



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2025 – 04:43 PM JST

PDB ID : 8Z96
Title : Crystal structure of CrtAgo/TIR-APAZ in complex with guide DNA and 21-nt target DNA
Authors : Hu, R.; Chen, J.; Liu, L.
Deposited on : 2024-04-22
Resolution : 3.36 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	:	4.02b-467
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.2

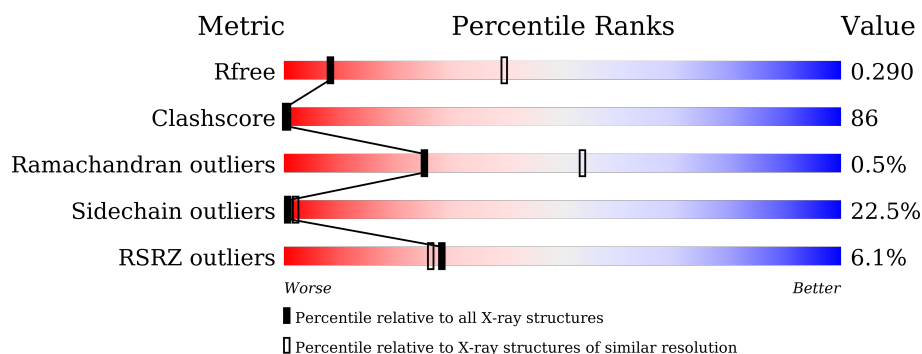
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.36 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}	164625	1012 (3.40-3.32)
Clashscore	180529	1035 (3.40-3.32)
Ramachandran outliers	177936	1037 (3.40-3.32)
Sidechain outliers	177891	1037 (3.40-3.32)
RSRZ outliers	164620	1012 (3.40-3.32)

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	507	<div> <div>4%</div> <div>25%</div> <div>52%</div> <div>16%</div> <div>7%</div> </div>
2	B	421	<div> <div>8%</div> <div>22%</div> <div>58%</div> <div>19%</div> </div>
3	C	21	<div> <div>5%</div> <div>67%</div> <div>29%</div> </div>
4	D	21	<div> <div>5%</div> <div>76%</div> <div>19%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8163 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 Piwi domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	0	0
			3827	2479	636	700	12			

- Molecule 2 is a protein called TIR domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	419	Total	C	N	O	S	0	0	0
			3452	2239	579	623	11			

- Molecule 3 is a DNA chain called DNA (5'-D(P*TP*GP*AP*GP*GP*TP*AP*GP*TP*AP*GP*GP*TP*TP*GP*TP*AP*TP*AP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	21	Total	C	N	O	P	0	0	0
			442	210	81	130	21			

- Molecule 4 is a DNA chain called DNA (5'-D(*CP*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*CP*TP*CP*AP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	21	Total	C	N	O	P	0	0	0
			416	202	71	123	20			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Mg	0	0
			1	1		

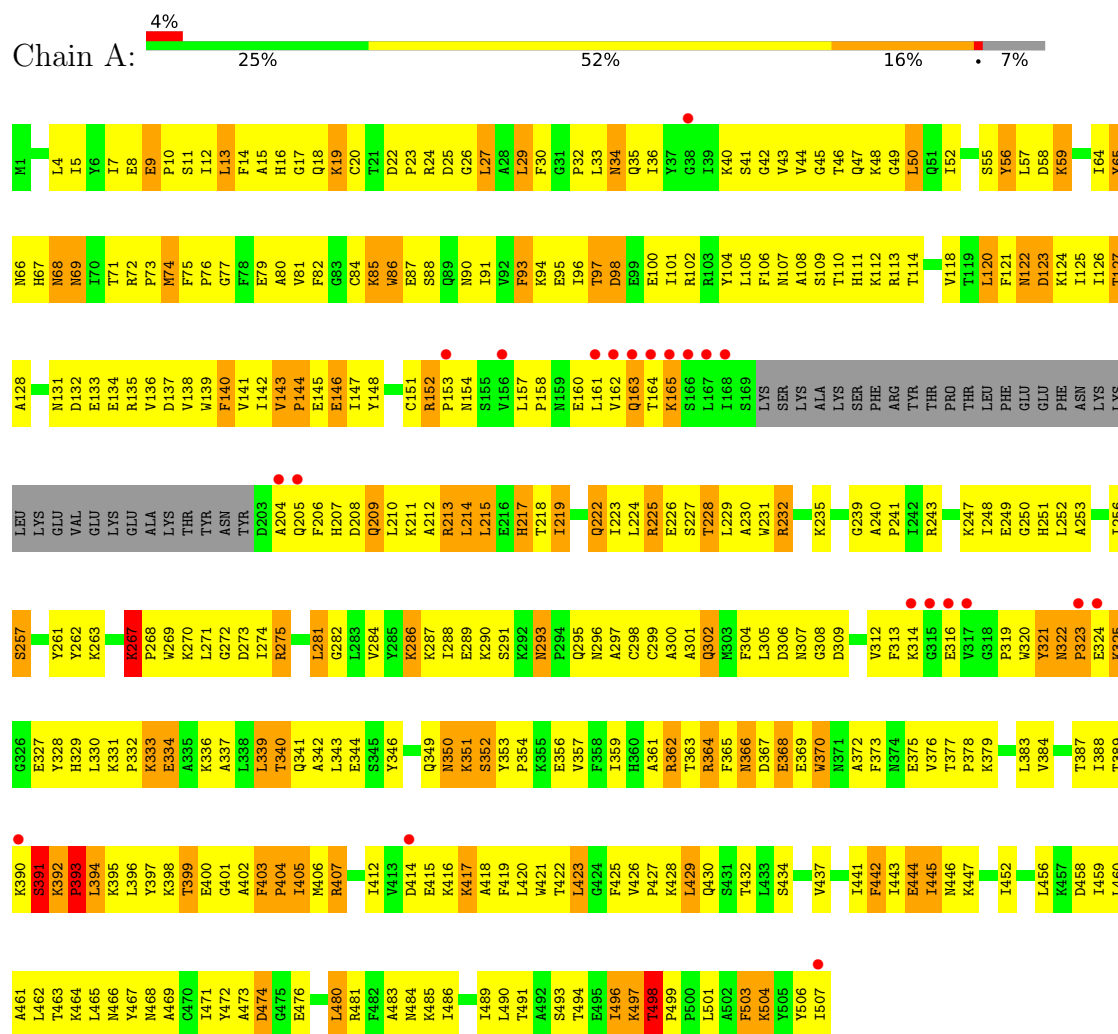
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	13	Total 13	O 13	0	0
6	B	10	Total 10	O 10	0	0
6	C	2	Total 2	O 2	0	0

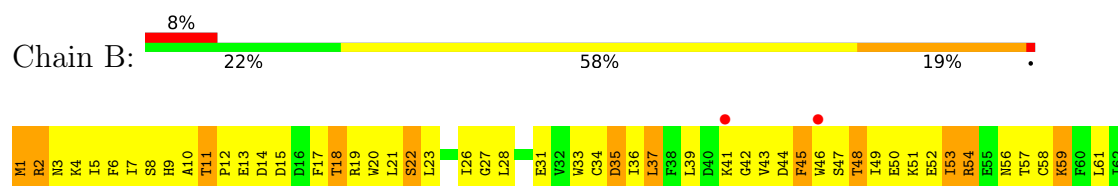
3 Residue-property plots

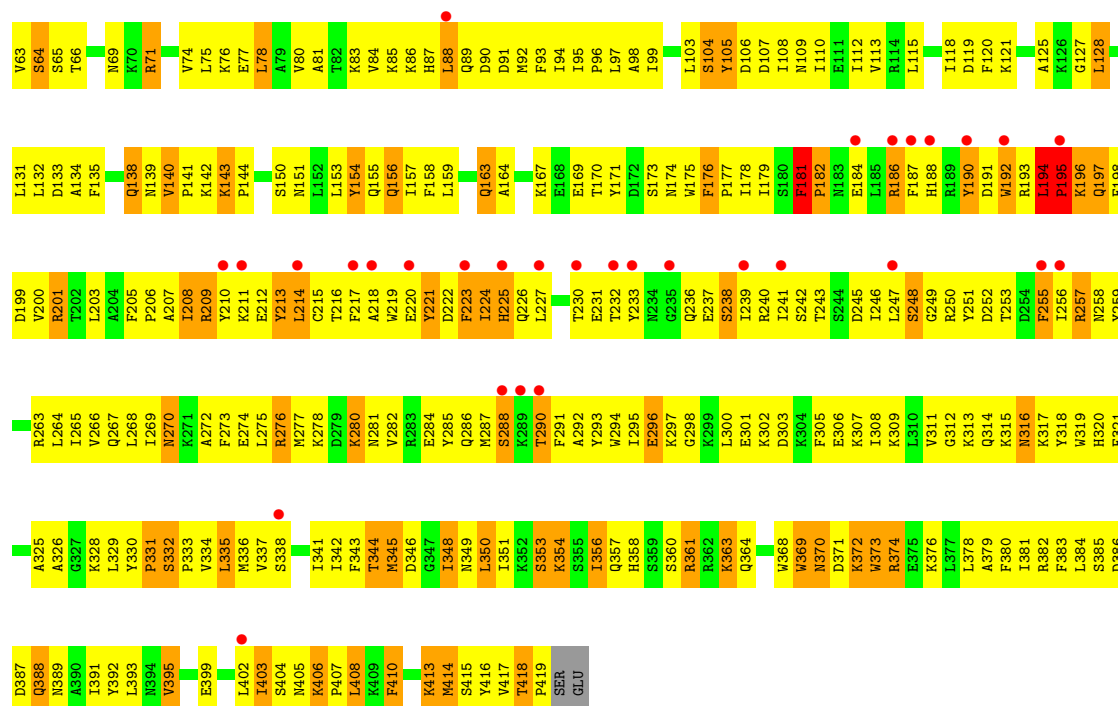
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Piwi domain-containing protein

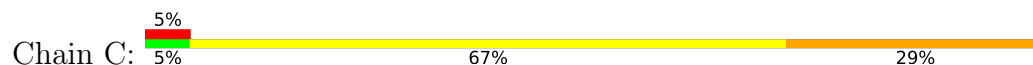


• Molecule 2: TIR domain-containing protein

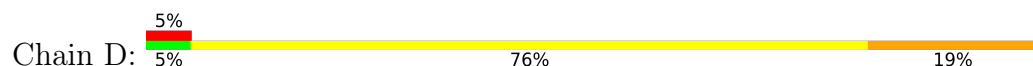




● Molecule 3: DNA (5'-D(P*TP*GP*AP*GP*GP*TP*AP*GP*TP*AP*GP*GP*TP*TP*GP*T
P*AP*TP*AP*GP*T)-3')



● Molecule 4: DNA (5'-D(*CP*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*
CP*TP*CP*AP*T)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.57Å 133.57Å 167.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.68 – 3.36 20.68 – 3.36	Depositor EDS
% Data completeness (in resolution range)	89.0 (20.68-3.36) 88.6 (20.68-3.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.20 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.247 , 0.287 0.247 , 0.290	Depositor DCC
R_{free} test set	1162 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.047 for -h,-k,l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	8163	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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: MG

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	0.83	7/3923 (0.2%)	0.84	19/5313 (0.4%)
2	B	0.67	3/3539 (0.1%)	0.78	13/4780 (0.3%)
3	C	1.48	6/496 (1.2%)	1.19	2/765 (0.3%)
4	D	1.22	4/464 (0.9%)	1.02	1/711 (0.1%)
All	All	0.85	20/8422 (0.2%)	0.86	35/11569 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	DT	OP3-P	-13.25	1.45	1.61
3	C	19	DA	C1'-N9	-12.20	1.30	1.47
1	A	86	TRP	CA-CB	-8.40	1.35	1.53
4	D	9	DC	C1'-N1	7.89	1.59	1.49
1	A	86	TRP	CB-CG	-6.83	1.38	1.50
3	C	1	DT	O3'-P	-6.65	1.53	1.61
4	D	5	DA	C3'-O3'	6.29	1.52	1.44
4	D	7	DA	N9-C4	-6.01	1.34	1.37
3	C	17	DA	C1'-N9	-5.95	1.39	1.47
3	C	17	DA	C3'-O3'	-5.71	1.36	1.44
1	A	151	CYS	CB-SG	-5.38	1.73	1.81
2	B	331	PRO	N-CD	5.37	1.55	1.47
2	B	182	PRO	N-CD	5.36	1.55	1.47
1	A	323	PRO	N-CD	5.36	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	16	DT	C3'-O3'	-5.34	1.37	1.44
1	A	499	PRO	N-CD	5.28	1.55	1.47
4	D	7	DA	C3'-O3'	-5.28	1.37	1.44
1	A	378	PRO	N-CD	5.14	1.55	1.47
2	B	141	PRO	N-CD	5.11	1.55	1.47
1	A	144	PRO	N-CD	5.02	1.54	1.47

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	391	SER	N-CA-C	-7.85	89.82	111.00
3	C	8	DG	O4'-C4'-C3'	-7.73	101.36	106.00
1	A	392	LYS	C-N-CD	6.38	141.79	128.40
1	A	219	ILE	C-N-CD	6.27	141.57	128.40
2	B	194	LEU	C-N-CD	6.22	141.45	128.40
1	A	403	PHE	C-N-CD	6.18	141.39	128.40
1	A	293	ASN	C-N-CD	6.15	141.31	128.40
2	B	176	PHE	C-N-CD	6.02	141.04	128.40
2	B	144	PRO	C-N-CD	5.98	140.96	128.40
1	A	267	LYS	C-N-CD	5.97	140.95	128.40
2	B	143	LYS	C-N-CD	5.92	140.82	128.40
1	A	240	ALA	C-N-CD	5.87	140.72	128.40
1	A	499	PRO	C-N-CD	5.86	140.70	128.40
1	A	429	LEU	CA-CB-CG	-5.85	101.84	115.30
1	A	143	VAL	C-N-CD	5.83	140.65	128.40
1	A	393	PRO	CA-N-CD	-5.82	103.36	111.50
1	A	152	ARG	C-N-CD	5.80	140.58	128.40
2	B	332	SER	C-N-CD	5.78	140.53	128.40
2	B	140	VAL	C-N-CD	5.75	140.48	128.40
1	A	331	LYS	C-N-CD	5.74	140.45	128.40
2	B	418	THR	C-N-CD	5.67	140.31	128.40
2	B	156	GLN	CB-CA-C	5.57	121.54	110.40
1	A	377	THR	C-N-CD	5.57	140.09	128.40
1	A	498	THR	C-N-CD	5.53	140.02	128.40
1	A	9	GLU	C-N-CD	5.53	140.01	128.40
2	B	335	LEU	CA-CB-CG	-5.52	102.61	115.30
1	A	322	ASN	C-N-CD	5.51	139.97	128.40
3	C	5	DG	O4'-C1'-N9	5.50	111.85	108.00
2	B	181	PHE	C-N-CD	5.45	139.84	128.40
2	B	12	PRO	CA-N-CD	-5.36	103.99	111.50
1	A	29	LEU	CA-CB-CG	-5.35	103.00	115.30
2	B	11	THR	C-N-CD	5.33	139.59	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	404	PRO	CA-N-CD	-5.26	104.14	111.50
4	D	12	DA	O4'-C4'-C3'	-5.20	102.42	104.50
2	B	195	PRO	CA-N-CD	-5.06	104.41	111.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	201	ARG	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	3827	0	3844	590	2
2	B	3452	0	3414	684	3
3	C	442	0	240	84	0
4	D	416	0	239	112	0
5	D	1	0	0	0	0
6	A	13	0	0	2	0
6	B	10	0	0	0	0
6	C	2	0	0	0	0
All	All	8163	0	7737	1358	3

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 86.

All (1358) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:HIS:CE1	4:D:20:DA:C2	1.89	1.57
2:B:393:LEU:HD11	2:B:403:ILE:CD1	1.26	1.57
2:B:178:ILE:HD13	2:B:403:ILE:CG2	1.44	1.47
2:B:225:HIS:CD2	2:B:226:GLN:HG3	1.52	1.45
1:A:267:LYS:NZ	1:A:307:ASN:CB	1.78	1.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:105:TYR:CE1	2:B:113:VAL:HG11	1.54	1.42
2:B:178:ILE:CD1	2:B:403:ILE:CG2	1.97	1.42
1:A:225:ARG:HH22	1:A:243:ARG:NH1	1.21	1.39
2:B:175:TRP:O	2:B:408:LEU:CD1	1.73	1.34
2:B:225:HIS:HD2	2:B:226:GLN:CG	1.40	1.33
2:B:393:LEU:CD1	2:B:403:ILE:HD11	1.61	1.31
2:B:108:ILE:CG2	2:B:113:VAL:HG22	1.60	1.30
2:B:151:ASN:ND2	2:B:155:GLN:OE1	1.61	1.30
2:B:49:ILE:O	2:B:53:ILE:HG13	1.27	1.30
2:B:108:ILE:HG22	2:B:113:VAL:CG2	1.60	1.30
2:B:188:HIS:CA	2:B:238:SER:OG	1.78	1.29
1:A:207:HIS:HE1	4:D:20:DA:C2	1.33	1.29
2:B:208:ILE:CD1	2:B:268:LEU:HD21	1.63	1.27
2:B:276:ARG:NH2	2:B:386:ASP:OD2	1.67	1.25
2:B:288:SER:OG	4:D:13:DC:H5'	1.09	1.25
1:A:468:ASN:HD21	1:A:507:ILE:CD1	1.49	1.24
2:B:294:TRP:HZ3	2:B:320:HIS:CE1	1.55	1.24
1:A:288:ILE:HB	1:A:296:ASN:O	1.34	1.23
2:B:11:THR:HG22	2:B:15:ASP:OD1	1.14	1.23
2:B:120:PHE:HE1	2:B:127:GLY:C	1.40	1.23
2:B:393:LEU:CD1	2:B:403:ILE:CD1	2.15	1.22
2:B:120:PHE:CD1	2:B:127:GLY:HA3	1.74	1.21
2:B:96:PRO:O	2:B:118:ILE:HG22	1.40	1.20
2:B:276:ARG:HD3	2:B:392:TYR:O	1.36	1.20
1:A:59:LYS:NZ	1:A:249:GLU:OE1	1.72	1.19
1:A:225:ARG:NH2	1:A:243:ARG:NH1	1.93	1.17
2:B:225:HIS:CD2	2:B:226:GLN:CG	2.21	1.17
1:A:468:ASN:ND2	1:A:507:ILE:HD13	1.57	1.17
2:B:209:ARG:HH21	2:B:209:ARG:HB3	1.08	1.17
2:B:187:PHE:O	2:B:238:SER:CB	1.93	1.16
2:B:178:ILE:HD12	2:B:403:ILE:HG23	1.20	1.16
2:B:49:ILE:HG22	2:B:53:ILE:HD11	1.19	1.16
2:B:208:ILE:CD1	2:B:268:LEU:CD2	2.23	1.16
1:A:390:LYS:CE	1:A:476:GLU:HG3	1.77	1.15
1:A:390:LYS:HG2	1:A:441:ILE:HG22	1.19	1.15
2:B:188:HIS:HA	2:B:238:SER:OG	0.99	1.15
1:A:288:ILE:CB	1:A:296:ASN:O	1.94	1.14
2:B:208:ILE:HD11	2:B:268:LEU:CD2	1.75	1.14
2:B:105:TYR:CE1	2:B:113:VAL:CG1	2.28	1.14
2:B:288:SER:OG	4:D:13:DC:C5'	1.93	1.14
1:A:366:ASN:HD21	1:A:369:GLU:CB	1.62	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:294:TRP:CZ3	2:B:320:HIS:ND1	2.17	1.13
1:A:393:PRO:HG2	1:A:419:PHE:HE1	1.10	1.12
2:B:178:ILE:HD13	2:B:403:ILE:HG22	1.19	1.11
4:D:17:DC:H2''	4:D:18:DT:H5''	1.27	1.11
1:A:362:ARG:NH2	1:A:476:GLU:OE2	1.82	1.11
1:A:405:ILE:HD11	1:A:421:TRP:NE1	1.65	1.11
2:B:276:ARG:CD	2:B:392:TYR:O	1.97	1.11
2:B:294:TRP:HZ3	2:B:320:HIS:ND1	1.48	1.11
2:B:328:LYS:HD2	2:B:336:MET:HE3	1.26	1.11
2:B:210:TYR:OH	2:B:256:ILE:CG2	1.98	1.11
1:A:267:LYS:NZ	1:A:307:ASN:HB2	1.48	1.10
2:B:19:ARG:HG3	2:B:158:PHE:HE2	1.11	1.10
1:A:262:TYR:OH	1:A:309:ASP:OD1	1.65	1.10
2:B:296:GLU:OE1	2:B:348:ILE:HG21	1.47	1.09
2:B:19:ARG:HG3	2:B:158:PHE:CE2	1.88	1.09
2:B:187:PHE:O	2:B:238:SER:OG	1.66	1.09
2:B:320:HIS:NE2	2:B:344:THR:OG1	1.84	1.08
2:B:44:ASP:O	2:B:47:SER:N	1.87	1.08
2:B:199:ASP:OD1	2:B:201:ARG:NH2	1.86	1.08
2:B:175:TRP:O	2:B:408:LEU:HD11	1.46	1.08
2:B:178:ILE:CD1	2:B:403:ILE:HG23	1.70	1.08
1:A:207:HIS:ND1	4:D:20:DA:C2	2.21	1.08
1:A:366:ASN:ND2	1:A:369:GLU:HB3	1.67	1.08
4:D:20:DA:H4'	4:D:21:DT:OP2	1.49	1.07
4:D:19:DC:H5''	4:D:19:DC:H6	1.15	1.07
2:B:190:TYR:HE2	2:B:227:LEU:HD11	1.09	1.07
2:B:135:PHE:O	2:B:138:GLN:O	1.70	1.06
2:B:163:GLN:OE1	2:B:164:ALA:N	1.88	1.06
3:C:17:DA:N6	4:D:3:DA:N6	2.03	1.06
1:A:267:LYS:NZ	1:A:307:ASN:HB3	1.49	1.06
1:A:268:PRO:HD2	1:A:467:TYR:CD1	1.90	1.06
1:A:133:GLU:OE1	1:A:133:GLU:N	1.88	1.06
2:B:175:TRP:O	2:B:408:LEU:HD12	1.51	1.06
2:B:119:ASP:OD2	2:B:121:LYS:NZ	1.88	1.05
2:B:267:GLN:OE1	2:B:267:GLN:N	1.88	1.05
1:A:322:ASN:OD1	1:A:325:LYS:N	1.88	1.05
2:B:249:GLY:HA2	2:B:258:ASN:HD22	1.11	1.05
2:B:343:PHE:HB2	2:B:357:GLN:HE21	1.17	1.05
2:B:408:LEU:HD12	2:B:408:LEU:H	1.18	1.05
3:C:19:DA:N6	4:D:2:DT:O4	1.90	1.04
1:A:10:PRO:HG3	1:A:461:ALA:HA	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:GLU:OE2	1:A:329:HIS:NE2	1.89	1.04
2:B:266:VAL:O	2:B:270:ASN:ND2	1.88	1.04
2:B:378:LEU:O	2:B:382:ARG:HG3	1.56	1.04
2:B:294:TRP:CE3	2:B:320:HIS:CG	2.46	1.03
2:B:354:LYS:H	2:B:354:LYS:HD2	1.20	1.03
2:B:37:LEU:H	2:B:37:LEU:HD22	1.23	1.02
2:B:203:LEU:HD12	2:B:223:PHE:HD1	1.21	1.02
2:B:200:VAL:O	2:B:203:LEU:HB2	1.57	1.02
2:B:294:TRP:CZ3	2:B:320:HIS:CE1	2.47	1.02
1:A:366:ASN:ND2	1:A:369:GLU:CB	2.22	1.02
2:B:120:PHE:CE1	2:B:127:GLY:C	2.33	1.02
2:B:266:VAL:CG2	2:B:329:LEU:HD21	1.90	1.01
2:B:286:GLN:HG3	2:B:291:PHE:CE1	1.95	1.01
2:B:108:ILE:HG22	2:B:113:VAL:HG22	1.24	1.01
2:B:108:ILE:HG22	2:B:113:VAL:HG23	1.39	1.01
2:B:109:ASN:O	2:B:113:VAL:HG23	1.59	1.01
1:A:366:ASN:HD21	1:A:369:GLU:HB2	1.22	1.01
2:B:219:TRP:HB3	2:B:221:TYR:CE2	1.96	1.01
2:B:120:PHE:CE1	2:B:127:GLY:HA3	1.95	1.00
2:B:236:GLN:N	2:B:236:GLN:OE1	1.94	1.00
2:B:255:PHE:CD2	2:B:256:ILE:HG23	1.95	1.00
1:A:9:GLU:OE1	1:A:464:LYS:NZ	1.93	1.00
4:D:17:DC:H2''	4:D:18:DT:C5'	1.90	1.00
2:B:178:ILE:CD1	2:B:403:ILE:HG21	1.89	0.99
2:B:197:GLN:O	2:B:197:GLN:NE2	1.95	0.99
1:A:18:GLN:OE1	2:B:151:ASN:OD1	1.80	0.99
1:A:390:LYS:HE3	1:A:476:GLU:HG3	1.40	0.99
2:B:49:ILE:CG2	2:B:53:ILE:HD11	1.91	0.99
1:A:288:ILE:CG1	1:A:296:ASN:O	2.11	0.99
2:B:17:PHE:CZ	2:B:120:PHE:CD2	2.49	0.99
2:B:105:TYR:HE1	2:B:113:VAL:HG11	0.89	0.99
2:B:11:THR:CG2	2:B:15:ASP:OD1	2.10	0.98
2:B:4:LYS:NZ	2:B:52:GLU:OE1	1.97	0.98
2:B:88:LEU:HD11	2:B:90:ASP:HB3	1.45	0.98
2:B:200:VAL:O	2:B:203:LEU:N	1.96	0.98
1:A:211:LYS:HD3	1:A:507:ILE:O	1.63	0.98
2:B:96:PRO:O	2:B:118:ILE:CG2	2.10	0.98
1:A:284:VAL:CG2	1:A:302:GLN:NE2	2.26	0.97
2:B:120:PHE:HD1	2:B:127:GLY:HA3	1.25	0.97
2:B:211:LYS:HG2	2:B:212:GLU:H	1.28	0.97
2:B:210:TYR:OH	2:B:256:ILE:HG22	1.61	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:LYS:HG2	1:A:441:ILE:CG2	1.94	0.97
1:A:393:PRO:HG2	1:A:419:PHE:CE1	2.00	0.97
2:B:88:LEU:CD1	2:B:90:ASP:HB3	1.95	0.97
1:A:225:ARG:HH22	1:A:243:ARG:HH12	1.08	0.96
1:A:484:ASN:OD1	3:C:7:DA:OP1	1.83	0.96
1:A:52:ILE:HD12	1:A:226:GLU:HG2	1.45	0.96
1:A:323:PRO:HB2	4:D:9:DC:P	2.05	0.96
3:C:11:DG:H22	4:D:11:DT:H3	1.14	0.95
1:A:405:ILE:CD1	1:A:421:TRP:NE1	2.30	0.95
1:A:42:GLY:N	1:A:136:VAL:HG11	1.82	0.95
1:A:40:LYS:HG3	1:A:90:ASN:HD21	1.29	0.95
2:B:251:TYR:OH	2:B:256:ILE:HD11	1.66	0.95
2:B:294:TRP:HE3	2:B:320:HIS:CB	1.80	0.95
2:B:49:ILE:O	2:B:53:ILE:CG1	2.14	0.95
2:B:120:PHE:CE1	2:B:127:GLY:CA	2.50	0.95
2:B:190:TYR:CE2	2:B:227:LEU:HD11	2.02	0.95
1:A:336:LYS:O	1:A:340:THR:OG1	1.85	0.95
2:B:246:ILE:O	2:B:258:ASN:ND2	2.00	0.94
2:B:286:GLN:HG3	2:B:291:PHE:HE1	1.29	0.94
2:B:220:GLU:OE2	2:B:220:GLU:N	2.00	0.94
1:A:267:LYS:HZ2	1:A:307:ASN:CB	1.52	0.94
2:B:97:LEU:HA	2:B:118:ILE:CG2	1.98	0.94
2:B:300:LEU:HD22	2:B:305:PHE:HB2	1.48	0.94
3:C:17:DA:C6	4:D:3:DA:N6	2.36	0.94
1:A:123:ASP:O	1:A:127:THR:OG1	1.85	0.94
2:B:112:ILE:HA	2:B:115:LEU:HD12	1.46	0.94
2:B:210:TYR:OH	2:B:256:ILE:HG21	1.66	0.93
2:B:81:ALA:O	2:B:85:LYS:N	2.01	0.93
3:C:14:DT:H3	4:D:7:DA:H61	1.15	0.93
2:B:247:LEU:HD12	2:B:248:SER:N	1.84	0.93
1:A:349:GLN:HB3	1:A:350:ASN:ND2	1.82	0.93
2:B:17:PHE:HZ	2:B:120:PHE:CE2	1.86	0.93
2:B:208:ILE:HD11	2:B:268:LEU:HD21	0.95	0.93
2:B:219:TRP:N	2:B:222:ASP:OD2	2.01	0.93
2:B:306:GLU:O	2:B:307:LYS:HG2	1.69	0.92
2:B:253:THR:OG1	2:B:256:ILE:O	1.85	0.92
1:A:72:ARG:NH2	3:C:1:DT:OP2	2.03	0.92
2:B:255:PHE:CE2	2:B:256:ILE:HG23	2.03	0.92
1:A:404:PRO:O	2:B:416:TYR:OH	1.86	0.92
2:B:14:ASP:O	2:B:18:THR:OG1	1.85	0.92
2:B:17:PHE:HZ	2:B:120:PHE:CD2	1.86	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:88:LEU:CG	2:B:90:ASP:HB3	1.98	0.92
2:B:206:PRO:HG3	2:B:395:VAL:HG12	1.49	0.92
1:A:267:LYS:HZ1	1:A:307:ASN:HB3	1.09	0.92
1:A:501:LEU:HD13	1:A:506:TYR:HE2	1.32	0.91
2:B:190:TYR:HE2	2:B:227:LEU:CD1	1.84	0.91
1:A:388:ILE:HD12	1:A:480:LEU:HD11	1.53	0.91
1:A:468:ASN:HD21	1:A:507:ILE:HD13	0.75	0.91
3:C:2:DG:O6	4:D:18:DT:C7	2.19	0.91
1:A:275:ARG:NH2	1:A:356:GLU:OE2	2.04	0.91
1:A:390:LYS:CE	1:A:476:GLU:CG	2.47	0.91
1:A:225:ARG:HH22	1:A:243:ARG:HH11	1.18	0.90
1:A:295:GLN:HG2	1:A:321:TYR:O	1.71	0.90
2:B:187:PHE:O	2:B:238:SER:HB3	1.71	0.90
2:B:296:GLU:HB3	2:B:348:ILE:HG22	1.52	0.90
2:B:294:TRP:CZ3	2:B:320:HIS:CG	2.59	0.90
2:B:81:ALA:CB	2:B:94:ILE:HD11	2.01	0.90
2:B:296:GLU:OE1	2:B:348:ILE:CG2	2.19	0.90
1:A:507:ILE:HG22	1:A:507:ILE:OXT	1.72	0.90
2:B:249:GLY:HA2	2:B:258:ASN:ND2	1.86	0.90
2:B:285:TYR:N	2:B:292:ALA:O	2.05	0.89
2:B:233:TYR:CZ	2:B:237:GLU:HB3	2.07	0.89
2:B:315:LYS:HD3	2:B:316:ASN:HD21	1.36	0.89
1:A:207:HIS:HE1	4:D:20:DA:H2	1.00	0.89
2:B:49:ILE:HG22	2:B:53:ILE:CD1	2.01	0.89
1:A:207:HIS:CE1	4:D:20:DA:N1	2.40	0.89
2:B:276:ARG:NE	2:B:392:TYR:O	2.06	0.89
1:A:399:THR:OG1	2:B:170:THR:O	1.89	0.88
2:B:225:HIS:HD2	2:B:226:GLN:HG3	0.72	0.88
1:A:12:ILE:HG13	1:A:14:PHE:CZ	2.09	0.88
2:B:344:THR:HG22	2:B:349:ASN:O	1.73	0.88
2:B:393:LEU:HD11	2:B:403:ILE:HD13	1.52	0.87
2:B:108:ILE:CG2	2:B:113:VAL:CG2	2.32	0.87
1:A:323:PRO:HB2	4:D:9:DC:OP2	1.75	0.87
3:C:5:DG:C2'	3:C:6:DT:H72	2.04	0.87
1:A:13:LEU:HD13	1:A:17:GLY:HA2	1.55	0.87
1:A:268:PRO:HD2	1:A:467:TYR:CE1	2.11	0.86
3:C:11:DG:N2	4:D:11:DT:O2	2.09	0.86
4:D:19:DC:H5''	4:D:19:DC:C6	2.08	0.86
1:A:144:PRO:HD2	1:A:147:ILE:CD1	2.05	0.85
1:A:267:LYS:HZ2	1:A:307:ASN:HB2	1.07	0.85
1:A:405:ILE:CD1	1:A:421:TRP:CD1	2.60	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:330:TYR:CG	2:B:331:PRO:HA	2.11	0.85
4:D:10:DC:H2"	4:D:11:DT:OP2	1.73	0.85
1:A:152:ARG:HG3	1:A:152:ARG:HH11	1.40	0.85
2:B:14:ASP:OD2	2:B:63:VAL:HG11	1.75	0.85
2:B:66:THR:HA	2:B:103:LEU:HD11	1.59	0.85
2:B:294:TRP:HB3	2:B:342:ILE:HG13	1.59	0.85
2:B:332:SER:O	2:B:334:VAL:HG13	1.77	0.85
2:B:28:LEU:O	2:B:142:LYS:HE3	1.77	0.84
1:A:122:ASN:O	1:A:126:ILE:N	2.09	0.84
1:A:153:PRO:HG3	1:A:204:ALA:HB3	1.57	0.84
2:B:353:SER:O	2:B:356:ILE:HD12	1.77	0.84
2:B:9:HIS:CB	2:B:18:THR:HG21	2.06	0.84
1:A:120:LEU:O	1:A:120:LEU:HD12	1.76	0.84
1:A:66:ASN:ND2	1:A:250:GLY:HA3	1.92	0.84
2:B:22:SER:O	2:B:26:ILE:HG13	1.78	0.84
2:B:209:ARG:HB3	2:B:209:ARG:NH2	1.91	0.84
2:B:9:HIS:CG	2:B:18:THR:HG21	2.13	0.83
2:B:294:TRP:CE3	2:B:320:HIS:CB	2.61	0.83
2:B:88:LEU:CD2	2:B:90:ASP:H	1.91	0.83
2:B:328:LYS:HD2	2:B:336:MET:CE	2.05	0.83
1:A:346:TYR:CD2	1:A:354:PRO:HD3	2.12	0.83
4:D:2:DT:H1'	4:D:3:DA:C8	2.13	0.83
1:A:68:ASN:OD1	1:A:71:THR:OG1	1.96	0.83
1:A:105:LEU:O	1:A:113:ARG:HD3	1.79	0.83
1:A:74:MET:HE2	1:A:76:PRO:N	1.94	0.83
2:B:66:THR:OG1	2:B:103:LEU:CD1	2.27	0.83
1:A:468:ASN:OD1	1:A:507:ILE:HG21	1.79	0.82
1:A:481:ARG:HH12	4:D:19:DC:P	2.01	0.82
2:B:208:ILE:CD1	2:B:268:LEU:HD23	2.08	0.82
2:B:251:TYR:OH	2:B:256:ILE:CD1	2.27	0.82
1:A:443:ILE:HD12	1:A:456:LEU:CD2	2.10	0.82
1:A:94:LYS:NZ	1:A:124:LYS:HZ3	1.77	0.82
2:B:97:LEU:HD23	2:B:118:ILE:HG21	1.62	0.82
1:A:207:HIS:CE1	4:D:20:DA:N3	2.47	0.82
1:A:74:MET:CE	1:A:75:PHE:C	2.47	0.81
1:A:393:PRO:CG	1:A:419:PHE:HE1	1.92	0.81
1:A:94:LYS:HD2	1:A:124:LYS:HD3	1.60	0.81
2:B:52:GLU:O	2:B:57:THR:OG1	1.99	0.81
1:A:390:LYS:HE2	1:A:476:GLU:CG	2.10	0.81
2:B:54:ARG:HH11	2:B:54:ARG:HG3	1.46	0.81
1:A:316:GLU:OE2	1:A:497:LYS:HD3	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:SER:CB	2:B:77:GLU:OE1	2.29	0.81
2:B:7:ILE:CD1	2:B:21:LEU:HD23	2.11	0.81
2:B:88:LEU:HD21	2:B:90:ASP:O	1.81	0.81
2:B:28:LEU:O	2:B:142:LYS:CE	2.29	0.81
2:B:128:LEU:O	2:B:132:LEU:HG	1.81	0.80
1:A:323:PRO:CB	4:D:9:DC:OP2	2.30	0.80
2:B:176:PHE:CD1	2:B:407:PRO:CA	2.54	0.80
1:A:248:ILE:CD1	3:C:1:DT:C2	2.64	0.80
1:A:108:ALA:HB2	1:A:162:VAL:HG11	1.63	0.80
2:B:187:PHE:C	2:B:238:SER:OG	2.19	0.80
1:A:86:TRP:HZ2	1:A:140:PHE:CE1	2.00	0.80
2:B:294:TRP:CE3	2:B:320:HIS:ND1	2.48	0.80
1:A:405:ILE:HD12	1:A:421:TRP:CD1	2.16	0.80
2:B:208:ILE:HD13	2:B:268:LEU:CD2	2.11	0.80
1:A:74:MET:HE2	1:A:75:PHE:C	2.02	0.80
2:B:203:LEU:HD12	2:B:223:PHE:CD1	2.14	0.79
2:B:214:LEU:HD13	2:B:215:CYS:H	1.46	0.79
1:A:225:ARG:NH2	1:A:243:ARG:HH11	1.73	0.79
2:B:151:ASN:CG	2:B:155:GLN:OE1	2.21	0.79
2:B:343:PHE:HB2	2:B:357:GLN:NE2	1.95	0.79
2:B:8:SER:OG	2:B:77:GLU:OE1	1.99	0.79
1:A:351:LYS:N	1:A:351:LYS:HD2	1.94	0.79
1:A:390:LYS:HE3	1:A:476:GLU:CG	2.09	0.79
2:B:242:SER:O	2:B:246:ILE:CD1	2.31	0.79
2:B:330:TYR:CD2	2:B:331:PRO:HA	2.18	0.79
1:A:252:LEU:O	1:A:256:ILE:HG13	1.83	0.79
4:D:19:DC:H6	4:D:19:DC:C5'	1.95	0.79
1:A:284:VAL:HG23	1:A:302:GLN:NE2	1.94	0.78
1:A:66:ASN:ND2	1:A:250:GLY:CA	2.47	0.78
2:B:120:PHE:HE1	2:B:127:GLY:CA	1.89	0.78
2:B:219:TRP:HB3	2:B:221:TYR:CD2	2.17	0.78
1:A:43:VAL:HG23	1:A:91:ILE:CG2	2.14	0.78
1:A:391:SER:O	1:A:393:PRO:HD3	1.82	0.78
1:A:40:LYS:HD3	1:A:135:ARG:O	1.83	0.78
2:B:66:THR:OG1	2:B:103:LEU:HD12	1.83	0.78
2:B:345:MET:HG2	2:B:351:ILE:CD1	2.14	0.78
1:A:364:ARG:HG3	1:A:364:ARG:HH11	1.47	0.77
3:C:5:DG:H2''	3:C:6:DT:C7	2.15	0.77
2:B:341:ILE:HD13	2:B:364:GLN:HG3	1.66	0.77
1:A:493:SER:O	1:A:496:ILE:HD11	1.83	0.77
3:C:5:DG:H2'	3:C:6:DT:H72	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:17:PHE:CZ	2:B:120:PHE:HD2	1.98	0.77
2:B:45:PHE:CD1	2:B:46:TRP:N	2.53	0.77
2:B:108:ILE:HG21	2:B:113:VAL:HG22	1.66	0.77
1:A:132:ASP:OD2	1:A:134:GLU:HB2	1.85	0.77
1:A:484:ASN:CG	3:C:7:DA:OP1	2.21	0.77
2:B:200:VAL:O	2:B:203:LEU:CB	2.33	0.77
2:B:242:SER:O	2:B:246:ILE:HD11	1.85	0.77
2:B:190:TYR:HB3	2:B:194:LEU:HB3	1.65	0.77
2:B:287:MET:HE1	2:B:292:ALA:HB2	1.67	0.76
1:A:42:GLY:N	1:A:136:VAL:CG1	2.47	0.76
2:B:1:MET:HA	2:B:2:ARG:NH1	2.00	0.76
2:B:108:ILE:CB	2:B:113:VAL:HG22	2.14	0.76
1:A:268:PRO:HB2	1:A:269:TRP:CE3	2.20	0.76
2:B:81:ALA:HB1	2:B:94:ILE:HD11	1.67	0.76
2:B:273:PHE:HD2	2:B:393:LEU:HD21	1.48	0.76
1:A:94:LYS:HZ1	1:A:124:LYS:HZ3	1.33	0.76
2:B:209:ARG:HH21	2:B:209:ARG:CB	1.93	0.76
2:B:270:ASN:HD22	2:B:270:ASN:H	1.34	0.76
1:A:267:LYS:HZ3	1:A:307:ASN:HB2	1.42	0.76
2:B:88:LEU:HG	2:B:90:ASP:HB3	1.68	0.76
2:B:393:LEU:HD11	2:B:403:ILE:CG1	2.14	0.76
1:A:127:THR:O	1:A:131:ASN:HB2	1.86	0.76
2:B:350:LEU:HD13	2:B:350:LEU:N	2.01	0.76
2:B:393:LEU:CD1	2:B:403:ILE:HD13	2.10	0.76
1:A:165:LYS:HD3	1:A:165:LYS:N	2.01	0.76
2:B:178:ILE:HD12	2:B:403:ILE:CG2	1.86	0.76
3:C:19:DA:C2	4:D:3:DA:C2	2.73	0.76
1:A:128:ALA:O	1:A:132:ASP:HB2	1.84	0.75
1:A:209:GLN:NE2	1:A:213:ARG:HH12	1.82	0.75
1:A:507:ILE:OXT	1:A:507:ILE:CG2	2.33	0.75
3:C:7:DA:C8	3:C:8:DG:N2	2.55	0.75
1:A:267:LYS:HZ3	1:A:307:ASN:CB	1.90	0.75
3:C:11:DG:N2	4:D:11:DT:H3	1.83	0.75
1:A:107:ASN:ND2	1:A:112:LYS:HD3	2.01	0.75
2:B:285:TYR:HB3	2:B:292:ALA:HB3	1.68	0.75
2:B:2:ARG:HD3	2:B:2:ARG:N	2.02	0.75
2:B:44:ASP:O	2:B:47:SER:CA	2.34	0.75
2:B:80:VAL:O	2:B:84:VAL:HG23	1.86	0.75
2:B:176:PHE:HB3	2:B:404:SER:O	1.86	0.75
1:A:86:TRP:CZ2	1:A:140:PHE:CE1	2.75	0.74
1:A:157:LEU:HG	1:A:161:LEU:HD12	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:HIS:HE1	1:A:364:ARG:O	1.71	0.74
1:A:288:ILE:HG13	1:A:296:ASN:O	1.86	0.74
2:B:379:ALA:O	2:B:383:PHE:N	2.20	0.74
2:B:255:PHE:CE2	2:B:256:ILE:CG2	2.71	0.74
1:A:44:VAL:HG21	1:A:125:ILE:HG12	1.67	0.74
1:A:52:ILE:CD1	1:A:226:GLU:HG2	2.17	0.74
1:A:284:VAL:HG21	1:A:302:GLN:NE2	2.00	0.74
1:A:344:GLU:OE2	1:A:353:TYR:OH	2.04	0.74
4:D:4:DT:H6	4:D:4:DT:H5''	1.53	0.74
1:A:210:LEU:HD23	1:A:210:LEU:O	1.87	0.74
2:B:1:MET:HA	2:B:2:ARG:HH11	1.50	0.74
1:A:207:HIS:ND1	4:D:20:DA:C4	2.56	0.74
2:B:97:LEU:HA	2:B:118:ILE:HG23	1.68	0.74
2:B:251:TYR:CE2	2:B:253:THR:HG23	2.23	0.74
1:A:504:LYS:HA	1:A:507:ILE:HD12	1.69	0.73
2:B:211:LYS:HG2	2:B:212:GLU:N	2.02	0.73
2:B:225:HIS:CD2	2:B:226:GLN:HG2	2.21	0.73
1:A:248:ILE:HG13	1:A:252:LEU:CD1	2.18	0.73
1:A:366:ASN:ND2	1:A:369:GLU:OE2	2.21	0.73
1:A:430:GLN:OE1	2:B:419:PRO:HB3	1.88	0.73
2:B:85:LYS:O	2:B:88:LEU:HD23	1.89	0.73
1:A:94:LYS:NZ	1:A:124:LYS:NZ	2.35	0.73
1:A:393:PRO:HB2	2:B:175:TRP:CZ2	2.23	0.73
1:A:496:ILE:N	1:A:496:ILE:HD12	2.04	0.73
2:B:354:LYS:HB3	2:B:358:HIS:NE2	2.04	0.73
1:A:157:LEU:CD2	1:A:162:VAL:HG22	2.17	0.73
2:B:277:MET:HG3	2:B:293:TYR:CE2	2.24	0.73
3:C:11:DG:N2	4:D:11:DT:C2	2.56	0.73
1:A:52:ILE:HD12	1:A:226:GLU:CG	2.18	0.73
2:B:354:LYS:HB2	2:B:358:HIS:CE1	2.24	0.73
1:A:501:LEU:HD13	1:A:506:TYR:CE2	2.22	0.73
1:A:57:LEU:HD12	1:A:88:SER:HA	1.70	0.73
1:A:142:ILE:N	1:A:142:ILE:HD13	2.04	0.73
2:B:1:MET:HG3	2:B:2:ARG:HH12	1.53	0.73
2:B:266:VAL:CG2	2:B:329:LEU:CD2	2.66	0.73
2:B:288:SER:HG	4:D:13:DC:H5''	1.48	0.73
3:C:4:DG:H2'	3:C:5:DG:C8	2.24	0.73
1:A:417:LYS:HD3	1:A:444:GLU:CG	2.19	0.72
4:D:18:DT:H2''	4:D:19:DC:C6	2.24	0.72
1:A:414:ASP:OD1	1:A:417:LYS:HE3	1.88	0.72
2:B:2:ARG:HH11	2:B:2:ARG:H	1.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:200:VAL:HG21	2:B:207:ALA:HB3	1.70	0.72
2:B:325:ALA:HB1	2:B:335:LEU:HD11	1.72	0.72
2:B:37:LEU:N	2:B:37:LEU:HD13	2.03	0.72
1:A:271:LEU:HG	1:A:465:LEU:HD21	1.70	0.71
2:B:81:ALA:HB3	2:B:94:ILE:HD11	1.71	0.71
2:B:178:ILE:HD13	2:B:403:ILE:HG21	1.56	0.71
1:A:66:ASN:HD21	1:A:250:GLY:CA	2.03	0.71
2:B:66:THR:CA	2:B:103:LEU:HD11	2.19	0.71
2:B:205:PHE:CD1	2:B:395:VAL:O	2.43	0.71
2:B:294:TRP:CZ2	2:B:350:LEU:HD12	2.26	0.71
1:A:390:LYS:CG	1:A:441:ILE:HG22	2.11	0.71
2:B:188:HIS:HA	2:B:238:SER:CB	2.18	0.71
2:B:264:LEU:HA	2:B:267:GLN:HE22	1.56	0.71
1:A:207:HIS:ND1	4:D:20:DA:N3	2.38	0.71
2:B:176:PHE:CD1	2:B:407:PRO:HB3	2.24	0.71
1:A:14:PHE:HE2	1:A:20:CYS:HG	1.36	0.70
1:A:43:VAL:CG2	1:A:91:ILE:CG2	2.69	0.70
2:B:61:LEU:HB3	2:B:97:LEU:HD11	1.73	0.70
2:B:243:THR:HA	2:B:246:ILE:HG12	1.72	0.70
2:B:246:ILE:N	2:B:246:ILE:HD13	2.04	0.70
2:B:287:MET:CE	2:B:292:ALA:HB2	2.21	0.70
3:C:15:DG:C2	4:D:7:DA:C2	2.78	0.70
3:C:15:DG:N2	4:D:7:DA:C2	2.58	0.70
1:A:74:MET:HE1	1:A:76:PRO:HA	1.73	0.70
1:A:393:PRO:HB2	2:B:175:TRP:HZ2	1.54	0.70
1:A:72:ARG:HH11	1:A:72:ARG:HG2	1.56	0.70
1:A:95:GLU:HG2	1:A:96:ILE:N	2.05	0.70
3:C:10:DA:N1	3:C:11:DG:C2	2.59	0.70
2:B:7:ILE:HD13	2:B:21:LEU:HD23	1.72	0.70
2:B:354:LYS:H	2:B:354:LYS:CD	1.96	0.70
1:A:284:VAL:HG23	1:A:302:GLN:HE21	1.56	0.70
2:B:315:LYS:HG2	2:B:316:ASN:ND2	2.06	0.70
2:B:329:LEU:N	2:B:329:LEU:HD22	2.07	0.70
3:C:19:DA:H2	4:D:3:DA:C4	2.08	0.70
1:A:30:PHE:HZ	2:B:151:ASN:HB3	1.56	0.70
4:D:15:DA:H2''	4:D:16:DC:H5''	1.74	0.70
1:A:390:LYS:NZ	1:A:441:ILE:HG21	2.07	0.69
2:B:44:ASP:O	2:B:47:SER:CB	2.41	0.69
2:B:188:HIS:N	2:B:238:SER:OG	2.25	0.69
1:A:42:GLY:H	1:A:136:VAL:HG11	1.56	0.69
1:A:98:ASP:HB3	1:A:102:ARG:HE	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:ASN:HD21	1:A:250:GLY:C	1.95	0.69
1:A:212:ALA:O	1:A:215:LEU:HB2	1.92	0.69
1:A:143:VAL:HG13	1:A:147:ILE:HB	1.73	0.69
1:A:468:ASN:ND2	1:A:507:ILE:CD1	2.32	0.69
2:B:14:ASP:OD2	2:B:63:VAL:CG1	2.40	0.69
2:B:167:LYS:O	2:B:414:MET:N	2.25	0.69
2:B:191:ASP:O	2:B:194:LEU:HG	1.92	0.69
1:A:163:GLN:HA	1:A:163:GLN:NE2	2.08	0.69
1:A:66:ASN:HD21	1:A:251:HIS:N	1.88	0.69
2:B:298:GLY:N	2:B:303:ASP:OD1	2.23	0.69
1:A:5:ILE:HD11	1:A:412:ILE:HD11	1.73	0.69
1:A:40:LYS:HG3	1:A:90:ASN:ND2	2.05	0.69
1:A:284:VAL:CG2	1:A:302:GLN:HE22	2.03	0.69
3:C:14:DT:H3	4:D:7:DA:N6	1.90	0.69
1:A:13:LEU:C	1:A:13:LEU:HD12	2.14	0.69
2:B:408:LEU:CD1	2:B:408:LEU:H	1.95	0.68
2:B:345:MET:HG2	2:B:351:ILE:HD13	1.76	0.68
2:B:379:ALA:HA	2:B:382:ARG:HD2	1.75	0.68
2:B:405:ASN:OD1	2:B:406:LYS:N	2.26	0.68
1:A:97:THR:OG1	1:A:100:GLU:HG3	1.93	0.68
1:A:405:ILE:HD11	1:A:421:TRP:CD1	2.25	0.68
3:C:15:DG:C2	4:D:7:DA:H2	2.11	0.68
2:B:81:ALA:CB	2:B:94:ILE:CD1	2.71	0.68
2:B:219:TRP:HB3	2:B:221:TYR:HE2	1.52	0.68
2:B:294:TRP:HZ2	2:B:350:LEU:HD12	1.58	0.68
1:A:24:ARG:HD2	1:A:73:PRO:HD2	1.76	0.68
1:A:363:THR:O	1:A:387:THR:OG1	2.12	0.68
1:A:43:VAL:HG23	1:A:91:ILE:HG23	1.75	0.68
1:A:57:LEU:HB2	1:A:88:SER:HB3	1.74	0.68
3:C:19:DA:C2	4:D:3:DA:C6	2.82	0.68
1:A:364:ARG:HG3	1:A:364:ARG:NH1	2.02	0.67
1:A:365:PHE:N	1:A:446:ASN:OD1	2.23	0.67
1:A:122:ASN:HD22	1:A:213:ARG:HG2	1.59	0.67
2:B:176:PHE:CD1	2:B:407:PRO:CB	2.68	0.67
1:A:269:TRP:O	1:A:467:TYR:OH	2.09	0.67
2:B:1:MET:CG	2:B:2:ARG:HH12	2.07	0.67
2:B:326:ALA:HB3	2:B:336:MET:HB2	1.76	0.67
1:A:118:VAL:CG1	1:A:213:ARG:NH2	2.57	0.67
3:C:10:DA:C6	3:C:11:DG:N1	2.62	0.67
1:A:288:ILE:HD13	1:A:491:THR:HG23	1.76	0.67
2:B:315:LYS:HD3	2:B:316:ASN:ND2	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:314:GLN:NE2	2:B:363:LYS:HE3	2.10	0.67
2:B:328:LYS:CD	2:B:336:MET:HE3	2.16	0.67
3:C:17:DA:N6	4:D:3:DA:H62	1.91	0.67
1:A:55:SER:O	1:A:59:LYS:HB2	1.95	0.67
2:B:241:ILE:HD13	2:B:251:TYR:CE2	2.30	0.67
2:B:266:VAL:HG23	2:B:329:LEU:HD21	1.74	0.67
2:B:296:GLU:CB	2:B:348:ILE:HG22	2.24	0.67
2:B:17:PHE:CD1	2:B:99:ILE:HG21	2.30	0.67
1:A:339:LEU:O	1:A:343:LEU:HG	1.94	0.67
1:A:66:ASN:OD1	1:A:72:ARG:HB3	1.94	0.66
1:A:158:PRO:HD2	1:A:161:LEU:HD12	1.77	0.66
1:A:365:PHE:HB2	1:A:447:LYS:HG3	1.76	0.66
3:C:5:DG:C2'	3:C:6:DT:C7	2.70	0.66
1:A:120:LEU:HD12	1:A:120:LEU:C	2.15	0.66
2:B:108:ILE:HG21	2:B:113:VAL:HA	1.77	0.66
2:B:194:LEU:C	2:B:194:LEU:HD12	2.15	0.66
4:D:9:DC:H2''	4:D:10:DC:H5'	1.76	0.66
2:B:17:PHE:CZ	2:B:120:PHE:CE2	2.75	0.66
2:B:218:ALA:HB1	2:B:222:ASP:OD2	1.95	0.66
3:C:10:DA:N1	3:C:11:DG:N2	2.43	0.66
3:C:11:DG:N2	4:D:11:DT:N3	2.43	0.66
2:B:14:ASP:OD2	2:B:65:SER:OG	2.09	0.66
2:B:391:ILE:HG22	2:B:392:TYR:N	2.10	0.66
4:D:7:DA:C2'	4:D:8:DA:H5''	2.25	0.66
1:A:235:LYS:HD2	1:A:239:GLY:O	1.96	0.66
4:D:6:DC:H2''	4:D:7:DA:C8	2.30	0.66
1:A:405:ILE:HD11	1:A:421:TRP:HE1	1.53	0.66
1:A:443:ILE:CD1	1:A:456:LEU:HD23	2.26	0.66
2:B:200:VAL:HA	2:B:203:LEU:HD23	1.78	0.66
1:A:207:HIS:ND1	4:D:20:DA:N1	2.41	0.66
1:A:493:SER:OG	1:A:496:ILE:HG13	1.96	0.66
2:B:266:VAL:HG22	2:B:329:LEU:HD21	1.74	0.66
1:A:152:ARG:HG3	1:A:152:ARG:NH1	2.11	0.66
1:A:405:ILE:CD1	1:A:421:TRP:CE2	2.79	0.66
2:B:88:LEU:HD23	2:B:90:ASP:H	1.61	0.66
2:B:294:TRP:HE3	2:B:320:HIS:CG	1.97	0.66
1:A:132:ASP:OD2	1:A:134:GLU:CB	2.29	0.65
1:A:163:GLN:HA	1:A:163:GLN:HE21	1.60	0.65
2:B:288:SER:OG	4:D:13:DC:C4'	2.44	0.65
1:A:398:LYS:NZ	6:A:601:HOH:O	2.06	0.65
2:B:58:CYS:O	2:B:59:LYS:HD3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:354:LYS:CB	2:B:358:HIS:CE1	2.80	0.65
2:B:36:ILE:HG22	2:B:37:LEU:HD13	1.77	0.65
2:B:69:ASN:O	2:B:75:LEU:HD21	1.97	0.65
2:B:214:LEU:CD1	2:B:215:CYS:N	2.60	0.65
2:B:223:PHE:O	2:B:224:ILE:HD12	1.97	0.65
1:A:332:PRO:HB3	1:A:372:ALA:HB2	1.77	0.65
2:B:1:MET:HG3	2:B:2:ARG:NH1	2.12	0.65
2:B:218:ALA:C	2:B:222:ASP:OD2	2.34	0.64
2:B:393:LEU:HD11	2:B:403:ILE:HD11	0.66	0.64
1:A:484:ASN:ND2	3:C:7:DA:OP1	2.30	0.64
2:B:85:LYS:NZ	2:B:91:ASP:O	2.28	0.64
2:B:9:HIS:HB3	2:B:18:THR:HG21	1.79	0.64
2:B:193:ARG:CB	2:B:230:THR:HG23	2.28	0.64
1:A:210:LEU:CD2	1:A:214:LEU:HD12	2.28	0.64
4:D:9:DC:H2'	4:D:10:DC:C5	2.33	0.64
1:A:267:LYS:HZ1	1:A:307:ASN:CB	1.71	0.64
1:A:366:ASN:ND2	1:A:369:GLU:HB2	1.99	0.64
2:B:210:TYR:CZ	2:B:256:ILE:HG21	2.33	0.64
3:C:17:DA:H61	4:D:3:DA:N6	1.92	0.64
1:A:107:ASN:HD21	1:A:112:LYS:HD3	1.63	0.63
2:B:64:SER:HB3	2:B:98:ALA:HA	1.79	0.63
1:A:402:ALA:O	2:B:370:ASN:HB3	1.98	0.63
2:B:214:LEU:HD13	2:B:215:CYS:N	2.13	0.63
2:B:328:LYS:HD3	2:B:330:TYR:O	1.99	0.63
4:D:9:DC:H2''	4:D:10:DC:C5'	2.27	0.63
1:A:125:ILE:HD12	1:A:214:LEU:HD11	1.81	0.63
1:A:253:ALA:O	1:A:257:SER:OG	2.14	0.63
1:A:501:LEU:CD1	1:A:506:TYR:HE2	2.08	0.63
2:B:329:LEU:HD22	2:B:329:LEU:H	1.64	0.63
1:A:248:ILE:HD13	3:C:1:DT:C2	2.34	0.63
1:A:262:TYR:CE1	1:A:507:ILE:HD11	2.34	0.63
1:A:417:LYS:HD3	1:A:444:GLU:HG3	1.79	0.63
1:A:43:VAL:HG21	1:A:91:ILE:HG21	1.79	0.63
1:A:90:ASN:ND2	1:A:90:ASN:O	2.32	0.63
2:B:1:MET:CA	2:B:2:ARG:HH11	2.11	0.63
2:B:246:ILE:HG22	2:B:258:ASN:OD1	1.98	0.63
1:A:481:ARG:NH2	4:D:19:DC:OP2	2.32	0.63
2:B:313:LYS:HD2	2:B:318:TYR:CE1	2.34	0.63
2:B:353:SER:HB3	2:B:356:ILE:CD1	2.29	0.63
4:D:20:DA:C4'	4:D:21:DT:OP2	2.32	0.63
1:A:52:ILE:HG23	1:A:230:ALA:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:PRO:CD	1:A:467:TYR:CD1	2.76	0.63
1:A:122:ASN:O	1:A:126:ILE:HG13	1.99	0.62
1:A:157:LEU:CD2	1:A:162:VAL:CG2	2.76	0.62
1:A:235:LYS:HA	1:A:241:PRO:HA	1.79	0.62
2:B:151:ASN:CB	2:B:155:GLN:OE1	2.47	0.62
2:B:399:GLU:HA	2:B:399:GLU:OE2	2.00	0.62
1:A:144:PRO:HD2	1:A:147:ILE:HG13	1.79	0.62
1:A:468:ASN:CG	1:A:507:ILE:HG21	2.19	0.62
2:B:88:LEU:HD11	2:B:90:ASP:CB	2.26	0.62
2:B:214:LEU:CD1	2:B:215:CYS:H	2.13	0.62
1:A:215:LEU:HD12	1:A:498:THR:HG21	1.80	0.62
2:B:294:TRP:HZ2	2:B:350:LEU:CD1	2.12	0.62
1:A:47:GLN:HG3	1:A:95:GLU:OE1	2.00	0.62
1:A:144:PRO:HD2	1:A:147:ILE:CG1	2.29	0.62
1:A:364:ARG:HH11	1:A:364:ARG:CG	2.12	0.62
2:B:37:LEU:HA	2:B:157:ILE:HG21	1.82	0.62
2:B:218:ALA:CA	2:B:222:ASP:OD2	2.47	0.62
3:C:10:DA:C6	3:C:11:DG:C2	2.88	0.62
2:B:379:ALA:HA	2:B:382:ARG:HB2	1.82	0.62
2:B:381:ILE:HG21	2:B:405:ASN:O	1.99	0.62
1:A:10:PRO:HG3	1:A:461:ALA:CA	2.24	0.62
1:A:96:ILE:CD1	1:A:121:PHE:CE1	2.82	0.62
1:A:118:VAL:O	1:A:122:ASN:OD1	2.17	0.62
2:B:251:TYR:CZ	2:B:253:THR:HG23	2.35	0.62
2:B:369:TRP:HA	2:B:369:TRP:CE3	2.35	0.62
1:A:417:LYS:HB3	1:A:444:GLU:HG3	1.82	0.62
2:B:353:SER:CB	2:B:356:ILE:HD11	2.30	0.62
1:A:23:PRO:O	1:A:27:LEU:HD12	2.01	0.61
1:A:305:LEU:HD22	1:A:346:TYR:HE1	1.63	0.61
2:B:97:LEU:HA	2:B:118:ILE:HG21	1.79	0.61
2:B:176:PHE:CZ	2:B:407:PRO:HB3	2.34	0.61
4:D:2:DT:H1'	4:D:3:DA:H8	1.64	0.61
1:A:206:PHE:HB3	4:D:20:DA:N6	2.15	0.61
1:A:340:THR:HG23	1:A:376:VAL:CG1	2.30	0.61
2:B:44:ASP:O	2:B:48:THR:N	2.33	0.61
1:A:207:HIS:ND1	4:D:20:DA:C6	2.67	0.61
1:A:262:TYR:HE1	1:A:507:ILE:HD11	1.64	0.61
1:A:394:LEU:HD21	2:B:410:PHE:CZ	2.35	0.61
2:B:186:ARG:HG3	2:B:188:HIS:CE1	2.35	0.61
2:B:294:TRP:HE3	2:B:320:HIS:HB3	1.61	0.61
2:B:369:TRP:O	2:B:370:ASN:C	2.37	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:PHE:HD2	1:A:308:GLY:HA2	1.64	0.61
1:A:406:MET:HB3	2:B:416:TYR:CD2	2.35	0.61
1:A:468:ASN:HD21	1:A:507:ILE:CG1	2.13	0.61
2:B:39:LEU:HD12	2:B:39:LEU:O	2.00	0.61
4:D:11:DT:H2''	4:D:12:DA:O5'	2.00	0.61
1:A:30:PHE:CZ	2:B:151:ASN:HB3	2.34	0.61
2:B:81:ALA:HB1	2:B:94:ILE:CD1	2.29	0.61
3:C:18:DT:H3	4:D:3:DA:N6	1.98	0.61
3:C:19:DA:N6	4:D:2:DT:C4	2.58	0.61
1:A:126:ILE:HD13	1:A:217:HIS:CE1	2.35	0.61
1:A:405:ILE:HG22	2:B:171:TYR:CE1	2.36	0.61
2:B:219:TRP:HZ3	2:B:240:ARG:NH2	1.99	0.61
2:B:233:TYR:OH	2:B:237:GLU:HG2	2.00	0.61
4:D:4:DT:H6	4:D:4:DT:C5'	2.13	0.61
1:A:94:LYS:HZ2	1:A:124:LYS:NZ	1.98	0.61
1:A:287:LYS:N	1:A:328:TYR:OH	2.33	0.61
2:B:81:ALA:HB3	2:B:94:ILE:CD1	2.30	0.61
1:A:10:PRO:CG	1:A:461:ALA:HA	2.24	0.61
3:C:10:DA:C2	3:C:11:DG:N2	2.69	0.61
3:C:10:DA:C2	3:C:11:DG:C2	2.89	0.61
1:A:118:VAL:HG12	1:A:213:ARG:NH2	2.16	0.60
1:A:320:TRP:CZ2	1:A:330:LEU:HD23	2.36	0.60
1:A:443:ILE:CD1	1:A:456:LEU:CD2	2.79	0.60
1:A:398:LYS:NZ	1:A:400:GLU:O	2.33	0.60
2:B:252:ASP:OD1	2:B:257:ARG:HD3	2.01	0.60
2:B:294:TRP:CB	2:B:342:ILE:HG13	2.31	0.60
1:A:74:MET:CE	1:A:76:PRO:N	2.62	0.60
1:A:423:LEU:HG	1:A:434:SER:HB2	1.83	0.60
1:A:14:PHE:HE2	1:A:20:CYS:SG	2.24	0.60
1:A:81:VAL:HG12	1:A:82:PHE:CD2	2.37	0.60
1:A:406:MET:HE3	1:A:427:PRO:HD3	1.82	0.60
2:B:2:ARG:N	2:B:2:ARG:HH11	1.99	0.60
2:B:3:ASN:OD1	2:B:3:ASN:N	2.33	0.60
2:B:50:GLU:O	2:B:54:ARG:HB2	2.01	0.60
2:B:285:TYR:O	2:B:292:ALA:N	2.20	0.60
3:C:4:DG:H2'	3:C:5:DG:H8	1.67	0.60
1:A:407:ARG:NH1	1:A:422:THR:O	2.34	0.60
1:A:298:CYS:SG	1:A:490:LEU:HB3	2.42	0.60
2:B:18:THR:O	2:B:22:SER:OG	2.19	0.60
2:B:220:GLU:H	2:B:220:GLU:CD	1.99	0.60
2:B:320:HIS:CD2	2:B:344:THR:OG1	2.55	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:9:DC:H2''	4:D:10:DC:C6	2.37	0.60
1:A:5:ILE:CD1	1:A:412:ILE:HD11	2.30	0.60
1:A:158:PRO:HD2	1:A:161:LEU:CD1	2.32	0.59
2:B:88:LEU:HG	2:B:90:ASP:CB	2.32	0.59
1:A:218:THR:HG22	1:A:501:LEU:CD2	2.31	0.59
1:A:228:THR:OG1	4:D:21:DT:OP1	2.13	0.59
1:A:349:GLN:HB3	1:A:350:ASN:HD21	1.66	0.59
2:B:408:LEU:HD12	2:B:408:LEU:N	2.03	0.59
3:C:17:DA:C2	4:D:5:DA:C2	2.89	0.59
1:A:133:GLU:CD	1:A:134:GLU:H	2.05	0.59
1:A:398:LYS:HD2	2:B:169:GLU:CD	2.22	0.59
2:B:251:TYR:CZ	2:B:253:THR:CG2	2.85	0.59
2:B:344:THR:HB	2:B:346:ASP:O	2.02	0.59
1:A:43:VAL:CG2	1:A:91:ILE:HG21	2.31	0.59
1:A:209:GLN:HE21	1:A:213:ARG:HH12	1.49	0.59
2:B:197:GLN:HE21	2:B:197:GLN:C	2.06	0.59
2:B:343:PHE:H	2:B:357:GLN:HE22	1.48	0.59
4:D:12:DA:H2''	4:D:13:DC:H5'	1.84	0.59
1:A:284:VAL:HG21	1:A:302:GLN:HE22	1.64	0.59
2:B:41:LYS:HG2	2:B:41:LYS:O	2.02	0.59
2:B:200:VAL:CG2	2:B:207:ALA:HB3	2.32	0.59
2:B:175:TRP:CD1	2:B:336:MET:HG2	2.37	0.59
2:B:361:ARG:HD2	2:B:361:ARG:O	2.02	0.59
2:B:275:LEU:O	2:B:278:LYS:CB	2.51	0.59
1:A:43:VAL:HG21	1:A:50:LEU:CD1	2.33	0.59
1:A:388:ILE:HD12	1:A:480:LEU:CD1	2.29	0.59
2:B:151:ASN:ND2	2:B:155:GLN:CD	2.53	0.59
2:B:294:TRP:CE3	2:B:320:HIS:HB2	2.38	0.59
2:B:369:TRP:HA	2:B:369:TRP:HE3	1.67	0.59
1:A:81:VAL:CG1	1:A:82:PHE:CE2	2.86	0.59
1:A:138:VAL:HB	1:A:140:PHE:CE2	2.38	0.58
2:B:190:TYR:CE2	2:B:227:LEU:CD1	2.74	0.58
2:B:313:LYS:CE	2:B:318:TYR:CE1	2.86	0.58
1:A:231:TRP:CZ2	1:A:232:ARG:NH1	2.71	0.58
2:B:108:ILE:HB	2:B:113:VAL:HG22	1.85	0.58
2:B:177:PRO:HA	2:B:334:VAL:HA	1.85	0.58
2:B:354:LYS:O	2:B:358:HIS:N	2.31	0.58
2:B:381:ILE:CG2	2:B:405:ASN:HA	2.33	0.58
1:A:231:TRP:CH2	1:A:232:ARG:NH1	2.72	0.58
2:B:105:TYR:CZ	2:B:113:VAL:CG1	2.85	0.58
2:B:178:ILE:HA	2:B:403:ILE:CG2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:251:TYR:CE2	2:B:253:THR:CG2	2.86	0.58
1:A:52:ILE:O	1:A:55:SER:HB2	2.03	0.58
2:B:389:ASN:OD1	2:B:389:ASN:N	2.36	0.58
1:A:41:SER:HB3	1:A:86:TRP:HE1	1.68	0.58
2:B:118:ILE:HG23	2:B:118:ILE:O	2.04	0.58
2:B:305:PHE:CE1	2:B:306:GLU:HB2	2.39	0.58
1:A:503:PHE:O	1:A:507:ILE:HG13	2.03	0.58
2:B:210:TYR:CE2	2:B:256:ILE:HG21	2.39	0.58
2:B:306:GLU:O	2:B:307:LYS:CG	2.47	0.58
2:B:344:THR:HG22	2:B:349:ASN:C	2.23	0.58
3:C:3:DA:H61	4:D:17:DC:N4	2.02	0.58
1:A:141:VAL:HB	1:A:223:ILE:HG12	1.86	0.58
1:A:148:TYR:CE1	1:A:225:ARG:NH1	2.72	0.58
1:A:322:ASN:CG	1:A:325:LYS:HB2	2.24	0.58
2:B:206:PRO:CG	2:B:395:VAL:HG12	2.28	0.58
2:B:393:LEU:CD1	2:B:403:ILE:CG1	2.80	0.58
1:A:66:ASN:ND2	1:A:251:HIS:N	2.52	0.57
2:B:296:GLU:CB	2:B:348:ILE:CG2	2.82	0.57
1:A:393:PRO:CB	2:B:175:TRP:HZ2	2.17	0.57
4:D:17:DC:H2''	4:D:18:DT:O5'	2.03	0.57
1:A:307:ASN:OD1	1:A:308:GLY:N	2.37	0.57
1:A:418:ALA:HB3	1:A:452:ILE:HD11	1.86	0.57
4:D:18:DT:H2''	4:D:19:DC:C5	2.40	0.57
1:A:42:GLY:CA	1:A:136:VAL:HG11	2.34	0.57
1:A:384:VAL:CG1	1:A:445:ILE:CG2	2.82	0.57
1:A:36:ILE:HG23	1:A:261:TYR:OH	2.05	0.57
1:A:349:GLN:HB3	1:A:350:ASN:HD22	1.68	0.57
2:B:413:LYS:O	2:B:414:MET:HB2	2.04	0.57
1:A:108:ALA:CB	1:A:162:VAL:HG11	2.33	0.57
2:B:213:TYR:N	2:B:213:TYR:CD2	2.73	0.57
3:C:19:DA:C2	4:D:3:DA:N1	2.72	0.57
1:A:144:PRO:HD2	1:A:147:ILE:HD11	1.84	0.57
1:A:404:PRO:HD2	1:A:425:PHE:HB2	1.86	0.57
1:A:476:GLU:OE1	4:D:18:DT:OP1	2.23	0.57
2:B:296:GLU:HB3	2:B:348:ILE:CG2	2.31	0.57
1:A:140:PHE:CD2	1:A:140:PHE:N	2.73	0.57
1:A:163:GLN:HE21	1:A:163:GLN:CA	2.17	0.57
1:A:336:LYS:HA	1:A:376:VAL:HG21	1.87	0.57
1:A:389:THR:CG2	1:A:442:PHE:HB3	2.33	0.57
1:A:390:LYS:HZ3	1:A:441:ILE:HG21	1.69	0.57
2:B:200:VAL:O	2:B:203:LEU:CA	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:6:DT:H2''	3:C:7:DA:C8	2.40	0.57
1:A:262:TYR:CZ	1:A:309:ASP:OD1	2.55	0.57
1:A:287:LYS:HA	1:A:297:ALA:HB2	1.86	0.57
2:B:233:TYR:OH	2:B:238:SER:N	2.38	0.57
2:B:270:ASN:ND2	2:B:270:ASN:H	2.03	0.57
1:A:12:ILE:CG1	1:A:14:PHE:CZ	2.86	0.56
2:B:233:TYR:CE2	2:B:237:GLU:HB3	2.40	0.56
1:A:14:PHE:CE2	1:A:20:CYS:SG	2.98	0.56
1:A:52:ILE:CG2	1:A:229:LEU:HB2	2.34	0.56
2:B:253:THR:OG1	2:B:256:ILE:HG13	2.04	0.56
2:B:314:GLN:NE2	2:B:363:LYS:CE	2.67	0.56
1:A:305:LEU:CD2	1:A:346:TYR:HE1	2.19	0.56
1:A:332:PRO:HD3	1:A:368:GLU:OE1	2.05	0.56
1:A:414:ASP:HB2	1:A:417:LYS:H	1.70	0.56
1:A:425:PHE:HA	1:A:432:THR:HA	1.88	0.56
2:B:14:ASP:CG	2:B:63:VAL:HG11	2.24	0.56
2:B:151:ASN:HB2	2:B:155:GLN:OE1	2.04	0.56
2:B:192:TRP:CD1	2:B:193:ARG:N	2.73	0.56
2:B:353:SER:HB3	2:B:356:ILE:HD11	1.85	0.56
2:B:282:VAL:O	2:B:282:VAL:HG23	2.04	0.56
2:B:374:ARG:HG2	2:B:378:LEU:HD13	1.87	0.56
1:A:324:GLU:HG3	4:D:8:DA:H3'	1.87	0.56
1:A:389:THR:HG23	1:A:389:THR:O	2.05	0.56
1:A:389:THR:HG22	1:A:442:PHE:HB3	1.88	0.56
3:C:4:DG:O6	4:D:16:DC:N4	2.38	0.56
1:A:33:LEU:CD1	1:A:270:LYS:HB2	2.36	0.56
1:A:274:ILE:HG21	1:A:306:ASP:HB3	1.88	0.56
1:A:291:SER:HB3	1:A:296:ASN:HB2	1.88	0.56
1:A:217:HIS:H	1:A:217:HIS:CD2	2.24	0.56
2:B:84:VAL:HG12	2:B:84:VAL:O	2.04	0.56
2:B:379:ALA:O	2:B:382:ARG:HB2	2.06	0.56
1:A:284:VAL:HG22	1:A:483:ALA:CB	2.36	0.56
1:A:320:TRP:CE2	1:A:330:LEU:HD23	2.41	0.56
2:B:273:PHE:CD2	2:B:393:LEU:HD21	2.35	0.56
2:B:315:LYS:CD	2:B:316:ASN:HD21	2.15	0.56
1:A:19:LYS:HE2	1:A:273:ASP:OD2	2.07	0.55
1:A:339:LEU:CD1	1:A:343:LEU:HD11	2.36	0.55
2:B:343:PHE:N	2:B:357:GLN:HE22	2.03	0.55
3:C:17:DA:C2	4:D:5:DA:N1	2.74	0.55
2:B:9:HIS:HB3	2:B:18:THR:CG2	2.35	0.55
2:B:45:PHE:CD1	2:B:45:PHE:N	2.73	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:45:PHE:N	2:B:45:PHE:HD1	2.03	0.55
3:C:18:DT:H2''	3:C:19:DA:H5'	1.86	0.55
1:A:94:LYS:HZ1	1:A:124:LYS:NZ	1.98	0.55
1:A:390:LYS:HE2	1:A:476:GLU:HG2	1.86	0.55
4:D:9:DC:C2'	4:D:10:DC:C5	2.89	0.55
2:B:105:TYR:CE1	2:B:113:VAL:HG13	2.36	0.55
2:B:268:LEU:O	2:B:272:ALA:N	2.35	0.55
2:B:313:LYS:NZ	2:B:318:TYR:CE1	2.73	0.55
1:A:64:ILE:HG13	1:A:75:PHE:HB3	1.87	0.55
1:A:295:GLN:CG	1:A:321:TYR:O	2.48	0.55
2:B:27:GLY:CA	2:B:150:SER:HB2	2.37	0.55
2:B:176:PHE:HD1	2:B:406:LYS:C	2.10	0.55
2:B:305:PHE:N	2:B:308:ILE:O	2.39	0.55
2:B:54:ARG:HG3	2:B:54:ARG:NH1	2.20	0.55
2:B:197:GLN:NE2	2:B:197:GLN:C	2.60	0.55
1:A:320:TRP:CZ2	1:A:330:LEU:CD2	2.90	0.55
2:B:196:LYS:HD3	4:D:5:DA:H3'	1.88	0.55
3:C:19:DA:C2	4:D:3:DA:C5	2.95	0.55
1:A:25:ASP:OD2	1:A:428:LYS:HE2	2.07	0.55
1:A:249:GLU:HB2	6:A:603:HOH:O	2.07	0.54
2:B:188:HIS:CA	2:B:238:SER:HG	2.12	0.54
1:A:443:ILE:HD13	1:A:456:LEU:HD23	1.88	0.54
2:B:17:PHE:CE1	2:B:99:ILE:HG21	2.42	0.54
2:B:194:LEU:HD12	2:B:194:LEU:O	2.08	0.54
1:A:390:LYS:NZ	1:A:476:GLU:HG3	2.23	0.54
1:A:329:HIS:CE1	1:A:364:ARG:O	2.56	0.54
1:A:414:ASP:OD1	2:B:330:TYR:OH	2.26	0.54
2:B:86:LYS:O	2:B:89:GLN:N	2.40	0.54
1:A:81:VAL:HG12	1:A:82:PHE:CE2	2.42	0.54
1:A:361:ALA:O	1:A:387:THR:HA	2.06	0.54
1:A:366:ASN:H	1:A:366:ASN:HD22	1.56	0.54
1:A:490:LEU:O	1:A:493:SER:O	2.25	0.54
2:B:69:ASN:ND2	2:B:103:LEU:HD21	2.22	0.54
2:B:353:SER:CB	2:B:356:ILE:CD1	2.85	0.54
1:A:7:ILE:CD1	1:A:456:LEU:HB3	2.38	0.54
1:A:80:ALA:HB1	2:B:20:TRP:HZ2	1.72	0.54
2:B:213:TYR:H	2:B:213:TYR:HD2	1.53	0.54
2:B:315:LYS:HG2	2:B:316:ASN:HD22	1.70	0.54
2:B:135:PHE:CD1	2:B:140:VAL:HG21	2.43	0.54
2:B:176:PHE:CD1	2:B:406:LYS:C	2.77	0.54
3:C:15:DG:N2	4:D:7:DA:H2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:GLY:H	1:A:136:VAL:CG1	2.15	0.54
1:A:323:PRO:HB3	4:D:9:DC:OP2	2.06	0.54
1:A:332:PRO:O	1:A:336:LYS:HG3	2.08	0.54
2:B:120:PHE:HE1	2:B:128:LEU:N	2.02	0.54
3:C:19:DA:C2	4:D:3:DA:C4	2.95	0.54
1:A:390:LYS:HZ2	1:A:441:ILE:CG2	2.21	0.54
3:C:14:DT:H2''	3:C:15:DG:C8	2.43	0.54
2:B:35:ASP:N	2:B:35:ASP:OD1	2.41	0.54
2:B:264:LEU:HA	2:B:267:GLN:NE2	2.21	0.54
1:A:165:LYS:HD3	1:A:165:LYS:H	1.70	0.53
1:A:323:PRO:HB2	4:D:8:DA:O3'	2.08	0.53
2:B:368:TRP:HE3	2:B:373:TRP:CD1	2.25	0.53
1:A:320:TRP:CH2	1:A:330:LEU:HD23	2.44	0.53
1:A:405:ILE:HG22	2:B:171:TYR:CZ	2.43	0.53
3:C:4:DG:C6	3:C:5:DG:C6	2.96	0.53
1:A:496:ILE:HD12	1:A:496:ILE:H	1.73	0.53
2:B:17:PHE:CE2	2:B:120:PHE:CD2	2.96	0.53
2:B:176:PHE:CD1	2:B:407:PRO:HA	2.40	0.53
1:A:80:ALA:HB1	2:B:20:TRP:CZ2	2.44	0.53
1:A:86:TRP:CZ2	1:A:140:PHE:HE1	2.23	0.53
1:A:122:ASN:ND2	1:A:213:ARG:HG2	2.23	0.53
1:A:420:LEU:HB2	1:A:456:LEU:HD22	1.91	0.53
2:B:104:SER:N	2:B:107:ASP:OD1	2.41	0.53
2:B:54:ARG:HH11	2:B:54:ARG:CG	2.16	0.53
1:A:302:GLN:OE1	1:A:486:ILE:HD12	2.08	0.53
1:A:396:LEU:HD13	2:B:171:TYR:HB2	1.90	0.53
1:A:429:LEU:HD11	1:A:472:TYR:HB2	1.90	0.53
2:B:380:PHE:O	2:B:384:LEU:HG	2.08	0.53
2:B:7:ILE:HD11	2:B:21:LEU:HD23	1.87	0.53
2:B:153:LEU:O	2:B:157:ILE:N	2.40	0.53
1:A:7:ILE:HD11	1:A:456:LEU:HB3	1.90	0.53
1:A:305:LEU:CD2	1:A:346:TYR:CE1	2.92	0.53
2:B:248:SER:HB3	2:B:250:ARG:HG2	1.89	0.53
1:A:43:VAL:CG2	1:A:91:ILE:HG23	2.38	0.53
1:A:56:TYR:CE1	1:A:256:ILE:HD12	2.44	0.53
1:A:69:ASN:HA	1:A:72:ARG:O	2.08	0.53
2:B:71:ARG:O	2:B:75:LEU:HD12	2.09	0.53
2:B:42:GLY:O	2:B:45:PHE:HB3	2.09	0.53
2:B:191:ASP:H	2:B:194:LEU:HD23	1.73	0.52
1:A:275:ARG:NH1	1:A:458:ASP:OD2	2.42	0.52
1:A:316:GLU:OE2	1:A:497:LYS:CD	2.54	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:TYR:CE2	1:A:354:PRO:HD3	2.44	0.52
2:B:245:ASP:HB3	2:B:250:ARG:HB2	1.92	0.52
2:B:391:ILE:CG2	2:B:392:TYR:N	2.72	0.52
1:A:215:LEU:CD1	1:A:498:THR:HG21	2.39	0.52
1:A:286:LYS:O	1:A:297:ALA:HB1	2.09	0.52
2:B:233:TYR:CE2	2:B:237:GLU:HG2	2.45	0.52
1:A:267:LYS:NZ	1:A:307:ASN:CG	2.57	0.52
1:A:163:GLN:NE2	1:A:163:GLN:CA	2.73	0.52
1:A:225:ARG:NE	1:A:227:SER:OG	2.29	0.52
1:A:316:GLU:O	1:A:334:GLU:OE2	2.27	0.52
2:B:44:ASP:O	2:B:47:SER:HB3	2.09	0.52
2:B:218:ALA:CB	2:B:222:ASP:OD2	2.58	0.52
1:A:107:ASN:OD1	1:A:109:SER:N	2.42	0.52
1:A:210:LEU:HD23	1:A:214:LEU:HD12	1.91	0.52
1:A:282:GLY:O	1:A:302:GLN:HG2	2.09	0.52
2:B:5:ILE:HD13	2:B:135:PHE:CZ	2.45	0.52
2:B:81:ALA:O	2:B:85:LYS:HB2	2.09	0.52
2:B:241:ILE:HG22	2:B:246:ILE:HD11	1.91	0.52
1:A:33:LEU:N	1:A:268:PRO:O	2.43	0.52
1:A:313:PHE:CZ	1:A:342:ALA:HA	2.45	0.52
1:A:390:LYS:HE3	1:A:476:GLU:CD	2.30	0.52
2:B:308:ILE:HG21	2:B:376:LYS:HA	1.92	0.52
2:B:315:LYS:CG	2:B:316:ASN:ND2	2.73	0.52
1:A:284:VAL:HG22	1:A:483:ALA:HB2	1.92	0.52
1:A:350:ASN:HD22	1:A:350:ASN:N	2.07	0.52
2:B:26:ILE:HD13	2:B:153:LEU:CD2	2.40	0.52
2:B:173:SER:OG	2:B:174:ASN:N	2.41	0.52
2:B:217:PHE:HE2	2:B:268:LEU:HD12	1.75	0.52
1:A:160:GLU:N	1:A:160:GLU:OE2	2.42	0.52
1:A:248:ILE:O	1:A:251:HIS:HB3	2.10	0.52
2:B:158:PHE:CD1	2:B:158:PHE:N	2.78	0.52
3:C:3:DA:N6	4:D:17:DC:N4	2.57	0.52
4:D:19:DC:H2"	4:D:20:DA:OP1	2.09	0.52
1:A:64:ILE:HD11	1:A:253:ALA:CB	2.40	0.51
1:A:132:ASP:OD2	1:A:134:GLU:N	2.35	0.51
1:A:398:LYS:HD2	2:B:169:GLU:OE2	2.11	0.51
2:B:45:PHE:CG	2:B:46:TRP:N	2.78	0.51
1:A:210:LEU:HD23	1:A:210:LEU:C	2.30	0.51
1:A:484:ASN:ND2	3:C:6:DT:O3'	2.43	0.51
1:A:493:SER:C	1:A:496:ILE:HD11	2.31	0.51
2:B:313:LYS:HD2	2:B:318:TYR:CD1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:330:TYR:HA	2:B:331:PRO:C	2.30	0.51
2:B:410:PHE:N	2:B:410:PHE:CD2	2.76	0.51
3:C:13:DT:H2''	3:C:14:DT:O5'	2.09	0.51
1:A:314:LYS:HE3	1:A:496:ILE:HD13	1.92	0.51
2:B:88:LEU:HG	2:B:90:ASP:N	2.26	0.51
2:B:174:ASN:ND2	2:B:337:VAL:O	2.27	0.51
2:B:191:ASP:N	2:B:194:LEU:HD23	2.25	0.51
2:B:227:LEU:HD22	2:B:230:THR:OG1	2.10	0.51
2:B:255:PHE:CZ	2:B:256:ILE:HG12	2.45	0.51
2:B:277:MET:HG3	2:B:293:TYR:CD2	2.45	0.51
2:B:395:VAL:HG23	2:B:399:GLU:O	2.10	0.51
3:C:2:DG:O6	4:D:18:DT:H73	2.09	0.51
1:A:34:ASN:N	1:A:34:ASN:OD1	2.44	0.51
1:A:122:ASN:OD1	1:A:122:ASN:N	2.41	0.51
1:A:214:LEU:O	1:A:217:HIS:O	2.29	0.51
3:C:2:DG:N1	4:D:18:DT:N3	2.52	0.51
1:A:77:GLY:O	1:A:81:VAL:HG23	2.10	0.51
1:A:370:TRP:O	1:A:373:PHE:HB2	2.11	0.51
2:B:223:PHE:CD2	2:B:223:PHE:N	2.78	0.51
2:B:251:TYR:HH	2:B:256:ILE:HG13	1.75	0.51
2:B:378:LEU:O	2:B:382:ARG:CG	2.46	0.51
1:A:43:VAL:HG11	1:A:50:LEU:HD13	1.91	0.51
1:A:66:ASN:HD22	1:A:250:GLY:HA3	1.71	0.51
2:B:80:VAL:O	2:B:84:VAL:N	2.34	0.51
1:A:29:LEU:HD12	2:B:154:TYR:CD1	2.46	0.51
1:A:365:PHE:O	1:A:447:LYS:CE	2.58	0.51
1:A:414:ASP:HB2	1:A:417:LYS:HG2	1.93	0.51
2:B:178:ILE:HA	2:B:403:ILE:HG22	1.90	0.51
2:B:354:LYS:O	2:B:357:GLN:N	2.43	0.51
1:A:79:GLU:HG2	2:B:125:ALA:CB	2.41	0.51
1:A:85:LYS:HB2	1:A:87:GLU:HG3	1.93	0.51
1:A:12:ILE:HD11	1:A:14:PHE:HZ	1.76	0.51
1:A:30:PHE:HZ	2:B:151:ASN:CB	2.23	0.51
2:B:251:TYR:CZ	2:B:256:ILE:HD11	2.44	0.51
2:B:276:ARG:HG3	2:B:276:ARG:HH11	1.76	0.51
1:A:74:MET:CE	1:A:75:PHE:O	2.59	0.51
1:A:96:ILE:HD12	1:A:121:PHE:CE1	2.46	0.51
1:A:414:ASP:OD1	1:A:417:LYS:HG3	2.11	0.51
1:A:66:ASN:HD21	1:A:250:GLY:HA3	1.66	0.50
1:A:284:VAL:HG11	1:A:486:ILE:HG22	1.93	0.50
1:A:396:LEU:HD23	2:B:173:SER:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:132:LEU:O	2:B:135:PHE:HB2	2.11	0.50
2:B:275:LEU:O	2:B:278:LYS:HB2	2.11	0.50
1:A:57:LEU:HD21	1:A:86:TRP:CE2	2.46	0.50
1:A:95:GLU:CG	1:A:96:ILE:N	2.73	0.50
2:B:34:CYS:HB3	2:B:37:LEU:HD21	1.93	0.50
2:B:49:ILE:C	2:B:53:ILE:HG13	2.21	0.50
2:B:287:MET:HB3	4:D:14:DT:H5'	1.93	0.50
4:D:4:DT:H5''	4:D:4:DT:C6	2.40	0.50
1:A:138:VAL:HG12	1:A:140:PHE:CE2	2.46	0.50
1:A:364:ARG:HB3	1:A:446:ASN:OD1	2.10	0.50
2:B:7:ILE:HG12	2:B:61:LEU:HB2	1.92	0.50
2:B:208:ILE:HD13	2:B:268:LEU:HD23	1.83	0.50
1:A:64:ILE:HD11	1:A:253:ALA:HB2	1.93	0.50
1:A:66:ASN:HD22	1:A:66:ASN:N	2.08	0.50
1:A:481:ARG:NH1	4:D:19:DC:OP2	2.43	0.50
2:B:44:ASP:C	2:B:47:SER:H	2.15	0.50
2:B:230:THR:C	2:B:232:THR:H	2.15	0.50
2:B:319:TRP:HB3	2:B:343:PHE:CE1	2.46	0.50
1:A:15:ALA:O	1:A:16:HIS:HB2	2.11	0.50
1:A:398:LYS:HG3	2:B:171:TYR:CD1	2.46	0.50
1:A:443:ILE:HD12	1:A:456:LEU:HD23	1.87	0.50
1:A:157:LEU:HD23	1:A:162:VAL:CG2	2.42	0.50
1:A:309:ASP:O	1:A:503:PHE:HB2	2.11	0.50
2:B:2:ARG:NH1	2:B:2:ARG:H	2.06	0.50
1:A:350:ASN:ND2	1:A:350:ASN:N	2.60	0.50
2:B:219:TRP:HH2	2:B:240:ARG:NH1	2.09	0.50
2:B:214:LEU:HD12	2:B:215:CYS:N	2.27	0.50
2:B:316:ASN:ND2	2:B:316:ASN:H	2.09	0.50
2:B:358:HIS:NE2	4:D:14:DT:OP2	2.33	0.50
1:A:52:ILE:HG22	1:A:229:LEU:HB2	1.94	0.50
2:B:192:TRP:CD1	2:B:192:TRP:C	2.85	0.50
2:B:220:GLU:CD	2:B:221:TYR:CZ	2.85	0.50
2:B:247:LEU:HD12	2:B:247:LEU:C	2.33	0.50
2:B:350:LEU:HD13	2:B:350:LEU:H	1.75	0.50
1:A:57:LEU:CB	1:A:88:SER:HB3	2.42	0.49
1:A:223:ILE:O	1:A:224:LEU:HD23	2.12	0.49
2:B:8:SER:HA	2:B:77:GLU:OE1	2.12	0.49
2:B:270:ASN:ND2	2:B:270:ASN:N	2.60	0.49
4:D:9:DC:H2''	4:D:10:DC:O5'	2.11	0.49
2:B:1:MET:CA	2:B:2:ARG:NH1	2.73	0.49
2:B:275:LEU:O	2:B:278:LYS:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:280:LYS:O	2:B:281:ASN:HB2	2.12	0.49
2:B:233:TYR:CZ	2:B:237:GLU:CB	2.89	0.49
2:B:315:LYS:CD	2:B:316:ASN:ND2	2.73	0.49
2:B:316:ASN:ND2	2:B:316:ASN:N	2.60	0.49
2:B:80:VAL:HG12	2:B:84:VAL:CG2	2.42	0.49
2:B:200:VAL:HG21	2:B:207:ALA:CB	2.40	0.49
2:B:242:SER:O	2:B:246:ILE:HD13	2.09	0.49
2:B:255:PHE:CD2	2:B:255:PHE:C	2.85	0.49
2:B:265:ILE:HG22	2:B:269:ILE:HG13	1.93	0.49
2:B:343:PHE:O	2:B:351:ILE:HG12	2.12	0.49
4:D:7:DA:C3'	4:D:8:DA:H5''	2.43	0.49
2:B:54:ARG:NH1	2:B:54:ARG:CG	2.73	0.49
2:B:88:LEU:CD2	2:B:93:PHE:HB2	2.42	0.49
2:B:309:LYS:HE2	2:B:311:VAL:O	2.13	0.49
2:B:369:TRP:O	2:B:372:LYS:N	2.45	0.49
1:A:40:LYS:O	1:A:136:VAL:HG12	2.13	0.49
1:A:504:LYS:HA	1:A:507:ILE:CD1	2.42	0.49
2:B:1:MET:CG	2:B:2:ARG:NH1	2.73	0.49
2:B:225:HIS:CD2	2:B:225:HIS:C	2.85	0.49
2:B:251:TYR:CD1	2:B:251:TYR:C	2.85	0.49
2:B:333:PRO:C	2:B:334:VAL:HG13	2.32	0.49
1:A:152:ARG:NH1	1:A:152:ARG:CG	2.73	0.49
2:B:263:ARG:NH1	2:B:263:ARG:HB2	2.26	0.49
2:B:321:PHE:HD1	2:B:380:PHE:CD2	2.31	0.49
2:B:383:PHE:C	2:B:383:PHE:CD1	2.85	0.49
1:A:125:ILE:HG23	1:A:139:TRP:CD1	2.48	0.49
1:A:366:ASN:CG	1:A:369:GLU:HB3	2.30	0.49
2:B:9:HIS:CB	2:B:18:THR:CG2	2.85	0.49
3:C:4:DG:N2	4:D:18:DT:C2	2.81	0.49
1:A:14:PHE:CE2	1:A:26:GLY:HA3	2.48	0.49
1:A:140:PHE:N	1:A:140:PHE:HD2	2.11	0.49
1:A:148:TYR:O	1:A:152:ARG:NH1	2.46	0.49
1:A:267:LYS:NZ	1:A:307:ASN:ND2	2.61	0.49
2:B:173:SER:O	2:B:407:PRO:CG	2.61	0.49
2:B:195:PRO:O	2:B:209:ARG:NH1	2.45	0.49
2:B:345:MET:N	2:B:351:ILE:HD11	2.27	0.49
1:A:132:ASP:CG	1:A:134:GLU:HB2	2.33	0.48
2:B:233:TYR:CE2	2:B:237:GLU:CG	2.95	0.48
2:B:252:ASP:OD1	2:B:257:ARG:HG3	2.12	0.48
2:B:381:ILE:HG22	2:B:405:ASN:HB2	1.93	0.48
4:D:13:DC:H2''	4:D:14:DT:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:370:TRP:O	1:A:373:PHE:N	2.46	0.48
2:B:26:ILE:CD1	2:B:153:LEU:HD23	2.43	0.48
2:B:186:ARG:HG3	2:B:188:HIS:HE1	1.79	0.48
1:A:76:PRO:HD2	1:A:81:VAL:CG2	2.43	0.48
2:B:329:LEU:CD2	2:B:329:LEU:H	2.25	0.48
3:C:11:DG:H5'	3:C:12:DG:OP2	2.13	0.48
1:A:398:LYS:HE2	1:A:403:PHE:O	2.12	0.48
2:B:206:PRO:HB2	2:B:268:LEU:HD22	1.94	0.48
3:C:2:DG:O6	4:D:18:DT:H72	2.10	0.48
1:A:248:ILE:HG13	1:A:252:LEU:HD11	1.93	0.48
1:A:368:GLU:OE2	1:A:369:GLU:N	2.46	0.48
1:A:98:ASP:O	1:A:102:ARG:N	2.23	0.48
1:A:365:PHE:O	1:A:447:LYS:HE3	2.12	0.48
2:B:37:LEU:H	2:B:37:LEU:CD2	2.01	0.48
2:B:247:LEU:HD12	2:B:248:SER:CA	2.41	0.48
3:C:5:DG:C2	3:C:6:DT:C2	3.01	0.48
2:B:184:GLU:O	2:B:186:ARG:NH2	2.46	0.48
2:B:329:LEU:CD2	2:B:329:LEU:N	2.76	0.48
1:A:42:GLY:HA3	1:A:139:TRP:CZ3	2.49	0.48
1:A:218:THR:CG2	1:A:501:LEU:CD2	2.91	0.48
2:B:43:VAL:O	2:B:45:PHE:HD1	1.97	0.48
2:B:346:ASP:OD1	2:B:349:ASN:HB2	2.13	0.48
2:B:175:TRP:CZ2	2:B:336:MET:HE1	2.48	0.48
2:B:187:PHE:C	2:B:238:SER:HG	2.09	0.48
2:B:219:TRP:CH2	2:B:240:ARG:CZ	2.96	0.47
2:B:274:GLU:OE1	2:B:291:PHE:CD2	2.67	0.47
3:C:3:DA:N6	4:D:17:DC:H42	2.12	0.47
3:C:18:DT:C4	3:C:19:DA:C6	3.02	0.47
1:A:138:VAL:HG12	1:A:140:PHE:CD2	2.49	0.47
1:A:138:VAL:CG1	1:A:140:PHE:CE2	2.97	0.47
1:A:340:THR:HG23	1:A:376:VAL:HG12	1.96	0.47
1:A:72:ARG:HH11	1:A:72:ARG:CG	2.24	0.47
1:A:430:GLN:OE1	2:B:419:PRO:CB	2.61	0.47
3:C:12:DG:H2''	3:C:13:DT:OP2	2.15	0.47
1:A:105:LEU:O	1:A:113:ARG:CD	2.58	0.47
1:A:323:PRO:HG2	1:A:324:GLU:H	1.80	0.47
1:A:484:ASN:ND2	3:C:7:DA:P	2.87	0.47
2:B:354:LYS:HD2	2:B:354:LYS:N	2.05	0.47
4:D:10:DC:C2'	4:D:11:DT:OP2	2.53	0.47
1:A:67:HIS:N	1:A:247:LYS:O	2.43	0.47
1:A:364:ARG:CA	1:A:446:ASN:OD1	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:462:LEU:HD23	1:A:465:LEU:HD12	1.97	0.47
1:A:496:ILE:N	1:A:496:ILE:CD1	2.73	0.47
2:B:188:HIS:O	2:B:190:TYR:N	2.48	0.47
1:A:12:ILE:CD1	1:A:14:PHE:HZ	2.28	0.47
1:A:27:LEU:HD21	1:A:268:PRO:HB3	1.97	0.47
1:A:68:ASN:OD1	1:A:71:THR:HG23	2.13	0.47
1:A:100:GLU:O	1:A:104:TYR:HD2	1.97	0.47
1:A:332:PRO:HB3	1:A:372:ALA:CB	2.44	0.47
1:A:373:PHE:HB3	1:A:383:LEU:HD21	1.95	0.47
1:A:397:TYR:HB3	2:B:374:ARG:HB2	1.95	0.47
2:B:44:ASP:HB2	2:B:47:SER:HB3	1.97	0.47
2:B:134:ALA:O	2:B:138:GLN:HG2	2.15	0.47
2:B:369:TRP:O	2:B:371:ASP:N	2.47	0.47
4:D:5:DA:C6	4:D:6:DC:C2	3.03	0.47
1:A:267:LYS:HZ2	1:A:307:ASN:HB3	1.38	0.47
1:A:307:ASN:O	1:A:467:TYR:OH	2.32	0.47
1:A:319:PRO:HD2	1:A:320:TRP:CZ3	2.49	0.47
2:B:109:ASN:C	2:B:113:VAL:HG23	2.33	0.47
2:B:151:ASN:O	2:B:155:GLN:OE1	2.33	0.47
2:B:8:SER:OG	2:B:74:VAL:HG13	2.14	0.47
2:B:218:ALA:HB1	2:B:222:ASP:CB	2.45	0.47
2:B:220:GLU:HG2	2:B:221:TYR:N	2.30	0.47
2:B:318:TYR:HE2	2:B:346:ASP:HA	1.80	0.47
1:A:313:PHE:CE2	1:A:342:ALA:HA	2.50	0.47
2:B:5:ILE:CD1	2:B:135:PHE:CZ	2.98	0.47
2:B:179:ILE:N	2:B:402:LEU:O	2.28	0.47
3:C:15:DG:H2''	3:C:16:DT:OP2	2.15	0.47
1:A:388:ILE:HD11	1:A:459:ILE:HD13	1.97	0.46
2:B:118:ILE:HD11	2:B:131:LEU:CA	2.46	0.46
2:B:211:LYS:CG	2:B:212:GLU:N	2.70	0.46
1:A:267:LYS:NZ	1:A:307:ASN:HD22	2.13	0.46
2:B:88:LEU:CG	2:B:90:ASP:H	2.28	0.46
4:D:8:DA:H2''	4:D:9:DC:O5'	2.15	0.46
1:A:81:VAL:HG11	1:A:82:PHE:CE2	2.50	0.46
1:A:305:LEU:HD22	1:A:346:TYR:CE1	2.46	0.46
1:A:443:ILE:HD12	1:A:456:LEU:HD22	1.95	0.46
2:B:5:ILE:HG22	2:B:5:ILE:O	2.14	0.46
2:B:118:ILE:HD11	2:B:131:LEU:N	2.30	0.46
1:A:288:ILE:HB	1:A:296:ASN:HB3	1.97	0.46
4:D:4:DT:H2''	4:D:5:DA:C8	2.51	0.46
1:A:94:LYS:HD2	1:A:124:LYS:CD	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:GLU:CG	1:A:134:GLU:N	2.78	0.46
2:B:280:LYS:HA	2:B:280:LYS:HD2	1.64	0.46
1:A:225:ARG:HE	1:A:227:SER:CB	2.28	0.46
2:B:44:ASP:HA	2:B:47:SER:HB2	1.98	0.46
2:B:184:GLU:OE1	2:B:240:ARG:HD3	2.15	0.46
2:B:219:TRP:CE3	2:B:221:TYR:CE2	3.04	0.46
2:B:343:PHE:N	2:B:357:GLN:NE2	2.63	0.46
2:B:417:VAL:HG23	2:B:417:VAL:O	2.14	0.46
1:A:44:VAL:HG12	1:A:121:PHE:HD1	1.81	0.46
1:A:58:ASP:OD1	1:A:88:SER:CB	2.64	0.46
1:A:401:GLY:O	2:B:371:ASP:HB3	2.16	0.46
2:B:287:MET:HE3	2:B:290:THR:O	2.16	0.46
1:A:337:ALA:O	1:A:341:GLN:HB2	2.16	0.46
1:A:396:LEU:HB2	1:A:421:TRP:CZ2	2.51	0.46
2:B:8:SER:CA	2:B:77:GLU:OE1	2.63	0.46
2:B:216:THR:HG23	2:B:218:ALA:H	1.81	0.46
4:D:2:DT:C1'	4:D:3:DA:C8	2.95	0.46
1:A:93:PHE:CE2	1:A:95:GLU:HA	2.50	0.46
1:A:339:LEU:CD2	1:A:359:ILE:HD11	2.45	0.46
3:C:19:DA:N1	4:D:3:DA:C6	2.84	0.46
1:A:471:ILE:HD12	1:A:473:ALA:O	2.16	0.46
2:B:344:THR:HG23	2:B:350:LEU:HA	1.98	0.46
1:A:321:TYR:HD2	1:A:322:ASN:H	1.64	0.45
2:B:80:VAL:HG12	2:B:84:VAL:HG23	1.97	0.45
2:B:88:LEU:CD2	2:B:90:ASP:HB3	2.47	0.45
3:C:5:DG:H2''	3:C:6:DT:H73	1.94	0.45
4:D:19:DC:C6	4:D:19:DC:C4'	2.99	0.45
1:A:40:LYS:HB3	1:A:136:VAL:HA	1.97	0.45
1:A:56:TYR:HE1	1:A:256:ILE:HD12	1.81	0.45
1:A:248:ILE:HD11	3:C:1:DT:C2	2.48	0.45
1:A:426:VAL:HG11	1:A:429:LEU:HD12	1.98	0.45
2:B:215:CYS:O	2:B:216:THR:HB	2.17	0.45
2:B:314:GLN:HE21	2:B:363:LYS:CE	2.28	0.45
1:A:4:LEU:HD21	2:B:410:PHE:HD1	1.81	0.45
1:A:141:VAL:C	1:A:142:ILE:HD13	2.37	0.45
2:B:17:PHE:HZ	2:B:120:PHE:HE2	1.57	0.45
2:B:371:ASP:OD1	2:B:372:LYS:N	2.48	0.45
2:B:388:GLN:H	2:B:388:GLN:HG3	1.56	0.45
3:C:9:DT:H2''	3:C:10:DA:O4'	2.17	0.45
1:A:25:ASP:O	1:A:29:LEU:HB2	2.17	0.45
1:A:143:VAL:HG21	4:D:20:DA:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:LEU:HD23	1:A:219:ILE:HD12	1.97	0.45
1:A:248:ILE:HG13	1:A:252:LEU:HD12	1.94	0.45
2:B:8:SER:HB2	2:B:77:GLU:OE1	2.13	0.45
2:B:313:LYS:CD	2:B:318:TYR:CE1	3.00	0.45
4:D:5:DA:H2''	4:D:6:DC:O5'	2.16	0.45
1:A:29:LEU:HA	1:A:29:LEU:HD23	1.40	0.45
1:A:339:LEU:HD13	1:A:343:LEU:HD11	1.98	0.45
1:A:429:LEU:HD11	1:A:472:TYR:CB	2.46	0.45
1:A:460:LEU:HD12	1:A:460:LEU:HA	1.72	0.45
1:A:468:ASN:ND2	1:A:507:ILE:HG21	2.31	0.45
2:B:345:MET:HG2	2:B:351:ILE:HD11	1.97	0.45
1:A:40:LYS:CD	1:A:135:ARG:O	2.62	0.45
1:A:74:MET:HE1	1:A:76:PRO:CA	2.44	0.45
1:A:290:LYS:CB	1:A:290:LYS:NZ	2.77	0.45
1:A:304:PHE:CD2	1:A:308:GLY:HA2	2.47	0.45
1:A:415:GLU:O	1:A:452:ILE:HB	2.16	0.45
2:B:276:ARG:HG3	2:B:276:ARG:NH1	2.32	0.45
3:C:18:DT:N3	4:D:3:DA:N6	2.63	0.45
1:A:466:ASN:ND2	1:A:469:ALA:HB3	2.31	0.45
2:B:321:PHE:HD1	2:B:380:PHE:HD2	1.65	0.45
2:B:321:PHE:CD1	2:B:380:PHE:HD2	2.35	0.45
3:C:19:DA:H2	4:D:3:DA:C2	2.31	0.45
1:A:4:LEU:HD21	2:B:410:PHE:CD1	2.52	0.45
1:A:113:ARG:NH1	1:A:157:LEU:HD13	2.32	0.45
1:A:122:ASN:ND2	1:A:213:ARG:HB3	2.32	0.45
2:B:2:ARG:N	2:B:2:ARG:CD	2.73	0.45
2:B:314:GLN:HE21	2:B:363:LYS:NZ	2.14	0.45
2:B:368:TRP:O	2:B:369:TRP:CE3	2.70	0.45
1:A:13:LEU:CD1	1:A:17:GLY:HA2	2.38	0.45
1:A:339:LEU:HD22	1:A:339:LEU:HA	1.82	0.45
1:A:485:LYS:O	1:A:489:ILE:HG13	2.16	0.45
2:B:223:PHE:C	2:B:224:ILE:CD1	2.86	0.45
1:A:97:THR:H	1:A:100:GLU:HG3	1.82	0.45
1:A:140:PHE:HA	1:A:222:GLN:O	2.17	0.45
2:B:270:ASN:HD22	2:B:270:ASN:N	2.08	0.45
2:B:350:LEU:N	2:B:350:LEU:CD1	2.73	0.45
1:A:100:GLU:O	1:A:104:TYR:CD2	2.70	0.44
1:A:207:HIS:CD2	1:A:208:ASP:OD1	2.70	0.44
1:A:222:GLN:HG3	1:A:263:LYS:CD	2.46	0.44
1:A:328:TYR:O	1:A:329:HIS:CG	2.70	0.44
2:B:58:CYS:O	2:B:59:LYS:CD	2.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:158:PHE:N	2:B:158:PHE:HD1	2.14	0.44
2:B:182:PRO:HG2	2:B:217:PHE:HB3	1.99	0.44
3:C:11:DG:H2'	3:C:12:DG:C4	2.52	0.44
1:A:65:TYR:N	1:A:65:TYR:CD2	2.85	0.44
1:A:288:ILE:N	1:A:296:ASN:O	2.50	0.44
1:A:364:ARG:HA	1:A:446:ASN:OD1	2.17	0.44
1:A:397:TYR:CD1	1:A:437:VAL:HG11	2.52	0.44
2:B:46:TRP:O	2:B:46:TRP:CD1	2.70	0.44
3:C:15:DG:N2	3:C:16:DT:C2	2.85	0.44
1:A:153:PRO:O	1:A:154:ASN:HB3	2.17	0.44
1:A:305:LEU:HD21	1:A:346:TYR:CD1	2.52	0.44
2:B:9:HIS:HD1	2:B:11:THR:HG23	1.82	0.44
2:B:23:LEU:CD1	2:B:154:TYR:HB2	2.47	0.44
2:B:219:TRP:CZ3	2:B:240:ARG:NH2	2.82	0.44
2:B:220:GLU:OE2	2:B:221:TYR:CE2	2.70	0.44
2:B:294:TRP:O	2:B:294:TRP:CG	2.71	0.44
2:B:26:ILE:HD12	2:B:153:LEU:HD23	2.00	0.44
2:B:206:PRO:CD	2:B:395:VAL:HA	2.48	0.44
2:B:251:TYR:OH	2:B:256:ILE:CG1	2.65	0.44
2:B:251:TYR:CZ	2:B:253:THR:OG1	2.70	0.44
2:B:251:TYR:HD1	2:B:251:TYR:O	2.01	0.44
1:A:22:ASP:HB2	1:A:428:LYS:HD2	1.98	0.44
1:A:333:LYS:HD2	1:A:333:LYS:HA	1.76	0.44
1:A:357:VAL:HB	1:A:383:LEU:HD12	2.00	0.44
2:B:96:PRO:O	2:B:118:ILE:HG21	2.11	0.44
2:B:233:TYR:CZ	2:B:237:GLU:HG2	2.52	0.44
2:B:266:VAL:HG22	2:B:329:LEU:CD2	2.39	0.44
2:B:305:PHE:O	2:B:308:ILE:N	2.41	0.44
1:A:122:ASN:HD21	1:A:213:ARG:HB3	1.82	0.44
2:B:42:GLY:O	2:B:45:PHE:CD1	2.70	0.44
2:B:43:VAL:O	2:B:45:PHE:CD1	2.70	0.44
2:B:295:ILE:HD13	2:B:300:LEU:HD11	1.98	0.44
2:B:393:LEU:CD1	2:B:403:ILE:HG12	2.47	0.44
1:A:339:LEU:HD21	1:A:359:ILE:HD11	1.98	0.44
2:B:305:PHE:CZ	2:B:306:GLU:OE1	2.70	0.44
3:C:18:DT:N3	3:C:19:DA:C6	2.86	0.44
1:A:15:ALA:HB2	1:A:32:PRO:O	2.17	0.44
2:B:192:TRP:HD1	2:B:193:ARG:N	2.14	0.44
2:B:251:TYR:CD1	2:B:251:TYR:O	2.70	0.44
2:B:309:LYS:NZ	2:B:312:GLY:HA2	2.33	0.44
1:A:94:LYS:HZ2	1:A:124:LYS:HZ2	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:LEU:O	1:A:105:LEU:HD12	2.17	0.44
2:B:220:GLU:OE1	2:B:221:TYR:CZ	2.70	0.44
1:A:46:THR:O	1:A:49:GLY:N	2.51	0.43
2:B:318:TYR:N	2:B:344:THR:O	2.51	0.43
2:B:364:GLN:NE2	2:B:364:GLN:HA	2.32	0.43
1:A:463:THR:HB	1:A:474:ASP:O	2.18	0.43
1:A:468:ASN:ND2	1:A:507:ILE:CG1	2.77	0.43
2:B:413:LYS:H	2:B:413:LYS:HG3	1.67	0.43
3:C:19:DA:H2	4:D:3:DA:N3	2.15	0.43
1:A:102:ARG:O	1:A:106:PHE:CD2	2.70	0.43
1:A:393:PRO:CG	1:A:419:PHE:CE1	2.82	0.43
2:B:182:PRO:HG2	2:B:217:PHE:CD1	2.53	0.43
2:B:309:LYS:O	2:B:319:TRP:HH2	2.01	0.43
1:A:402:ALA:O	2:B:370:ASN:N	2.51	0.43
2:B:173:SER:OG	2:B:175:TRP:N	2.32	0.43
1:A:212:ALA:HB1	1:A:493:SER:HB2	2.00	0.43
1:A:468:ASN:CG	1:A:507:ILE:CG2	2.86	0.43
2:B:42:GLY:O	2:B:45:PHE:CG	2.70	0.43
2:B:69:ASN:HD21	2:B:103:LEU:HD21	1.83	0.43
2:B:219:TRP:CB	2:B:221:TYR:CE2	2.85	0.43
1:A:282:GLY:O	1:A:301:ALA:HA	2.19	0.43
1:A:418:ALA:HB3	1:A:456:LEU:HD21	2.00	0.43
2:B:34:CYS:O	2:B:37:LEU:HD22	2.18	0.43
2:B:142:LYS:HG2	2:B:143:LYS:O	2.19	0.43
3:C:11:DG:H2'	3:C:12:DG:C8	2.53	0.43
1:A:105:LEU:HD12	1:A:113:ARG:HD2	2.01	0.43
2:B:2:ARG:HD3	2:B:2:ARG:H	1.78	0.43
2:B:103:LEU:HD12	2:B:103:LEU:HA	1.72	0.43
2:B:236:GLN:H	2:B:236:GLN:CD	2.12	0.43
1:A:271:LEU:HA	1:A:271:LEU:HD23	1.81	0.43
2:B:14:ASP:CB	2:B:63:VAL:HG11	2.48	0.43
2:B:219:TRP:CZ3	2:B:240:ARG:CZ	3.02	0.43
3:C:18:DT:O4	3:C:19:DA:N6	2.52	0.43
1:A:312:VAL:HG11	1:A:506:TYR:CE1	2.54	0.43
2:B:41:LYS:HE2	2:B:41:LYS:HB3	1.71	0.43
2:B:176:PHE:CG	2:B:407:PRO:HB3	2.54	0.43
2:B:195:PRO:O	2:B:195:PRO:HD2	2.19	0.43
2:B:368:TRP:CD1	2:B:368:TRP:N	2.84	0.43
1:A:146:GLU:H	1:A:146:GLU:HG2	1.60	0.42
2:B:61:LEU:HD22	2:B:95:ILE:HB	2.01	0.42
2:B:217:PHE:CE2	2:B:268:LEU:HD12	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:321:PHE:CD1	2:B:380:PHE:CD2	3.07	0.42
2:B:231:GLU:H	2:B:231:GLU:HG3	1.64	0.42
2:B:258:ASN:O	2:B:259:TYR:C	2.57	0.42
1:A:120:LEU:C	1:A:120:LEU:CD1	2.85	0.42
1:A:406:MET:HE3	1:A:406:MET:HB2	1.60	0.42
2:B:9:HIS:CD2	2:B:34:CYS:SG	3.12	0.42
2:B:381:ILE:CG2	2:B:405:ASN:O	2.68	0.42
1:A:262:TYR:CE2	1:A:309:ASP:OD1	2.73	0.42
2:B:27:GLY:HA3	2:B:150:SER:HB2	2.02	0.42
2:B:181:PHE:HZ	2:B:269:ILE:HD11	1.84	0.42
2:B:255:PHE:CE2	2:B:256:ILE:HG12	2.54	0.42
3:C:11:DG:H2'	3:C:12:DG:C5	2.54	0.42
1:A:11:SER:O	1:A:272:GLY:N	2.51	0.42
2:B:4:LYS:NZ	2:B:52:GLU:CD	2.72	0.42
1:A:12:ILE:HG21	1:A:464:LYS:HB3	2.00	0.42
1:A:138:VAL:CB	1:A:140:PHE:CE2	3.02	0.42
1:A:214:LEU:CD2	1:A:219:ILE:HD12	2.50	0.42
1:A:464:LYS:HZ2	1:A:473:ALA:HB2	1.84	0.42
1:A:503:PHE:O	1:A:506:TYR:N	2.53	0.42
2:B:78:LEU:O	2:B:78:LEU:HD23	2.19	0.42
2:B:120:PHE:CE1	2:B:128:LEU:N	2.83	0.42
1:A:57:LEU:CD1	1:A:88:SER:HA	2.45	0.42
1:A:93:PHE:HD2	1:A:94:LYS:N	2.17	0.42
1:A:206:PHE:HB3	4:D:20:DA:H62	1.81	0.42
1:A:74:MET:CE	1:A:76:PRO:CA	2.98	0.42
1:A:74:MET:CE	1:A:76:PRO:HA	2.46	0.42
1:A:133:GLU:HG2	1:A:134:GLU:HG2	2.02	0.42
1:A:429:LEU:HD23	1:A:429:LEU:HA	1.87	0.42
2:B:142:LYS:CG	2:B:143:LYS:N	2.83	0.42
2:B:221:TYR:O	2:B:224:ILE:HD13	2.19	0.42
2:B:370:ASN:C	2:B:370:ASN:ND2	2.72	0.42
3:C:6:DT:H2''	3:C:7:DA:H8	1.82	0.42
1:A:365:PHE:HB2	1:A:447:LYS:CG	2.46	0.42
2:B:211:LYS:HE2	2:B:213:TYR:HE2	1.85	0.42
3:C:10:DA:H2'	3:C:11:DG:C1'	2.49	0.42
3:C:18:DT:H2''	3:C:19:DA:C5'	2.49	0.42
1:A:12:ILE:CD1	1:A:14:PHE:CZ	3.03	0.42
1:A:302:GLN:HG2	1:A:302:GLN:H	1.75	0.42
1:A:394:LEU:HD23	1:A:394:LEU:HA	1.84	0.42
1:A:416:LYS:O	1:A:445:ILE:HG13	2.19	0.42
2:B:53:ILE:HA	2:B:57:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:210:TYR:HH	2:B:256:ILE:HG22	1.76	0.42
2:B:284:GLU:HG3	2:B:284:GLU:O	2.20	0.42
1:A:66:ASN:ND2	1:A:66:ASN:N	2.68	0.41
1:A:133:GLU:CD	1:A:134:GLU:N	2.73	0.41
1:A:351:LYS:HD2	1:A:351:LYS:H	1.82	0.41
2:B:219:TRP:CE3	2:B:221:TYR:HE2	2.38	0.41
2:B:295:ILE:CD1	2:B:300:LEU:HD11	2.50	0.41
2:B:410:PHE:N	2:B:410:PHE:HD2	2.18	0.41
4:D:9:DC:H2''	4:D:10:DC:C5	2.55	0.41
1:A:396:LEU:HD23	1:A:396:LEU:HA	1.82	0.41
1:A:13:LEU:HD12	1:A:13:LEU:O	2.19	0.41
1:A:328:TYR:O	1:A:329:HIS:ND1	2.52	0.41
2:B:273:PHE:CE1	2:B:325:ALA:HB2	2.55	0.41
2:B:353:SER:HB2	2:B:356:ILE:HD11	2.02	0.41
2:B:6:PHE:HE2	2:B:33:TRP:CE3	2.38	0.41
2:B:120:PHE:CE1	2:B:127:GLY:O	2.69	0.41
2:B:300:LEU:HD21	2:B:383:PHE:CD2	2.56	0.41
1:A:40:LYS:HE2	1:A:90:ASN:OD1	2.21	0.41
1:A:110:THR:O	1:A:114:THR:N	2.42	0.41
1:A:207:HIS:HB2	1:A:223:ILE:HD12	2.01	0.41
1:A:390:LYS:NZ	1:A:441:ILE:CG2	2.77	0.41
1:A:418:ALA:HB1	1:A:456:LEU:HD11	2.02	0.41
2:B:216:THR:HG23	2:B:218:ALA:N	2.36	0.41
2:B:218:ALA:HB1	2:B:222:ASP:HB2	2.02	0.41
2:B:393:LEU:HD12	2:B:403:ILE:HG12	2.03	0.41
3:C:19:DA:H2''	3:C:20:DG:C8	2.55	0.41
1:A:101:ILE:O	1:A:105:LEU:HB3	2.20	0.41
1:A:322:ASN:OD1	1:A:325:LYS:HB2	2.21	0.41
1:A:323:PRO:HG2	1:A:324:GLU:N	2.36	0.41
2:B:48:THR:O	2:B:52:GLU:HG2	2.21	0.41
2:B:198:PHE:CD1	2:B:199:ASP:N	2.89	0.41
2:B:219:TRP:HE3	2:B:221:TYR:CE2	2.38	0.41
1:A:10:PRO:HG2	1:A:464:LYS:HG3	2.03	0.41
1:A:295:GLN:O	1:A:319:PRO:HA	2.20	0.41
1:A:398:LYS:HE3	1:A:398:LYS:HB3	1.87	0.41
2:B:374:ARG:O	2:B:378:LEU:HD13	2.21	0.41
1:A:135:ARG:HD2	1:A:135:ARG:HA	1.67	0.41
1:A:281:LEU:HB3	1:A:359:ILE:HG12	2.03	0.41
1:A:501:LEU:CD1	1:A:506:TYR:CE2	2.93	0.41
2:B:19:ARG:CG	2:B:158:PHE:CE2	2.81	0.41
2:B:26:ILE:CD1	2:B:153:LEU:CD2	2.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:81:ALA:O	2:B:85:LYS:CA	2.67	0.41
2:B:192:TRP:HZ2	2:B:232:THR:HG21	1.85	0.41
2:B:219:TRP:CB	2:B:221:TYR:CD2	2.98	0.41
2:B:266:VAL:HG21	2:B:329:LEU:CD2	2.48	0.41
2:B:418:THR:HG23	2:B:418:THR:O	2.19	0.41
1:A:398:LYS:HG3	2:B:171:TYR:CE1	2.56	0.41
2:B:10:ALA:CB	2:B:71:ARG:HD3	2.51	0.41
2:B:333:PRO:C	2:B:334:VAL:CG1	2.90	0.41
1:A:24:ARG:CZ	1:A:73:PRO:HD3	2.51	0.40
1:A:274:ILE:HG21	1:A:306:ASP:CB	2.50	0.40
1:A:391:SER:C	1:A:393:PRO:HD3	2.40	0.40
1:A:415:GLU:O	1:A:452:ILE:CG2	2.68	0.40
2:B:187:PHE:O	2:B:238:SER:CA	2.65	0.40
1:A:157:LEU:HD23	1:A:162:VAL:HG23	2.04	0.40
1:A:365:PHE:O	1:A:447:LYS:HE2	2.21	0.40
1:A:393:PRO:O	1:A:393:PRO:CD	2.69	0.40
1:A:406:MET:HB3	2:B:416:TYR:CE2	2.55	0.40
2:B:294:TRP:CZ3	2:B:320:HIS:CD2	3.08	0.40
4:D:17:DC:H4'	4:D:18:DT:OP1	2.22	0.40
1:A:12:ILE:CG2	1:A:464:LYS:HB3	2.51	0.40
1:A:45:GLY:O	1:A:93:PHE:CE2	2.75	0.40
1:A:366:ASN:CG	1:A:369:GLU:CB	2.88	0.40
2:B:118:ILE:CG2	2:B:118:ILE:O	2.70	0.40
2:B:177:PRO:HA	2:B:334:VAL:HG12	2.02	0.40
4:D:5:DA:N1	4:D:6:DC:O2	2.54	0.40
4:D:19:DC:C6	4:D:19:DC:C3'	3.04	0.40
1:A:102:ARG:O	1:A:106:PHE:HD2	2.04	0.40
1:A:210:LEU:CD2	1:A:210:LEU:C	2.90	0.40
1:A:307:ASN:O	1:A:467:TYR:CZ	2.75	0.40
2:B:6:PHE:CE2	2:B:33:TRP:CE3	3.09	0.40
2:B:88:LEU:HG	2:B:90:ASP:H	1.86	0.40
2:B:175:TRP:HB2	2:B:408:LEU:HD13	2.02	0.40
2:B:219:TRP:CB	2:B:221:TYR:HE2	2.26	0.40
2:B:220:GLU:CD	2:B:221:TYR:CE2	2.95	0.40
2:B:296:GLU:HB2	2:B:348:ILE:CG2	2.51	0.40
1:A:300:ALA:HB2	1:A:490:LEU:HD21	2.03	0.40
1:A:468:ASN:ND2	1:A:507:ILE:CG2	2.84	0.40
2:B:320:HIS:CD2	2:B:320:HIS:N	2.89	0.40
2:B:381:ILE:CG2	2:B:405:ASN:CA	3.00	0.40
3:C:10:DA:N6	3:C:11:DG:N1	2.69	0.40
4:D:7:DA:H2'	4:D:8:DA:H5''	2.02	0.40

All (3) 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:A:352:SER:OG	2:B:156:GLN:OE1[4_555]	1.55	0.65
1:A:325:LYS:NZ	2:B:301:GLU:OE2[3_565]	1.56	0.64
2:B:103:LEU:O	2:B:105:TYR:N[6_554]	2.17	0.03

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	470/507 (93%)	451 (96%)	17 (4%)	2 (0%)	30	59
2	B	417/421 (99%)	396 (95%)	19 (5%)	2 (0%)	25	53
All	All	887/928 (96%)	847 (96%)	36 (4%)	4 (0%)	25	53

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	392	LYS
2	B	414	MET
1	A	393	PRO
2	B	195	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	414/446 (93%)	327 (79%)	87 (21%)	1	2
2	B	372/387 (96%)	282 (76%)	90 (24%)	0	1
All	All	786/833 (94%)	609 (78%)	177 (22%)	1	2

All (177) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	GLU
1	A	13	LEU
1	A	19	LYS
1	A	27	LEU
1	A	34	ASN
1	A	35	GLN
1	A	48	LYS
1	A	50	LEU
1	A	56	TYR
1	A	59	LYS
1	A	65	TYR
1	A	68	ASN
1	A	69	ASN
1	A	74	MET
1	A	84	CYS
1	A	85	LYS
1	A	93	PHE
1	A	97	THR
1	A	98	ASP
1	A	111	HIS
1	A	120	LEU
1	A	122	ASN
1	A	123	ASP
1	A	127	THR
1	A	137	ASP
1	A	140	PHE
1	A	145	GLU
1	A	146	GLU
1	A	163	GLN
1	A	164	THR
1	A	165	LYS
1	A	205	GLN
1	A	209	GLN
1	A	213	ARG
1	A	214	LEU

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Mol	Chain	Res	Type
1	A	215	LEU
1	A	217	HIS
1	A	222	GLN
1	A	225	ARG
1	A	228	THR
1	A	232	ARG
1	A	257	SER
1	A	267	LYS
1	A	275	ARG
1	A	281	LEU
1	A	286	LYS
1	A	289	GLU
1	A	293	ASN
1	A	299	CYS
1	A	302	GLN
1	A	321	TYR
1	A	325	LYS
1	A	333	LYS
1	A	334	GLU
1	A	339	LEU
1	A	340	THR
1	A	350	ASN
1	A	351	LYS
1	A	352	SER
1	A	362	ARG
1	A	364	ARG
1	A	366	ASN
1	A	367	ASP
1	A	368	GLU
1	A	370	TRP
1	A	375	GLU
1	A	379	LYS
1	A	391	SER
1	A	393	PRO
1	A	394	LEU
1	A	395	LYS
1	A	399	THR
1	A	405	ILE
1	A	407	ARG
1	A	417	LYS
1	A	423	LEU
1	A	442	PHE

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Mol	Chain	Res	Type
1	A	444	GLU
1	A	445	ILE
1	A	474	ASP
1	A	480	LEU
1	A	494	THR
1	A	496	ILE
1	A	497	LYS
1	A	498	THR
1	A	503	PHE
1	A	504	LYS
2	B	1	MET
2	B	2	ARG
2	B	13	GLU
2	B	18	THR
2	B	22	SER
2	B	31	GLU
2	B	35	ASP
2	B	37	LEU
2	B	45	PHE
2	B	48	THR
2	B	51	LYS
2	B	53	ILE
2	B	54	ARG
2	B	56	ASN
2	B	59	LYS
2	B	64	SER
2	B	71	ARG
2	B	76	LYS
2	B	78	LEU
2	B	83	LYS
2	B	87	HIS
2	B	88	LEU
2	B	92	MET
2	B	104	SER
2	B	105	TYR
2	B	106	ASP
2	B	110	ILE
2	B	128	LEU
2	B	133	ASP
2	B	138	GLN
2	B	139	ASN
2	B	154	TYR

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Mol	Chain	Res	Type
2	B	159	LEU
2	B	163	GLN
2	B	181	PHE
2	B	186	ARG
2	B	190	TYR
2	B	192	TRP
2	B	194	LEU
2	B	196	LYS
2	B	197	GLN
2	B	208	ILE
2	B	209	ARG
2	B	213	TYR
2	B	214	LEU
2	B	221	TYR
2	B	223	PHE
2	B	224	ILE
2	B	225	HIS
2	B	238	SER
2	B	239	ILE
2	B	248	SER
2	B	255	PHE
2	B	257	ARG
2	B	270	ASN
2	B	276	ARG
2	B	280	LYS
2	B	288	SER
2	B	290	THR
2	B	296	GLU
2	B	297	LYS
2	B	302	LYS
2	B	316	ASN
2	B	317	LYS
2	B	338	SER
2	B	344	THR
2	B	345	MET
2	B	348	ILE
2	B	350	LEU
2	B	353	SER
2	B	354	LYS
2	B	356	ILE
2	B	360	SER
2	B	361	ARG

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Mol	Chain	Res	Type
2	B	363	LYS
2	B	369	TRP
2	B	370	ASN
2	B	372	LYS
2	B	373	TRP
2	B	374	ARG
2	B	385	SER
2	B	387	ASP
2	B	388	GLN
2	B	395	VAL
2	B	403	ILE
2	B	406	LYS
2	B	408	LEU
2	B	410	PHE
2	B	413	LYS
2	B	415	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	ASN
1	A	163	GLN
1	A	209	GLN
1	A	217	HIS
1	A	302	GLN
1	A	341	GLN
1	A	350	ASN
1	A	366	ASN
1	A	468	ASN
1	A	484	ASN
2	B	69	ASN
2	B	138	GLN
2	B	139	ASN
2	B	188	HIS
2	B	197	GLN
2	B	225	HIS
2	B	226	GLN
2	B	270	ASN
2	B	314	GLN
2	B	316	ASN
2	B	357	GLN
2	B	364	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	474/507 (93%)	0.24	22 (4%) 38 33	14, 43, 96, 139	0
2	B	419/421 (99%)	0.55	33 (7%) 20 20	21, 60, 132, 154	0
3	C	21/21 (100%)	1.08	1 (4%) 36 32	52, 76, 96, 105	0
4	D	21/21 (100%)	1.02	1 (4%) 36 32	55, 73, 85, 90	0
All	All	935/970 (96%)	0.42	57 (6%) 28 26	14, 52, 122, 154	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	166	SER	5.7
1	A	164	THR	5.0
1	A	167	LEU	4.1
2	B	192	TRP	3.7
1	A	161	LEU	3.6
2	B	232	THR	3.6
2	B	41	LYS	3.5
2	B	187	PHE	3.5
1	A	165	LYS	3.4
2	B	289	LYS	3.4
2	B	218	ALA	3.2
2	B	235	GLY	3.2
2	B	241	ILE	3.2
2	B	255	PHE	3.1
2	B	46	TRP	2.9
1	A	315	GLY	2.9
2	B	88	LEU	2.9
2	B	188	HIS	2.8
1	A	38	GLY	2.7
2	B	195	PRO	2.7
1	A	156	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	227	LEU	2.6
1	A	163	GLN	2.6
2	B	230	THR	2.6
1	A	323	PRO	2.5
1	A	205	GLN	2.5
1	A	168	ILE	2.5
2	B	290	THR	2.4
2	B	247	LEU	2.4
1	A	204	ALA	2.4
1	A	153	PRO	2.4
2	B	214	LEU	2.4
2	B	239	ILE	2.4
2	B	184	GLU	2.4
1	A	162	VAL	2.4
2	B	217	PHE	2.3
1	A	316	GLU	2.3
2	B	220	GLU	2.3
1	A	317	VAL	2.3
1	A	324	GLU	2.3
2	B	190	TYR	2.2
1	A	390	LYS	2.2
2	B	210	TYR	2.2
2	B	225	HIS	2.2
1	A	414	ASP	2.2
4	D	9	DC	2.2
2	B	233	TYR	2.2
2	B	186	ARG	2.1
2	B	288	SER	2.1
2	B	338	SER	2.1
2	B	211	LYS	2.1
1	A	507	ILE	2.1
2	B	256	ILE	2.1
1	A	314	LYS	2.1
3	C	11	DG	2.1
2	B	223	PHE	2.0
2	B	402	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
5	MG	D	101	1/1	0.94	0.32	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.