28, 51, 102, 136	0
1	B	316/347 (91%)	-0.47	0	100	100	29, 67, 127, 137	0
1	C	314/347 (90%)	-0.45	0	100	100	26, 59, 121, 135	0
1	D	328/347 (94%)	-0.52	0	100	100	28, 55, 112, 143	0
1	E	329/347 (94%)	-0.49	1 (0%)	90	79	22, 58, 128, 144	0
1	F	333/347 (95%)	-0.51	1 (0%)	90	79	23, 52, 119, 148	0
1	G	329/347 (94%)	-0.50	0	100	100	30, 61, 127, 149	0
All	All	2277/2429 (93%)	-0.48	2 (0%)	92	86	22, 57, 123, 149	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	565	CYS	2.3
1	E	230	ALA	2.3

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(Å ²)	Q<0.9
2	SO4	A	1	5/5	0.79	0.14	68,72,86,94	0
2	SO4	B	4	5/5	0.79	0.07	75,79,82,89	0
2	SO4	A	5	5/5	0.86	0.06	72,75,93,93	0
2	SO4	A	2	5/5	0.92	0.10	47,58,60,63	0
2	SO4	A	3	5/5	0.97	0.07	41,46,53,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.