



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 03:57 AM UTC

PDB ID : 3UUS / pdb_00003uus
Title : Crystal structure of the dATP inhibited E. coli class Ia ribonucleotide reductase complex
Authors : Zimanyi, C.M.; Drennan, C.L.
Deposited on : 2011-11-28
Resolution : 5.65 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

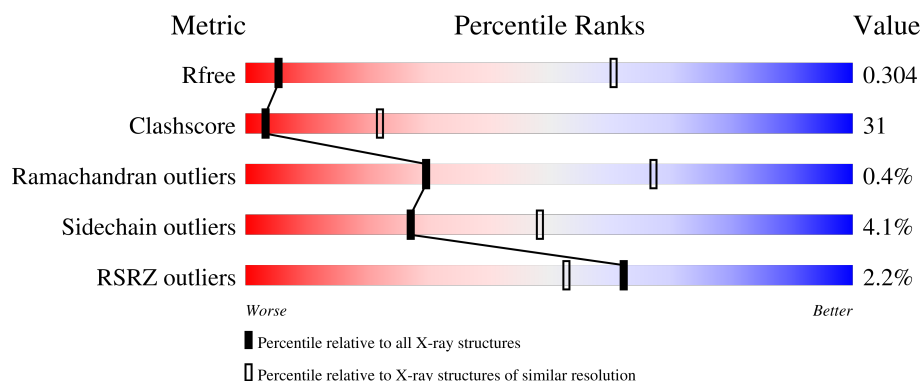
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.65 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	1104 (7.32-4.00)
Clashscore	190562	1165 (7.32-4.00)
Ramachandran outliers	187476	1000 (7.32-4.00)
Sidechain outliers	187428	1031 (7.36-3.96)
RSRZ outliers	180081	1097 (7.32-4.00)

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	761	3% 47% 45% . .
1	B	761	2% 46% 47% . .
1	C	761	3% 49% 44% . .
1	D	761	2% 50% 43% . .
2	E	375	% 48% 43% . 7%

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Mol	Chain	Length	Quality of chain
2	F	375	% 49% 43% 7%
2	G	375	% 49% 44% 6%
2	H	375	% 47% 45% 7%

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
3	DTP	A	800	-	-	X	-
3	DTP	C	800	-	-	X	-
3	DTP	D	800	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 35029 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.

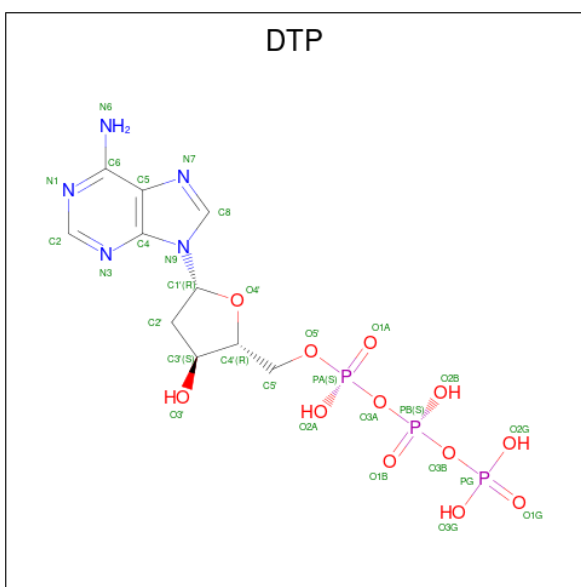
- Molecule 1 is a protein called Ribonucleoside-diphosphate reductase 1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	732	Total	C	N	O	S	0	0	0
			5829	3702	1001	1102	24			
1	B	732	Total	C	N	O	S	0	0	0
			5829	3702	1001	1102	24			
1	C	732	Total	C	N	O	S	0	0	0
			5829	3702	1001	1102	24			
1	D	732	Total	C	N	O	S	0	0	0
			5829	3702	1001	1102	24			

- Molecule 2 is a protein called Ribonucleoside-diphosphate reductase 1 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	348	Total	C	N	O	S	0	0	0
			2855	1824	474	544	13			
2	F	348	Total	C	N	O	S	0	0	0
			2855	1824	474	544	13			
2	G	352	Total	C	N	O	S	0	0	0
			2885	1841	478	553	13			
2	H	350	Total	C	N	O	S	0	0	0
			2870	1833	476	548	13			

- Molecule 3 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$)



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	A	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	B	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	B	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	C	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	C	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	D	1	Total 30	C 10	N 5	O 12	P 3	0	0
3	D	1	Total 30	C 10	N 5	O 12	P 3	0	0

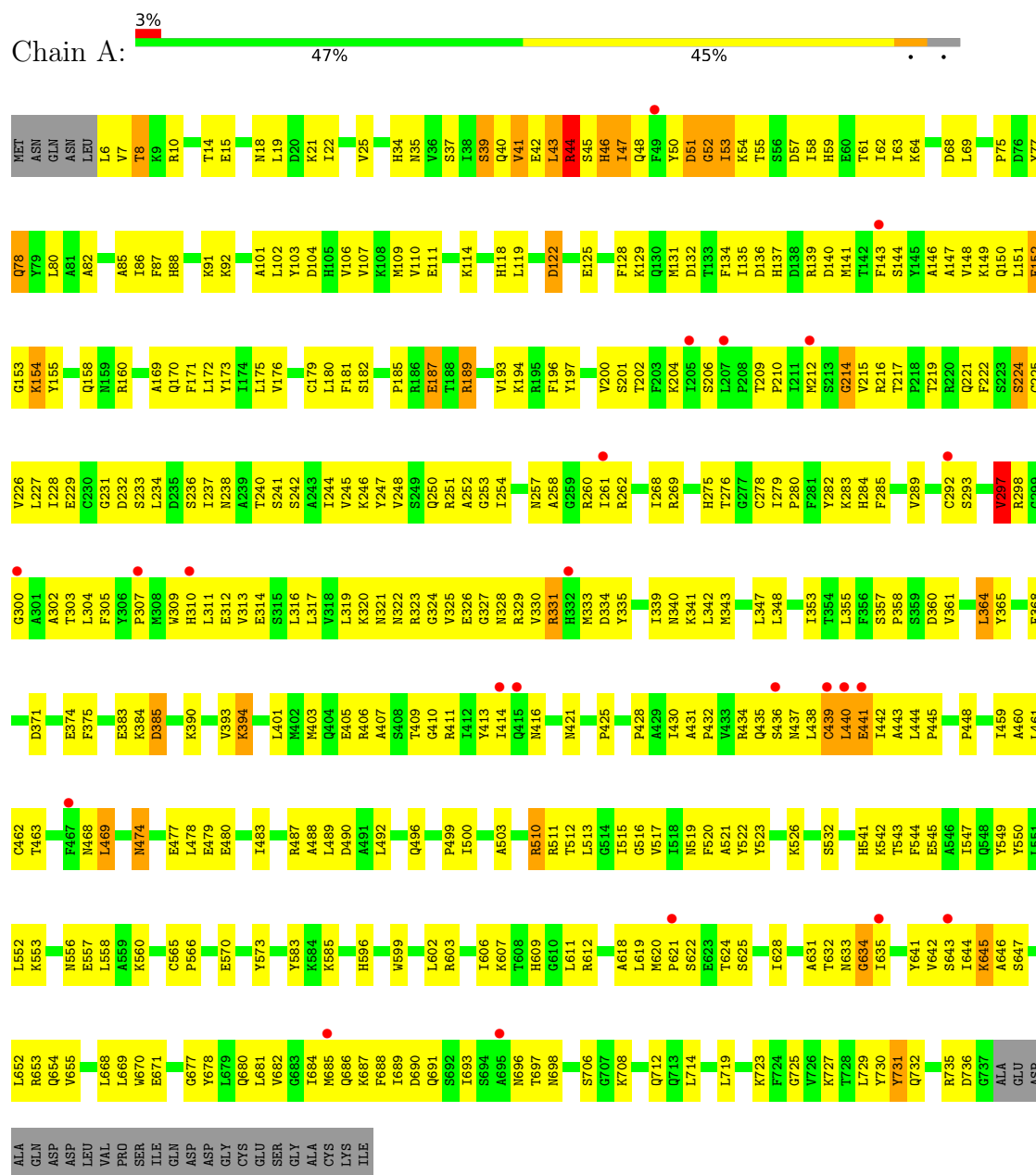
- Molecule 4 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	2	Total Fe 2 2	0	0
4	F	2	Total Fe 2 2	0	0
4	G	2	Total Fe 2 2	0	0
4	H	2	Total Fe 2 2	0	0

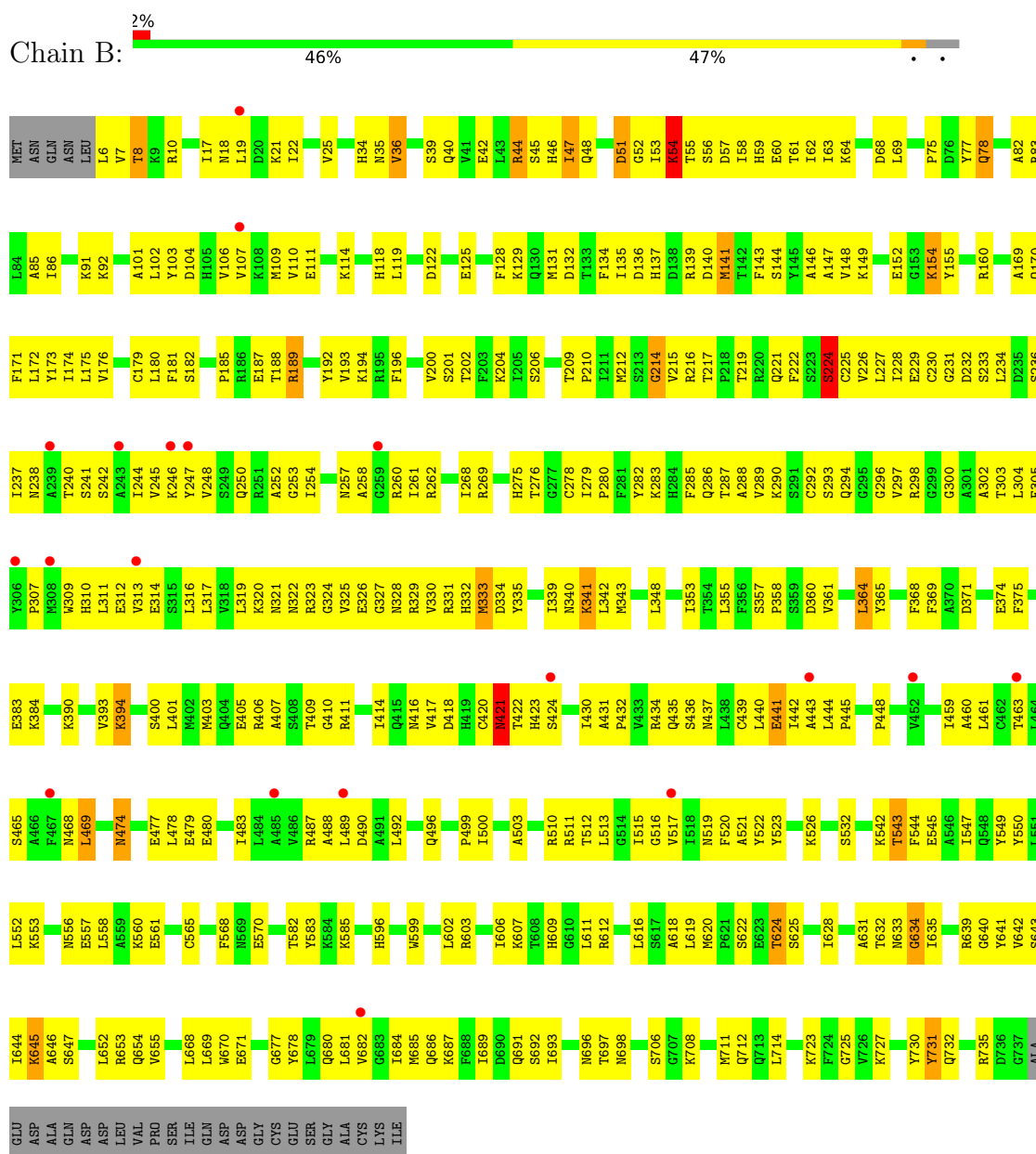
3 Residue-property plots

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.

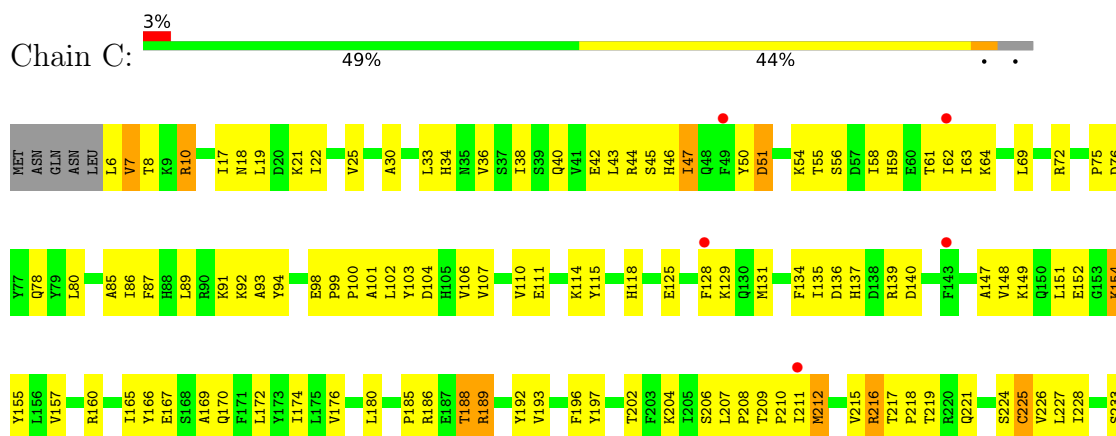
- Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha



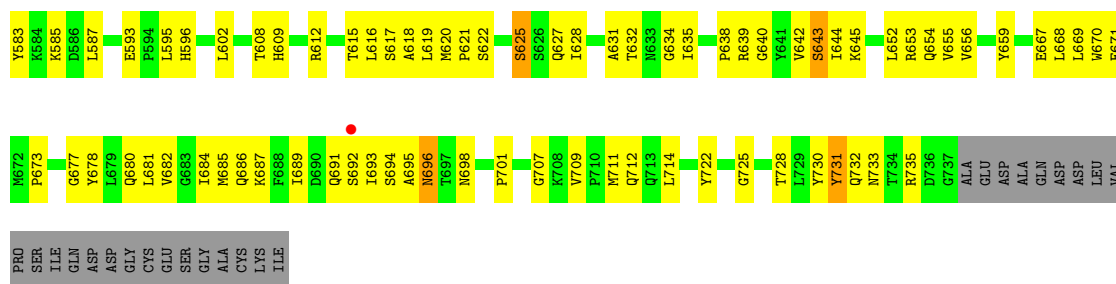
- Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha



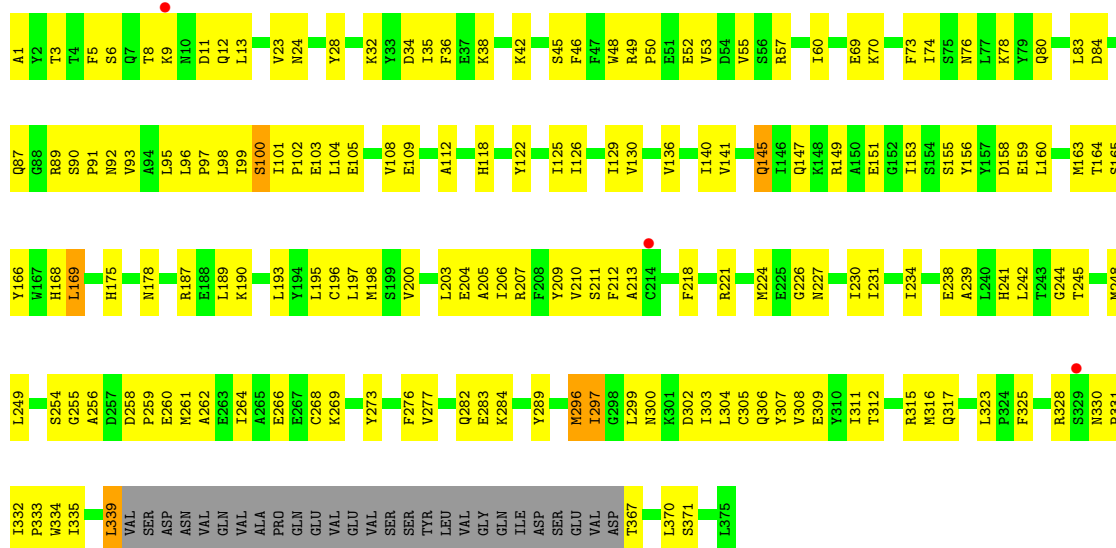
• Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha



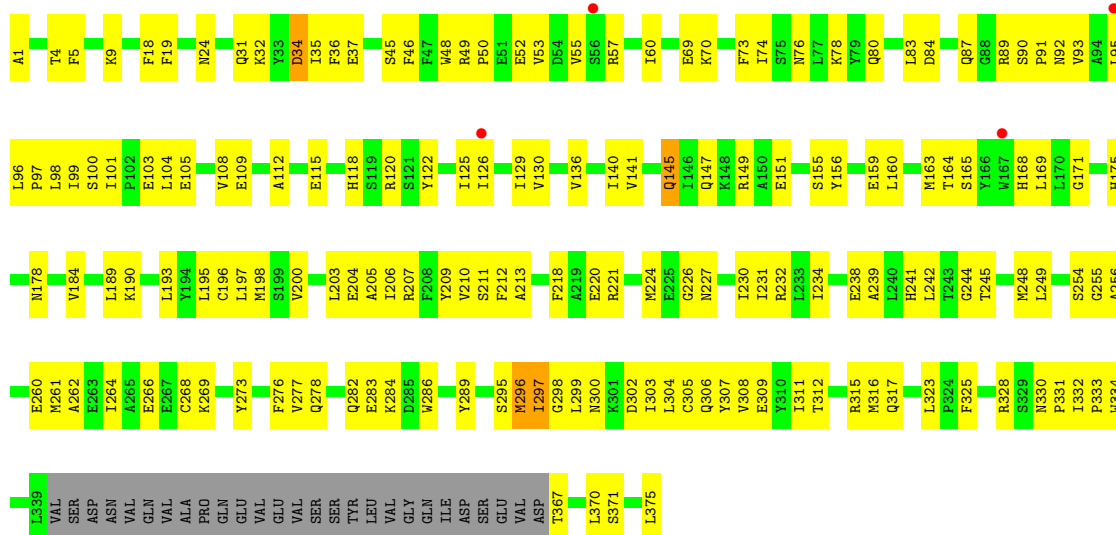




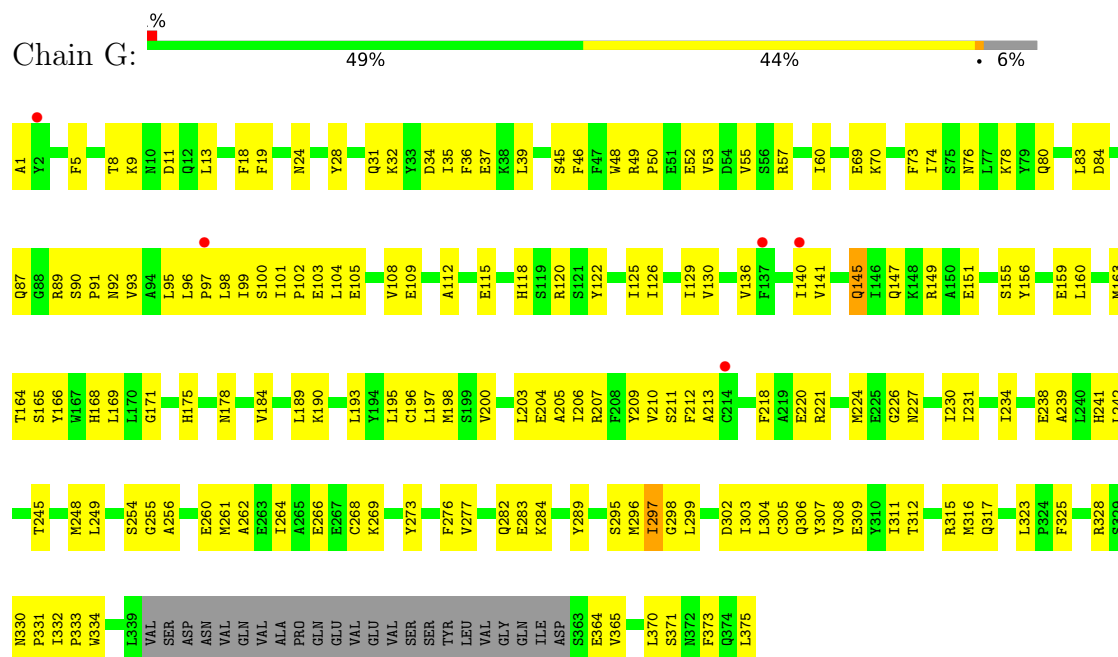
• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



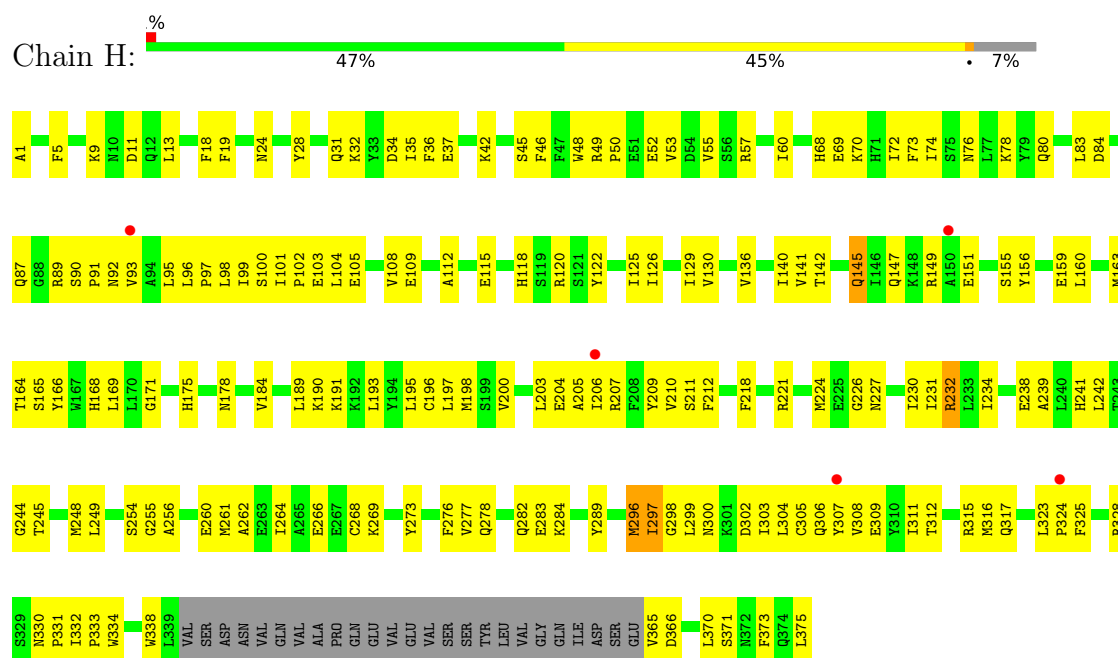
• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



- Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



- Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	287.36Å 153.46Å 169.42Å 90.00° 119.91° 90.00°	Depositor
Resolution (Å)	50.00 – 5.65 50.00 – 5.65	Depositor EDS
% Data completeness (in resolution range)	91.2 (50.00-5.65) 91.0 (50.00-5.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 5.73Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.257 , 0.303 0.257 , 0.304	Depositor DCC
R_{free} test set	967 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	194.8	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 203.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	35029	wwPDB-VP
Average B, all atoms (Å ²)	242.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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: FE, DTP

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	0.32	1/5957 (0.0%)	0.80	7/8068 (0.1%)
1	B	0.30	1/5957 (0.0%)	0.80	8/8068 (0.1%)
1	C	0.29	0/5957	0.78	5/8068 (0.1%)
1	D	0.30	1/5957 (0.0%)	0.80	9/8068 (0.1%)
2	E	0.28	0/2919	0.76	3/3957 (0.1%)
2	F	0.28	0/2919	0.74	2/3957 (0.1%)
2	G	0.28	0/2949	0.74	2/3998 (0.1%)
2	H	0.28	0/2934	0.74	2/3978 (0.1%)
All	All	0.29	3/35549 (0.0%)	0.78	38/48162 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	48	GLN	C-N	5.92	1.41	1.33
1	D	48	GLN	C-N	5.91	1.41	1.33
1	B	48	GLN	C-N	5.83	1.41	1.33

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	543	THR	N-CA-C	7.44	119.03	111.07
1	D	429	ALA	N-CA-C	7.12	119.12	111.36
1	D	48	GLN	O-C-N	7.03	132.15	123.01
1	B	48	GLN	O-C-N	6.99	132.09	123.01
1	A	48	GLN	O-C-N	6.96	132.05	123.01
1	D	430	ILE	N-CA-C	6.77	118.38	111.00
1	B	297	VAL	N-CA-C	6.75	117.53	110.72
1	D	608	THR	N-CA-C	6.72	118.40	111.14
1	A	385	ASP	N-CA-C	-6.64	100.20	110.10
1	C	46	HIS	N-CA-C	-6.60	102.83	111.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	46	HIS	N-CA-C	-6.48	102.73	111.54
1	D	46	HIS	N-CA-C	-6.44	102.79	111.54
1	A	46	HIS	N-CA-C	-6.41	102.82	111.54
1	C	608	THR	N-CA-C	6.38	118.31	111.36
1	C	51	ASP	N-CA-C	-6.12	100.99	110.10
2	F	70	LYS	N-CA-C	-6.00	104.82	111.36
2	G	70	LYS	N-CA-C	-6.00	104.82	111.36
2	E	70	LYS	N-CA-C	-5.96	104.78	111.28
2	H	70	LYS	N-CA-C	-5.96	104.78	111.28
1	C	532	SER	N-CA-C	5.87	120.06	113.01
1	D	532	SER	N-CA-C	5.85	120.03	113.01
1	B	421	ASN	N-CA-C	5.64	117.51	111.36
1	B	224	SER	N-CA-C	5.62	117.48	111.36
1	D	99	PRO	O-C-N	5.60	123.78	121.15
1	D	485	ALA	N-CA-C	5.52	117.10	111.14
1	A	44	ARG	N-CA-C	-5.49	105.29	111.28
1	B	441	GLU	N-CA-C	5.45	117.30	111.36
2	E	169	LEU	N-CA-C	5.39	117.24	111.36
1	D	279	ILE	CB-CA-C	-5.32	108.65	113.70
1	C	279	ILE	CB-CA-C	-5.29	108.68	113.70
2	G	32	LYS	N-CA-C	-5.23	105.75	111.82
1	B	469	LEU	N-CA-C	-5.22	105.71	111.71
2	H	32	LYS	N-CA-C	-5.22	105.77	111.82
2	E	32	LYS	N-CA-C	-5.21	105.78	111.82
2	F	32	LYS	N-CA-C	-5.19	105.80	111.82
1	A	297	VAL	N-CA-C	5.19	115.96	110.72
1	A	469	LEU	N-CA-C	-5.18	105.75	111.71
1	A	331	ARG	N-CA-C	5.07	116.81	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5829	0	5753	417	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5829	0	5751	378	0
1	C	5829	0	5751	423	0
1	D	5829	0	5751	416	0
2	E	2855	0	2789	154	0
2	F	2855	0	2789	144	0
2	G	2885	0	2813	143	0
2	H	2870	0	2802	144	0
3	A	60	0	22	19	0
3	B	60	0	22	13	0
3	C	60	0	22	20	0
3	D	60	0	22	18	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
All	All	35029	0	34287	2115	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 (2115) 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:C:206:SER:HB2	1:C:466:ALA:CB	1.42	1.48
2:E:5:PHE:CD1	2:E:24:ASN:HB2	1.61	1.34
1:C:432:PRO:CG	1:C:434:ARG:HD2	1.62	1.30
1:C:206:SER:CB	1:C:466:ALA:HB3	1.63	1.28
1:A:544:PHE:CE2	1:A:685:MET:HG2	1.69	1.25
1:B:303:THR:HA	1:B:334:ASP:O	1.39	1.22
1:C:441:GLU:HB2	1:C:619:LEU:O	1.38	1.22
1:D:7:VAL:CG2	1:D:17:ILE:HG12	1.70	1.20
1:C:208:PRO:CB	1:C:464:LEU:HD11	1.76	1.15
1:A:227:LEU:HB3	1:A:435:GLN:NE2	1.59	1.15
1:A:55:THR:OG1	3:A:800:DTP:H8	1.44	1.15
1:C:6:LEU:CD2	1:C:51:ASP:HB2	1.80	1.12
1:C:432:PRO:CB	1:C:434:ARG:HD2	1.78	1.12
1:B:244:ILE:HG23	1:B:254:ILE:HG13	1.33	1.11
1:C:430:ILE:HG21	1:C:570:GLU:HB3	1.21	1.11
1:A:7:VAL:HB	1:A:15:GLU:O	1.51	1.10
1:B:185:PRO:HG2	1:B:188:THR:OG1	1.50	1.10
1:C:6:LEU:HD22	1:C:51:ASP:CB	1.81	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:THR:HB	1:A:54:LYS:HA	1.30	1.10
1:D:560:LYS:HD3	1:D:609:HIS:CE1	1.86	1.10
1:A:6:LEU:HD13	1:A:51:ASP:OD1	1.49	1.08
1:A:437:ASN:HD21	1:A:439:CYS:HB2	1.15	1.08
1:D:427:ASP:OD1	1:D:428:PRO:HD2	1.52	1.08
1:A:244:ILE:HG23	1:A:254:ILE:HG13	1.32	1.07
1:C:208:PRO:HB3	1:C:464:LEU:CD1	1.83	1.07
1:C:208:PRO:HB3	1:C:464:LEU:HD11	1.14	1.07
2:E:5:PHE:CE1	2:E:24:ASN:HB2	1.90	1.05
1:D:249:SER:HA	1:D:292:CYS:SG	1.96	1.04
1:A:463:THR:CG2	1:A:492:LEU:HD23	1.88	1.02
1:A:293:SER:HB3	1:A:298:ARG:O	1.57	1.02
1:C:432:PRO:HG2	1:C:434:ARG:HD2	1.35	1.02
1:D:40:GLN:OE1	2:E:334:TRP:HB3	1.60	1.01
1:C:227:LEU:HB3	1:C:435:GLN:NE2	1.76	1.01
1:D:186:ARG:HH21	1:D:189:ARG:HH22	1.06	1.01
1:D:514:GLY:CA	1:D:618:ALA:HB3	1.91	1.00
1:C:532:SER:HA	1:C:677:GLY:HA3	1.42	1.00
1:B:6:LEU:HB2	1:B:52:GLY:H	1.26	0.99
1:B:155:TYR:CE1	1:B:209:THR:HG23	1.97	0.99
1:D:532:SER:HA	1:D:677:GLY:HA3	1.43	0.98
1:C:431:ALA:HB1	1:C:445:PRO:HB3	1.45	0.98
1:C:432:PRO:HB2	1:C:434:ARG:HD2	1.42	0.98
1:D:514:GLY:HA2	1:D:618:ALA:HB3	1.45	0.98
1:C:322:ASN:HA	1:C:331:ARG:HE	1.28	0.97
1:D:618:ALA:O	1:D:620:MET:HE3	1.65	0.96
1:B:36:VAL:HG12	1:B:77:TYR:CZ	2.01	0.96
1:D:322:ASN:HA	1:D:331:ARG:HE	1.29	0.95
1:C:6:LEU:HD22	1:C:51:ASP:HB2	0.95	0.95
1:D:7:VAL:HG21	1:D:17:ILE:HG12	1.47	0.95
1:B:40:GLN:O	1:B:44:ARG:HG2	1.68	0.94
1:D:215:VAL:O	1:D:216:ARG:HG2	1.66	0.94
1:A:53:ILE:HD11	1:A:58:ILE:CD1	1.98	0.94
1:B:320:LYS:HB3	1:B:409:THR:HG21	1.47	0.94
1:A:297:VAL:HG12	1:A:298:ARG:CG	1.98	0.94
1:A:670:TRP:CZ2	1:A:735:ARG:HB2	2.03	0.93
1:C:619:LEU:HD13	1:C:693:ILE:HG23	1.50	0.93
1:D:55:THR:OG1	3:D:800:DTP:H8	1.69	0.93
1:D:189:ARG:O	1:D:193:VAL:HG23	1.67	0.93
1:D:290:LYS:HG2	1:D:296:GLY:O	1.69	0.93
1:A:50:TYR:O	1:A:53:ILE:HG22	1.69	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:VAL:HG22	1:D:17:ILE:HG12	1.48	0.93
1:A:439:CYS:HB3	1:A:441:GLU:OE1	1.68	0.92
1:C:185:PRO:HG2	1:C:188:THR:OG1	1.68	0.92
1:D:301:ALA:O	1:D:438:LEU:HD13	1.68	0.92
1:A:618:ALA:HB2	1:A:691:GLN:HB2	1.49	0.92
1:C:427:ASP:HB3	1:C:430:ILE:HD12	1.51	0.92
1:C:155:TYR:OH	1:C:624:THR:HG22	1.69	0.92
1:C:206:SER:CB	1:C:466:ALA:CB	2.36	0.91
1:A:297:VAL:HG12	1:A:298:ARG:HG3	1.49	0.91
1:C:430:ILE:HG21	1:C:570:GLU:CB	2.00	0.91
1:C:619:LEU:HD13	1:C:693:ILE:CG2	2.01	0.91
1:A:439:CYS:SG	1:A:441:GLU:OE1	2.29	0.90
1:D:276:THR:HG22	3:D:900:DTP:H2	1.54	0.89
1:C:42:GLU:OE1	2:G:298:GLY:HA2	1.71	0.89
1:D:7:VAL:CG2	1:D:17:ILE:CG1	2.49	0.89
1:D:290:LYS:CG	1:D:296:GLY:O	2.20	0.89
1:B:618:ALA:HB2	1:B:691:GLN:HB2	1.52	0.89
1:D:696:ASN:ND2	1:D:730:TYR:HB3	1.87	0.89
1:A:44:ARG:HH11	1:A:69:LEU:CD2	1.86	0.89
2:H:92:ASN:HA	2:H:96:LEU:HD23	1.56	0.88
1:B:441:GLU:HG2	1:B:442:ILE:HG12	1.55	0.88
1:C:465:SER:CB	1:C:515:ILE:HG12	2.04	0.88
1:D:514:GLY:HA2	1:D:618:ALA:CB	2.04	0.88
1:A:439:CYS:SG	1:A:621:PRO:HD2	2.13	0.88
1:D:40:GLN:OE1	2:E:334:TRP:CD1	2.27	0.88
1:B:303:THR:CA	1:B:334:ASP:O	2.21	0.88
1:A:439:CYS:CB	1:A:441:GLU:OE1	2.22	0.87
1:A:437:ASN:O	1:A:440:LEU:HD22	1.73	0.87
1:A:463:THR:HG23	1:A:492:LEU:HD23	1.53	0.87
1:C:432:PRO:HG2	1:C:434:ARG:CD	2.04	0.87
1:D:560:LYS:HG2	1:D:609:HIS:CD2	2.09	0.87
1:C:621:PRO:HD3	1:C:694:SER:OG	1.73	0.87
1:C:432:PRO:CG	1:C:434:ARG:CD	2.52	0.87
1:D:50:TYR:O	1:D:53:ILE:CG2	2.22	0.87
1:A:689:ILE:HG22	1:A:691:GLN:O	1.75	0.87
1:A:53:ILE:CD1	1:A:58:ILE:CD1	2.53	0.86
2:F:92:ASN:HA	2:F:96:LEU:HD23	1.57	0.86
1:C:441:GLU:CB	1:C:619:LEU:O	2.23	0.86
1:A:437:ASN:ND2	1:A:439:CYS:HB2	1.89	0.86
1:C:18:ASN:O	3:C:800:DTP:H2	1.75	0.86
1:A:151:LEU:HA	1:A:155:TYR:HB2	1.56	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:253:GLY:HA3	1:C:438:LEU:HD22	1.58	0.85
1:B:215:VAL:O	1:B:216:ARG:HG2	1.77	0.85
1:B:618:ALA:HB2	1:B:691:GLN:CB	2.06	0.85
1:D:249:SER:CA	1:D:292:CYS:SG	2.64	0.85
1:A:22:ILE:HG13	3:A:800:DTP:H2'1	1.57	0.85
1:D:430:ILE:HG21	1:D:570:GLU:HG2	1.59	0.85
1:A:7:VAL:CB	1:A:15:GLU:O	2.24	0.85
1:B:154:LYS:HA	1:B:160:ARG:HH22	1.39	0.85
1:C:217:THR:OG1	1:C:219:THR:HG22	1.77	0.84
1:B:320:LYS:HE3	1:B:411:ARG:CB	2.07	0.84
1:C:206:SER:HB2	1:C:466:ALA:HB1	1.53	0.84
1:A:438:LEU:O	1:A:440:LEU:HD23	1.78	0.84
2:G:92:ASN:HA	2:G:96:LEU:HD23	1.58	0.84
1:A:712:GLN:HE22	2:F:370:LEU:HG	1.41	0.84
1:B:293:SER:HB3	1:B:298:ARG:O	1.77	0.84
1:C:22:ILE:HG12	3:C:800:DTP:H2'1	1.60	0.84
1:C:427:ASP:CB	1:C:430:ILE:HD12	2.09	0.83
1:A:227:LEU:CB	1:A:435:GLN:NE2	2.42	0.83
1:D:558:LEU:HD23	1:D:612:ARG:HG2	1.61	0.83
2:E:1:ALA:HB3	2:E:168:HIS:HA	1.59	0.83
1:B:320:LYS:HE3	1:B:411:ARG:HB2	1.58	0.83
1:C:430:ILE:CG2	1:C:570:GLU:HB3	2.09	0.82
1:B:6:LEU:HD12	1:B:51:ASP:HB2	1.62	0.82
1:A:320:LYS:HE2	1:A:333:MET:O	1.80	0.82
1:B:420:CYS:O	1:B:424:SER:HB3	1.80	0.82
1:C:208:PRO:HB3	1:C:464:LEU:CG	2.10	0.82
1:D:585:LYS:H	1:D:585:LYS:HD3	1.45	0.82
1:C:558:LEU:HD23	1:C:612:ARG:HG2	1.62	0.82
1:B:154:LYS:HD2	1:B:155:TYR:HE1	1.43	0.81
1:C:427:ASP:OD1	1:C:428:PRO:HD2	1.80	0.81
1:A:189:ARG:O	1:A:193:VAL:HG23	1.79	0.81
1:A:441:GLU:OE1	1:A:620:MET:HB2	1.80	0.81
1:C:155:TYR:OH	1:C:624:THR:CG2	2.28	0.81
1:C:689:ILE:HG21	1:C:691:GLN:O	1.81	0.81
1:D:40:GLN:OE1	2:E:334:TRP:CB	2.28	0.81
1:D:186:ARG:HH21	1:D:189:ARG:NH2	1.78	0.81
1:D:276:THR:CG2	3:D:900:DTP:H2	2.10	0.81
1:A:432:PRO:HG2	1:A:434:ARG:HD2	1.62	0.81
1:C:585:LYS:HD3	1:C:585:LYS:H	1.44	0.81
1:C:234:LEU:HB3	1:D:246:LYS:HZ3	1.44	0.81
1:C:463:THR:HG22	1:C:489:LEU:HD22	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:215:VAL:O	1:D:216:ARG:CG	2.29	0.80
1:A:55:THR:HA	1:A:58:ILE:CG1	2.11	0.80
1:C:280:PRO:HB3	1:D:291:SER:O	1.80	0.80
1:B:642:VAL:HG22	1:B:655:VAL:HG22	1.63	0.80
1:D:730:TYR:O	1:D:731:TYR:O	2.00	0.80
1:B:188:THR:O	1:B:192:TYR:HD2	1.65	0.80
1:C:432:PRO:HB2	1:C:434:ARG:CD	2.11	0.80
1:A:730:TYR:O	1:A:731:TYR:O	1.99	0.80
1:C:206:SER:HB2	1:C:466:ALA:HB3	0.80	0.80
1:A:55:THR:C	1:A:58:ILE:HG12	2.07	0.79
1:B:418:ASP:O	1:B:422:THR:HG23	1.82	0.79
1:D:293:SER:CB	1:D:298:ARG:O	2.30	0.79
1:D:551:LEU:O	1:D:616:LEU:CD1	2.30	0.79
2:F:1:ALA:HB3	2:F:168:HIS:HA	1.64	0.79
1:A:618:ALA:CB	1:A:691:GLN:HB2	2.12	0.79
1:D:689:ILE:HG21	1:D:691:GLN:O	1.81	0.79
1:A:50:TYR:O	1:A:53:ILE:CG2	2.31	0.79
1:C:465:SER:HB2	1:C:514:GLY:O	1.82	0.79
1:D:6:LEU:CD2	1:D:14:THR:HG21	2.12	0.79
2:E:92:ASN:HA	2:E:96:LEU:HD23	1.63	0.79
1:A:325:VAL:HG22	1:A:327:GLY:H	1.48	0.79
1:D:560:LYS:CD	1:D:609:HIS:NE2	2.46	0.79
1:A:53:ILE:HD11	1:A:58:ILE:HD12	1.62	0.79
1:A:544:PHE:HE2	1:A:685:MET:HG2	1.42	0.79
1:B:432:PRO:HG2	1:B:434:ARG:HD2	1.65	0.79
1:D:155:TYR:CE1	1:D:209:THR:HG23	2.18	0.79
1:D:551:LEU:O	1:D:616:LEU:HD13	1.82	0.79
2:G:1:ALA:HB3	2:G:168:HIS:HA	1.64	0.79
1:C:513:LEU:HD12	1:C:616:LEU:HD23	1.63	0.78
1:C:208:PRO:HD3	1:C:464:LEU:HD12	1.63	0.78
1:D:560:LYS:HD3	1:D:609:HIS:NE2	1.97	0.78
2:E:255:GLY:HA2	2:E:258:ASP:O	1.83	0.78
1:D:211:ILE:O	1:D:215:VAL:HG23	1.83	0.78
1:C:151:LEU:HA	1:C:155:TYR:HB2	1.66	0.78
1:D:50:TYR:O	1:D:53:ILE:HG22	1.82	0.78
1:D:301:ALA:HB1	1:D:438:LEU:HD11	1.66	0.78
2:H:1:ALA:HB3	2:H:168:HIS:HA	1.64	0.78
1:A:463:THR:HG21	1:A:492:LEU:HD23	1.66	0.78
1:A:642:VAL:HG22	1:A:655:VAL:HG22	1.65	0.78
1:C:7:VAL:CG2	1:C:17:ILE:HG12	2.13	0.77
1:A:55:THR:OG1	3:A:800:DTP:C8	2.30	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:LEU:HB3	1:A:435:GLN:HE21	1.49	0.77
2:G:195:LEU:HD21	2:G:268:CYS:HB3	1.66	0.77
1:C:55:THR:OG1	3:C:800:DTP:H8	1.82	0.77
1:A:436:SER:OG	1:A:440:LEU:HA	1.84	0.77
1:A:696:ASN:ND2	1:A:730:TYR:HB3	1.99	0.77
2:F:195:LEU:HD21	2:F:268:CYS:HB3	1.66	0.77
1:B:155:TYR:CZ	1:B:209:THR:HG23	2.20	0.77
1:D:619:LEU:HD12	1:D:693:ILE:HG12	1.66	0.77
2:H:5:PHE:CE1	2:H:24:ASN:O	2.37	0.77
1:C:276:THR:HB	3:C:900:DTP:H2	1.65	0.77
1:B:36:VAL:HG12	1:B:77:TYR:CE2	2.20	0.77
1:B:325:VAL:HG22	1:B:327:GLY:H	1.48	0.77
1:A:439:CYS:O	1:A:440:LEU:HB2	1.84	0.77
1:B:442:ILE:HG23	1:B:691:GLN:OE1	1.84	0.77
1:D:432:PRO:HG2	1:D:434:ARG:HD2	1.67	0.77
2:F:5:PHE:CE1	2:F:24:ASN:O	2.37	0.77
1:A:544:PHE:CE2	1:A:685:MET:CG	2.62	0.76
1:B:268:ILE:HD11	1:B:275:HIS:HA	1.67	0.76
1:C:208:PRO:CA	1:C:464:LEU:HD11	2.15	0.76
1:D:45:SER:OG	1:D:61:THR:HG22	1.84	0.76
1:B:44:ARG:HG3	1:B:69:LEU:HD21	1.66	0.76
1:C:21:LYS:HD2	3:C:800:DTP:N1	1.99	0.76
1:C:432:PRO:HG2	1:C:434:ARG:HH11	1.51	0.76
2:E:195:LEU:HD21	2:E:268:CYS:HB3	1.67	0.76
2:H:195:LEU:HD21	2:H:268:CYS:HB3	1.68	0.76
1:C:287:THR:HB	1:D:284:HIS:HA	1.67	0.76
1:A:34:HIS:O	1:A:35:ASN:HB2	1.86	0.76
1:A:44:ARG:NH1	1:A:69:LEU:HD23	2.00	0.76
1:C:51:ASP:OD1	1:C:51:ASP:O	2.04	0.76
2:E:5:PHE:CE1	2:E:24:ASN:CB	2.69	0.76
1:D:622:SER:HB2	1:D:625:SER:HB2	1.69	0.75
1:C:689:ILE:CG2	1:C:691:GLN:O	2.34	0.75
1:A:233:SER:O	1:A:237:ILE:HG13	1.85	0.75
2:E:165:SER:O	2:E:169:LEU:HG	1.87	0.75
1:A:53:ILE:CD1	1:A:58:ILE:HD11	2.15	0.75
1:A:268:ILE:HD11	1:A:275:HIS:HA	1.69	0.75
1:D:53:ILE:HG13	1:D:58:ILE:HD11	1.69	0.75
1:D:276:THR:HG23	1:D:280:PRO:HG2	1.66	0.75
1:D:463:THR:HG22	1:D:489:LEU:HD22	1.68	0.75
2:E:5:PHE:CD1	2:E:24:ASN:CB	2.57	0.75
2:E:245:THR:HA	2:E:248:MET:HE3	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:SER:CB	1:A:298:ARG:O	2.34	0.75
1:D:249:SER:CB	1:D:292:CYS:SG	2.75	0.75
1:B:185:PRO:HG2	1:B:188:THR:HG1	1.48	0.74
1:B:234:LEU:N	3:B:900:DTP:H3'	2.02	0.74
1:D:53:ILE:CG1	1:D:58:ILE:HD11	2.17	0.74
2:F:18:PHE:CZ	2:F:104:LEU:HD21	2.22	0.74
1:A:10:ARG:HE	1:A:91:LYS:NZ	1.85	0.74
1:D:551:LEU:C	1:D:616:LEU:HD13	2.12	0.74
1:D:689:ILE:CG2	1:D:691:GLN:O	2.35	0.74
1:A:619:LEU:HD12	1:A:693:ILE:HG12	1.69	0.74
3:A:800:DTP:H8	3:A:800:DTP:H5'2	1.69	0.74
1:A:18:ASN:H	3:A:800:DTP:H2	1.50	0.74
1:D:441:GLU:HB2	1:D:619:LEU:O	1.88	0.74
2:G:5:PHE:CE1	2:G:24:ASN:O	2.41	0.74
1:B:233:SER:O	1:B:237:ILE:HG13	1.88	0.74
1:D:7:VAL:HG22	1:D:17:ILE:CG1	2.17	0.74
1:A:125:GLU:HG2	1:A:129:LYS:HE2	1.69	0.73
1:A:499:PRO:HG2	1:A:500:ILE:HD12	1.68	0.73
1:B:125:GLU:HG2	1:B:129:LYS:HE2	1.68	0.73
1:C:465:SER:HB2	1:C:515:ILE:HG12	1.69	0.73
1:A:719:LEU:HD22	2:F:375:LEU:HD21	1.70	0.73
1:C:225:CYS:H	1:C:462:CYS:HB2	1.53	0.73
1:B:499:PRO:HG2	1:B:500:ILE:HD12	1.69	0.73
1:D:364:LEU:HD23	1:D:378:LEU:HB2	1.71	0.73
1:B:188:THR:O	1:B:192:TYR:CD2	2.41	0.73
1:C:513:LEU:HD11	1:C:613:ASN:ND2	2.04	0.73
1:D:19:LEU:HD13	2:E:297:ILE:HG22	1.69	0.73
1:D:6:LEU:HD22	1:D:14:THR:HG21	1.70	0.73
1:B:21:LYS:HB2	3:B:800:DTP:C2	2.19	0.73
1:C:465:SER:N	1:C:514:GLY:O	2.22	0.73
1:C:622:SER:HB2	1:C:625:SER:HB2	1.69	0.73
1:A:44:ARG:HH11	1:A:69:LEU:HD23	1.50	0.72
1:D:6:LEU:HA	1:D:14:THR:HG22	1.70	0.72
1:D:689:ILE:HG22	1:D:691:GLN:H	1.54	0.72
1:A:441:GLU:CD	1:A:620:MET:HB2	2.15	0.72
1:D:556:ASN:HD21	1:D:609:HIS:HB2	1.54	0.72
1:B:543:THR:O	1:B:547:ILE:HG13	1.90	0.72
1:C:45:SER:OG	1:C:61:THR:HG22	1.89	0.72
1:D:430:ILE:HG21	1:D:570:GLU:CG	2.19	0.72
1:D:430:ILE:HD12	1:D:570:GLU:HA	1.71	0.72
1:A:442:ILE:HG23	1:A:691:GLN:OE1	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:GLN:OE1	2:E:334:TRP:HD1	1.69	0.72
1:D:678:TYR:OH	1:D:695:ALA:HB1	1.90	0.72
2:G:18:PHE:CZ	2:G:104:LEU:HD21	2.24	0.72
1:C:293:SER:HB2	1:C:296:GLY:HA2	1.72	0.72
1:C:489:LEU:HB3	1:C:513:LEU:HD22	1.71	0.72
1:A:8:THR:CB	1:A:54:LYS:HA	2.14	0.72
1:A:19:LEU:HA	1:A:22:ILE:HD12	1.70	0.72
1:C:44:ARG:HA	1:C:44:ARG:HE	1.54	0.72
1:C:364:LEU:HD23	1:C:378:LEU:HB2	1.71	0.72
1:D:348:LEU:O	2:E:371:SER:HB3	1.89	0.72
1:C:276:THR:HG23	1:C:280:PRO:HG2	1.72	0.71
1:A:233:SER:OG	1:A:236:SER:CB	2.39	0.71
1:C:268:ILE:HD11	1:C:275:HIS:HA	1.72	0.71
1:B:685:MET:O	1:B:689:ILE:HG12	1.90	0.71
1:D:157:VAL:HG23	1:D:167:GLU:OE2	1.90	0.71
1:D:268:ILE:HD11	1:D:275:HIS:HA	1.71	0.71
2:E:69:GLU:HG2	2:E:296:MET:HG3	1.72	0.71
1:A:18:ASN:H	3:A:800:DTP:C2	2.03	0.71
1:D:225:CYS:H	1:D:462:CYS:HB2	1.54	0.71
2:F:69:GLU:HG2	2:F:296:MET:HG3	1.73	0.71
1:A:55:THR:HA	1:A:58:ILE:HG12	1.72	0.71
1:D:430:ILE:CG2	1:D:570:GLU:HG2	2.20	0.71
1:D:560:LYS:CD	1:D:609:HIS:CE1	2.72	0.71
2:E:90:SER:HB2	2:E:91:PRO:HD3	1.73	0.71
1:C:465:SER:HB3	1:C:515:ILE:HG23	1.72	0.71
2:E:311:ILE:HG23	2:E:312:THR:H	1.55	0.71
1:C:227:LEU:HD23	1:C:435:GLN:HG3	1.73	0.70
1:B:215:VAL:O	1:B:216:ARG:CG	2.39	0.70
1:C:215:VAL:O	1:C:216:ARG:CG	2.40	0.70
1:D:670:TRP:CH2	1:D:735:ARG:HB2	2.27	0.70
1:C:689:ILE:HG22	1:C:691:GLN:H	1.56	0.70
1:C:297:VAL:O	1:C:297:VAL:HG12	1.92	0.70
1:D:441:GLU:HG3	1:D:620:MET:HB3	1.72	0.70
1:D:464:LEU:HA	1:D:514:GLY:O	1.91	0.70
1:D:514:GLY:CA	1:D:618:ALA:CB	2.66	0.70
1:C:44:ARG:NH2	2:G:220:GLU:OE1	2.22	0.70
1:B:6:LEU:HB2	1:B:52:GLY:N	2.04	0.70
1:A:185:PRO:HB2	1:A:187:GLU:HG2	1.74	0.70
1:B:276:THR:HB	3:B:900:DTP:H2	1.74	0.70
1:B:439:CYS:HB2	1:B:441:GLU:OE1	1.92	0.70
1:C:293:SER:HB3	1:C:298:ARG:O	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:431:ALA:HB1	1:C:445:PRO:CB	2.20	0.70
1:D:233:SER:HA	3:D:900:DTP:H5'1	1.74	0.70
2:H:18:PHE:CZ	2:H:104:LEU:HD21	2.27	0.70
1:C:7:VAL:HG22	1:C:17:ILE:HG12	1.72	0.70
1:D:510:ARG:HG2	1:D:567:TRP:HE3	1.56	0.70
1:A:407:ALA:HA	1:A:732:GLN:OE1	1.91	0.69
3:A:800:DTP:C8	3:A:800:DTP:H5'2	2.22	0.69
1:B:442:ILE:HD12	1:B:691:GLN:OE1	1.91	0.69
2:F:90:SER:HB2	2:F:91:PRO:HD3	1.74	0.69
1:A:45:SER:OG	1:A:61:THR:HG22	1.92	0.69
1:C:196:PHE:HD1	1:C:484:LEU:HB3	1.57	0.69
1:D:287:THR:O	1:D:291:SER:HB3	1.93	0.69
1:A:317:LEU:HD23	1:A:401:LEU:HD23	1.73	0.69
1:D:430:ILE:HG21	1:D:570:GLU:CB	2.23	0.69
1:A:441:GLU:CD	1:A:620:MET:CB	2.65	0.69
1:C:186:ARG:HH21	1:C:189:ARG:HH22	1.41	0.69
2:G:90:SER:HB2	2:G:91:PRO:HD3	1.74	0.69
2:H:90:SER:HB2	2:H:91:PRO:HD3	1.74	0.69
2:H:218:PHE:CZ	2:H:296:MET:SD	2.85	0.69
2:E:307:TYR:HA	2:E:331:PRO:HG3	1.74	0.69
1:B:320:LYS:CE	1:B:411:ARG:HB2	2.23	0.69
2:G:69:GLU:HG2	2:G:296:MET:HG3	1.72	0.69
2:H:311:ILE:HG23	2:H:312:THR:H	1.56	0.69
1:B:558:LEU:HD23	1:B:612:ARG:HG2	1.75	0.69
1:C:370:ALA:HA	1:C:428:PRO:HB2	1.74	0.69
1:A:41:VAL:HG22	1:A:69:LEU:HD12	1.74	0.69
1:B:407:ALA:HA	1:B:732:GLN:OE1	1.93	0.69
1:C:520:PHE:O	1:C:523:TYR:N	2.25	0.69
1:A:7:VAL:HG11	3:A:800:DTP:C6	2.24	0.68
2:F:245:THR:HA	2:F:248:MET:HE3	1.73	0.68
2:G:307:TYR:HA	2:G:331:PRO:HG3	1.75	0.68
2:H:221:ARG:HH12	2:H:296:MET:HG2	1.58	0.68
1:B:19:LEU:HA	1:B:22:ILE:HD12	1.76	0.68
1:D:40:GLN:O	1:D:44:ARG:HG2	1.92	0.68
1:B:521:ALA:HB3	1:B:632:THR:HG21	1.75	0.68
2:G:9:LYS:HA	2:H:141:VAL:HG11	1.74	0.68
1:C:10:ARG:HD2	1:C:91:LYS:HE2	1.75	0.68
1:D:320:LYS:HB3	1:D:409:THR:HG21	1.76	0.68
2:H:5:PHE:HE1	2:H:24:ASN:O	1.76	0.68
1:A:40:GLN:O	1:A:44:ARG:N	2.25	0.68
1:A:55:THR:CA	1:A:58:ILE:HG12	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:GLU:OE1	2:G:298:GLY:CA	2.41	0.68
1:A:297:VAL:HG12	1:A:298:ARG:HG2	1.73	0.68
1:C:246:LYS:HZ3	1:D:234:LEU:C	2.01	0.68
2:F:311:ILE:HG23	2:F:312:THR:H	1.59	0.68
1:C:55:THR:CB	3:C:800:DTP:H8	2.23	0.68
1:C:510:ARG:HG2	1:C:567:TRP:HE3	1.59	0.68
1:D:301:ALA:O	1:D:438:LEU:CD1	2.42	0.68
1:A:292:CYS:HA	1:B:276:THR:HG21	1.74	0.68
1:B:294:GLN:C	1:B:296:GLY:H	2.02	0.68
1:D:185:PRO:HB2	1:D:187:GLU:HG2	1.76	0.68
1:B:229:GLU:HG3	1:B:257:ASN:HD22	1.59	0.67
1:B:459:ILE:HB	1:B:503:ALA:HA	1.76	0.67
2:G:311:ILE:HG23	2:G:312:THR:H	1.57	0.67
1:A:40:GLN:O	1:A:44:ARG:HB2	1.93	0.67
1:A:55:THR:O	1:A:58:ILE:HG12	1.92	0.67
1:A:558:LEU:HD23	1:A:612:ARG:HG2	1.77	0.67
2:G:245:THR:HA	2:G:248:MET:HE3	1.75	0.67
1:C:290:LYS:HE2	1:C:332:HIS:HB3	1.76	0.67
1:A:521:ALA:HB3	1:A:632:THR:HG21	1.75	0.67
1:C:234:LEU:HB3	1:D:246:LYS:NZ	2.08	0.67
2:F:5:PHE:HE1	2:F:24:ASN:O	1.77	0.67
1:C:712:GLN:HE22	2:G:370:LEU:HG	1.59	0.67
1:B:44:ARG:HA	1:B:44:ARG:HE	1.58	0.67
1:C:513:LEU:CD1	1:C:613:ASN:ND2	2.57	0.67
2:F:307:TYR:HA	2:F:331:PRO:HG3	1.76	0.67
2:H:245:THR:HA	2:H:248:MET:HE3	1.76	0.67
1:B:332:HIS:O	1:B:333:MET:HG2	1.95	0.67
1:D:618:ALA:O	1:D:620:MET:CE	2.41	0.67
1:D:627:GLN:HA	1:D:654:GLN:HE22	1.58	0.67
2:E:203:LEU:HG	2:E:207:ARG:HD2	1.78	0.67
1:B:307:PRO:HG2	1:B:310:HIS:HB2	1.77	0.66
2:E:83:LEU:HD22	2:E:203:LEU:HD21	1.78	0.66
2:H:76:ASN:HD21	2:H:211:SER:HA	1.60	0.66
1:D:33:LEU:HD13	1:D:80:LEU:HB2	1.77	0.66
1:D:560:LYS:CD	1:D:609:HIS:CD2	2.77	0.66
1:B:58:ILE:HG21	3:B:800:DTP:H1'	1.77	0.66
1:B:585:LYS:H	1:B:585:LYS:HD3	1.60	0.66
1:A:53:ILE:HG13	1:A:53:ILE:O	1.91	0.66
1:C:689:ILE:HG22	1:C:691:GLN:N	2.10	0.66
1:D:689:ILE:HG22	1:D:691:GLN:N	2.09	0.66
1:C:475:LEU:HD21	1:C:543:THR:HG23	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ARG:HH11	1:A:69:LEU:HD21	1.59	0.66
1:B:294:GLN:O	1:B:296:GLY:N	2.25	0.66
2:H:307:TYR:HA	2:H:331:PRO:HG3	1.76	0.66
1:B:321:ASN:ND2	1:B:323:ARG:O	2.28	0.66
1:B:442:ILE:CD1	1:B:691:GLN:OE1	2.43	0.66
1:D:560:LYS:CG	1:D:609:HIS:CD2	2.78	0.66
1:B:36:VAL:HG12	1:B:77:TYR:CE1	2.31	0.66
1:B:210:PRO:HG3	1:B:224:SER:OG	1.95	0.66
1:C:432:PRO:HB2	1:C:434:ARG:CG	2.26	0.66
1:A:53:ILE:HD11	1:A:58:ILE:HD11	1.73	0.66
1:B:40:GLN:O	1:B:44:ARG:CG	2.42	0.66
1:D:516:GLY:HA2	1:D:619:LEU:HD23	1.78	0.66
1:B:154:LYS:HD2	1:B:155:TYR:CE1	2.28	0.66
1:B:317:LEU:HD23	1:B:401:LEU:HD23	1.76	0.66
3:B:800:DTP:H5'1	3:B:800:DTP:O2B	1.96	0.66
1:C:627:GLN:HA	1:C:654:GLN:HE22	1.58	0.66
2:E:74:ILE:HG13	2:E:78:LYS:HE3	1.78	0.65
1:A:40:GLN:HE22	2:F:334:TRP:N	1.95	0.65
1:D:10:ARG:HD2	1:D:91:LYS:HE2	1.75	0.65
1:D:696:ASN:HD22	1:D:730:TYR:HB3	1.62	0.65
1:A:229:GLU:HG3	1:A:257:ASN:HD22	1.61	0.65
1:A:459:ILE:HB	1:A:503:ALA:HA	1.77	0.65
1:C:154:LYS:HG2	1:C:155:TYR:HD1	1.62	0.65
1:C:7:VAL:CG2	1:C:17:ILE:CG1	2.75	0.65
1:C:621:PRO:HD3	1:C:694:SER:CB	2.25	0.65
1:D:301:ALA:CB	1:D:438:LEU:HD11	2.26	0.65
1:A:206:SER:OG	1:A:625:SER:HB3	1.96	0.65
1:D:489:LEU:HB3	1:D:513:LEU:HD22	1.77	0.65
1:C:208:PRO:HD3	1:C:464:LEU:CD1	2.26	0.65
1:C:33:LEU:HD13	1:C:80:LEU:HB2	1.77	0.65
1:C:268:ILE:HD13	3:C:900:DTP:C8	2.27	0.65
1:D:217:THR:OG1	1:D:219:THR:HG22	1.97	0.65
1:D:260:ARG:NH1	1:D:448:PRO:HG3	2.12	0.65
1:D:560:LYS:HG2	1:D:609:HIS:CG	2.31	0.65
1:C:427:ASP:HB3	1:C:430:ILE:CD1	2.26	0.65
2:E:118:HIS:CE1	2:E:234:ILE:HG23	2.32	0.65
2:F:76:ASN:HD21	2:F:211:SER:HA	1.62	0.65
2:G:76:ASN:HD21	2:G:211:SER:HA	1.62	0.65
1:C:320:LYS:HB3	1:C:409:THR:HG21	1.77	0.65
1:D:427:ASP:OD1	1:D:428:PRO:CD	2.40	0.65
1:D:290:LYS:NZ	1:D:297:VAL:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:5:PHE:HE1	2:G:24:ASN:O	1.80	0.64
2:G:74:ILE:HG13	2:G:78:LYS:HE3	1.79	0.64
1:B:437:ASN:HD21	1:B:441:GLU:CD	2.05	0.64
2:F:171:GLY:O	2:F:184:VAL:HG11	1.97	0.64
2:F:203:LEU:HG	2:F:207:ARG:HD2	1.79	0.64
2:H:171:GLY:O	2:H:184:VAL:HG11	1.97	0.64
1:A:585:LYS:HD3	1:A:585:LYS:H	1.61	0.64
1:C:281:PHE:CZ	3:C:900:DTP:H2'1	2.31	0.64
1:D:430:ILE:CG2	1:D:570:GLU:CG	2.76	0.64
1:B:320:LYS:O	1:B:321:ASN:C	2.41	0.64
1:C:6:LEU:HB2	1:C:51:ASP:HA	1.79	0.64
1:B:206:SER:OG	1:B:625:SER:HB3	1.97	0.64
1:B:320:LYS:HE3	1:B:411:ARG:CG	2.26	0.64
2:E:307:TYR:O	2:E:311:ILE:HG22	1.98	0.64
1:A:307:PRO:HG2	1:A:310:HIS:HB2	1.78	0.64
1:B:441:GLU:HA	1:B:692:SER:O	1.98	0.64
2:G:45:SER:HB3	2:H:49:ARG:HH12	1.61	0.64
2:G:203:LEU:HG	2:G:207:ARG:HD2	1.80	0.64
2:H:99:ILE:HD13	2:H:105:GLU:HA	1.80	0.64
1:A:227:LEU:C	1:A:435:GLN:HE22	2.05	0.64
2:H:365:VAL:HG12	2:H:366:ASP:H	1.62	0.64
1:A:260:ARG:NH1	1:A:448:PRO:HG3	2.13	0.64
1:C:284:HIS:HA	1:D:287:THR:HB	1.79	0.64
2:G:218:PHE:CZ	2:G:296:MET:SD	2.91	0.64
2:G:307:TYR:O	2:G:311:ILE:HG22	1.97	0.64
1:A:131:MET:SD	1:A:193:VAL:HG11	2.39	0.63
2:F:307:TYR:O	2:F:311:ILE:HG22	1.98	0.63
2:H:118:HIS:CE1	2:H:234:ILE:HG23	2.33	0.63
1:B:8:THR:CB	1:B:54:LYS:HA	2.28	0.63
1:C:215:VAL:O	1:C:216:ARG:HD3	1.97	0.63
2:H:307:TYR:O	2:H:311:ILE:HG22	1.98	0.63
1:C:260:ARG:NH1	1:C:448:PRO:HG3	2.14	0.63
1:B:443:ALA:H	1:B:691:GLN:HG2	1.62	0.63
3:B:900:DTP:H8	3:B:900:DTP:H5'1	1.81	0.63
1:C:276:THR:HB	3:C:900:DTP:C2	2.28	0.63
1:C:432:PRO:HB2	1:C:434:ARG:HG3	1.80	0.63
1:B:34:HIS:O	1:B:35:ASN:HB3	1.98	0.63
1:B:618:ALA:CB	1:B:691:GLN:CB	2.77	0.63
1:C:693:ILE:HG22	1:C:694:SER:N	2.12	0.63
1:D:40:GLN:OE1	2:E:334:TRP:CG	2.52	0.63
1:D:233:SER:HA	3:D:900:DTP:C5'	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:CB	1:B:52:GLY:H	2.07	0.63
1:D:475:LEU:HD21	1:D:543:THR:HG23	1.79	0.63
1:B:8:THR:HB	1:B:54:LYS:HA	1.79	0.63
1:B:712:GLN:HE22	2:H:370:LEU:HG	1.64	0.63
1:C:238:ASN:CG	1:D:246:LYS:HE2	2.23	0.63
1:C:669:LEU:HD11	1:C:698:ASN:ND2	2.14	0.63
1:D:228:ILE:HD12	1:D:244:ILE:HG12	1.81	0.63
2:E:12:GLN:NE2	2:E:23:VAL:HG13	2.14	0.63
1:C:215:VAL:O	1:C:216:ARG:CD	2.47	0.62
1:D:370:ALA:HA	1:D:428:PRO:HB2	1.81	0.62
2:E:76:ASN:HD21	2:E:211:SER:HA	1.62	0.62
2:G:99:ILE:HD13	2:G:105:GLU:HA	1.81	0.62
1:A:151:LEU:HD23	1:A:155:TYR:CG	2.34	0.62
1:C:227:LEU:CB	1:C:435:GLN:NE2	2.59	0.62
1:A:320:LYS:HE3	1:A:411:ARG:CB	2.30	0.62
1:A:285:PHE:O	1:A:289:VAL:HG23	2.00	0.62
1:B:474:ASN:H	1:B:474:ASN:HD22	1.47	0.62
1:B:131:MET:SD	1:B:193:VAL:HG11	2.40	0.62
1:B:260:ARG:NH1	1:B:448:PRO:HG3	2.14	0.62
1:D:524:LEU:HB3	1:D:529:LYS:O	2.00	0.62
2:E:218:PHE:CZ	2:E:296:MET:SD	2.93	0.62
2:H:207:ARG:HH22	2:H:282:GLN:NE2	1.98	0.62
1:A:441:GLU:HB2	1:A:619:LEU:O	1.99	0.62
1:A:723:LYS:HG3	2:F:375:LEU:OXT	2.00	0.62
1:C:465:SER:O	1:C:516:GLY:N	2.23	0.62
1:D:125:GLU:HG2	1:D:129:LYS:HE2	1.81	0.62
1:A:150:GLN:O	1:A:154:LYS:HG3	1.99	0.62
1:A:439:CYS:HB3	1:A:441:GLU:CD	2.23	0.62
1:A:463:THR:HG23	1:A:492:LEU:CD2	2.27	0.62
1:D:249:SER:HB3	1:D:292:CYS:SG	2.39	0.62
2:H:83:LEU:HD22	2:H:203:LEU:HD21	1.81	0.62
2:E:198:MET:SD	2:E:249:LEU:HD13	2.39	0.62
2:F:53:VAL:HG11	2:F:230:ILE:HG13	1.82	0.62
2:G:171:GLY:O	2:G:184:VAL:HG11	2.00	0.62
1:D:189:ARG:NH1	1:D:189:ARG:HG2	2.14	0.62
1:D:520:PHE:HB3	1:D:635:ILE:HA	1.80	0.62
1:A:227:LEU:HD23	1:A:435:GLN:HG3	1.80	0.61
2:E:49:ARG:O	2:E:52:GLU:HG2	1.99	0.61
1:A:474:ASN:H	1:A:474:ASN:HD22	1.48	0.61
1:B:369:PHE:O	1:B:421:ASN:CG	2.43	0.61
2:E:207:ARG:HH22	2:E:282:GLN:NE2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:218:PHE:CZ	2:F:296:MET:SD	2.93	0.61
2:G:83:LEU:HD22	2:G:203:LEU:HD21	1.82	0.61
1:A:439:CYS:CB	1:A:441:GLU:CD	2.74	0.61
1:C:125:GLU:HG2	1:C:129:LYS:HE2	1.82	0.61
1:C:524:LEU:HB3	1:C:529:LYS:O	2.00	0.61
1:C:530:ARG:HH11	1:C:667:GLU:HB2	1.65	0.61
1:D:694:SER:O	1:D:696:ASN:ND2	2.33	0.61
1:A:224:SER:O	1:A:252:ALA:HA	1.99	0.61
1:C:573:TYR:HE1	1:C:578:LEU:HD23	1.65	0.61
2:E:311:ILE:HG23	2:E:312:THR:N	2.16	0.61
2:F:49:ARG:O	2:F:52:GLU:HG2	2.00	0.61
2:F:74:ILE:HG13	2:F:78:LYS:HE3	1.81	0.61
2:H:203:LEU:HG	2:H:207:ARG:HD2	1.81	0.61
1:C:276:THR:O	1:D:294:GLN:HG3	2.00	0.61
1:D:53:ILE:CD1	1:D:58:ILE:HD11	2.31	0.61
1:D:189:ARG:CG	1:D:189:ARG:HH11	2.13	0.61
2:H:49:ARG:O	2:H:52:GLU:HG2	2.01	0.61
1:A:215:VAL:O	1:A:216:ARG:CG	2.49	0.61
1:B:221:GLN:NE2	1:B:250:GLN:HG2	2.16	0.61
1:D:115:TYR:HA	1:D:216:ARG:O	2.01	0.61
1:D:348:LEU:HB3	2:E:371:SER:HA	1.81	0.61
1:A:154:LYS:HA	1:A:160:ARG:HH22	1.64	0.61
1:B:320:LYS:HE3	1:B:411:ARG:HG3	1.81	0.61
1:D:122:ASP:O	1:D:189:ARG:NH2	2.33	0.61
1:A:221:GLN:NE2	1:A:250:GLN:HG2	2.16	0.61
1:A:442:ILE:HG22	1:A:444:LEU:HG	1.81	0.61
1:B:10:ARG:HG2	1:B:55:THR:HG21	1.82	0.61
1:D:290:LYS:HG3	1:D:296:GLY:O	2.00	0.61
1:D:669:LEU:HD11	1:D:698:ASN:ND2	2.15	0.61
2:H:74:ILE:HG13	2:H:78:LYS:HE3	1.81	0.61
1:A:233:SER:OG	1:A:236:SER:HB3	1.99	0.61
1:A:246:LYS:HG2	1:B:238:ASN:HD21	1.66	0.61
1:B:6:LEU:HD12	1:B:51:ASP:CB	2.30	0.61
1:B:18:ASN:O	3:B:800:DTP:H2	2.01	0.61
1:B:319:LEU:O	1:B:329:ARG:HD2	2.00	0.61
2:F:118:HIS:CE1	2:F:234:ILE:HG23	2.35	0.61
1:A:55:THR:HA	1:A:58:ILE:HG13	1.80	0.61
1:D:15:GLU:HG2	3:D:800:DTP:N6	2.16	0.61
1:C:211:ILE:O	1:C:215:VAL:HG23	2.00	0.60
1:D:573:TYR:HE1	1:D:578:LEU:HD23	1.65	0.60
2:G:99:ILE:HD11	2:G:108:VAL:HG21	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:36:VAL:CG1	1:B:77:TYR:CE2	2.85	0.60
1:B:696:ASN:ND2	1:B:730:TYR:HB3	2.16	0.60
2:G:118:HIS:CE1	2:G:234:ILE:HG23	2.36	0.60
2:H:53:VAL:HG11	2:H:230:ILE:HG13	1.83	0.60
1:B:233:SER:C	3:B:900:DTP:H3'	2.26	0.60
1:C:228:ILE:HD12	1:C:244:ILE:HG12	1.82	0.60
1:D:694:SER:O	1:D:730:TYR:CB	2.48	0.60
1:B:520:PHE:HB3	1:B:635:ILE:HA	1.84	0.60
1:C:115:TYR:HA	1:C:216:ARG:O	2.02	0.60
1:C:619:LEU:CD1	1:C:693:ILE:HD13	2.31	0.60
1:A:209:THR:N	1:A:210:PRO:HD2	2.17	0.60
1:C:465:SER:HB3	1:C:515:ILE:HG12	1.83	0.60
1:B:209:THR:N	1:B:210:PRO:HD2	2.17	0.60
1:C:619:LEU:HB3	1:C:693:ILE:HA	1.83	0.60
1:D:186:ARG:NH2	1:D:189:ARG:HH22	1.87	0.60
2:G:53:VAL:HG11	2:G:230:ILE:HG13	1.83	0.60
1:A:68:ASP:HA	1:A:653:ARG:NH1	2.16	0.60
1:D:249:SER:HA	1:D:292:CYS:HG	1.63	0.60
2:F:91:PRO:HB2	2:F:112:ALA:HB2	1.83	0.60
2:G:18:PHE:O	2:G:19:PHE:HB2	2.01	0.60
2:G:98:LEU:HD21	2:G:164:THR:HG23	1.83	0.60
2:G:311:ILE:HG23	2:G:312:THR:N	2.16	0.60
1:C:425:PRO:HB2	1:C:615:THR:HG22	1.83	0.60
1:C:128:PHE:HA	1:C:131:MET:HE3	1.84	0.59
1:C:294:GLN:HB2	1:C:298:ARG:HD2	1.83	0.59
1:C:407:ALA:HA	1:C:732:GLN:OE1	2.02	0.59
1:D:670:TRP:CZ2	1:D:735:ARG:HB2	2.37	0.59
2:E:53:VAL:HG11	2:E:230:ILE:HG13	1.84	0.59
2:E:98:LEU:HD21	2:E:164:THR:HG23	1.84	0.59
2:F:99:ILE:HD13	2:F:105:GLU:HA	1.82	0.59
2:F:101:ILE:HG13	2:F:104:LEU:HB3	1.84	0.59
2:H:99:ILE:HD11	2:H:108:VAL:HG21	1.84	0.59
1:B:185:PRO:CG	1:B:188:THR:OG1	2.39	0.59
1:D:53:ILE:HD11	1:D:58:ILE:HD11	1.83	0.59
2:E:23:VAL:HG22	2:E:100:SER:O	2.02	0.59
2:H:18:PHE:O	2:H:19:PHE:HB2	2.02	0.59
1:A:53:ILE:HD12	1:A:58:ILE:CD1	2.30	0.59
1:A:150:GLN:OE1	1:A:154:LYS:HE3	2.01	0.59
1:B:285:PHE:O	1:B:289:VAL:HG23	2.01	0.59
1:B:689:ILE:HG22	1:B:691:GLN:O	2.01	0.59
1:D:301:ALA:HB1	1:D:438:LEU:CD1	2.30	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:317:GLN:HB2	2:G:323:LEU:HD21	1.84	0.59
1:B:276:THR:CB	3:B:900:DTP:H2	2.32	0.59
1:C:30:ALA:HA	1:C:33:LEU:HD12	1.82	0.59
1:D:7:VAL:N	1:D:15:GLU:O	2.35	0.59
1:D:301:ALA:CB	1:D:438:LEU:CD1	2.80	0.59
1:D:530:ARG:HH11	1:D:667:GLU:HB2	1.67	0.59
2:H:302:ASP:O	2:H:306:GLN:HG2	2.03	0.59
1:C:513:LEU:HD11	1:C:613:ASN:HD21	1.65	0.59
1:D:21:LYS:HD2	3:D:800:DTP:C2	2.32	0.59
1:D:459:ILE:HB	1:D:503:ALA:HA	1.84	0.59
2:E:91:PRO:O	2:E:95:LEU:HB2	2.03	0.59
2:E:99:ILE:HD13	2:E:105:GLU:HA	1.83	0.59
2:G:91:PRO:HB2	2:G:112:ALA:HB2	1.84	0.59
2:H:311:ILE:HG23	2:H:312:THR:N	2.16	0.59
1:C:341:LYS:HG2	1:C:722:TYR:OH	2.03	0.59
1:D:290:LYS:HE2	1:D:332:HIS:HB3	1.82	0.59
1:A:441:GLU:HG2	1:A:442:ILE:N	2.18	0.59
1:A:469:LEU:HD12	1:A:520:PHE:HA	1.85	0.59
1:B:171:PHE:O	1:B:175:LEU:HD12	2.02	0.59
2:F:302:ASP:O	2:F:306:GLN:HG2	2.02	0.59
2:F:207:ARG:HH22	2:F:282:GLN:NE2	2.01	0.59
1:D:430:ILE:CG2	1:D:570:GLU:HB3	2.33	0.59
2:F:83:LEU:HD22	2:F:203:LEU:HD21	1.84	0.59
2:F:98:LEU:HD21	2:F:164:THR:HG23	1.84	0.59
2:H:57:ARG:HG2	2:H:60:ILE:HD11	1.84	0.59
2:E:302:ASP:O	2:E:306:GLN:HG2	2.03	0.59
2:G:49:ARG:O	2:G:52:GLU:HG2	2.02	0.59
2:H:92:ASN:O	2:H:96:LEU:HB2	2.03	0.59
1:A:254:ILE:O	1:A:302:ALA:HB1	2.02	0.58
1:C:21:LYS:HB2	3:C:800:DTP:C2	2.32	0.58
1:C:189:ARG:O	1:C:193:VAL:HG23	2.03	0.58
1:D:55:THR:HG21	3:D:800:DTP:O1B	2.03	0.58
1:D:407:ALA:HA	1:D:732:GLN:OE1	2.03	0.58
1:A:461:LEU:HD11	1:A:503:ALA:HB1	1.86	0.58
1:B:8:THR:OG1	1:B:54:LYS:HA	2.03	0.58
1:B:276:THR:N	3:B:900:DTP:H2	2.16	0.58
1:C:426:PHE:HE1	1:C:510:ARG:HE	1.50	0.58
1:D:30:ALA:HA	1:D:33:LEU:HD12	1.84	0.58
2:E:221:ARG:HH12	2:E:296:MET:HG2	1.68	0.58
2:G:302:ASP:O	2:G:306:GLN:HG2	2.03	0.58
1:B:215:VAL:O	1:B:216:ARG:CB	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:442:ILE:HG22	1:B:444:LEU:HG	1.85	0.58
1:D:427:ASP:HB3	1:D:430:ILE:HG13	1.86	0.58
2:F:18:PHE:O	2:F:19:PHE:HB2	2.01	0.58
2:F:19:PHE:CE2	2:F:190:LYS:HG2	2.38	0.58
2:F:221:ARG:HH12	2:F:296:MET:HG2	1.68	0.58
2:G:198:MET:HG2	2:G:249:LEU:HD22	1.85	0.58
1:D:50:TYR:O	1:D:53:ILE:HG23	2.03	0.58
2:F:311:ILE:HG23	2:F:312:THR:N	2.18	0.58
2:G:91:PRO:O	2:G:95:LEU:HB2	2.04	0.58
1:A:171:PHE:O	1:A:175:LEU:HD12	2.03	0.58
1:C:368:PHE:CE2	1:C:417:VAL:HG21	2.38	0.58
1:D:365:TYR:O	1:D:368:PHE:HB3	2.03	0.58
1:B:282:TYR:HA	1:B:285:PHE:HD2	1.69	0.58
1:B:212:MET:HA	1:B:212:MET:HE2	1.86	0.58
1:B:276:THR:H	3:B:900:DTP:H2	1.69	0.58
1:C:459:ILE:HB	1:C:503:ALA:HA	1.86	0.58
1:C:465:SER:CB	1:C:515:ILE:HA	2.34	0.58
1:D:196:PHE:HD1	1:D:484:LEU:HB3	1.68	0.58
1:D:551:LEU:O	1:D:616:LEU:HD11	2.03	0.58
2:E:101:ILE:HG13	2:E:104:LEU:HB3	1.85	0.58
2:H:296:MET:O	2:H:299:LEU:O	2.22	0.58
1:A:520:PHE:HB3	1:A:635:ILE:HA	1.84	0.58
1:C:622:SER:HB2	1:C:625:SER:CB	2.33	0.58
1:C:693:ILE:HG22	1:C:694:SER:H	1.68	0.58
1:D:622:SER:HB2	1:D:625:SER:CB	2.32	0.58
2:E:8:THR:CG2	2:E:9:LYS:N	2.67	0.58
2:F:317:GLN:HB2	2:F:323:LEU:HD21	1.86	0.58
1:B:320:LYS:CB	1:B:409:THR:HG21	2.29	0.58
1:D:694:SER:O	1:D:730:TYR:HB3	2.03	0.58
1:B:42:GLU:OE1	2:H:298:GLY:HA2	2.03	0.58
1:B:56:SER:O	1:B:60:GLU:HG2	2.04	0.58
1:C:613:ASN:CG	1:C:616:LEU:HD21	2.28	0.58
1:D:62:ILE:HG13	1:D:63:ILE:N	2.19	0.58
2:F:92:ASN:O	2:F:96:LEU:HB2	2.04	0.58
2:F:99:ILE:HD11	2:F:108:VAL:HG21	1.86	0.58
2:H:198:MET:SD	2:H:249:LEU:HD13	2.44	0.58
1:A:10:ARG:HG3	1:A:91:LYS:HE2	1.85	0.57
1:A:62:ILE:HG13	1:A:63:ILE:N	2.18	0.57
1:C:72:ARG:HG2	1:C:642:VAL:HG23	1.85	0.57
2:E:198:MET:HG2	2:E:249:LEU:HD22	1.85	0.57
1:C:62:ILE:HG13	1:C:63:ILE:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:VAL:O	1:C:297:VAL:CG1	2.51	0.57
1:C:441:GLU:HA	1:C:692:SER:O	2.05	0.57
2:E:317:GLN:HB2	2:E:323:LEU:HD21	1.85	0.57
1:C:54:LYS:O	1:C:58:ILE:HG12	2.04	0.57
2:E:305:CYS:O	2:E:309:GLU:HG3	2.04	0.57
2:G:165:SER:O	2:G:169:LEU:HG	2.04	0.57
2:G:19:PHE:CE2	2:G:190:LYS:HG2	2.40	0.57
2:G:57:ARG:HG2	2:G:60:ILE:HD11	1.86	0.57
1:A:254:ILE:O	1:A:302:ALA:CB	2.52	0.57
1:A:543:THR:O	1:A:547:ILE:HG13	2.04	0.57
1:B:303:THR:HG23	1:B:334:ASP:C	2.30	0.57
1:D:18:ASN:HD22	1:D:21:LYS:HE3	1.69	0.57
1:D:520:PHE:CB	1:D:635:ILE:HA	2.34	0.57
1:D:712:GLN:HE22	2:E:370:LEU:HG	1.69	0.57
2:G:296:MET:O	2:G:299:LEU:O	2.23	0.57
1:B:619:LEU:HD12	1:B:693:ILE:HG12	1.87	0.57
1:D:227:LEU:HB3	1:D:435:GLN:NE2	2.20	0.57
2:F:57:ARG:HG2	2:F:60:ILE:HD11	1.87	0.57
2:G:101:ILE:HG13	2:G:104:LEU:HB3	1.86	0.57
1:A:44:ARG:NH1	1:A:69:LEU:CD2	2.57	0.57
1:B:101:ALA:HB3	1:B:104:ASP:OD2	2.04	0.57
1:B:258:ALA:HB1	1:B:261:ILE:HD12	1.86	0.57
1:C:619:LEU:HD13	1:C:693:ILE:HD13	1.86	0.57
1:D:465:SER:O	1:D:515:ILE:HA	2.05	0.57
2:H:305:CYS:O	2:H:309:GLU:HG3	2.05	0.57
1:A:101:ALA:HB3	1:A:104:ASP:OD2	2.05	0.57
1:C:44:ARG:HG3	1:C:69:LEU:HD21	1.87	0.57
1:C:208:PRO:HB3	1:C:464:LEU:CD2	2.35	0.57
1:C:208:PRO:HB3	1:C:464:LEU:HD21	1.86	0.57
1:D:560:LYS:HD2	1:D:609:HIS:NE2	2.19	0.57
2:G:160:LEU:HD21	2:G:193:LEU:HD22	1.87	0.57
2:G:190:LYS:HB3	2:G:261:MET:SD	2.44	0.57
2:G:207:ARG:HH22	2:G:282:GLN:NE2	2.03	0.57
1:B:439:CYS:O	1:B:440:LEU:HB2	2.03	0.57
1:C:44:ARG:HA	1:C:44:ARG:NE	2.20	0.57
1:D:18:ASN:H	3:D:800:DTP:H2	1.68	0.57
1:D:441:GLU:HA	1:D:692:SER:O	2.05	0.57
2:E:3:THR:OG1	2:E:5:PHE:O	2.20	0.57
2:F:197:LEU:HB2	2:F:249:LEU:HD21	1.87	0.57
1:A:234:LEU:HG	3:A:900:DTP:H2'2	1.87	0.57
1:B:618:ALA:CB	1:B:691:GLN:HB2	2.29	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:ASN:HD22	1:C:21:LYS:HE3	1.70	0.57
1:C:348:LEU:HB3	2:G:371:SER:HA	1.85	0.57
2:E:296:MET:O	2:E:299:LEU:O	2.23	0.57
2:G:221:ARG:HH12	2:G:296:MET:HG2	1.69	0.57
1:A:212:MET:HE2	1:A:212:MET:HA	1.85	0.56
1:C:209:THR:N	1:C:210:PRO:HD2	2.20	0.56
1:C:280:PRO:CB	1:D:291:SER:O	2.51	0.56
1:C:305:PHE:CZ	1:C:436:SER:HB3	2.40	0.56
1:C:441:GLU:HG3	1:C:620:MET:HB3	1.87	0.56
1:D:209:THR:N	1:D:210:PRO:HD2	2.20	0.56
1:D:286:GLN:CD	1:D:332:HIS:HB2	2.29	0.56
1:D:341:LYS:HG2	1:D:722:TYR:OH	2.03	0.56
2:E:8:THR:HG22	2:E:9:LYS:N	2.18	0.56
2:E:45:SER:HB3	2:F:49:ARG:HH12	1.69	0.56
2:F:296:MET:O	2:F:299:LEU:O	2.23	0.56
1:B:279:ILE:HB	1:B:280:PRO:HD3	1.86	0.56
1:B:286:GLN:CD	1:B:332:HIS:HB2	2.29	0.56
1:A:21:LYS:O	1:A:25:VAL:HG23	2.05	0.56
1:A:173:TYR:CZ	1:A:201:SER:HA	2.40	0.56
1:A:258:ALA:HB1	1:A:261:ILE:HD12	1.86	0.56
1:A:279:ILE:HB	1:A:280:PRO:HD3	1.87	0.56
1:B:317:LEU:O	1:B:405:GLU:HG3	2.06	0.56
1:B:441:GLU:O	1:B:692:SER:O	2.24	0.56
1:B:682:VAL:HA	1:B:685:MET:HE3	1.86	0.56
1:C:93:ALA:HB1	1:C:166:TYR:O	2.05	0.56
1:D:403:MET:HE2	1:D:714:LEU:HB3	1.87	0.56
1:D:621:PRO:HD3	1:D:694:SER:CB	2.35	0.56
2:G:305:CYS:O	2:G:309:GLU:HG3	2.05	0.56
2:H:19:PHE:CE2	2:H:190:LYS:HG2	2.41	0.56
2:H:101:ILE:HG13	2:H:104:LEU:HB3	1.88	0.56
2:H:160:LEU:HD21	2:H:193:LEU:HD22	1.87	0.56
2:F:311:ILE:HD11	2:F:315:ARG:HE	1.69	0.56
2:G:92:ASN:O	2:G:96:LEU:HB2	2.05	0.56
1:B:62:ILE:HG13	1:B:63:ILE:N	2.19	0.56
1:C:529:LYS:HB3	1:C:536:ALA:HB2	1.88	0.56
1:C:639:ARG:HH22	1:C:733:ASN:HB3	1.71	0.56
2:F:198:MET:HG2	2:F:249:LEU:HD22	1.87	0.56
2:H:317:GLN:HB2	2:H:323:LEU:HD21	1.87	0.56
1:A:19:LEU:HA	1:A:22:ILE:CD1	2.36	0.56
1:A:215:VAL:O	1:A:216:ARG:HG2	2.05	0.56
1:B:231:GLY:HA2	1:B:260:ARG:HD3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:279:ILE:HD12	1:B:319:LEU:HD21	1.88	0.56
1:C:7:VAL:HG22	1:C:17:ILE:CG1	2.34	0.56
1:C:467:PHE:HB2	1:C:517:VAL:HG12	1.86	0.56
2:F:91:PRO:O	2:F:95:LEU:HB2	2.06	0.56
2:G:304:LEU:O	2:G:308:VAL:HG23	2.06	0.56
1:A:320:LYS:HB3	1:A:409:THR:HG21	1.87	0.56
1:B:68:ASP:HA	1:B:653:ARG:NH1	2.21	0.56
1:C:21:LYS:HD2	3:C:800:DTP:C6	2.35	0.56
1:C:530:ARG:NH1	1:C:667:GLU:HB2	2.20	0.56
1:D:39:SER:O	1:D:43:LEU:HG	2.06	0.56
1:D:128:PHE:HA	1:D:131:MET:HE3	1.87	0.56
2:E:12:GLN:HE21	2:E:23:VAL:HG13	1.69	0.56
2:H:255:GLY:CA	2:H:262:ALA:HB2	2.36	0.56
1:A:217:THR:OG1	1:A:219:THR:HG22	2.06	0.56
1:A:253:GLY:C	1:A:254:ILE:HD13	2.31	0.56
1:B:417:VAL:O	1:B:421:ASN:ND2	2.38	0.56
1:C:286:GLN:CD	1:C:332:HIS:HB2	2.31	0.56
1:D:6:LEU:CA	1:D:14:THR:HG22	2.36	0.56
2:E:91:PRO:HB2	2:E:112:ALA:HB2	1.87	0.56
1:A:215:VAL:O	1:A:216:ARG:CB	2.53	0.56
1:A:439:CYS:SG	1:A:621:PRO:CD	2.92	0.56
1:B:106:VAL:O	1:B:110:VAL:HG23	2.05	0.56
1:B:154:LYS:HA	1:B:160:ARG:NH2	2.16	0.56
1:B:173:TYR:CE2	1:B:201:SER:HA	2.41	0.56
1:B:229:GLU:HG3	1:B:257:ASN:ND2	2.20	0.56
1:C:154:LYS:HG2	1:C:155:TYR:CD1	2.41	0.56
1:D:430:ILE:CG2	1:D:570:GLU:CB	2.83	0.56
1:D:639:ARG:HH22	1:D:733:ASN:HB3	1.71	0.56
2:H:198:MET:HG2	2:H:249:LEU:HD22	1.87	0.56
1:A:682:VAL:HA	1:A:685:MET:HE3	1.86	0.56
1:B:342:LEU:HG	1:B:343:MET:HE2	1.87	0.56
1:C:154:LYS:HA	1:C:160:ARG:HH22	1.71	0.56
1:C:215:VAL:O	1:C:216:ARG:HG2	2.06	0.56
1:D:72:ARG:HG2	1:D:642:VAL:HG23	1.86	0.56
1:D:93:ALA:HB1	1:D:166:TYR:O	2.05	0.56
2:F:165:SER:O	2:F:169:LEU:HG	2.06	0.56
2:G:198:MET:SD	2:G:249:LEU:HD13	2.46	0.56
1:A:441:GLU:CD	1:A:620:MET:HB3	2.31	0.55
1:B:643:SER:C	1:B:644:ILE:HD12	2.32	0.55
1:C:439:CYS:HB2	1:C:441:GLU:OE1	2.06	0.55
1:C:467:PHE:CE2	1:C:515:ILE:HG21	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:49:ARG:HH12	2:F:45:SER:HB3	1.72	0.55
2:E:196:CYS:O	2:E:200:VAL:HG23	2.06	0.55
1:A:618:ALA:HA	1:A:689:ILE:CG2	2.36	0.55
1:A:670:TRP:CE2	1:A:735:ARG:HB2	2.41	0.55
1:B:10:ARG:HE	1:B:91:LYS:NZ	2.03	0.55
1:C:719:LEU:HB3	2:G:373:PHE:CD2	2.40	0.55
1:D:18:ASN:H	3:D:800:DTP:C2	2.19	0.55
1:D:44:ARG:HA	1:D:44:ARG:HE	1.71	0.55
1:D:189:ARG:HG2	1:D:189:ARG:HH11	1.70	0.55
2:E:306:GLN:HB3	2:E:328:ARG:NH1	2.20	0.55
2:F:255:GLY:CA	2:F:262:ALA:HB2	2.36	0.55
1:B:253:GLY:C	1:B:254:ILE:HD13	2.32	0.55
1:B:469:LEU:HD12	1:B:520:PHE:HA	1.87	0.55
2:E:92:ASN:O	2:E:96:LEU:HB2	2.05	0.55
2:F:330:ASN:HB3	2:F:333:PRO:HG3	1.88	0.55
2:H:95:LEU:O	2:H:99:ILE:HG13	2.06	0.55
1:B:463:THR:HG23	1:B:492:LEU:HD23	1.88	0.55
1:D:530:ARG:NH1	1:D:667:GLU:HB2	2.22	0.55
2:E:57:ARG:HG2	2:E:60:ILE:HD11	1.87	0.55
2:G:89:ARG:O	2:G:93:VAL:HG23	2.07	0.55
2:H:190:LYS:HB3	2:H:261:MET:SD	2.46	0.55
1:A:282:TYR:HA	1:A:285:PHE:HD2	1.71	0.55
1:B:35:ASN:O	1:B:35:ASN:ND2	2.39	0.55
1:B:173:TYR:CZ	1:B:201:SER:HA	2.42	0.55
1:B:254:ILE:O	1:B:302:ALA:HB1	2.05	0.55
1:C:465:SER:HB3	1:C:515:ILE:HA	1.88	0.55
1:C:520:PHE:CB	1:C:635:ILE:HA	2.36	0.55
1:D:106:VAL:O	1:D:110:VAL:HG23	2.06	0.55
1:D:530:ARG:HB2	1:D:533:ASP:OD2	2.07	0.55
2:E:99:ILE:HD11	2:E:108:VAL:HG21	1.87	0.55
2:E:190:LYS:HB3	2:E:261:MET:SD	2.47	0.55
2:F:305:CYS:O	2:F:309:GLU:HG3	2.04	0.55
2:H:91:PRO:HB2	2:H:112:ALA:HB2	1.87	0.55
2:H:98:LEU:HD21	2:H:164:THR:HG23	1.87	0.55
1:A:173:TYR:CE2	1:A:201:SER:HA	2.42	0.55
1:A:619:LEU:HD12	1:A:693:ILE:CG1	2.37	0.55
1:C:196:PHE:CD1	1:C:484:LEU:HB3	2.40	0.55
2:G:255:GLY:CA	2:G:262:ALA:HB2	2.37	0.55
1:A:181:PHE:O	1:A:189:ARG:HD2	2.07	0.55
1:A:185:PRO:HB2	1:A:187:GLU:CG	2.37	0.55
1:A:278:CYS:HB3	1:A:282:TYR:CE1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:SER:OG	1:B:61:THR:HG22	2.06	0.55
1:B:254:ILE:O	1:B:302:ALA:HA	2.07	0.55
1:D:685:MET:O	1:D:689:ILE:HG12	2.07	0.55
2:G:8:THR:HG22	2:G:9:LYS:N	2.22	0.55
2:G:49:ARG:HH12	2:H:45:SER:HB3	1.72	0.55
1:B:6:LEU:O	1:B:53:ILE:HG22	2.07	0.55
1:B:102:LEU:HD23	1:B:128:PHE:O	2.07	0.55
1:C:106:VAL:O	1:C:110:VAL:HG23	2.07	0.55
2:E:95:LEU:O	2:E:99:ILE:HG13	2.07	0.55
2:H:91:PRO:O	2:H:95:LEU:HB2	2.06	0.55
1:B:403:MET:CE	1:B:714:LEU:HB3	2.36	0.55
1:B:515:ILE:O	1:B:618:ALA:O	2.24	0.55
1:D:40:GLN:O	1:D:44:ARG:N	2.38	0.55
1:D:439:CYS:HB2	1:D:441:GLU:OE1	2.07	0.55
1:D:441:GLU:HG3	1:D:619:LEU:O	2.06	0.55
1:A:7:VAL:CG2	1:A:15:GLU:O	2.54	0.55
1:A:106:VAL:O	1:A:110:VAL:HG23	2.07	0.55
1:A:242:SER:HB3	1:B:238:ASN:HB3	1.89	0.55
1:A:689:ILE:CG2	1:A:691:GLN:O	2.51	0.55
1:C:281:PHE:HZ	3:C:900:DTP:H2'1	1.73	0.55
2:F:160:LEU:HD21	2:F:193:LEU:HD22	1.87	0.55
2:F:273:TYR:O	2:F:277:VAL:HG23	2.07	0.55
1:A:10:ARG:HH22	1:A:88:HIS:CE1	2.26	0.54
1:C:403:MET:HE2	1:C:714:LEU:HB3	1.88	0.54
1:C:432:PRO:HG2	1:C:434:ARG:NH1	2.21	0.54
1:C:433:VAL:HG11	1:C:443:ALA:HB1	1.89	0.54
1:C:619:LEU:CD1	1:C:693:ILE:HG12	2.37	0.54
1:D:529:LYS:HB3	1:D:536:ALA:HB2	1.88	0.54
1:D:560:LYS:HD3	1:D:609:HIS:CD2	2.41	0.54
2:E:23:VAL:HG22	2:E:100:SER:C	2.32	0.54
1:A:244:ILE:HG12	1:A:254:ILE:HG21	1.90	0.54
1:B:21:LYS:O	1:B:25:VAL:HG23	2.07	0.54
1:B:35:ASN:O	1:B:35:ASN:CG	2.50	0.54
1:C:21:LYS:O	1:C:25:VAL:HG23	2.06	0.54
1:C:287:THR:CB	1:D:284:HIS:HA	2.37	0.54
1:C:619:LEU:HD12	1:C:693:ILE:HG12	1.88	0.54
1:D:430:ILE:CD1	1:D:570:GLU:HA	2.37	0.54
1:B:217:THR:OG1	1:B:219:THR:HG22	2.08	0.54
1:B:647:SER:HB2	1:B:652:LEU:HD11	1.89	0.54
1:D:368:PHE:CD2	1:D:369:PHE:CZ	2.95	0.54
1:D:678:TYR:OH	1:D:695:ALA:CB	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:273:TYR:O	2:E:277:VAL:HG23	2.08	0.54
2:H:196:CYS:O	2:H:200:VAL:HG23	2.07	0.54
2:H:306:GLN:HB3	2:H:328:ARG:NH1	2.22	0.54
1:A:516:GLY:N	1:A:620:MET:HE1	2.23	0.54
1:C:685:MET:O	1:C:689:ILE:HG12	2.07	0.54
1:D:290:LYS:CE	1:D:332:HIS:HB3	2.37	0.54
2:E:160:LEU:HD21	2:E:193:LEU:HD22	1.87	0.54
2:H:206:ILE:HG12	2:H:315:ARG:HG3	1.90	0.54
1:A:238:ASN:HB3	1:B:242:SER:HB3	1.89	0.54
1:B:254:ILE:O	1:B:302:ALA:CB	2.55	0.54
1:C:154:LYS:CG	1:C:155:TYR:HD1	2.20	0.54
1:D:425:PRO:HG2	1:D:615:THR:HG22	1.88	0.54
2:H:165:SER:O	2:H:169:LEU:HG	2.07	0.54
1:C:87:PHE:HE1	3:C:800:DTP:O2A	1.90	0.54
2:F:306:GLN:HB3	2:F:328:ARG:NH1	2.23	0.54
1:A:229:GLU:HG3	1:A:257:ASN:ND2	2.21	0.54
1:A:254:ILE:O	1:A:302:ALA:HA	2.07	0.54
1:B:304:LEU:HD23	1:B:305:PHE:N	2.23	0.54
2:F:190:LYS:HB3	2:F:261:MET:SD	2.47	0.54
1:A:483:ILE:O	1:A:487:ARG:HB2	2.08	0.54
1:A:542:LYS:HG3	1:A:596:HIS:CD2	2.42	0.54
1:B:483:ILE:O	1:B:487:ARG:HB2	2.08	0.54
1:B:511:ARG:HG2	1:B:511:ARG:HH11	1.73	0.54
1:C:432:PRO:CG	1:C:434:ARG:HH11	2.21	0.54
1:C:719:LEU:HD22	2:G:375:LEU:HD21	1.89	0.54
1:D:6:LEU:HD23	1:D:14:THR:HG21	1.89	0.54
2:E:255:GLY:CA	2:E:262:ALA:HB2	2.37	0.54
2:G:141:VAL:HG11	2:H:9:LYS:HA	1.90	0.54
2:G:197:LEU:HB2	2:G:249:LEU:HD21	1.89	0.54
2:H:129:ILE:HG13	2:H:130:VAL:HG13	1.89	0.54
1:A:228:ILE:HG21	1:A:240:THR:HG23	1.90	0.54
1:A:231:GLY:HA2	1:A:260:ARG:HD3	1.90	0.54
1:A:321:ASN:ND2	1:A:323:ARG:O	2.41	0.54
1:C:208:PRO:CD	1:C:464:LEU:CD1	2.85	0.54
1:C:520:PHE:O	1:C:523:TYR:HB3	2.08	0.54
1:C:530:ARG:HB2	1:C:533:ASP:OD2	2.08	0.54
1:D:233:SER:HA	3:D:900:DTP:O5'	2.08	0.54
1:D:545:GLU:OE1	1:D:595:LEU:HA	2.08	0.54
2:F:163:MET:HB3	2:F:189:LEU:HD13	1.90	0.54
2:F:196:CYS:O	2:F:200:VAL:HG23	2.07	0.54
2:F:227:ASN:O	2:F:231:ILE:HG12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:306:GLN:HB3	2:G:328:ARG:NH1	2.23	0.54
1:C:565:CYS:SG	1:C:568:PHE:HB2	2.47	0.54
1:D:18:ASN:N	3:D:800:DTP:H2	2.22	0.54
1:D:151:LEU:HA	1:D:155:TYR:HB2	1.90	0.54
2:E:129:ILE:HG13	2:E:130:VAL:HG13	1.89	0.54
2:G:273:TYR:O	2:G:277:VAL:HG23	2.08	0.54
1:B:214:GLY:O	1:B:215:VAL:C	2.50	0.53
1:B:689:ILE:CG2	1:B:691:GLN:O	2.56	0.53
1:D:228:ILE:CG2	1:D:240:THR:HG23	2.39	0.53
1:A:7:VAL:HG11	3:A:800:DTP:N6	2.22	0.53
1:A:544:PHE:CZ	1:A:685:MET:HG2	2.34	0.53
1:C:92:LYS:HD3	1:C:165:ILE:HD12	1.88	0.53
1:C:185:PRO:HG2	1:C:188:THR:HG1	1.72	0.53
1:C:425:PRO:CB	1:C:615:THR:HG22	2.37	0.53
1:D:642:VAL:HG22	1:D:655:VAL:HG22	1.90	0.53
2:E:36:PHE:CZ	2:E:104:LEU:HD13	2.43	0.53
2:E:141:VAL:HG11	2:F:9:LYS:HA	1.89	0.53
2:G:330:ASN:HB3	2:G:333:PRO:HG3	1.89	0.53
2:H:197:LEU:HB2	2:H:249:LEU:HD21	1.89	0.53
1:A:54:LYS:HB2	1:A:57:ASP:OD2	2.07	0.53
1:B:403:MET:HE3	1:B:714:LEU:HB3	1.90	0.53
1:C:107:VAL:O	1:C:111:GLU:HG3	2.09	0.53
1:D:565:CYS:SG	1:D:568:PHE:HB2	2.48	0.53
2:H:5:PHE:CD1	2:H:24:ASN:O	2.61	0.53
1:A:670:TRP:CH2	1:A:735:ARG:HB2	2.43	0.53
1:B:542:LYS:HG3	1:B:596:HIS:CD2	2.43	0.53
2:F:5:PHE:CD1	2:F:24:ASN:O	2.61	0.53
2:H:273:TYR:O	2:H:277:VAL:HG23	2.08	0.53
1:A:125:GLU:O	1:A:129:LYS:HG3	2.08	0.53
1:B:290:LYS:CG	1:B:296:GLY:O	2.57	0.53
1:B:552:LEU:HB3	1:B:602:LEU:HD21	1.91	0.53
1:C:701:PRO:O	1:C:707:GLY:HA2	2.09	0.53
1:D:430:ILE:HG22	1:D:570:GLU:OE1	2.09	0.53
1:D:701:PRO:O	1:D:707:GLY:HA2	2.08	0.53
2:G:8:THR:CG2	2:G:9:LYS:N	2.72	0.53
1:A:102:LEU:O	1:A:106:VAL:HG23	2.08	0.53
1:B:418:ASP:HA	1:B:421:ASN:HD22	1.73	0.53
1:D:226:VAL:HG21	1:D:247:TYR:CG	2.44	0.53
2:G:169:LEU:HD22	2:H:166:TYR:CE2	2.43	0.53
1:B:517:VAL:O	1:B:634:GLY:HA2	2.09	0.53
2:E:78:LYS:HE2	2:E:136:VAL:HG13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:78:LYS:HE2	2:G:136:VAL:HG13	1.91	0.53
1:A:140:ASP:OD1	1:A:169:ALA:HB3	2.09	0.53
1:A:317:LEU:O	1:A:405:GLU:HG3	2.09	0.53
1:B:7:VAL:HG23	1:B:17:ILE:HG12	1.89	0.53
1:C:544:PHE:HA	1:C:547:ILE:HD12	1.90	0.53
2:H:36:PHE:CZ	2:H:104:LEU:HD13	2.44	0.53
1:B:137:HIS:HA	1:B:170:GLN:HG3	1.89	0.53
1:C:403:MET:HB2	1:C:711:MET:HE1	1.91	0.53
1:C:474:ASN:OD1	1:C:476:ASP:HB2	2.09	0.53
1:C:510:ARG:HG2	1:C:567:TRP:CE3	2.41	0.53
1:C:545:GLU:OE1	1:C:595:LEU:HA	2.08	0.53
1:D:317:LEU:HD23	1:D:401:LEU:HD23	1.90	0.53
2:G:196:CYS:O	2:G:200:VAL:HG23	2.07	0.53
1:B:102:LEU:O	1:B:106:VAL:HG23	2.09	0.53
1:C:226:VAL:HG21	1:C:247:TYR:CG	2.44	0.53
1:C:430:ILE:CG2	1:C:570:GLU:OE1	2.57	0.53
1:C:670:TRP:CH2	1:C:735:ARG:HB2	2.44	0.53
1:D:92:LYS:HD3	1:D:165:ILE:HD12	1.91	0.53
1:D:107:VAL:O	1:D:111:GLU:HG3	2.08	0.53
1:D:364:LEU:HD23	1:D:378:LEU:CB	2.38	0.53
1:A:102:LEU:HD23	1:A:128:PHE:O	2.08	0.52
1:A:152:GLU:O	1:A:158:GLN:NE2	2.42	0.52
1:A:242:SER:HA	1:B:238:ASN:OD1	2.09	0.52
1:A:317:LEU:HD23	1:A:401:LEU:CD2	2.39	0.52
1:A:320:LYS:HE3	1:A:411:ARG:HB2	1.91	0.52
1:B:140:ASP:OD1	1:B:169:ALA:HB3	2.09	0.52
1:B:293:SER:CB	1:B:298:ARG:O	2.53	0.52
1:C:87:PHE:CE1	3:C:800:DTP:O2A	2.62	0.52
1:C:642:VAL:HG22	1:C:655:VAL:HG22	1.91	0.52
2:H:227:ASN:O	2:H:231:ILE:HG12	2.09	0.52
1:A:18:ASN:N	3:A:800:DTP:H2	2.22	0.52
1:A:276:THR:HG21	1:B:292:CYS:HA	1.90	0.52
1:A:403:MET:CE	1:A:714:LEU:HB3	2.39	0.52
2:E:206:ILE:HG12	2:E:315:ARG:HG3	1.91	0.52
2:E:304:LEU:O	2:E:308:VAL:HG23	2.08	0.52
1:B:125:GLU:O	1:B:129:LYS:HG3	2.08	0.52
1:B:140:ASP:HA	1:B:143:PHE:CE2	2.43	0.52
1:C:573:TYR:CE1	1:C:578:LEU:HD23	2.44	0.52
1:D:21:LYS:O	1:D:25:VAL:HG23	2.08	0.52
1:D:464:LEU:HD13	1:D:620:MET:HG3	1.90	0.52
1:D:519:ASN:HB2	1:D:631:ALA:HB1	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:620:MET:HB2	1:D:621:PRO:HD2	1.90	0.52
2:F:78:LYS:HE2	2:F:136:VAL:HG13	1.91	0.52
1:B:82:ALA:O	1:B:86:ILE:HG12	2.09	0.52
1:B:618:ALA:CB	1:B:691:GLN:HB3	2.39	0.52
1:C:38:ILE:O	1:C:42:GLU:HG3	2.09	0.52
1:D:316:LEU:HA	1:D:319:LEU:HG	1.92	0.52
1:D:510:ARG:HG2	1:D:567:TRP:CE3	2.39	0.52
2:G:175:HIS:CD2	2:H:178:ASN:HD21	2.28	0.52
2:H:89:ARG:O	2:H:93:VAL:HG23	2.09	0.52
1:B:290:LYS:HG3	1:B:296:GLY:O	2.09	0.52
1:C:317:LEU:HD23	1:C:401:LEU:HD23	1.90	0.52
1:C:432:PRO:CG	1:C:434:ARG:NH1	2.72	0.52
2:F:95:LEU:O	2:F:99:ILE:HG13	2.09	0.52
2:F:198:MET:SD	2:F:249:LEU:HD13	2.50	0.52
1:A:10:ARG:HE	1:A:91:LYS:CE	2.22	0.52
1:B:224:SER:O	1:B:252:ALA:HA	2.10	0.52
1:C:464:LEU:HD12	1:C:464:LEU:O	2.10	0.52
1:D:189:ARG:O	1:D:193:VAL:CG2	2.49	0.52
1:D:638:PRO:O	1:D:668:LEU:HA	2.10	0.52
2:G:206:ILE:HG12	2:G:315:ARG:HG3	1.92	0.52
1:A:342:LEU:HG	1:A:343:MET:HE2	1.90	0.52
1:B:669:LEU:HD11	1:B:698:ASN:ND2	2.25	0.52
1:C:463:THR:CG2	1:C:489:LEU:HD22	2.35	0.52
1:C:617:SER:OG	1:C:690:ASP:N	2.27	0.52
2:E:197:LEU:HB2	2:E:249:LEU:HD21	1.90	0.52
2:F:304:LEU:O	2:F:308:VAL:HG23	2.08	0.52
2:G:129:ILE:HG13	2:G:130:VAL:HG13	1.90	0.52
2:G:163:MET:HB3	2:G:189:LEU:HD13	1.92	0.52
2:H:330:ASN:HB3	2:H:333:PRO:HG3	1.92	0.52
1:D:136:ASP:HB3	1:D:139:ARG:NE	2.25	0.52
1:A:478:LEU:HB2	1:A:550:TYR:CD2	2.45	0.52
1:B:244:ILE:CG2	1:B:254:ILE:HG13	2.24	0.52
1:B:474:ASN:HD22	1:B:474:ASN:N	2.06	0.52
1:C:206:SER:CA	1:C:466:ALA:HB3	2.38	0.52
1:C:279:ILE:HB	1:C:280:PRO:HD3	1.92	0.52
1:D:368:PHE:CZ	1:D:417:VAL:HG21	2.45	0.52
1:D:403:MET:HB2	1:D:711:MET:HE1	1.91	0.52
2:E:89:ARG:O	2:E:93:VAL:HG23	2.10	0.52
1:A:91:LYS:HD2	3:A:800:DTP:O2A	2.10	0.52
1:A:140:ASP:HA	1:A:143:PHE:CE2	2.45	0.52
1:A:553:LYS:O	1:A:557:GLU:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:647:SER:HB2	1:A:652:LEU:HD11	1.92	0.52
1:A:678:TYR:O	1:A:682:VAL:HG23	2.10	0.52
1:C:638:PRO:O	1:C:668:LEU:HA	2.10	0.52
1:D:279:ILE:HB	1:D:280:PRO:HD3	1.92	0.52
1:D:544:PHE:HA	1:D:547:ILE:HD12	1.91	0.52
1:A:6:LEU:HB2	1:A:52:GLY:N	2.24	0.51
1:A:279:ILE:HD12	1:A:319:LEU:HD21	1.92	0.51
1:A:305:PHE:CZ	1:A:436:SER:HB3	2.45	0.51
1:A:322:ASN:HA	1:A:331:ARG:HE	1.75	0.51
1:A:384:LYS:N	1:A:384:LYS:HD2	2.25	0.51
1:A:474:ASN:HD22	1:A:474:ASN:N	2.07	0.51
1:A:517:VAL:O	1:A:634:GLY:HA2	2.10	0.51
1:B:51:ASP:C	1:B:51:ASP:OD2	2.52	0.51
1:C:19:LEU:HD12	2:G:295:SER:O	2.10	0.51
1:C:131:MET:HA	1:C:134:PHE:CD2	2.44	0.51
1:C:228:ILE:CG2	1:C:240:THR:HG23	2.40	0.51
1:C:364:LEU:HD23	1:C:378:LEU:CB	2.38	0.51
1:C:371:ASP:HB3	1:C:374:GLU:HB3	1.93	0.51
1:D:189:ARG:NH1	1:D:189:ARG:CG	2.72	0.51
1:A:515:ILE:O	1:A:618:ALA:O	2.29	0.51
1:A:622:SER:HB2	1:A:625:SER:HB2	1.92	0.51
1:B:244:ILE:HG12	1:B:254:ILE:HG21	1.92	0.51
1:B:670:TRP:CZ2	1:B:735:ARG:HB2	2.46	0.51
1:B:678:TYR:O	1:B:682:VAL:HG23	2.10	0.51
1:C:135:ILE:HD11	1:C:174:ILE:HG21	1.92	0.51
1:C:147:ALA:CB	1:C:628:ILE:HA	2.41	0.51
1:C:151:LEU:HD23	1:C:155:TYR:CD2	2.45	0.51
1:D:293:SER:HB2	1:D:298:ARG:O	2.07	0.51
1:A:59:HIS:CD2	3:A:800:DTP:H4'	2.46	0.51
1:A:219:THR:HA	1:B:269:ARG:HH22	1.74	0.51
1:B:305:PHE:CZ	1:B:436:SER:HB3	2.45	0.51
1:B:444:LEU:HD12	1:B:460:ALA:HB1	1.93	0.51
1:D:542:LYS:HG3	1:D:596:HIS:CD2	2.45	0.51
2:E:258:ASP:OD1	2:E:259:PRO:HD2	2.11	0.51
1:C:180:LEU:HD13	1:C:488:ALA:HB1	1.92	0.51
1:C:426:PHE:O	1:C:572:THR:HG23	2.10	0.51
1:C:686:GLN:HG2	1:C:725:GLY:O	2.11	0.51
1:D:147:ALA:CB	1:D:628:ILE:HA	2.40	0.51
1:A:137:HIS:HA	1:A:170:GLN:HG3	1.92	0.51
1:A:490:ASP:CG	1:A:511:ARG:HH21	2.18	0.51
1:C:188:THR:O	1:C:192:TYR:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:206:ILE:HG12	2:F:315:ARG:HG3	1.91	0.51
1:A:44:ARG:HG3	1:A:69:LEU:HD21	1.93	0.51
1:A:247:TYR:OH	1:A:461:LEU:HD21	2.10	0.51
1:B:278:CYS:HB3	1:B:282:TYR:CE1	2.45	0.51
1:C:245:VAL:HB	1:D:238:ASN:HD21	1.76	0.51
1:D:305:PHE:CZ	1:D:436:SER:HB3	2.45	0.51
2:H:145:GLN:HG2	2:H:289:TYR:CG	2.46	0.51
1:A:304:LEU:HD23	1:A:305:PHE:N	2.25	0.51
1:A:347:LEU:O	2:F:367:THR:HG21	2.11	0.51
1:B:119:LEU:HD21	1:B:179:CYS:SG	2.50	0.51
1:B:384:LYS:HD2	1:B:384:LYS:N	2.24	0.51
1:B:544:PHE:CE2	1:B:685:MET:HG2	2.46	0.51
1:B:686:GLN:HG2	1:B:725:GLY:O	2.11	0.51
1:C:33:LEU:HD22	1:C:76:ASP:HB3	1.92	0.51
1:C:513:LEU:HD12	1:C:616:LEU:CD2	2.35	0.51
1:C:543:THR:O	1:C:547:ILE:HG13	2.10	0.51
1:D:573:TYR:CE1	1:D:578:LEU:HD23	2.44	0.51
2:G:227:ASN:O	2:G:231:ILE:HG12	2.10	0.51
1:A:421:ASN:HB3	1:A:428:PRO:HB3	1.93	0.51
1:A:442:ILE:CG2	1:A:444:LEU:HG	2.40	0.51
1:A:469:LEU:HB3	1:A:523:TYR:CD1	2.45	0.51
1:B:553:LYS:O	1:B:557:GLU:HG2	2.10	0.51
1:C:151:LEU:HG	1:C:628:ILE:HD12	1.93	0.51
1:D:215:VAL:O	1:D:216:ARG:CB	2.58	0.51
1:D:293:SER:HB3	1:D:298:ARG:O	2.09	0.51
1:D:560:LYS:HD3	1:D:609:HIS:ND1	2.22	0.51
2:E:84:ASP:HA	2:E:87:GLN:HB2	1.92	0.51
2:E:311:ILE:HD11	2:E:315:ARG:HE	1.75	0.51
2:F:36:PHE:CZ	2:F:104:LEU:HD13	2.45	0.51
1:A:8:THR:HG21	1:A:54:LYS:HG2	1.93	0.51
1:B:619:LEU:HB2	1:B:693:ILE:HG23	1.92	0.51
1:D:686:GLN:HG2	1:D:725:GLY:O	2.10	0.51
2:E:330:ASN:HB3	2:E:333:PRO:HG3	1.92	0.51
2:F:89:ARG:O	2:F:93:VAL:HG23	2.11	0.51
2:G:95:LEU:O	2:G:99:ILE:HG13	2.11	0.51
1:A:606:ILE:HG23	1:A:611:LEU:HG	1.92	0.51
1:B:247:TYR:OH	1:B:461:LEU:HD21	2.10	0.51
1:C:136:ASP:HB3	1:C:139:ARG:NE	2.25	0.51
1:D:131:MET:HA	1:D:134:PHE:CD2	2.45	0.51
2:H:332:ILE:HB	2:H:334:TRP:NE1	2.26	0.51
1:A:19:LEU:CD1	2:F:295:SER:O	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:THR:O	1:A:58:ILE:CG1	2.59	0.50
1:B:322:ASN:HA	1:B:331:ARG:HE	1.75	0.50
1:B:723:LYS:HD2	2:H:373:PHE:CZ	2.45	0.50
1:C:208:PRO:CD	1:C:464:LEU:HD11	2.41	0.50
1:C:515:ILE:HD12	1:C:551:LEU:HD22	1.92	0.50
1:D:180:LEU:HD13	1:D:488:ALA:HB1	1.92	0.50
1:D:474:ASN:OD1	1:D:476:ASP:HB2	2.12	0.50
2:G:175:HIS:HD2	2:H:178:ASN:HD21	1.59	0.50
1:A:50:TYR:H	1:A:53:ILE:HG21	1.75	0.50
1:A:109:MET:HE3	1:A:114:LYS:HB2	1.93	0.50
1:A:276:THR:HB	3:A:900:DTP:H2	1.93	0.50
1:A:320:LYS:CD	1:A:411:ARG:HB2	2.40	0.50
1:D:148:VAL:HA	1:D:151:LEU:HD12	1.94	0.50
2:F:74:ILE:O	2:F:78:LYS:HG3	2.11	0.50
2:H:311:ILE:HD11	2:H:315:ARG:HE	1.76	0.50
1:A:46:HIS:HE1	2:F:220:GLU:O	1.94	0.50
1:A:686:GLN:HG2	1:A:725:GLY:O	2.10	0.50
1:B:680:GLN:O	1:B:684:ILE:HG13	2.11	0.50
1:C:293:SER:CB	1:C:298:ARG:O	2.59	0.50
2:E:178:ASN:HD21	2:F:175:HIS:CD2	2.29	0.50
2:F:129:ILE:HG13	2:F:130:VAL:HG13	1.92	0.50
2:G:311:ILE:HD11	2:G:315:ARG:HE	1.75	0.50
1:A:196:PHE:O	1:A:200:VAL:HG22	2.11	0.50
1:A:441:GLU:OE1	1:A:620:MET:CB	2.54	0.50
1:C:55:THR:HB	3:C:800:DTP:H8	1.92	0.50
1:C:313:VAL:HG13	1:C:314:GLU:N	2.26	0.50
1:D:303:THR:HG21	1:D:440:LEU:HD21	1.94	0.50
2:F:332:ILE:HB	2:F:334:TRP:NE1	2.25	0.50
2:H:163:MET:HB3	2:H:189:LEU:HD13	1.93	0.50
1:B:103:TYR:O	1:B:107:VAL:HG23	2.12	0.50
1:B:327:GLY:C	1:B:328:ASN:HD22	2.19	0.50
1:C:430:ILE:HG22	1:C:431:ALA:N	2.26	0.50
1:D:313:VAL:HG13	1:D:314:GLU:N	2.27	0.50
2:E:332:ILE:HB	2:E:334:TRP:NE1	2.27	0.50
2:G:5:PHE:CD1	2:G:24:ASN:O	2.65	0.50
2:H:304:LEU:O	2:H:308:VAL:HG23	2.11	0.50
1:A:227:LEU:CA	1:A:435:GLN:NE2	2.73	0.50
1:B:53:ILE:O	1:B:53:ILE:HG23	2.11	0.50
1:C:135:ILE:HA	1:C:197:TYR:CZ	2.46	0.50
1:C:316:LEU:HA	1:C:319:LEU:HG	1.92	0.50
1:D:217:THR:O	1:D:218:PRO:C	2.55	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:36:PHE:CZ	2:G:104:LEU:HD13	2.47	0.50
1:A:82:ALA:O	1:A:86:ILE:HG12	2.10	0.50
1:A:151:LEU:HD23	1:A:155:TYR:CD2	2.47	0.50
1:A:618:ALA:HB2	1:A:691:GLN:CB	2.32	0.50
1:D:55:THR:OG1	3:D:800:DTP:H5'1	2.11	0.50
1:D:135:ILE:HD11	1:D:174:ILE:HG21	1.93	0.50
1:D:368:PHE:HD2	1:D:369:PHE:CZ	2.29	0.50
1:A:680:GLN:O	1:A:684:ILE:HG13	2.11	0.50
1:B:469:LEU:HB3	1:B:523:TYR:CD1	2.46	0.50
1:C:619:LEU:CD1	1:C:693:ILE:CD1	2.90	0.50
1:C:656:VAL:HG23	1:C:659:TYR:HB2	1.94	0.50
2:E:255:GLY:CA	2:E:258:ASP:O	2.57	0.50
1:A:153:GLY:O	1:A:160:ARG:NH1	2.45	0.50
1:B:622:SER:HB2	1:B:625:SER:HB2	1.94	0.50
1:C:303:THR:HG21	1:C:440:LEU:HD21	1.94	0.50
2:E:175:HIS:CD2	2:F:178:ASN:HD21	2.29	0.50
2:F:160:LEU:HD21	2:F:193:LEU:CD2	2.41	0.50
2:G:160:LEU:HD21	2:G:193:LEU:CD2	2.41	0.50
1:A:643:SER:C	1:A:644:ILE:HD12	2.37	0.49
1:D:469:LEU:HB3	1:D:523:TYR:CD1	2.47	0.49
1:D:656:VAL:HG23	1:D:659:TYR:HB2	1.93	0.49
2:E:74:ILE:O	2:E:78:LYS:HG3	2.11	0.49
2:F:147:GLN:O	2:F:151:GLU:N	2.45	0.49
2:G:55:VAL:HG12	2:G:226:GLY:HA3	1.94	0.49
2:H:147:GLN:O	2:H:151:GLU:N	2.46	0.49
1:A:224:SER:O	1:A:252:ALA:CA	2.60	0.49
1:A:463:THR:CG2	1:A:492:LEU:CD2	2.78	0.49
1:C:348:LEU:O	2:G:371:SER:HB3	2.12	0.49
1:C:619:LEU:CD1	1:C:693:ILE:HG23	2.32	0.49
1:D:33:LEU:HD22	1:D:76:ASP:HB3	1.93	0.49
2:H:78:LYS:HE2	2:H:136:VAL:HG13	1.93	0.49
1:A:103:TYR:O	1:A:107:VAL:HG23	2.13	0.49
1:A:247:TYR:CZ	1:A:461:LEU:HD21	2.47	0.49
1:A:254:ILE:O	1:A:302:ALA:CA	2.60	0.49
1:B:109:MET:HE3	1:B:114:LYS:HB2	1.95	0.49
1:C:276:THR:CB	3:C:900:DTP:H2	2.39	0.49
1:D:227:LEU:HD23	1:D:435:GLN:HG3	1.93	0.49
1:D:514:GLY:HA2	1:D:618:ALA:HB2	1.91	0.49
1:D:519:ASN:HA	1:D:632:THR:H	1.77	0.49
1:D:681:LEU:O	1:D:685:MET:HG3	2.13	0.49
1:A:227:LEU:CB	1:A:435:GLN:HE21	2.17	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:ILE:CG2	1:A:240:THR:HG23	2.42	0.49
1:A:669:LEU:HD11	1:A:698:ASN:ND2	2.28	0.49
1:B:324:GLY:HA3	1:B:329:ARG:NH2	2.28	0.49
1:B:645:LYS:HB2	1:B:645:LYS:NZ	2.27	0.49
1:D:543:THR:O	1:D:547:ILE:HG13	2.11	0.49
2:H:74:ILE:O	2:H:78:LYS:HG3	2.12	0.49
1:A:40:GLN:HE22	2:F:334:TRP:H	1.60	0.49
1:A:269:ARG:HH22	1:B:219:THR:HA	1.77	0.49
1:B:196:PHE:O	1:B:200:VAL:HG22	2.12	0.49
1:C:234:LEU:C	1:D:246:LYS:HZ3	2.21	0.49
1:C:247:TYR:O	1:C:252:ALA:HB3	2.13	0.49
1:D:54:LYS:O	1:D:58:ILE:HG12	2.13	0.49
1:D:114:LYS:HE2	1:D:166:TYR:CE2	2.47	0.49
1:D:433:VAL:HG11	1:D:443:ALA:HB1	1.94	0.49
2:G:332:ILE:HB	2:G:334:TRP:NE1	2.28	0.49
1:A:327:GLY:C	1:A:328:ASN:HD22	2.20	0.49
1:A:552:LEU:HB3	1:A:602:LEU:HD21	1.93	0.49
1:B:478:LEU:HB2	1:B:550:TYR:CD2	2.47	0.49
1:B:696:ASN:HD22	1:B:696:ASN:N	2.11	0.49
1:C:342:LEU:HD21	1:C:379:TYR:CD2	2.47	0.49
1:C:469:LEU:HB3	1:C:523:TYR:CD1	2.47	0.49
1:B:522:TYR:CZ	1:B:526:LYS:HD3	2.48	0.49
1:C:154:LYS:CG	1:C:155:TYR:CD1	2.96	0.49
1:C:583:TYR:HD2	1:C:587:LEU:HD12	1.77	0.49
1:D:135:ILE:HA	1:D:197:TYR:CZ	2.47	0.49
2:E:160:LEU:HD21	2:E:193:LEU:CD2	2.43	0.49
1:A:238:ASN:OD1	1:B:242:SER:HA	2.12	0.49
1:A:520:PHE:CB	1:A:635:ILE:HA	2.43	0.49
1:B:107:VAL:O	1:B:111:GLU:HG3	2.11	0.49
1:B:520:PHE:CB	1:B:635:ILE:HA	2.43	0.49
1:C:542:LYS:HG3	1:C:596:HIS:CD2	2.46	0.49
1:D:368:PHE:HD2	1:D:369:PHE:CE1	2.31	0.49
1:A:119:LEU:HD21	1:A:179:CYS:SG	2.53	0.49
1:A:144:SER:O	1:A:148:VAL:HG23	2.12	0.49
1:B:134:PHE:HB3	1:B:194:LYS:HG3	1.95	0.49
1:C:43:LEU:HD12	2:G:334:TRP:CD1	2.48	0.49
1:C:379:TYR:O	1:C:383:GLU:HG3	2.13	0.49
1:D:517:VAL:O	1:D:634:GLY:HA2	2.12	0.49
2:E:55:VAL:HG12	2:E:226:GLY:HA3	1.94	0.49
2:E:155:SER:O	2:E:159:GLU:HG3	2.13	0.49
2:G:155:SER:O	2:G:159:GLU:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:SER:HB3	1:A:40:GLN:HG2	1.93	0.49
1:A:403:MET:HE3	1:A:714:LEU:HB3	1.94	0.49
1:A:618:ALA:HA	1:A:689:ILE:HG23	1.93	0.49
1:B:227:LEU:HB3	1:B:435:GLN:NE2	2.28	0.49
1:B:441:GLU:HG2	1:B:442:ILE:CG1	2.33	0.49
1:B:606:ILE:HG23	1:B:611:LEU:HG	1.94	0.49
1:C:248:VAL:HG11	1:C:289:VAL:HA	1.95	0.49
2:E:227:ASN:O	2:E:231:ILE:HG12	2.13	0.49
2:H:84:ASP:HA	2:H:87:GLN:HB2	1.95	0.49
2:H:147:GLN:HA	2:H:147:GLN:NE2	2.27	0.49
2:H:204:GLU:OE2	2:H:241:HIS:HB3	2.13	0.49
1:A:244:ILE:CG2	1:A:254:ILE:HG13	2.24	0.48
1:B:361:VAL:O	1:B:364:LEU:HB2	2.13	0.48
1:C:40:GLN:HG2	1:C:44:ARG:HG3	1.95	0.48
1:D:103:TYR:O	1:D:107:VAL:HG23	2.12	0.48
1:D:379:TYR:O	1:D:383:GLU:HG3	2.12	0.48
1:D:437:ASN:HB3	1:D:442:ILE:HB	1.94	0.48
1:D:689:ILE:CG2	1:D:691:GLN:H	2.25	0.48
2:H:155:SER:O	2:H:159:GLU:HG3	2.13	0.48
1:A:151:LEU:CA	1:A:155:TYR:HB2	2.35	0.48
1:D:94:TYR:CD1	1:D:100:PRO:CD	2.96	0.48
1:D:151:LEU:HG	1:D:628:ILE:HD12	1.94	0.48
1:D:248:VAL:HG11	1:D:289:VAL:HA	1.95	0.48
2:G:145:GLN:HG2	2:G:289:TYR:CG	2.49	0.48
2:H:149:ARG:HH21	2:H:283:GLU:CD	2.20	0.48
2:H:160:LEU:HD21	2:H:193:LEU:CD2	2.42	0.48
1:B:290:LYS:HE3	1:B:332:HIS:HB3	1.95	0.48
1:B:532:SER:HA	1:B:677:GLY:HA3	1.95	0.48
1:D:367:ALA:O	1:D:371:ASP:O	2.31	0.48
2:E:147:GLN:O	2:E:151:GLU:N	2.47	0.48
1:A:437:ASN:HD21	1:A:439:CYS:CB	2.05	0.48
1:C:42:GLU:OE1	2:G:298:GLY:N	2.46	0.48
1:C:103:TYR:O	1:C:107:VAL:HG23	2.13	0.48
1:C:301:ALA:HB1	1:C:438:LEU:HD11	1.95	0.48
1:C:437:ASN:HB3	1:C:442:ILE:HB	1.93	0.48
1:D:248:VAL:C	1:D:250:GLN:H	2.22	0.48
1:D:692:SER:OG	1:D:728:THR:HG23	2.14	0.48
2:G:147:GLN:HA	2:G:147:GLN:NE2	2.29	0.48
1:A:312:GLU:O	1:A:316:LEU:HG	2.12	0.48
1:A:324:GLY:HA3	1:A:329:ARG:NH2	2.29	0.48
1:A:645:LYS:HB2	1:A:645:LYS:NZ	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:SER:O	1:B:148:VAL:HG23	2.14	0.48
1:B:254:ILE:O	1:B:302:ALA:CA	2.61	0.48
1:C:233:SER:HA	3:C:900:DTP:O5'	2.13	0.48
1:D:583:TYR:HD2	1:D:587:LEU:HD12	1.77	0.48
1:B:430:ILE:HG21	1:B:570:GLU:HG2	1.94	0.48
1:B:441:GLU:HG2	1:B:442:ILE:N	2.29	0.48
1:C:208:PRO:CB	1:C:464:LEU:CD1	2.60	0.48
1:C:425:PRO:HG2	1:C:615:THR:HG22	1.95	0.48
1:D:695:ALA:C	1:D:696:ASN:HD22	2.21	0.48
2:G:74:ILE:O	2:G:78:LYS:HG3	2.14	0.48
1:C:148:VAL:HA	1:C:151:LEU:HD12	1.94	0.48
1:C:458:GLU:OE1	1:C:567:TRP:CZ3	2.67	0.48
1:D:125:GLU:O	1:D:129:LYS:HG3	2.13	0.48
1:D:403:MET:CE	1:D:714:LEU:HB3	2.44	0.48
1:D:572:THR:HB	1:D:577:ILE:HB	1.95	0.48
1:D:644:ILE:HA	1:D:652:LEU:O	2.14	0.48
2:E:35:ILE:HG23	2:E:36:PHE:N	2.29	0.48
2:F:92:ASN:OD1	2:F:109:GLU:HG2	2.13	0.48
2:G:9:LYS:HD3	2:H:142:THR:HG23	1.94	0.48
1:A:383:GLU:O	1:A:390:LYS:HE2	2.14	0.48
1:A:444:LEU:HD12	1:A:460:ALA:HB1	1.95	0.48
1:A:696:ASN:HD22	1:A:696:ASN:N	2.11	0.48
1:C:86:ILE:HD11	1:C:148:VAL:HG22	1.95	0.48
1:C:294:GLN:CB	1:C:298:ARG:HD2	2.43	0.48
1:D:668:LEU:HB2	1:D:671:GLU:HG3	1.96	0.48
1:D:693:ILE:HG22	1:D:694:SER:N	2.28	0.48
2:E:118:HIS:ND1	2:E:234:ILE:HG23	2.28	0.48
2:E:163:MET:HB3	2:E:189:LEU:HD13	1.95	0.48
2:G:92:ASN:OD1	2:G:109:GLU:HG2	2.14	0.48
2:G:204:GLU:OE2	2:G:241:HIS:HB3	2.14	0.48
1:A:55:THR:CB	3:A:800:DTP:H8	2.42	0.48
1:A:132:ASP:HA	1:A:135:ILE:HD12	1.96	0.48
1:A:182:SER:HA	1:A:189:ARG:HE	1.79	0.48
1:A:214:GLY:O	1:A:215:VAL:C	2.53	0.48
1:A:441:GLU:OE1	1:A:621:PRO:HD2	2.14	0.48
1:A:730:TYR:O	1:A:731:TYR:C	2.57	0.48
1:B:231:GLY:N	1:B:236:SER:OG	2.46	0.48
1:B:312:GLU:O	1:B:316:LEU:HG	2.13	0.48
1:B:644:ILE:HG13	1:B:653:ARG:HG2	1.95	0.48
2:H:122:TYR:O	2:H:126:ILE:HG13	2.14	0.48
1:A:6:LEU:HB2	1:A:52:GLY:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:342:LEU:HD21	1:D:379:TYR:CD2	2.49	0.48
1:D:689:ILE:HG22	1:D:691:GLN:O	2.12	0.48
2:E:145:GLN:HG2	2:E:289:TYR:CG	2.49	0.48
2:G:147:GLN:O	2:G:151:GLU:N	2.47	0.48
1:A:361:VAL:O	1:A:364:LEU:HB2	2.13	0.47
1:B:19:LEU:HA	1:B:22:ILE:CD1	2.44	0.47
1:B:317:LEU:HD23	1:B:401:LEU:CD2	2.42	0.47
1:C:94:TYR:CD1	1:C:100:PRO:HG3	2.49	0.47
1:D:207:LEU:CD1	1:D:212:MET:HE3	2.43	0.47
2:E:245:THR:CA	2:E:248:MET:HE3	2.43	0.47
2:F:206:ILE:O	2:F:210:VAL:HG23	2.14	0.47
1:A:87:PHE:HE1	3:A:800:DTP:O2A	1.97	0.47
1:C:441:GLU:CA	1:C:692:SER:O	2.62	0.47
2:E:149:ARG:HH21	2:E:283:GLU:CD	2.21	0.47
2:F:84:ASP:HA	2:F:87:GLN:HB2	1.96	0.47
2:F:126:ILE:O	2:F:130:VAL:HG22	2.14	0.47
2:G:9:LYS:HD3	2:H:142:THR:CG2	2.44	0.47
2:H:255:GLY:HA2	2:H:262:ALA:HB2	1.96	0.47
1:A:107:VAL:O	1:A:111:GLU:HG3	2.14	0.47
1:C:437:ASN:O	1:C:440:LEU:HD22	2.15	0.47
2:F:55:VAL:HG12	2:F:226:GLY:HA3	1.97	0.47
2:G:204:GLU:HG2	2:G:238:GLU:OE2	2.14	0.47
1:A:532:SER:HA	1:A:677:GLY:HA3	1.96	0.47
1:B:51:ASP:OD2	1:B:51:ASP:O	2.32	0.47
1:D:155:TYR:HE1	1:D:209:THR:HG23	1.72	0.47
1:D:514:GLY:C	1:D:618:ALA:HB3	2.39	0.47
2:F:145:GLN:HG2	2:F:289:TYR:CG	2.49	0.47
2:H:102:PRO:HG2	2:H:103:GLU:OE1	2.14	0.47
1:B:180:LEU:HD13	1:B:488:ALA:HB1	1.96	0.47
1:B:303:THR:HG23	1:B:334:ASP:O	2.14	0.47
1:C:186:ARG:HH21	1:C:189:ARG:NH2	2.08	0.47
1:C:668:LEU:HB2	1:C:671:GLU:HG3	1.96	0.47
1:D:561:GLU:HG2	1:D:562:GLN:HG3	1.96	0.47
2:E:8:THR:O	2:F:141:VAL:HG11	2.14	0.47
2:G:255:GLY:HA2	2:G:262:ALA:HB2	1.96	0.47
1:A:231:GLY:N	1:A:236:SER:OG	2.45	0.47
1:A:560:LYS:HG2	1:A:609:HIS:CB	2.44	0.47
1:A:618:ALA:HB2	1:A:691:GLN:CD	2.39	0.47
1:A:644:ILE:HG13	1:A:653:ARG:HG2	1.95	0.47
1:B:181:PHE:O	1:B:189:ARG:HD2	2.15	0.47
1:C:7:VAL:HG21	1:C:17:ILE:HG12	1.91	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:285:PHE:O	1:C:289:VAL:HG23	2.15	0.47
1:C:287:THR:HB	1:D:284:HIS:ND1	2.30	0.47
1:C:309:TRP:O	1:C:355:LEU:HA	2.14	0.47
1:C:403:MET:CE	1:C:714:LEU:HB3	2.45	0.47
1:C:558:LEU:HD11	1:C:562:GLN:NE2	2.30	0.47
1:C:689:ILE:CG2	1:C:691:GLN:H	2.26	0.47
1:D:441:GLU:CB	1:D:619:LEU:O	2.59	0.47
1:D:441:GLU:CA	1:D:692:SER:O	2.63	0.47
1:A:63:ILE:HD13	1:A:85:ALA:HA	1.97	0.47
1:A:320:LYS:HE3	1:A:411:ARG:HB3	1.96	0.47
1:A:668:LEU:HB2	1:A:671:GLU:HG3	1.97	0.47
1:B:244:ILE:O	1:B:248:VAL:HG13	2.15	0.47
1:B:459:ILE:HB	1:B:503:ALA:CA	2.44	0.47
1:B:490:ASP:CG	1:B:511:ARG:HH21	2.21	0.47
1:C:114:LYS:HE2	1:C:166:TYR:CE2	2.49	0.47
1:C:125:GLU:O	1:C:129:LYS:HG3	2.14	0.47
1:C:157:VAL:HG23	1:C:167:GLU:OE2	2.14	0.47
1:C:619:LEU:CD1	1:C:693:ILE:CG1	2.93	0.47
1:C:681:LEU:O	1:C:685:MET:HG3	2.14	0.47
1:D:15:GLU:HG3	1:D:16:ARG:N	2.28	0.47
1:D:44:ARG:HG3	1:D:69:LEU:HD21	1.96	0.47
1:D:519:ASN:CB	1:D:631:ALA:HB1	2.45	0.47
2:E:93:VAL:HG13	2:F:97:PRO:HG3	1.97	0.47
2:E:266:GLU:OE2	2:E:269:LYS:HD2	2.15	0.47
2:F:255:GLY:HA2	2:F:262:ALA:HB2	1.95	0.47
2:G:126:ILE:O	2:G:130:VAL:HG22	2.15	0.47
2:H:204:GLU:HG2	2:H:238:GLU:OE2	2.15	0.47
1:B:309:TRP:O	1:B:355:LEU:HA	2.14	0.47
1:B:339:ILE:O	1:B:416:ASN:HA	2.15	0.47
1:B:516:GLY:N	1:B:620:MET:HE1	2.30	0.47
1:B:603:ARG:O	1:B:607:LYS:HB2	2.15	0.47
1:C:567:TRP:O	1:C:569:ASN:N	2.48	0.47
1:D:25:VAL:HG21	3:D:800:DTP:O3'	2.15	0.47
2:H:1:ALA:HB3	2:H:168:HIS:CA	2.42	0.47
1:A:522:TYR:CZ	1:A:526:LYS:HD3	2.50	0.47
1:D:247:TYR:O	1:D:252:ALA:HB3	2.15	0.47
2:E:5:PHE:CE1	2:E:24:ASN:CG	2.93	0.47
2:F:155:SER:O	2:F:159:GLU:HG3	2.15	0.47
2:G:84:ASP:HA	2:G:87:GLN:HB2	1.95	0.47
1:A:431:ALA:HB1	1:A:445:PRO:CB	2.44	0.47
1:A:438:LEU:C	1:A:440:LEU:HD23	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:ARG:HD3	1:B:55:THR:CG2	2.45	0.47
1:C:234:LEU:HD22	1:D:246:LYS:HD3	1.96	0.47
1:C:264:LEU:HD13	1:C:276:THR:O	2.15	0.47
1:C:520:PHE:O	1:C:521:ALA:C	2.58	0.47
1:D:85:ALA:O	1:D:89:LEU:HG	2.15	0.47
2:G:48:TRP:CZ3	2:G:50:PRO:HG3	2.49	0.47
2:G:206:ILE:O	2:G:210:VAL:HG23	2.15	0.47
2:H:205:ALA:HB1	2:H:315:ARG:HD2	1.97	0.47
1:A:42:GLU:O	2:F:297:ILE:CD1	2.63	0.46
1:B:59:HIS:O	1:B:62:ILE:HG12	2.15	0.46
1:B:258:ALA:C	1:B:260:ARG:H	2.23	0.46
1:C:135:ILE:HG23	1:C:170:GLN:HB3	1.97	0.46
1:C:561:GLU:HG2	1:C:562:GLN:HG3	1.96	0.46
2:E:147:GLN:HA	2:E:147:GLN:NE2	2.30	0.46
1:B:383:GLU:O	1:B:390:LYS:HE2	2.15	0.46
1:B:463:THR:HG22	1:B:489:LEU:HD22	1.97	0.46
1:C:585:LYS:HD3	1:C:585:LYS:N	2.23	0.46
1:D:458:GLU:OE1	1:D:567:TRP:CZ3	2.69	0.46
2:F:122:TYR:O	2:F:126:ILE:HG13	2.15	0.46
2:H:118:HIS:ND1	2:H:234:ILE:HG23	2.30	0.46
1:A:180:LEU:HD13	1:A:488:ALA:HB1	1.97	0.46
1:A:233:SER:OG	1:A:236:SER:N	2.40	0.46
1:A:258:ALA:O	1:A:260:ARG:N	2.49	0.46
1:A:304:LEU:HB3	1:A:335:TYR:HD1	1.81	0.46
1:A:342:LEU:HD23	1:A:375:PHE:HE2	1.81	0.46
1:A:371:ASP:HB3	1:A:374:GLU:HB3	1.97	0.46
1:B:140:ASP:HA	1:B:143:PHE:CD2	2.51	0.46
1:B:560:LYS:HG2	1:B:609:HIS:CB	2.45	0.46
1:C:248:VAL:C	1:C:250:GLN:H	2.23	0.46
1:C:617:SER:O	1:C:690:ASP:HB2	2.15	0.46
1:D:400:SER:HA	1:D:711:MET:HE3	1.97	0.46
2:E:126:ILE:O	2:E:130:VAL:HG22	2.15	0.46
2:H:55:VAL:HG12	2:H:226:GLY:HA3	1.96	0.46
1:A:394:LYS:HB2	1:A:394:LYS:NZ	2.30	0.46
1:A:603:ARG:O	1:A:607:LYS:HB2	2.14	0.46
1:B:146:ALA:HB3	1:B:654:GLN:NE2	2.31	0.46
1:B:258:ALA:O	1:B:260:ARG:N	2.49	0.46
1:B:519:ASN:HA	1:B:632:THR:H	1.81	0.46
1:C:50:TYR:O	1:C:51:ASP:C	2.56	0.46
1:D:135:ILE:HG23	1:D:170:GLN:HB3	1.97	0.46
1:D:176:VAL:HG22	1:D:215:VAL:HB	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:350:GLY:HA3	2:E:367:THR:HG21	1.98	0.46
1:A:202:THR:OG1	1:A:204:LYS:HD3	2.15	0.46
1:A:253:GLY:O	1:A:254:ILE:HD13	2.16	0.46
1:C:400:SER:HA	1:C:711:MET:HE3	1.98	0.46
1:C:572:THR:HB	1:C:577:ILE:HB	1.97	0.46
1:D:86:ILE:HD11	1:D:148:VAL:HG22	1.96	0.46
1:D:185:PRO:HB2	1:D:187:GLU:CG	2.45	0.46
1:D:567:TRP:O	1:D:569:ASN:N	2.49	0.46
2:F:1:ALA:HB3	2:F:168:HIS:CA	2.43	0.46
2:F:260:GLU:O	2:F:264:ILE:HG13	2.15	0.46
1:A:226:VAL:HG21	1:A:247:TYR:CG	2.51	0.46
1:A:706:SER:HB2	1:A:708:LYS:CD	2.46	0.46
1:B:320:LYS:CD	1:B:411:ARG:HB2	2.46	0.46
1:B:431:ALA:HB1	1:B:445:PRO:CB	2.46	0.46
1:C:40:GLN:O	1:C:44:ARG:N	2.43	0.46
1:C:233:SER:HA	3:C:900:DTP:PA	2.56	0.46
1:C:246:LYS:NZ	1:D:234:LEU:HB3	2.30	0.46
1:C:317:LEU:O	1:C:405:GLU:HG3	2.15	0.46
1:D:6:LEU:O	1:D:14:THR:HG23	2.15	0.46
1:D:102:LEU:O	1:D:106:VAL:HG23	2.16	0.46
1:D:367:ALA:C	1:D:369:PHE:N	2.73	0.46
1:D:583:TYR:CB	1:D:687:LYS:HG3	2.46	0.46
2:E:122:TYR:O	2:E:126:ILE:HG13	2.15	0.46
2:E:204:GLU:OE2	2:E:241:HIS:HB3	2.16	0.46
2:E:260:GLU:O	2:E:264:ILE:HG13	2.16	0.46
2:F:239:ALA:O	2:F:242:LEU:HG	2.15	0.46
2:H:126:ILE:O	2:H:130:VAL:HG22	2.15	0.46
1:A:258:ALA:C	1:A:260:ARG:H	2.22	0.46
1:B:228:ILE:HG21	1:B:240:THR:HG23	1.97	0.46
1:C:422:THR:O	1:C:582:THR:HB	2.15	0.46
2:E:136:VAL:O	2:E:140:ILE:HG13	2.16	0.46
1:A:353:ILE:HB	1:A:393:VAL:HG23	1.98	0.46
1:B:172:LEU:O	1:B:176:VAL:HG23	2.16	0.46
1:B:294:GLN:C	1:B:296:GLY:N	2.69	0.46
1:C:85:ALA:O	1:C:89:LEU:HG	2.15	0.46
1:C:207:LEU:CD1	1:C:212:MET:HE3	2.45	0.46
1:C:680:GLN:O	1:C:684:ILE:HG13	2.16	0.46
1:D:53:ILE:HG13	1:D:58:ILE:CD1	2.44	0.46
1:D:264:LEU:HD13	1:D:276:THR:O	2.15	0.46
2:F:203:LEU:HA	2:F:207:ARG:HD2	1.98	0.46
2:G:166:TYR:CE2	2:H:169:LEU:HD22	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LEU:O	1:A:176:VAL:HG23	2.16	0.46
1:B:403:MET:HE2	1:B:714:LEU:O	2.16	0.46
1:C:102:LEU:O	1:C:106:VAL:HG23	2.16	0.46
1:C:215:VAL:O	1:C:216:ARG:CB	2.64	0.46
1:D:240:THR:O	1:D:244:ILE:HG13	2.16	0.46
2:F:147:GLN:NE2	2:F:147:GLN:HA	2.30	0.46
2:G:260:GLU:O	2:G:264:ILE:HG13	2.16	0.46
2:H:48:TRP:CZ3	2:H:50:PRO:HG3	2.51	0.46
1:A:45:SER:O	1:A:46:HIS:C	2.59	0.46
1:A:244:ILE:O	1:A:248:VAL:HG13	2.15	0.46
1:A:357:SER:HB3	1:A:360:ASP:OD2	2.16	0.46
1:A:686:GLN:CD	1:A:727:LYS:HG3	2.41	0.46
1:B:182:SER:HA	1:B:189:ARG:HE	1.80	0.46
1:B:706:SER:HB2	1:B:708:LYS:CD	2.45	0.46
1:C:137:HIS:HA	1:C:170:GLN:HG3	1.98	0.46
1:C:339:ILE:HD12	1:C:414:ILE:HG23	1.98	0.46
1:C:520:PHE:O	1:C:523:TYR:CB	2.63	0.46
1:C:692:SER:OG	1:C:728:THR:HG23	2.16	0.46
1:D:152:GLU:O	1:D:158:GLN:NE2	2.48	0.46
1:D:309:TRP:O	1:D:355:LEU:HA	2.15	0.46
1:D:437:ASN:O	1:D:440:LEU:HD22	2.16	0.46
1:D:544:PHE:CE2	1:D:685:MET:HG2	2.51	0.46
1:D:696:ASN:ND2	1:D:696:ASN:N	2.62	0.46
2:E:255:GLY:HA2	2:E:262:ALA:HB2	1.97	0.46
2:F:103:GLU:HG2	2:F:104:LEU:N	2.30	0.46
1:A:41:VAL:HG22	1:A:69:LEU:CD1	2.44	0.45
1:A:365:TYR:O	1:A:368:PHE:HB3	2.16	0.45
1:A:440:LEU:N	1:A:440:LEU:CD2	2.78	0.45
1:B:253:GLY:O	1:B:254:ILE:HD13	2.16	0.45
1:B:365:TYR:O	1:B:368:PHE:HB3	2.17	0.45
1:B:371:ASP:HB3	1:B:374:GLU:HB3	1.98	0.45
1:B:511:ARG:HG2	1:B:511:ARG:NH1	2.30	0.45
1:B:681:LEU:O	1:B:685:MET:HG3	2.16	0.45
1:C:226:VAL:HG21	1:C:247:TYR:CD1	2.51	0.45
1:D:217:THR:O	1:D:219:THR:N	2.49	0.45
2:E:46:PHE:O	2:E:48:TRP:HD1	1.99	0.45
2:E:97:PRO:HG3	2:F:93:VAL:HG13	1.98	0.45
2:G:103:GLU:HG2	2:G:104:LEU:N	2.30	0.45
2:G:118:HIS:ND1	2:G:234:ILE:HG23	2.31	0.45
2:G:239:ALA:O	2:G:242:LEU:HG	2.16	0.45
2:H:260:GLU:O	2:H:264:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:276:PHE:HB3	2:H:316:MET:SD	2.56	0.45
1:A:59:HIS:NE2	3:A:800:DTP:H4'	2.30	0.45
1:A:233:SER:OG	1:A:236:SER:HB2	2.15	0.45
1:B:202:THR:OG1	1:B:204:LYS:HD3	2.17	0.45
1:B:357:SER:O	1:B:358:PRO:C	2.58	0.45
1:B:418:ASP:HA	1:B:421:ASN:ND2	2.31	0.45
1:B:619:LEU:CB	1:B:693:ILE:HG23	2.46	0.45
1:C:59:HIS:CD2	3:C:800:DTP:H4'	2.50	0.45
2:F:266:GLU:OE2	2:F:269:LYS:HD2	2.17	0.45
1:A:10:ARG:HG2	1:A:91:LYS:HZ1	1.82	0.45
1:A:39:SER:O	1:A:40:GLN:C	2.58	0.45
1:A:511:ARG:HG2	1:A:511:ARG:HH11	1.81	0.45
1:C:310:HIS:O	1:C:355:LEU:HB3	2.17	0.45
1:C:644:ILE:HA	1:C:652:LEU:O	2.16	0.45
1:D:137:HIS:HA	1:D:170:GLN:HG3	1.97	0.45
1:D:320:LYS:HE2	1:D:333:MET:O	2.17	0.45
2:E:28:TYR:CD2	2:F:120:ARG:HA	2.51	0.45
2:F:136:VAL:O	2:F:140:ILE:HG13	2.16	0.45
2:F:309:GLU:HB3	2:F:325:PHE:HB3	1.99	0.45
1:A:106:VAL:HG21	1:A:128:PHE:CE1	2.52	0.45
1:A:146:ALA:HB3	1:A:654:GLN:NE2	2.31	0.45
1:B:341:LYS:HE3	2:H:375:LEU:HB2	1.98	0.45
1:B:633:ASN:O	1:B:634:GLY:C	2.60	0.45
1:C:56:SER:O	1:C:59:HIS:HB2	2.17	0.45
1:C:242:SER:O	1:D:238:ASN:ND2	2.50	0.45
1:C:689:ILE:HG22	1:C:691:GLN:O	2.11	0.45
1:D:339:ILE:HD12	1:D:414:ILE:HG23	1.97	0.45
1:A:68:ASP:HA	1:A:653:ARG:HH12	1.78	0.45
1:A:430:ILE:HG21	1:A:570:GLU:HG2	1.98	0.45
1:B:34:HIS:O	1:B:36:VAL:HG22	2.17	0.45
1:C:465:SER:CB	1:C:489:LEU:HD11	2.47	0.45
1:C:619:LEU:HD13	1:C:693:ILE:CG1	2.47	0.45
1:C:693:ILE:CG2	1:C:694:SER:N	2.79	0.45
2:E:73:PHE:CZ	2:E:224:MET:HE2	2.51	0.45
2:F:73:PHE:CZ	2:F:224:MET:HE2	2.52	0.45
2:H:266:GLU:OE2	2:H:269:LYS:HD2	2.16	0.45
1:A:43:LEU:CD2	2:F:298:GLY:HA3	2.45	0.45
1:A:309:TRP:O	1:A:355:LEU:HA	2.17	0.45
1:C:136:ASP:HB3	1:C:139:ARG:HE	1.82	0.45
1:C:613:ASN:HB2	1:C:616:LEU:HG	1.98	0.45
2:F:204:GLU:HG2	2:F:238:GLU:OE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ILE:O	1:A:416:ASN:HA	2.16	0.45
1:A:512:THR:O	1:A:513:LEU:HD23	2.16	0.45
1:A:696:ASN:HD21	1:A:730:TYR:HB3	1.81	0.45
1:B:226:VAL:C	1:B:227:LEU:HD12	2.42	0.45
1:B:342:LEU:HD23	1:B:375:PHE:HE2	1.81	0.45
1:B:552:LEU:HD12	1:B:599:TRP:HZ3	1.82	0.45
1:C:544:PHE:CE2	1:C:685:MET:HG2	2.52	0.45
2:E:34:ASP:O	2:E:38:LYS:HG3	2.17	0.45
2:E:239:ALA:O	2:E:242:LEU:HG	2.17	0.45
2:F:284:LYS:HE3	2:F:325:PHE:CE1	2.52	0.45
2:H:92:ASN:OD1	2:H:109:GLU:HG2	2.17	0.45
1:A:519:ASN:HA	1:A:632:THR:H	1.81	0.45
1:C:135:ILE:HA	1:C:197:TYR:CE2	2.52	0.45
1:C:583:TYR:CB	1:C:687:LYS:HG3	2.47	0.45
1:D:422:THR:O	1:D:582:THR:HB	2.17	0.45
1:D:558:LEU:HD11	1:D:562:GLN:NE2	2.32	0.45
1:D:670:TRP:CZ3	1:D:735:ARG:HB2	2.52	0.45
2:E:175:HIS:HD2	2:F:178:ASN:HD21	1.65	0.45
2:F:149:ARG:HH21	2:F:283:GLU:CD	2.25	0.45
2:G:73:PHE:CZ	2:G:224:MET:HE2	2.52	0.45
2:G:284:LYS:HE3	2:G:325:PHE:CE1	2.52	0.45
2:H:136:VAL:O	2:H:140:ILE:HG13	2.16	0.45
2:H:203:LEU:O	2:H:207:ARG:HB2	2.17	0.45
1:C:98:GLU:HA	1:C:99:PRO:HD3	1.81	0.45
1:C:441:GLU:O	1:C:692:SER:O	2.34	0.45
1:C:510:ARG:HB2	1:C:512:THR:HG23	1.99	0.45
1:D:551:LEU:C	1:D:616:LEU:CD1	2.84	0.45
1:D:680:GLN:O	1:D:684:ILE:HG13	2.17	0.45
2:E:103:GLU:HG2	2:E:104:LEU:N	2.31	0.45
2:F:46:PHE:O	2:F:48:TRP:HD1	1.99	0.45
2:G:120:ARG:HA	2:H:28:TYR:CD2	2.52	0.45
1:A:438:LEU:O	1:A:440:LEU:CD2	2.59	0.45
1:A:696:ASN:OD1	1:A:731:TYR:HB2	2.17	0.45
1:B:40:GLN:O	1:B:44:ARG:N	2.32	0.45
1:B:339:ILE:HG22	1:B:340:ASN:N	2.32	0.45
1:B:706:SER:HB2	1:B:708:LYS:HD2	1.99	0.45
1:D:6:LEU:CA	1:D:14:THR:CG2	2.94	0.45
1:D:33:LEU:CD1	1:D:80:LEU:HB2	2.45	0.45
1:D:524:LEU:HD22	1:D:529:LYS:HB2	1.97	0.45
1:D:585:LYS:HD3	1:D:585:LYS:N	2.23	0.45
2:G:276:PHE:HB3	2:G:316:MET:SD	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:HIS:CE1	3:A:800:DTP:O2A	2.71	0.44
1:A:134:PHE:HB3	1:A:194:LYS:HG3	1.99	0.44
1:A:140:ASP:HA	1:A:143:PHE:CD2	2.52	0.44
1:B:311:LEU:HA	1:B:355:LEU:HB3	1.99	0.44
1:B:512:THR:O	1:B:513:LEU:HD23	2.17	0.44
1:D:254:ILE:HG22	1:D:255:GLY:N	2.32	0.44
2:G:122:TYR:O	2:G:126:ILE:HG13	2.16	0.44
2:G:136:VAL:O	2:G:140:ILE:HG13	2.17	0.44
2:H:103:GLU:HG2	2:H:104:LEU:N	2.32	0.44
2:H:365:VAL:HG12	2:H:366:ASP:N	2.30	0.44
1:A:348:LEU:O	2:F:371:SER:HB3	2.17	0.44
1:B:55:THR:HA	1:B:58:ILE:HG12	1.98	0.44
1:B:222:PHE:HD2	1:B:496:GLN:HB3	1.81	0.44
1:C:240:THR:O	1:C:244:ILE:HG13	2.17	0.44
1:C:431:ALA:CB	1:C:445:PRO:HB3	2.32	0.44
1:C:500:ILE:HG22	1:C:502:ALA:H	1.83	0.44
1:D:730:TYR:O	1:D:731:TYR:C	2.59	0.44
2:F:76:ASN:HD21	2:F:211:SER:CA	2.30	0.44
2:G:149:ARG:HH21	2:G:283:GLU:CD	2.25	0.44
2:G:203:LEU:HA	2:G:207:ARG:HD2	1.98	0.44
2:H:254:SER:C	2:H:256:ALA:H	2.25	0.44
1:A:241:SER:O	1:A:245:VAL:HG23	2.18	0.44
1:A:545:GLU:HA	1:A:688:PHE:CE2	2.53	0.44
1:B:63:ILE:HD13	1:B:85:ALA:HA	1.99	0.44
1:B:357:SER:HB3	1:B:360:ASP:OD2	2.17	0.44
1:B:556:ASN:O	1:B:560:LYS:HG3	2.17	0.44
1:B:686:GLN:CD	1:B:727:LYS:HG3	2.42	0.44
1:C:167:GLU:OE2	1:C:216:ARG:NH2	2.47	0.44
1:D:6:LEU:HB3	1:D:14:THR:CG2	2.47	0.44
1:D:538:ASN:HB3	1:D:593:GLU:OE1	2.18	0.44
1:D:585:LYS:H	1:D:585:LYS:CD	2.25	0.44
2:H:284:LYS:HE3	2:H:325:PHE:CE1	2.52	0.44
1:A:697:THR:OG1	1:A:732:GLN:HG3	2.18	0.44
1:A:712:GLN:NE2	2:F:370:LEU:HG	2.21	0.44
1:B:10:ARG:HE	1:B:91:LYS:HZ3	1.65	0.44
1:B:54:LYS:HE2	1:B:57:ASP:CG	2.42	0.44
1:B:188:THR:HB	1:B:192:TYR:HE2	1.82	0.44
1:B:479:GLU:O	1:B:483:ILE:HG13	2.18	0.44
1:D:348:LEU:HD22	2:E:370:LEU:O	2.18	0.44
1:D:694:SER:O	1:D:730:TYR:HB2	2.16	0.44
2:E:284:LYS:HE3	2:E:325:PHE:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:48:TRP:CZ3	2:F:50:PRO:HG3	2.52	0.44
2:H:203:LEU:HA	2:H:207:ARG:HD2	1.98	0.44
1:C:307:PRO:HG2	1:C:310:HIS:HB2	2.00	0.44
1:D:75:PRO:O	1:D:78:GLN:HB2	2.18	0.44
1:D:226:VAL:HG21	1:D:247:TYR:CD1	2.53	0.44
2:F:204:GLU:OE2	2:F:241:HIS:HB3	2.18	0.44
2:G:205:ALA:HB1	2:G:315:ARG:HD2	2.00	0.44
2:H:273:TYR:OH	2:H:324:PRO:HB3	2.17	0.44
1:A:339:ILE:HG22	1:A:340:ASN:N	2.32	0.44
1:A:685:MET:O	1:A:689:ILE:HG12	2.18	0.44
1:B:670:TRP:CH2	1:B:735:ARG:HB2	2.53	0.44
1:C:254:ILE:HG22	1:C:255:GLY:N	2.32	0.44
1:C:320:LYS:HE2	1:C:333:MET:O	2.17	0.44
1:D:45:SER:O	1:D:46:HIS:C	2.59	0.44
1:D:307:PRO:HG2	1:D:310:HIS:HB2	2.00	0.44
2:G:309:GLU:HB3	2:G:325:PHE:HB3	1.99	0.44
1:A:46:HIS:CE1	2:F:220:GLU:O	2.71	0.44
1:A:232:ASP:OD2	1:A:262:ARG:NH2	2.50	0.44
1:A:357:SER:O	1:A:358:PRO:C	2.59	0.44
1:A:545:GLU:CD	1:A:596:HIS:H	2.25	0.44
1:B:320:LYS:HD2	1:B:411:ARG:HB2	2.00	0.44
1:C:172:LEU:O	1:C:176:VAL:HG23	2.18	0.44
1:C:553:LYS:HA	1:C:602:LEU:HD11	2.00	0.44
1:A:232:ASP:OD2	1:A:262:ARG:NE	2.49	0.44
1:A:439:CYS:O	1:A:440:LEU:CB	2.58	0.44
1:A:706:SER:HB2	1:A:708:LYS:HD2	2.00	0.44
1:B:40:GLN:C	1:B:44:ARG:HG2	2.37	0.44
1:C:155:TYR:OH	1:C:624:THR:HG21	2.14	0.44
1:C:669:LEU:HD12	1:C:672:MET:HE2	2.00	0.44
1:D:228:ILE:HG21	1:D:240:THR:HG23	1.99	0.44
1:D:350:GLY:CA	2:E:367:THR:HG21	2.48	0.44
1:D:441:GLU:CG	1:D:620:MET:HB3	2.46	0.44
2:E:23:VAL:CG2	2:E:100:SER:C	2.91	0.44
2:E:206:ILE:O	2:E:210:VAL:HG23	2.17	0.44
1:A:468:ASN:O	1:A:469:LEU:C	2.60	0.44
1:A:510:ARG:HE	1:A:510:ARG:HB3	1.60	0.44
1:B:44:ARG:HA	1:B:44:ARG:NE	2.31	0.44
1:B:304:LEU:HB3	1:B:335:TYR:HD1	1.83	0.44
1:C:244:ILE:HG23	1:C:254:ILE:HG13	2.00	0.44
1:C:500:ILE:N	1:C:500:ILE:HD12	2.32	0.44
1:C:538:ASN:HB3	1:C:593:GLU:OE1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:317:LEU:O	1:D:405:GLU:HG3	2.18	0.44
2:E:166:TYR:CE2	2:F:169:LEU:HD22	2.53	0.44
2:G:209:TYR:HA	2:G:212:PHE:CD2	2.53	0.44
2:G:266:GLU:OE2	2:G:269:LYS:HD2	2.17	0.44
1:A:384:LYS:O	1:A:385:ASP:C	2.58	0.43
1:A:519:ASN:CG	1:A:631:ALA:HB1	2.43	0.43
1:B:55:THR:HG23	1:B:56:SER:N	2.33	0.43
1:B:91:LYS:NZ	3:B:800:DTP:O3A	2.51	0.43
1:B:230:CYS:SG	1:B:237:ILE:HA	2.58	0.43
1:B:290:LYS:HG2	1:B:296:GLY:O	2.18	0.43
1:D:102:LEU:HD23	1:D:128:PHE:O	2.18	0.43
1:D:136:ASP:HB3	1:D:139:ARG:HE	1.82	0.43
1:D:228:ILE:HG22	1:D:240:THR:HG23	1.99	0.43
1:D:248:VAL:C	1:D:250:GLN:N	2.76	0.43
1:D:313:VAL:O	1:D:317:LEU:HB2	2.18	0.43
2:E:254:SER:C	2:E:256:ALA:H	2.26	0.43
2:F:96:LEU:HB2	2:F:97:PRO:HD3	1.99	0.43
1:A:222:PHE:HD2	1:A:496:GLN:HB3	1.82	0.43
1:B:468:ASN:O	1:B:469:LEU:C	2.60	0.43
1:C:248:VAL:C	1:C:250:GLN:N	2.77	0.43
1:C:640:GLY:HA2	1:C:668:LEU:HD22	2.00	0.43
1:D:172:LEU:C	1:D:172:LEU:HD23	2.43	0.43
1:D:172:LEU:O	1:D:176:VAL:HG23	2.18	0.43
2:G:18:PHE:O	2:G:19:PHE:CB	2.66	0.43
2:H:209:TYR:HA	2:H:212:PHE:CD2	2.53	0.43
1:A:50:TYR:O	1:A:51:ASP:C	2.61	0.43
1:A:59:HIS:HA	1:A:62:ILE:HG12	1.99	0.43
1:A:172:LEU:C	1:A:172:LEU:HD23	2.43	0.43
1:B:152:GLU:O	1:B:152:GLU:HG2	2.17	0.43
1:B:644:ILE:HA	1:B:652:LEU:O	2.18	0.43
1:B:668:LEU:HB2	1:B:671:GLU:HG3	2.00	0.43
1:B:697:THR:OG1	1:B:732:GLN:HG3	2.18	0.43
1:C:75:PRO:O	1:C:78:GLN:HB2	2.18	0.43
1:D:514:GLY:HA3	1:D:618:ALA:HB3	1.90	0.43
1:D:520:PHE:O	1:D:523:TYR:HB3	2.17	0.43
2:F:18:PHE:O	2:F:19:PHE:CB	2.66	0.43
2:F:96:LEU:CB	2:F:97:PRO:HD3	2.47	0.43
2:F:171:GLY:O	2:F:184:VAL:CG1	2.65	0.43
2:G:254:SER:C	2:G:256:ALA:H	2.26	0.43
2:H:46:PHE:O	2:H:48:TRP:HD1	2.01	0.43
2:H:73:PHE:CZ	2:H:224:MET:HE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:206:ILE:O	2:H:210:VAL:HG23	2.18	0.43
1:A:131:MET:HA	1:A:134:PHE:CD2	2.53	0.43
1:A:549:TYR:CD1	1:A:602:LEU:HD22	2.54	0.43
1:B:106:VAL:HG21	1:B:128:PHE:CE1	2.53	0.43
1:B:189:ARG:O	1:B:193:VAL:HG23	2.18	0.43
1:B:244:ILE:O	1:B:248:VAL:HG22	2.17	0.43
1:B:320:LYS:HD3	1:B:409:THR:HB	2.00	0.43
1:B:545:GLU:CD	1:B:596:HIS:H	2.26	0.43
1:D:18:ASN:O	3:D:800:DTP:H2	2.17	0.43
2:E:309:GLU:HB3	2:E:325:PHE:HB3	2.00	0.43
2:G:96:LEU:HB2	2:G:97:PRO:HD3	2.00	0.43
2:H:239:ALA:O	2:H:242:LEU:HG	2.18	0.43
2:H:309:GLU:HB3	2:H:325:PHE:HB3	2.00	0.43
1:A:459:ILE:HB	1:A:503:ALA:CA	2.44	0.43
1:A:681:LEU:O	1:A:685:MET:HG3	2.18	0.43
1:B:131:MET:HA	1:B:134:PHE:CD2	2.54	0.43
1:B:132:ASP:HA	1:B:135:ILE:HD12	1.99	0.43
1:B:179:CYS:HB2	1:B:215:VAL:HG12	2.00	0.43
1:B:423:HIS:HB2	1:B:582:THR:O	2.18	0.43
1:D:202:THR:OG1	1:D:204:LYS:HD3	2.19	0.43
1:D:500:ILE:HG22	1:D:502:ALA:H	1.81	0.43
2:E:92:ASN:OD1	2:E:109:GLU:HG2	2.18	0.43
2:H:76:ASN:HD21	2:H:211:SER:CA	2.29	0.43
2:H:221:ARG:NH1	2:H:296:MET:HG2	2.30	0.43
2:H:297:ILE:O	2:H:297:ILE:HG13	2.18	0.43
1:A:556:ASN:O	1:A:560:LYS:HG3	2.18	0.43
1:B:394:LYS:HB2	1:B:394:LYS:NZ	2.33	0.43
1:B:403:MET:HB2	1:B:711:MET:HE1	2.01	0.43
1:C:151:LEU:CA	1:C:155:TYR:HB2	2.41	0.43
1:C:543:THR:HG22	1:C:547:ILE:HD11	2.01	0.43
1:D:320:LYS:HE2	1:D:334:ASP:HA	2.01	0.43
1:D:500:ILE:HD12	1:D:500:ILE:N	2.33	0.43
1:D:640:GLY:HA2	1:D:668:LEU:HD22	2.01	0.43
1:D:678:TYR:CZ	1:D:695:ALA:HB1	2.54	0.43
2:E:166:TYR:CZ	2:F:169:LEU:HD13	2.53	0.43
2:E:204:GLU:HG2	2:E:238:GLU:OE2	2.18	0.43
1:A:238:ASN:HB3	1:B:242:SER:CB	2.49	0.43
1:B:348:LEU:HB3	2:H:371:SER:HA	2.00	0.43
1:C:361:VAL:HG23	1:C:361:VAL:O	2.19	0.43
1:D:244:ILE:HG23	1:D:254:ILE:HG13	1.99	0.43
1:D:474:ASN:HD22	1:D:474:ASN:N	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:ASN:O	1:A:19:LEU:C	2.61	0.43
1:A:43:LEU:HD21	2:F:298:GLY:HA3	2.00	0.43
1:A:227:LEU:HB3	1:A:435:GLN:CD	2.35	0.43
1:A:560:LYS:HG2	1:A:609:HIS:HB3	1.99	0.43
1:B:40:GLN:NE2	2:H:334:TRP:HB3	2.33	0.43
1:B:47:ILE:C	1:B:47:ILE:HD13	2.44	0.43
1:B:172:LEU:HD23	1:B:172:LEU:C	2.43	0.43
1:B:353:ILE:HB	1:B:393:VAL:HG23	2.01	0.43
1:B:442:ILE:HD13	1:B:691:GLN:OE1	2.19	0.43
1:C:465:SER:HB3	1:C:515:ILE:CG2	2.43	0.43
1:D:56:SER:O	1:D:59:HIS:HB2	2.18	0.43
2:E:1:ALA:HB3	2:E:168:HIS:CA	2.37	0.43
2:E:205:ALA:HB1	2:E:315:ARG:HD2	2.01	0.43
2:F:125:ILE:O	2:F:129:ILE:HG12	2.18	0.43
2:G:178:ASN:HD21	2:H:175:HIS:HD2	1.65	0.43
1:A:339:ILE:HD12	1:A:414:ILE:HG23	2.00	0.43
1:A:544:PHE:CZ	1:A:685:MET:CG	3.00	0.43
1:B:8:THR:O	1:B:55:THR:HB	2.18	0.43
1:B:283:LYS:HG3	1:B:330:VAL:HG22	2.01	0.43
1:B:474:ASN:HD21	1:B:477:GLU:HG3	1.83	0.43
1:C:524:LEU:HD22	1:C:529:LYS:HB2	2.00	0.43
1:D:135:ILE:HA	1:D:197:TYR:CE2	2.53	0.43
1:D:361:VAL:HG23	1:D:361:VAL:O	2.19	0.43
1:D:441:GLU:O	1:D:692:SER:O	2.36	0.43
2:G:102:PRO:HG2	2:G:103:GLU:OE1	2.19	0.43
1:A:19:LEU:HD12	2:F:295:SER:O	2.18	0.43
1:A:147:ALA:HB1	1:A:628:ILE:HA	2.00	0.43
1:A:425:PRO:HG2	1:A:690:ASP:HB3	2.01	0.43
1:A:633:ASN:O	1:A:634:GLY:C	2.60	0.43
1:B:561:GLU:O	1:B:561:GLU:HG2	2.18	0.43
2:F:115:GLU:OE1	2:F:115:GLU:HA	2.19	0.43
2:F:118:HIS:ND1	2:F:234:ILE:HG23	2.32	0.43
2:H:1:ALA:N	2:H:168:HIS:O	2.49	0.43
1:A:474:ASN:HD21	1:A:477:GLU:HG3	1.84	0.42
1:B:83:ARG:HG2	1:B:141:MET:HG3	2.01	0.42
1:B:92:LYS:HG2	1:B:92:LYS:O	2.19	0.42
1:C:55:THR:OG1	3:C:800:DTP:O4'	2.31	0.42
1:C:172:LEU:HD23	1:C:172:LEU:C	2.44	0.42
1:C:553:LYS:O	1:C:557:GLU:HG2	2.19	0.42
1:D:510:ARG:HB2	1:D:512:THR:HG23	2.00	0.42
2:E:213:ALA:O	2:E:334:TRP:HH2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:311:ILE:HD11	2:F:315:ARG:NE	2.33	0.42
2:G:46:PHE:O	2:G:48:TRP:HD1	2.01	0.42
1:A:303:THR:HA	1:A:334:ASP:O	2.19	0.42
1:A:479:GLU:O	1:A:483:ILE:HG13	2.19	0.42
1:A:644:ILE:HA	1:A:652:LEU:O	2.18	0.42
1:B:36:VAL:CG1	1:B:77:TYR:CD2	3.03	0.42
1:B:155:TYR:OH	1:B:624:THR:CG2	2.67	0.42
1:C:467:PHE:CE2	1:C:515:ILE:CG2	3.02	0.42
1:D:286:GLN:OE1	1:D:332:HIS:HB2	2.19	0.42
1:D:430:ILE:HG21	1:D:570:GLU:HA	2.01	0.42
2:F:104:LEU:O	2:F:108:VAL:HG23	2.19	0.42
2:G:92:ASN:HB3	2:H:92:ASN:HB3	2.01	0.42
2:H:76:ASN:O	2:H:80:GLN:HG3	2.19	0.42
1:A:37:SER:HB3	1:A:40:GLN:CG	2.49	0.42
1:A:353:ILE:N	1:A:393:VAL:O	2.51	0.42
1:A:552:LEU:HD12	1:A:599:TRP:HZ3	1.84	0.42
1:C:532:SER:OG	1:C:673:PRO:HD2	2.20	0.42
1:D:444:LEU:HA	1:D:445:PRO:HD3	1.90	0.42
1:D:620:MET:SD	1:D:620:MET:N	2.92	0.42
1:D:696:ASN:HD21	1:D:730:TYR:HB3	1.76	0.42
2:E:92:ASN:HB3	2:F:92:ASN:HB3	2.00	0.42
2:G:28:TYR:CD2	2:H:120:ARG:HA	2.54	0.42
1:A:47:ILE:HD13	1:A:47:ILE:C	2.44	0.42
1:A:284:HIS:CE1	1:B:288:ALA:HB2	2.54	0.42
1:A:311:LEU:HA	1:A:355:LEU:HB3	2.00	0.42
1:C:320:LYS:HE2	1:C:334:ASP:HA	2.00	0.42
1:C:619:LEU:HB3	1:C:693:ILE:HG23	2.01	0.42
1:D:94:TYR:CG	1:D:100:PRO:HD3	2.54	0.42
1:D:217:THR:C	1:D:219:THR:N	2.75	0.42
2:F:203:LEU:O	2:F:207:ARG:HB2	2.19	0.42
2:F:300:ASN:OD1	2:F:302:ASP:HB2	2.20	0.42
2:G:178:ASN:HD21	2:H:175:HIS:CD2	2.37	0.42
2:G:245:THR:CA	2:G:248:MET:HE3	2.48	0.42
1:A:50:TYR:H	1:A:53:ILE:CG2	2.32	0.42
1:A:320:LYS:CE	1:A:411:ARG:HB2	2.49	0.42
1:A:334:ASP:OD1	1:A:411:ARG:HB3	2.20	0.42
1:B:54:LYS:HE2	1:B:57:ASP:OD2	2.20	0.42
1:B:147:ALA:HB1	1:B:628:ILE:HA	2.01	0.42
1:B:240:THR:O	1:B:244:ILE:HG13	2.19	0.42
1:B:304:LEU:N	1:B:334:ASP:O	2.53	0.42
1:B:640:GLY:HA2	1:B:668:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:LYS:O	1:C:91:LYS:HG2	2.19	0.42
1:C:94:TYR:CG	1:C:100:PRO:HD3	2.55	0.42
1:C:520:PHE:HB3	1:C:635:ILE:HA	2.01	0.42
2:E:203:LEU:O	2:E:207:ARG:HB2	2.20	0.42
2:G:1:ALA:HB3	2:G:168:HIS:CA	2.41	0.42
2:G:96:LEU:CB	2:G:97:PRO:HD3	2.50	0.42
2:G:213:ALA:O	2:G:334:TRP:HH2	2.03	0.42
1:A:258:ALA:C	1:A:260:ARG:N	2.78	0.42
1:B:478:LEU:HD13	1:B:547:ILE:HA	2.01	0.42
1:B:565:CYS:SG	1:B:568:PHE:HB2	2.59	0.42
1:C:228:ILE:HG22	1:C:240:THR:HG23	2.01	0.42
1:C:693:ILE:CG2	1:C:694:SER:H	2.31	0.42
1:D:140:ASP:OD1	1:D:169:ALA:HB3	2.20	0.42
1:D:553:LYS:HA	1:D:602:LEU:HD11	2.01	0.42
2:E:96:LEU:HB2	2:E:97:PRO:HD3	2.00	0.42
2:F:276:PHE:HB3	2:F:316:MET:SD	2.59	0.42
2:G:11:ASP:OD1	2:G:13:LEU:HB2	2.19	0.42
2:G:31:GLN:HG2	2:G:37:GLU:HB2	2.02	0.42
1:A:179:CYS:HB2	1:A:215:VAL:HG12	2.00	0.42
1:A:641:TYR:O	1:A:655:VAL:HA	2.20	0.42
1:B:139:ARG:NH1	1:B:202:THR:HG23	2.34	0.42
1:B:210:PRO:HG3	1:B:224:SER:HG	1.83	0.42
1:C:7:VAL:CG2	1:C:17:ILE:HG13	2.49	0.42
1:C:154:LYS:HD2	1:C:209:THR:CG2	2.49	0.42
1:C:444:LEU:HA	1:C:445:PRO:HD3	1.90	0.42
1:C:617:SER:OG	1:C:690:ASP:OD2	2.38	0.42
1:D:47:ILE:C	1:D:47:ILE:HD13	2.44	0.42
1:D:695:ALA:C	1:D:696:ASN:ND2	2.78	0.42
2:E:42:LYS:HE3	2:E:46:PHE:CZ	2.55	0.42
2:E:76:ASN:HD21	2:E:211:SER:CA	2.31	0.42
2:E:96:LEU:HA	2:E:99:ILE:HD12	2.01	0.42
2:E:102:PRO:HG2	2:E:103:GLU:OE1	2.19	0.42
2:E:203:LEU:HA	2:E:207:ARG:HD2	2.02	0.42
2:F:209:TYR:HA	2:F:212:PHE:CD2	2.54	0.42
1:A:7:VAL:HG11	3:A:800:DTP:C5	2.49	0.42
1:A:240:THR:O	1:A:244:ILE:HG13	2.20	0.42
1:A:403:MET:HE2	1:A:714:LEU:O	2.19	0.42
1:A:480:GLU:CD	1:A:480:GLU:H	2.28	0.42
1:C:140:ASP:OD1	1:C:169:ALA:HB3	2.20	0.42
1:C:467:PHE:O	1:C:518:ILE:N	2.37	0.42
1:D:304:LEU:HD23	1:D:305:PHE:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:310:HIS:O	1:D:355:LEU:HB3	2.18	0.42
1:D:467:PHE:CE1	1:D:481:LEU:HB3	2.54	0.42
1:D:518:ILE:HD12	1:D:631:ALA:HB3	2.02	0.42
1:D:543:THR:HG22	1:D:547:ILE:HD11	2.02	0.42
2:E:11:ASP:OD1	2:E:13:LEU:HB2	2.19	0.42
2:E:335:ILE:O	2:E:339:LEU:HG	2.18	0.42
2:F:213:ALA:O	2:F:334:TRP:HH2	2.03	0.42
2:F:244:GLY:O	2:F:248:MET:HG3	2.20	0.42
2:H:191:LYS:HG3	2:H:264:ILE:HG23	2.02	0.42
1:A:519:ASN:CB	1:A:631:ALA:HB1	2.50	0.42
1:B:228:ILE:CG2	1:B:240:THR:HG23	2.49	0.42
1:B:303:THR:CG2	1:B:334:ASP:O	2.67	0.42
1:B:317:LEU:HD12	1:B:317:LEU:HA	1.89	0.42
1:B:406:ARG:O	1:B:410:GLY:HA2	2.20	0.42
1:C:33:LEU:CD1	1:C:80:LEU:HB2	2.46	0.42
1:C:47:ILE:HD13	1:C:47:ILE:C	2.44	0.42
1:C:228:ILE:HG21	1:C:240:THR:HG23	2.00	0.42
1:C:436:SER:OG	1:C:440:LEU:HD13	2.20	0.42
1:C:723:LYS:HG3	2:G:375:LEU:OXT	2.19	0.42
1:D:91:LYS:O	1:D:91:LYS:HG2	2.20	0.42
1:D:464:LEU:HB3	1:D:620:MET:HE2	2.00	0.42
1:D:669:LEU:HD11	1:D:698:ASN:CG	2.45	0.42
2:E:125:ILE:O	2:E:129:ILE:HG12	2.20	0.42
2:E:165:SER:HB3	2:F:165:SER:HB3	2.02	0.42
2:E:187:ARG:NH1	2:E:260:GLU:HG3	2.35	0.42
2:F:149:ARG:HD2	2:F:286:TRP:HB2	2.02	0.42
1:A:75:PRO:O	1:A:78:GLN:HB2	2.19	0.42
1:A:173:TYR:HB3	1:A:197:TYR:HD1	1.84	0.42
1:B:136:ASP:OD2	1:B:139:ARG:HG3	2.18	0.42
1:B:480:GLU:H	1:B:480:GLU:CD	2.28	0.42
1:B:560:LYS:HG2	1:B:609:HIS:HB3	2.01	0.42
1:C:482:ALA:O	1:C:486:VAL:CG2	2.68	0.42
1:C:482:ALA:O	1:C:486:VAL:HG23	2.20	0.42
1:D:410:GLY:O	1:D:411:ARG:HD2	2.20	0.42
1:D:498:TYR:CB	1:D:504:LYS:HB2	2.50	0.42
2:H:96:LEU:HB2	2:H:97:PRO:HD3	2.01	0.42
1:A:645:LYS:HG2	1:A:646:ALA:N	2.35	0.41
1:B:519:ASN:CB	1:B:631:ALA:HB1	2.50	0.41
1:C:169:ALA:O	1:C:172:LEU:HB3	2.20	0.41
1:C:410:GLY:O	1:C:411:ARG:HD2	2.20	0.41
1:D:560:LYS:HD3	1:D:609:HIS:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:643:SER:O	1:D:653:ARG:HA	2.20	0.41
2:E:35:ILE:HG23	2:E:36:PHE:H	1.84	0.41
2:E:96:LEU:CB	2:E:97:PRO:HD3	2.50	0.41
2:H:96:LEU:CB	2:H:97:PRO:HD3	2.50	0.41
1:A:478:LEU:HD13	1:A:547:ILE:HA	2.02	0.41
1:B:334:ASP:OD1	1:B:411:ARG:HB3	2.20	0.41
1:B:339:ILE:HD12	1:B:414:ILE:HG23	2.02	0.41
1:B:639:ARG:O	1:B:668:LEU:HB3	2.19	0.41
1:C:217:THR:O	1:C:218:PRO:C	2.62	0.41
1:D:260:ARG:HH12	1:D:448:PRO:HG3	1.85	0.41
1:A:463:THR:O	1:A:489:LEU:HD22	2.20	0.41
1:B:146:ALA:HB2	1:B:654:GLN:HB2	2.02	0.41
1:B:241:SER:O	1:B:245:VAL:HG23	2.19	0.41
1:B:686:GLN:NE2	1:B:727:LYS:HE3	2.35	0.41
1:C:152:GLU:O	1:C:152:GLU:HG2	2.20	0.41
1:C:430:ILE:HG21	1:C:570:GLU:CG	2.50	0.41
1:C:567:TRP:C	1:C:569:ASN:N	2.78	0.41
1:C:619:LEU:HD13	1:C:693:ILE:CD1	2.50	0.41
1:D:275:HIS:ND1	3:D:900:DTP:H1'	2.35	0.41
2:E:209:TYR:HA	2:E:212:PHE:CD2	2.55	0.41
2:E:300:ASN:OD1	2:E:302:ASP:HB2	2.21	0.41
2:F:76:ASN:O	2:F:80:GLN:HG3	2.20	0.41
2:F:254:SER:C	2:F:256:ALA:H	2.29	0.41
2:G:76:ASN:O	2:G:80:GLN:HG3	2.20	0.41
2:G:171:GLY:O	2:G:184:VAL:CG1	2.66	0.41
2:H:18:PHE:O	2:H:19:PHE:CB	2.66	0.41
2:H:31:GLN:HG2	2:H:37:GLU:HB2	2.02	0.41
1:A:139:ARG:NH1	1:A:202:THR:HG23	2.36	0.41
1:A:313:VAL:HG13	1:A:314:GLU:N	2.36	0.41
1:B:160:ARG:HD3	1:B:160:ARG:HA	1.91	0.41
1:B:619:LEU:HD12	1:B:693:ILE:CD1	2.51	0.41
1:C:202:THR:OG1	1:C:204:LYS:HD3	2.19	0.41
1:D:521:ALA:HB3	1:D:632:THR:HG21	2.02	0.41
2:G:115:GLU:HA	2:G:115:GLU:OE1	2.21	0.41
2:G:125:ILE:O	2:G:129:ILE:HG12	2.20	0.41
1:A:413:TYR:HB3	1:A:729:LEU:O	2.21	0.41
1:A:583:TYR:CB	1:A:687:LYS:HG3	2.51	0.41
1:B:258:ALA:C	1:B:260:ARG:N	2.78	0.41
1:B:353:ILE:N	1:B:393:VAL:O	2.52	0.41
1:B:442:ILE:CG2	1:B:444:LEU:HG	2.50	0.41
1:B:549:TYR:CD1	1:B:602:LEU:HD22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:425:PRO:CG	1:C:615:THR:HG22	2.50	0.41
1:C:515:ILE:HD12	1:C:551:LEU:CD2	2.50	0.41
1:D:169:ALA:O	1:D:172:LEU:HB3	2.21	0.41
1:D:207:LEU:HD13	1:D:212:MET:HE3	2.02	0.41
1:D:224:SER:O	1:D:252:ALA:HA	2.20	0.41
1:D:437:ASN:OD1	1:D:441:GLU:OE1	2.39	0.41
2:E:276:PHE:HB3	2:E:316:MET:SD	2.60	0.41
2:G:203:LEU:O	2:G:207:ARG:HB2	2.19	0.41
1:B:641:TYR:O	1:B:655:VAL:HA	2.21	0.41
1:B:644:ILE:HD12	1:B:644:ILE:N	2.36	0.41
1:C:221:GLN:OE1	1:C:250:GLN:HG2	2.21	0.41
1:C:227:LEU:HB3	1:C:435:GLN:HE21	1.72	0.41
1:C:304:LEU:HD23	1:C:305:PHE:N	2.36	0.41
1:C:313:VAL:O	1:C:317:LEU:HB2	2.19	0.41
1:C:669:LEU:HD11	1:C:698:ASN:CG	2.45	0.41
1:D:367:ALA:HB1	1:D:375:PHE:HB2	2.02	0.41
1:D:463:THR:CG2	1:D:489:LEU:HD22	2.46	0.41
1:D:556:ASN:ND2	1:D:609:HIS:HB2	2.27	0.41
2:E:48:TRP:CZ3	2:E:50:PRO:HG3	2.55	0.41
2:E:332:ILE:HG22	2:E:334:TRP:HE1	1.85	0.41
2:G:9:LYS:CA	2:H:141:VAL:HG11	2.45	0.41
2:G:297:ILE:O	2:G:297:ILE:HG13	2.21	0.41
1:A:92:LYS:O	1:A:92:LYS:HG2	2.20	0.41
1:A:284:HIS:HA	1:B:287:THR:CB	2.50	0.41
1:A:558:LEU:CD2	1:A:612:ARG:HG2	2.49	0.41
1:A:565:CYS:HA	1:A:566:PRO:HD3	1.96	0.41
1:B:39:SER:O	1:B:40:GLN:C	2.64	0.41
1:C:224:SER:O	1:C:252:ALA:HA	2.21	0.41
1:C:431:ALA:HA	1:C:432:PRO:HD2	1.85	0.41
1:D:426:PHE:HE1	1:D:510:ARG:HE	1.65	0.41
2:E:244:GLY:O	2:E:248:MET:HG3	2.21	0.41
2:F:245:THR:CA	2:F:248:MET:HE3	2.47	0.41
1:A:10:ARG:CG	1:A:91:LYS:HZ1	2.34	0.41
1:A:77:TYR:CD1	1:A:80:LEU:HD23	2.55	0.41
1:B:68:ASP:HA	1:B:653:ARG:HH12	1.85	0.41
1:B:400:SER:HA	1:B:711:MET:HE3	2.03	0.41
1:B:645:LYS:HG2	1:B:646:ALA:N	2.36	0.41
1:C:465:SER:CB	1:C:514:GLY:O	2.61	0.41
1:C:498:TYR:CB	1:C:504:LYS:HB2	2.51	0.41
1:C:645:LYS:HG2	1:C:646:ALA:N	2.36	0.41
1:D:437:ASN:OD1	1:D:442:ILE:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:31:GLN:HG2	2:F:37:GLU:HB2	2.02	0.41
2:F:34:ASP:OD1	2:F:34:ASP:N	2.54	0.41
2:F:205:ALA:HB1	2:F:315:ARG:HD2	2.03	0.41
2:H:36:PHE:HZ	2:H:248:MET:HG2	1.85	0.41
2:H:278:GLN:O	2:H:282:GLN:HG3	2.21	0.41
1:A:227:LEU:C	1:A:435:GLN:NE2	2.76	0.41
1:A:406:ARG:O	1:A:410:GLY:HA2	2.21	0.41
1:A:425:PRO:HB3	1:A:573:TYR:CE2	2.55	0.41
1:A:437:ASN:ND2	1:A:439:CYS:H	2.18	0.41
1:A:541:HIS:O	1:A:545:GLU:HB2	2.21	0.41
1:A:619:LEU:HD12	1:A:693:ILE:CD1	2.50	0.41
1:B:441:GLU:O	1:B:692:SER:N	2.54	0.41
1:B:619:LEU:HD12	1:B:693:ILE:CG1	2.51	0.41
1:C:34:HIS:O	1:C:36:VAL:HG13	2.21	0.41
1:C:102:LEU:HD23	1:C:128:PHE:O	2.21	0.41
1:C:260:ARG:HH11	1:C:448:PRO:HG3	1.86	0.41
1:C:437:ASN:OD1	1:C:441:GLU:OE1	2.39	0.41
1:C:639:ARG:NH2	1:C:733:ASN:HB3	2.33	0.41
2:H:11:ASP:OD1	2:H:13:LEU:HB2	2.20	0.41
2:H:69:GLU:HG2	2:H:296:MET:HG3	2.03	0.41
2:H:125:ILE:O	2:H:129:ILE:HG12	2.20	0.41
2:H:332:ILE:HG22	2:H:334:TRP:HE1	1.84	0.41
1:B:53:ILE:O	1:B:54:LYS:O	2.39	0.41
1:B:232:ASP:OD2	1:B:262:ARG:NH2	2.53	0.41
1:B:583:TYR:CB	1:B:687:LYS:HG3	2.51	0.41
1:C:474:ASN:N	1:C:474:ASN:HD22	2.19	0.41
1:C:524:LEU:HD12	1:C:531:TYR:CE1	2.55	0.41
1:D:18:ASN:N	3:D:800:DTP:C2	2.82	0.41
1:D:524:LEU:HD12	1:D:531:TYR:CE1	2.56	0.41
1:D:553:LYS:O	1:D:557:GLU:HG2	2.20	0.41
1:D:567:TRP:C	1:D:569:ASN:N	2.78	0.41
1:D:583:TYR:CG	1:D:687:LYS:HG3	2.56	0.41
2:E:76:ASN:O	2:E:80:GLN:HG3	2.21	0.41
2:E:153:ILE:HD13	2:E:203:LEU:CD1	2.51	0.41
2:E:178:ASN:HD21	2:F:175:HIS:HD2	1.67	0.41
2:F:278:GLN:O	2:F:282:GLN:HG3	2.21	0.41
1:A:44:ARG:O	1:A:46:HIS:CD2	2.74	0.40
1:A:136:ASP:OD2	1:A:139:ARG:HG3	2.20	0.40
1:A:443:ALA:O	1:A:444:LEU:HD23	2.21	0.40
1:C:354:THR:HG21	1:C:390:LYS:HD3	2.03	0.40
1:C:640:GLY:CA	1:C:668:LEU:HD22	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:442:ILE:HD11	1:D:464:LEU:HD21	2.01	0.40
1:D:678:TYR:O	1:D:682:VAL:HG23	2.21	0.40
2:G:364:GLU:HG3	2:G:365:VAL:N	2.36	0.40
1:A:238:ASN:HD21	1:B:246:LYS:HG2	1.86	0.40
1:A:244:ILE:O	1:A:248:VAL:HG22	2.21	0.40
1:B:21:LYS:HD2	3:B:800:DTP:C6	2.52	0.40
1:B:174:ILE:HG23	1:B:175:LEU:N	2.36	0.40
1:B:227:LEU:HD11	1:B:437:ASN:HB3	2.03	0.40
1:B:403:MET:HE2	1:B:714:LEU:HB3	2.04	0.40
1:C:101:ALA:HB3	1:C:104:ASP:OD2	2.20	0.40
1:C:583:TYR:CG	1:C:687:LYS:HG3	2.57	0.40
1:D:55:THR:OG1	3:D:800:DTP:C5'	2.68	0.40
1:D:441:GLU:CG	1:D:619:LEU:O	2.70	0.40
2:G:36:PHE:O	2:G:39:LEU:HB2	2.22	0.40
2:G:76:ASN:HD21	2:G:211:SER:CA	2.29	0.40
2:H:42:LYS:HE3	2:H:46:PHE:CZ	2.56	0.40
2:H:232:ARG:HD2	2:H:338:TRP:HE3	1.87	0.40
2:H:244:GLY:O	2:H:248:MET:HG3	2.21	0.40
1:B:313:VAL:HG13	1:B:314:GLU:N	2.37	0.40
1:C:643:SER:O	1:C:653:ARG:HA	2.21	0.40
1:C:678:TYR:O	1:C:682:VAL:HG23	2.21	0.40
1:D:354:THR:HG21	1:D:390:LYS:HD3	2.03	0.40
1:D:367:ALA:O	1:D:369:PHE:N	2.54	0.40
2:E:158:ASP:OD1	2:F:4:THR:HG23	2.21	0.40
2:E:317:GLN:O	2:E:317:GLN:HG2	2.21	0.40
2:H:171:GLY:O	2:H:184:VAL:CG1	2.65	0.40
1:A:7:VAL:O	1:A:14:THR:HA	2.21	0.40
1:A:122:ASP:O	1:A:189:ARG:NH2	2.54	0.40
1:A:228:ILE:N	1:A:435:GLN:HE22	2.19	0.40
1:B:155:TYR:CD1	1:B:155:TYR:N	2.90	0.40
1:C:403:MET:HE2	1:C:714:LEU:O	2.22	0.40
1:C:696:ASN:ND2	1:C:730:TYR:HB3	2.36	0.40
1:D:430:ILE:HG21	1:D:570:GLU:CA	2.51	0.40
1:D:519:ASN:OD1	1:D:632:THR:HG23	2.21	0.40
1:D:532:SER:OG	1:D:673:PRO:HD2	2.20	0.40
2:G:93:VAL:HG13	2:H:97:PRO:HG3	2.04	0.40
2:G:104:LEU:O	2:G:108:VAL:HG23	2.21	0.40
2:H:300:ASN:OD1	2:H:302:ASP:HB2	2.21	0.40
1:A:283:LYS:HG3	1:A:330:VAL:HG22	2.04	0.40
1:A:735:ARG:HG2	1:A:736:ASP:N	2.36	0.40
1:B:75:PRO:O	1:B:78:GLN:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:696:ASN:OD1	1:B:731:TYR:HB2	2.21	0.40
1:C:246:LYS:HE2	1:D:238:ASN:CG	2.46	0.40
1:C:427:ASP:CG	1:C:430:ILE:HD12	2.47	0.40
2:E:6:SER:H	2:E:24:ASN:HB3	1.85	0.40
2:H:68:HIS:O	2:H:72:ILE:HG13	2.21	0.40
2:H:115:GLU:HA	2:H:115:GLU:OE1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	730/761 (96%)	688 (94%)	37 (5%)	5 (1%)	18	55
1	B	730/761 (96%)	684 (94%)	41 (6%)	5 (1%)	18	55
1	C	730/761 (96%)	686 (94%)	41 (6%)	3 (0%)	30	67
1	D	730/761 (96%)	685 (94%)	42 (6%)	3 (0%)	30	67
2	E	344/375 (92%)	326 (95%)	18 (5%)	0	100	100
2	F	344/375 (92%)	325 (94%)	19 (6%)	0	100	100
2	G	348/375 (93%)	330 (95%)	18 (5%)	0	100	100
2	H	346/375 (92%)	329 (95%)	17 (5%)	0	100	100
All	All	4302/4544 (95%)	4053 (94%)	233 (5%)	16 (0%)	30	67

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	731	TYR
1	B	54	LYS
1	D	731	TYR
1	A	52	GLY

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Mol	Chain	Res	Type
1	C	430	ILE
1	C	736	ASP
1	A	214	GLY
1	A	634	GLY
1	B	214	GLY
1	B	634	GLY
1	B	731	TYR
1	A	300	GLY
1	B	300	GLY
1	D	300	GLY
1	C	271	GLY
1	D	271	GLY

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	627/651 (96%)	593 (95%)	34 (5%)	20	41
1	B	627/651 (96%)	598 (95%)	29 (5%)	24	45
1	C	627/651 (96%)	600 (96%)	27 (4%)	26	47
1	D	627/651 (96%)	594 (95%)	33 (5%)	20	41
2	E	315/340 (93%)	308 (98%)	7 (2%)	45	64
2	F	315/340 (93%)	306 (97%)	9 (3%)	37	57
2	G	319/340 (94%)	312 (98%)	7 (2%)	45	64
2	H	317/340 (93%)	308 (97%)	9 (3%)	38	59
All	All	3774/3964 (95%)	3619 (96%)	155 (4%)	27	48

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	THR
1	A	39	SER
1	A	41	VAL

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Mol	Chain	Res	Type
1	A	43	LEU
1	A	44	ARG
1	A	47	ILE
1	A	51	ASP
1	A	53	ILE
1	A	64	LYS
1	A	78	GLN
1	A	118	HIS
1	A	122	ASP
1	A	141	MET
1	A	149	LYS
1	A	152	GLU
1	A	154	LYS
1	A	187	GLU
1	A	189	ARG
1	A	224	SER
1	A	225	CYS
1	A	251	ARG
1	A	297	VAL
1	A	326	GLU
1	A	341	LYS
1	A	364	LEU
1	A	394	LYS
1	A	439	CYS
1	A	440	LEU
1	A	441	GLU
1	A	462	CYS
1	A	474	ASN
1	A	510	ARG
1	A	624	THR
1	A	645	LYS
1	B	8	THR
1	B	36	VAL
1	B	44	ARG
1	B	47	ILE
1	B	51	ASP
1	B	54	LYS
1	B	64	LYS
1	B	78	GLN
1	B	118	HIS
1	B	122	ASP
1	B	141	MET

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Mol	Chain	Res	Type
1	B	149	LYS
1	B	154	LYS
1	B	187	GLU
1	B	189	ARG
1	B	224	SER
1	B	225	CYS
1	B	326	GLU
1	B	333	MET
1	B	341	LYS
1	B	364	LEU
1	B	394	LYS
1	B	421	ASN
1	B	465	SER
1	B	474	ASN
1	B	510	ARG
1	B	616	LEU
1	B	624	THR
1	B	645	LYS
1	C	7	VAL
1	C	8	THR
1	C	10	ARG
1	C	47	ILE
1	C	64	LYS
1	C	118	HIS
1	C	149	LYS
1	C	154	LYS
1	C	188	THR
1	C	189	ARG
1	C	212	MET
1	C	216	ARG
1	C	225	CYS
1	C	234	LEU
1	C	341	LYS
1	C	364	LEU
1	C	372	GLN
1	C	384	LYS
1	C	394	LYS
1	C	463	THR
1	C	465	SER
1	C	474	ASN
1	C	619	LEU
1	C	625	SER

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Mol	Chain	Res	Type
1	C	643	SER
1	C	645	LYS
1	C	709	VAL
1	D	8	THR
1	D	10	ARG
1	D	15	GLU
1	D	16	ARG
1	D	39	SER
1	D	47	ILE
1	D	53	ILE
1	D	64	LYS
1	D	118	HIS
1	D	149	LYS
1	D	154	LYS
1	D	187	GLU
1	D	189	ARG
1	D	212	MET
1	D	224	SER
1	D	225	CYS
1	D	234	LEU
1	D	276	THR
1	D	292	CYS
1	D	294	GLN
1	D	297	VAL
1	D	341	LYS
1	D	364	LEU
1	D	384	LYS
1	D	394	LYS
1	D	438	LEU
1	D	474	ASN
1	D	617	SER
1	D	625	SER
1	D	643	SER
1	D	645	LYS
1	D	696	ASN
1	D	709	VAL
2	E	100	SER
2	E	145	GLN
2	E	156	TYR
2	E	296	MET
2	E	297	ILE
2	E	303	ILE

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Mol	Chain	Res	Type
2	E	339	LEU
2	F	34	ASP
2	F	35	ILE
2	F	100	SER
2	F	145	GLN
2	F	156	TYR
2	F	232	ARG
2	F	296	MET
2	F	297	ILE
2	F	303	ILE
2	G	34	ASP
2	G	35	ILE
2	G	100	SER
2	G	145	GLN
2	G	156	TYR
2	G	297	ILE
2	G	303	ILE
2	H	34	ASP
2	H	35	ILE
2	H	100	SER
2	H	145	GLN
2	H	156	TYR
2	H	232	ARG
2	H	296	MET
2	H	297	ILE
2	H	303	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (110) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	HIS
1	A	40	GLN
1	A	46	HIS
1	A	78	GLN
1	A	130	GLN
1	A	137	HIS
1	A	257	ASN
1	A	321	ASN
1	A	328	ASN
1	A	435	GLN
1	A	474	ASN
1	A	541	HIS

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Mol	Chain	Res	Type
1	A	613	ASN
1	A	675	ASN
1	A	696	ASN
1	A	698	ASN
1	A	712	GLN
1	A	733	ASN
1	B	35	ASN
1	B	40	GLN
1	B	78	GLN
1	B	130	GLN
1	B	137	HIS
1	B	257	ASN
1	B	321	ASN
1	B	328	ASN
1	B	421	ASN
1	B	435	GLN
1	B	474	ASN
1	B	541	HIS
1	B	613	ASN
1	B	675	ASN
1	B	686	GLN
1	B	696	ASN
1	B	698	ASN
1	B	712	GLN
1	B	733	ASN
1	C	18	ASN
1	C	23	HIS
1	C	130	GLN
1	C	238	ASN
1	C	275	HIS
1	C	435	GLN
1	C	474	ASN
1	C	613	ASN
1	C	654	GLN
1	C	696	ASN
1	C	712	GLN
1	C	733	ASN
1	D	18	ASN
1	D	23	HIS
1	D	78	GLN
1	D	130	GLN
1	D	137	HIS

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Mol	Chain	Res	Type
1	D	238	ASN
1	D	250	GLN
1	D	275	HIS
1	D	294	GLN
1	D	435	GLN
1	D	474	ASN
1	D	562	GLN
1	D	613	ASN
1	D	654	GLN
1	D	691	GLN
1	D	696	ASN
1	D	712	GLN
1	D	733	ASN
2	E	10	ASN
2	E	12	GLN
2	E	30	GLN
2	E	43	GLN
2	E	68	HIS
2	E	76	ASN
2	E	87	GLN
2	E	124	HIS
2	E	147	GLN
2	E	175	HIS
2	E	201	ASN
2	E	246	GLN
2	E	282	GLN
2	F	21	GLN
2	F	30	GLN
2	F	68	HIS
2	F	76	ASN
2	F	87	GLN
2	F	124	HIS
2	F	147	GLN
2	F	175	HIS
2	F	201	ASN
2	F	246	GLN
2	F	282	GLN
2	G	21	GLN
2	G	30	GLN
2	G	68	HIS
2	G	76	ASN
2	G	87	GLN

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Mol	Chain	Res	Type
2	G	147	GLN
2	G	178	ASN
2	G	201	ASN
2	G	246	GLN
2	G	282	GLN
2	H	30	GLN
2	H	68	HIS
2	H	76	ASN
2	H	87	GLN
2	H	147	GLN
2	H	178	ASN
2	H	201	ASN
2	H	246	GLN
2	H	282	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 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DTP	A	800	-	31,32,32	1.74	6 (19%)	46,50,50	1.69	10 (21%)
3	DTP	A	900	-	31,32,32	1.72	6 (19%)	46,50,50	1.71	10 (21%)
3	DTP	B	900	-	31,32,32	1.73	6 (19%)	46,50,50	1.72	10 (21%)
3	DTP	C	800	-	31,32,32	1.72	6 (19%)	46,50,50	1.75	10 (21%)
3	DTP	C	900	-	31,32,32	1.72	6 (19%)	46,50,50	1.70	10 (21%)
3	DTP	D	900	-	31,32,32	1.78	7 (22%)	46,50,50	1.68	10 (21%)
3	DTP	B	800	-	31,32,32	1.73	6 (19%)	46,50,50	1.77	10 (21%)
3	DTP	D	800	-	31,32,32	1.75	7 (22%)	46,50,50	1.73	10 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DTP	A	800	-	-	8/22/34/34	0/3/3/3
3	DTP	A	900	-	-	3/22/34/34	0/3/3/3
3	DTP	B	900	-	-	5/22/34/34	0/3/3/3
3	DTP	C	800	-	-	8/22/34/34	0/3/3/3
3	DTP	C	900	-	-	11/22/34/34	0/3/3/3
3	DTP	D	900	-	-	5/22/34/34	0/3/3/3
3	DTP	B	800	-	-	2/22/34/34	0/3/3/3
3	DTP	D	800	-	-	8/22/34/34	0/3/3/3

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	800	DTP	C6-N6	5.07	1.47	1.34
3	B	900	DTP	C6-N6	5.06	1.47	1.34
3	C	900	DTP	C6-N6	5.04	1.47	1.34
3	D	800	DTP	C6-N6	5.04	1.47	1.34
3	C	800	DTP	C6-N6	5.02	1.47	1.34
3	D	900	DTP	C6-N6	5.01	1.47	1.34
3	B	800	DTP	C6-N6	5.00	1.47	1.34
3	A	900	DTP	C6-N6	4.93	1.46	1.34
3	D	800	DTP	O3'-C3'	-4.01	1.34	1.43
3	D	900	DTP	O3'-C3'	-3.97	1.35	1.43
3	B	800	DTP	O3'-C3'	-3.95	1.35	1.43
3	B	900	DTP	O3'-C3'	-3.95	1.35	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	800	DTP	O3'-C3'	-3.94	1.35	1.43
3	A	800	DTP	O3'-C3'	-3.93	1.35	1.43
3	A	900	DTP	O3'-C3'	-3.92	1.35	1.43
3	C	900	DTP	O3'-C3'	-3.90	1.35	1.43
3	B	800	DTP	C5'-C4'	-3.15	1.42	1.51
3	A	800	DTP	C5'-C4'	-3.08	1.42	1.51
3	D	800	DTP	C5'-C4'	-3.08	1.42	1.51
3	D	900	DTP	C5'-C4'	-3.05	1.42	1.51
3	A	900	DTP	C5'-C4'	-3.02	1.42	1.51
3	C	800	DTP	C5'-C4'	-2.95	1.42	1.51
3	C	900	DTP	C5'-C4'	-2.93	1.42	1.51
3	B	900	DTP	C5'-C4'	-2.88	1.42	1.51
3	A	800	DTP	O5'-C5'	-2.85	1.33	1.44
3	D	900	DTP	O5'-C5'	-2.82	1.33	1.44
3	B	800	DTP	O5'-C5'	-2.81	1.34	1.44
3	D	800	DTP	O5'-C5'	-2.79	1.34	1.44
3	B	900	DTP	O5'-C5'	-2.76	1.34	1.44
3	A	900	DTP	O5'-C5'	-2.75	1.34	1.44
3	C	900	DTP	O5'-C5'	-2.74	1.34	1.44
3	D	900	DTP	C2'-C3'	-2.73	1.45	1.52
3	C	900	DTP	C2'-C3'	-2.71	1.46	1.52
3	D	800	DTP	C2'-C3'	-2.71	1.46	1.52
3	C	800	DTP	O5'-C5'	-2.67	1.34	1.44
3	A	800	DTP	PA-O3A	-2.66	1.56	1.59
3	B	800	DTP	C2'-C3'	-2.66	1.46	1.52
3	A	900	DTP	C2'-C3'	-2.65	1.46	1.52
3	B	900	DTP	C2'-C3'	-2.62	1.46	1.52
3	C	800	DTP	C2'-C3'	-2.61	1.46	1.52
3	A	800	DTP	C2'-C3'	-2.55	1.46	1.52
3	D	900	DTP	C3'-C4'	-2.45	1.46	1.53
3	A	900	DTP	PA-O3A	-2.37	1.56	1.59
3	D	900	DTP	PA-O3A	-2.35	1.57	1.59
3	B	800	DTP	PA-O3A	-2.27	1.57	1.59
3	B	900	DTP	C3'-C4'	-2.27	1.47	1.53
3	C	900	DTP	PA-O3A	-2.24	1.57	1.59
3	C	800	DTP	PA-O3A	-2.22	1.57	1.59
3	D	800	DTP	PA-O3A	-2.19	1.57	1.59
3	D	800	DTP	C3'-C4'	-2.12	1.47	1.53

All (80) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	800	DTP	C5-C4-N3	-5.39	119.30	126.72
3	C	800	DTP	C5-C4-N3	-5.38	119.31	126.72
3	C	900	DTP	C5-C4-N3	-5.28	119.44	126.72
3	B	800	DTP	C5-C4-N3	-5.21	119.54	126.72
3	A	900	DTP	C5-C4-N3	-5.20	119.56	126.72
3	B	900	DTP	C5-C4-N3	-5.08	119.72	126.72
3	D	800	DTP	C5-C4-N3	-4.95	119.91	126.72
3	D	900	DTP	C5-C4-N3	-4.83	120.06	126.72
3	B	800	DTP	O4'-C1'-N9	4.17	115.45	107.96
3	D	900	DTP	O4'-C1'-N9	4.01	115.17	107.96
3	D	800	DTP	O4'-C1'-N9	3.94	115.04	107.96
3	A	800	DTP	N3-C4-N9	3.85	133.72	127.17
3	C	800	DTP	N3-C4-N9	3.82	133.67	127.17
3	C	900	DTP	N3-C4-N9	3.73	133.51	127.17
3	B	900	DTP	N3-C4-N9	3.65	133.38	127.17
3	A	900	DTP	N3-C4-N9	3.64	133.35	127.17
3	C	900	DTP	O4'-C1'-N9	3.63	114.47	107.96
3	A	900	DTP	O4'-C1'-N9	3.47	114.20	107.96
3	A	900	DTP	N3-C2-N1	-3.46	123.34	128.58
3	C	800	DTP	O4'-C1'-N9	3.45	114.17	107.96
3	D	800	DTP	N3-C4-N9	3.44	133.01	127.17
3	C	800	DTP	N3-C2-N1	-3.43	123.39	128.58
3	D	800	DTP	N9-C8-N7	-3.41	109.10	113.94
3	B	800	DTP	N3-C4-N9	3.40	132.95	127.17
3	B	800	DTP	N9-C8-N7	-3.39	109.13	113.94
3	B	900	DTP	N3-C2-N1	-3.38	123.46	128.58
3	B	800	DTP	N3-C2-N1	-3.38	123.47	128.58
3	D	900	DTP	N9-C8-N7	-3.38	109.14	113.94
3	D	800	DTP	N3-C2-N1	-3.37	123.49	128.58
3	B	900	DTP	N9-C8-N7	-3.34	109.20	113.94
3	B	900	DTP	O4'-C1'-N9	3.33	113.94	107.96
3	C	900	DTP	N3-C2-N1	-3.33	123.55	128.58
3	A	900	DTP	N9-C8-N7	-3.31	109.24	113.94
3	C	900	DTP	N9-C8-N7	-3.30	109.26	113.94
3	A	800	DTP	N3-C2-N1	-3.27	123.63	128.58
3	C	800	DTP	N9-C8-N7	-3.24	109.34	113.94
3	A	800	DTP	O4'-C1'-N9	3.17	113.65	107.96
3	C	800	DTP	C2-N3-C4	3.16	119.54	111.83
3	D	900	DTP	N3-C4-N9	3.16	132.53	127.17
3	B	800	DTP	C2-N3-C4	3.14	119.50	111.83
3	B	800	DTP	C4-C5-N7	-3.13	107.00	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	900	DTP	C2-N3-C4	3.09	119.38	111.83
3	A	800	DTP	C2-N3-C4	3.08	119.36	111.83
3	B	900	DTP	C2-N3-C4	3.07	119.33	111.83
3	C	900	DTP	C2-N3-C4	3.07	119.32	111.83
3	B	800	DTP	C5-N7-C8	3.06	108.27	103.45
3	D	900	DTP	N3-C2-N1	-3.02	124.01	128.58
3	D	800	DTP	C2-N3-C4	2.99	119.13	111.83
3	A	800	DTP	N9-C8-N7	-2.98	109.71	113.94
3	D	800	DTP	C5-N7-C8	2.96	108.10	103.45
3	D	900	DTP	C4-C5-N7	-2.95	107.21	110.58
3	C	900	DTP	C5-N7-C8	2.95	108.09	103.45
3	C	800	DTP	C5-N7-C8	2.94	108.08	103.45
3	A	900	DTP	C5-N7-C8	2.94	108.07	103.45
3	D	900	DTP	C5-N7-C8	2.91	108.02	103.45
3	B	900	DTP	C5-N7-C8	2.90	108.01	103.45
3	D	800	DTP	C4-C5-N7	-2.85	107.32	110.58
3	C	900	DTP	C4-C5-N7	-2.83	107.34	110.58
3	A	800	DTP	C5-N7-C8	2.83	107.90	103.45
3	D	900	DTP	C2-N3-C4	2.83	118.73	111.83
3	A	900	DTP	C4-C5-N7	-2.83	107.35	110.58
3	C	800	DTP	C4-C5-N7	-2.79	107.39	110.58
3	A	800	DTP	C4-C5-N7	-2.78	107.40	110.58
3	B	900	DTP	O5'-C5'-C4'	2.74	118.33	108.99
3	B	900	DTP	C4-C5-N7	-2.70	107.49	110.58
3	A	800	DTP	O5'-C5'-C4'	2.62	117.90	108.99
3	C	800	DTP	O5'-C5'-C4'	2.59	117.81	108.99
3	C	900	DTP	O5'-C5'-C4'	2.53	117.59	108.99
3	B	900	DTP	C4-N9-C8	2.52	108.39	105.74
3	D	800	DTP	C4-N9-C8	2.52	108.39	105.74
3	D	800	DTP	O5'-C5'-C4'	2.47	117.40	108.99
3	A	900	DTP	O5'-C5'-C4'	2.46	117.37	108.99
3	C	900	DTP	C4-N9-C8	2.41	108.27	105.74
3	A	900	DTP	C4-N9-C8	2.40	108.26	105.74
3	D	900	DTP	O5'-C5'-C4'	2.39	117.14	108.99
3	D	900	DTP	C4-N9-C8	2.37	108.23	105.74
3	C	800	DTP	C4-N9-C8	2.32	108.17	105.74
3	B	800	DTP	C4-N9-C8	2.25	108.10	105.74
3	A	800	DTP	C4-N9-C8	2.16	108.00	105.74
3	B	800	DTP	O5'-C5'-C4'	2.03	115.90	108.99

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	800	DTP	PB-O3B-PG-O2G
3	A	800	DTP	C5'-O5'-PA-O1A
3	A	800	DTP	C5'-O5'-PA-O3A
3	A	900	DTP	O4'-C4'-C5'-O5'
3	A	900	DTP	C3'-C4'-C5'-O5'
3	B	800	DTP	C5'-O5'-PA-O1A
3	B	900	DTP	C5'-O5'-PA-O1A
3	B	900	DTP	C5'-O5'-PA-O2A
3	B	900	DTP	C5'-O5'-PA-O3A
3	C	900	DTP	C5'-O5'-PA-O2A
3	D	900	DTP	C3'-C4'-C5'-O5'
3	A	800	DTP	C3'-C4'-C5'-O5'
3	A	800	DTP	O4'-C4'-C5'-O5'
3	D	900	DTP	O4'-C4'-C5'-O5'
3	B	900	DTP	O4'-C4'-C5'-O5'
3	C	800	DTP	PB-O3B-PG-O1G
3	A	900	DTP	PG-O3B-PB-O1B
3	C	900	DTP	C2'-C1'-N9-C4
3	C	900	DTP	C3'-C4'-C5'-O5'
3	D	800	DTP	O4'-C4'-C5'-O5'
3	C	800	DTP	O4'-C4'-C5'-O5'
3	C	900	DTP	PB-O3B-PG-O1G
3	B	900	DTP	C3'-C4'-C5'-O5'
3	C	900	DTP	O4'-C4'-C5'-O5'
3	A	800	DTP	C5'-O5'-PA-O2A
3	C	800	DTP	C5'-O5'-PA-O1A
3	C	800	DTP	C5'-O5'-PA-O2A
3	C	800	DTP	C5'-O5'-PA-O3A
3	C	900	DTP	C5'-O5'-PA-O1A
3	C	900	DTP	C5'-O5'-PA-O3A
3	D	800	DTP	C5'-O5'-PA-O1A
3	D	800	DTP	C5'-O5'-PA-O3A
3	D	800	DTP	PG-O3B-PB-O1B
3	D	900	DTP	O4'-C1'-N9-C4
3	D	900	DTP	O4'-C1'-N9-C8
3	C	900	DTP	PB-O3B-PG-O2G
3	C	900	DTP	PB-O3B-PG-O3G
3	A	800	DTP	PG-O3B-PB-O2B
3	C	800	DTP	PA-O3A-PB-O2B
3	D	800	DTP	PG-O3B-PB-O2B
3	C	800	DTP	C2'-C1'-N9-C4
3	D	800	DTP	C2'-C1'-N9-C4
3	B	800	DTP	O4'-C4'-C5'-O5'

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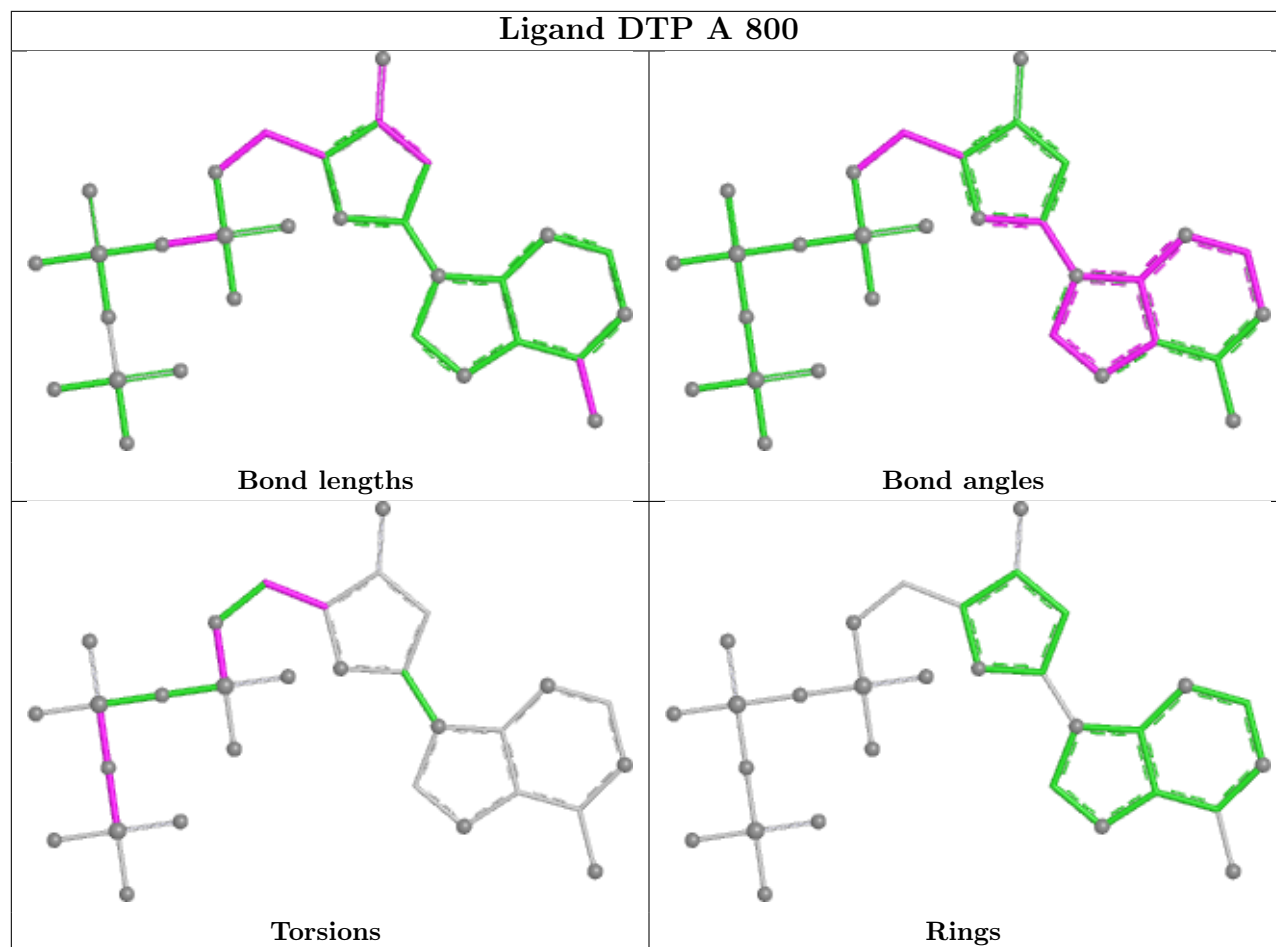
Mol	Chain	Res	Type	Atoms
3	D	800	DTP	C2'-C1'-N9-C8
3	C	900	DTP	O4'-C1'-N9-C4
3	D	800	DTP	O4'-C1'-N9-C4
3	C	800	DTP	C3'-C4'-C5'-O5'
3	C	900	DTP	PA-O3A-PB-O2B
3	D	900	DTP	PA-O3A-PB-O2B
3	A	800	DTP	PG-O3B-PB-O3A

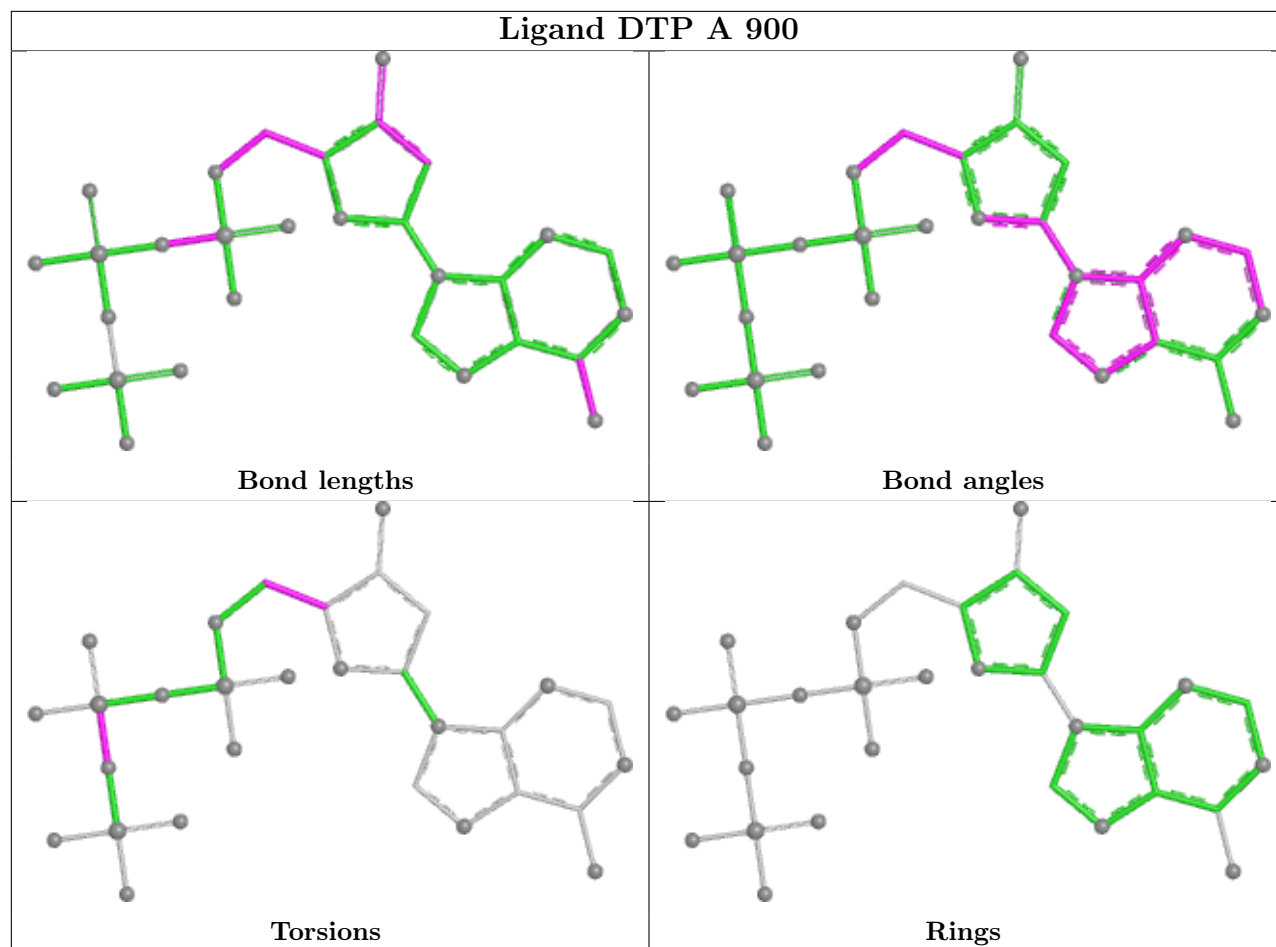
There are no ring outliers.

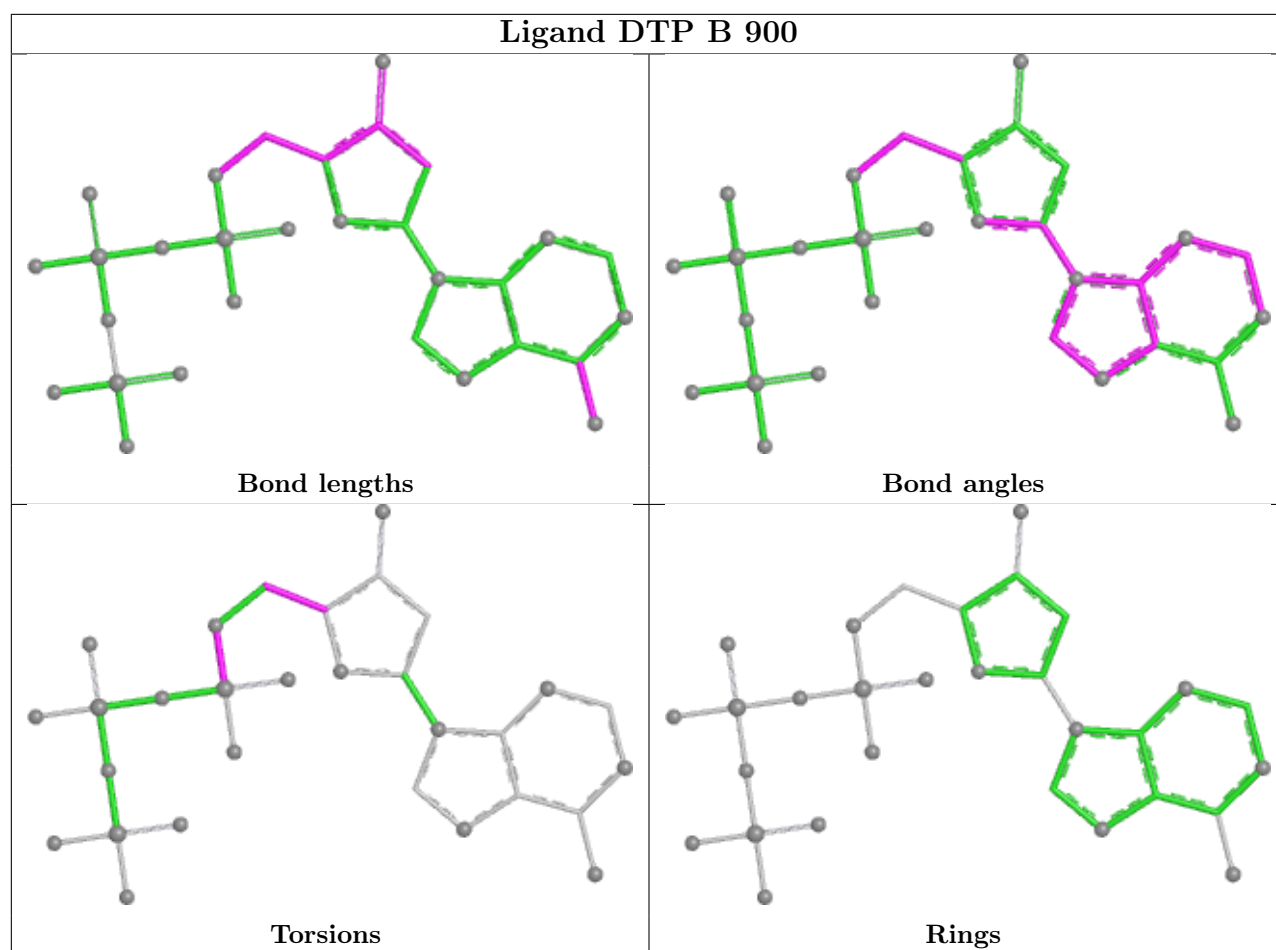
8 monomers are involved in 70 short contacts:

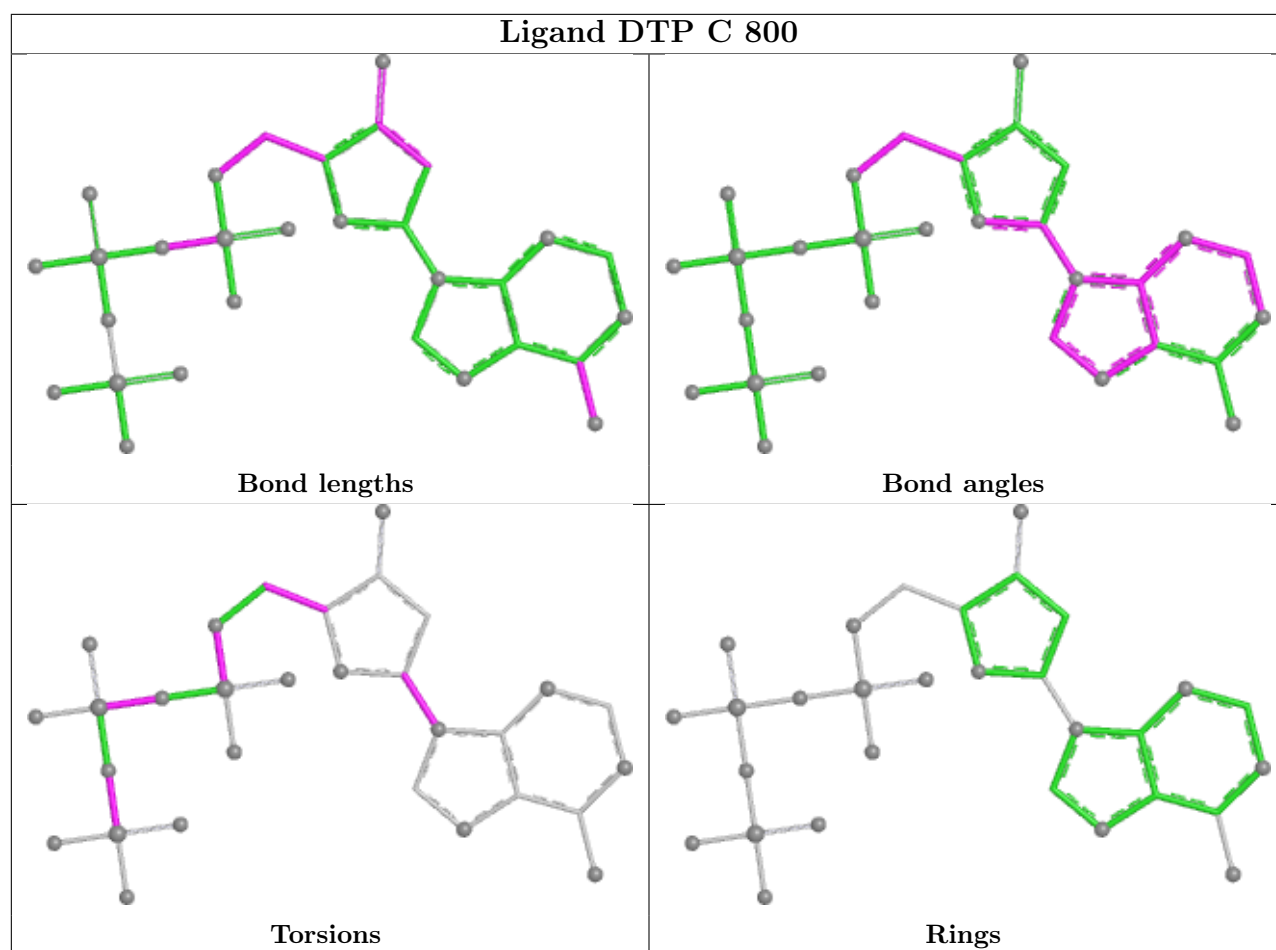
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	800	DTP	17	0
3	A	900	DTP	2	0
3	B	900	DTP	7	0
3	C	800	DTP	12	0
3	C	900	DTP	8	0
3	D	900	DTP	6	0
3	B	800	DTP	6	0
3	D	800	DTP	12	0

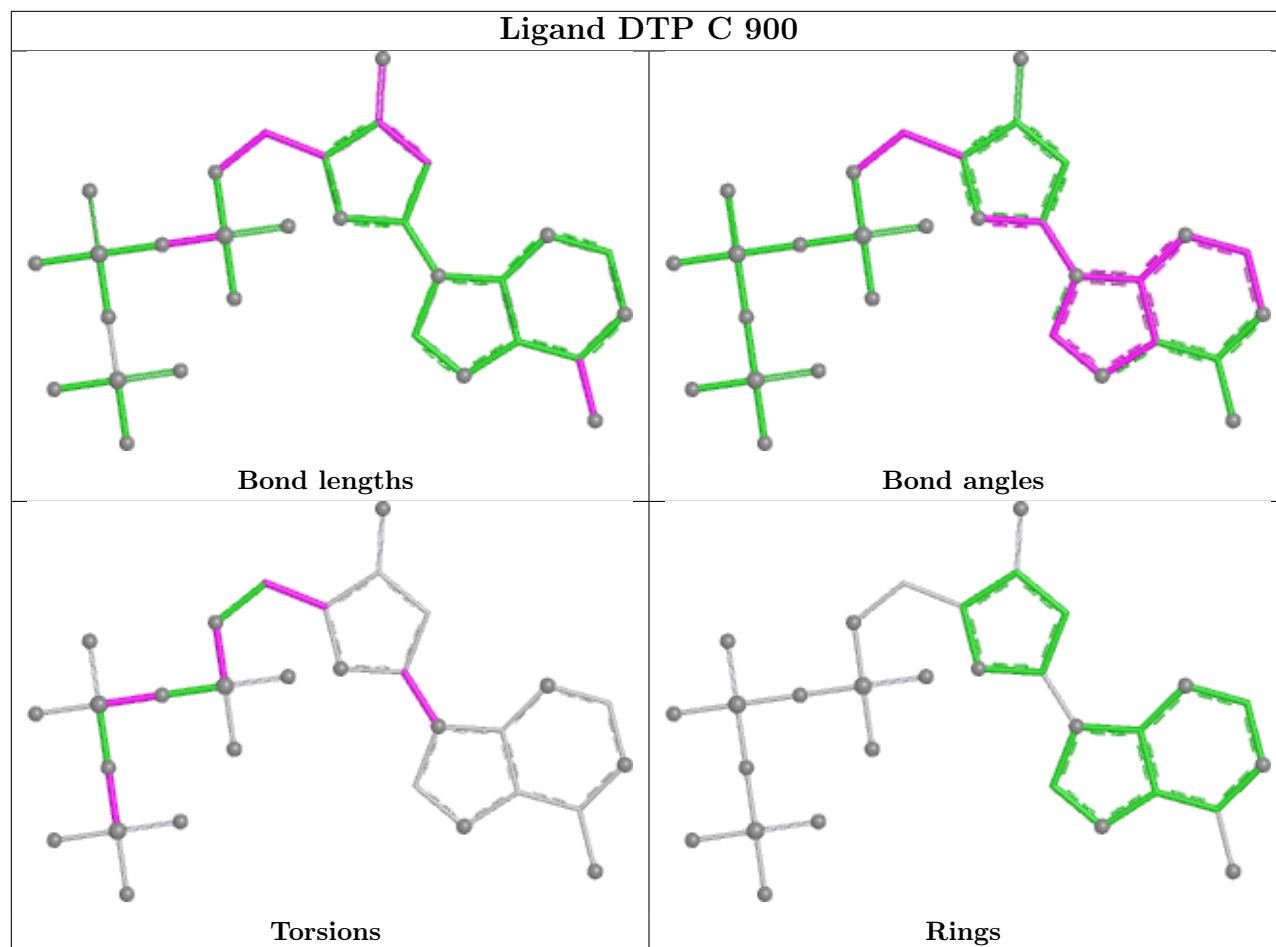
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

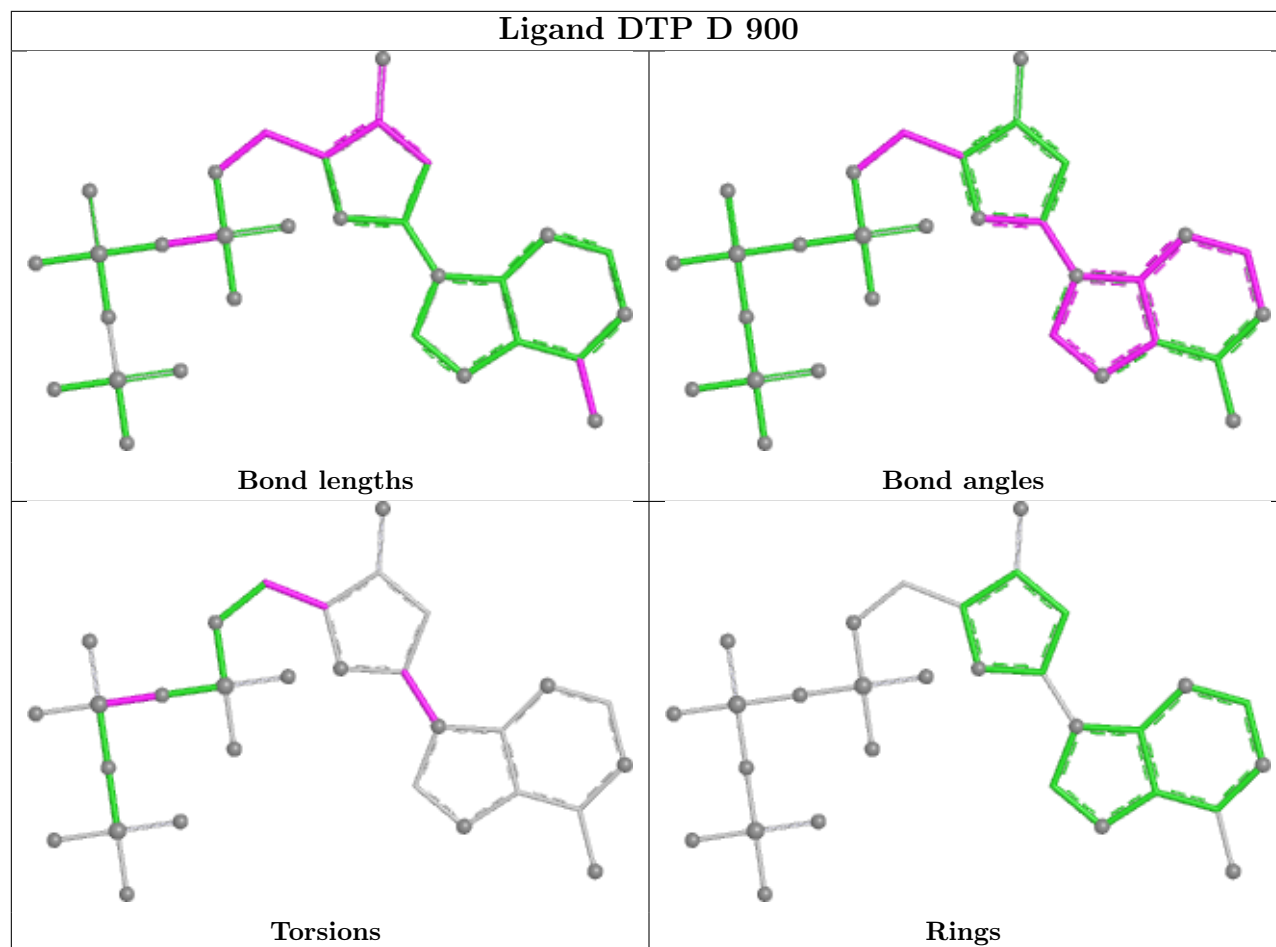


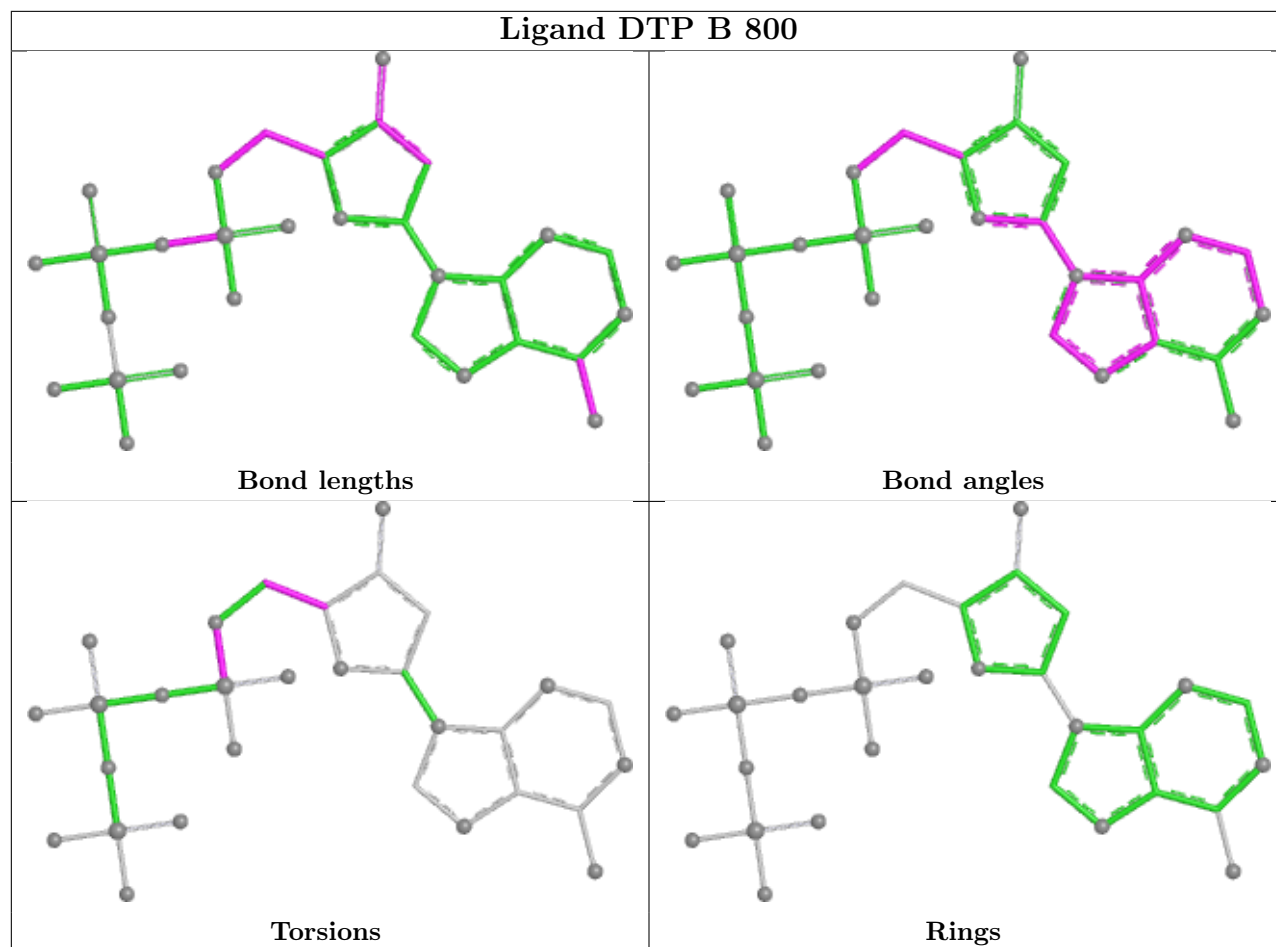


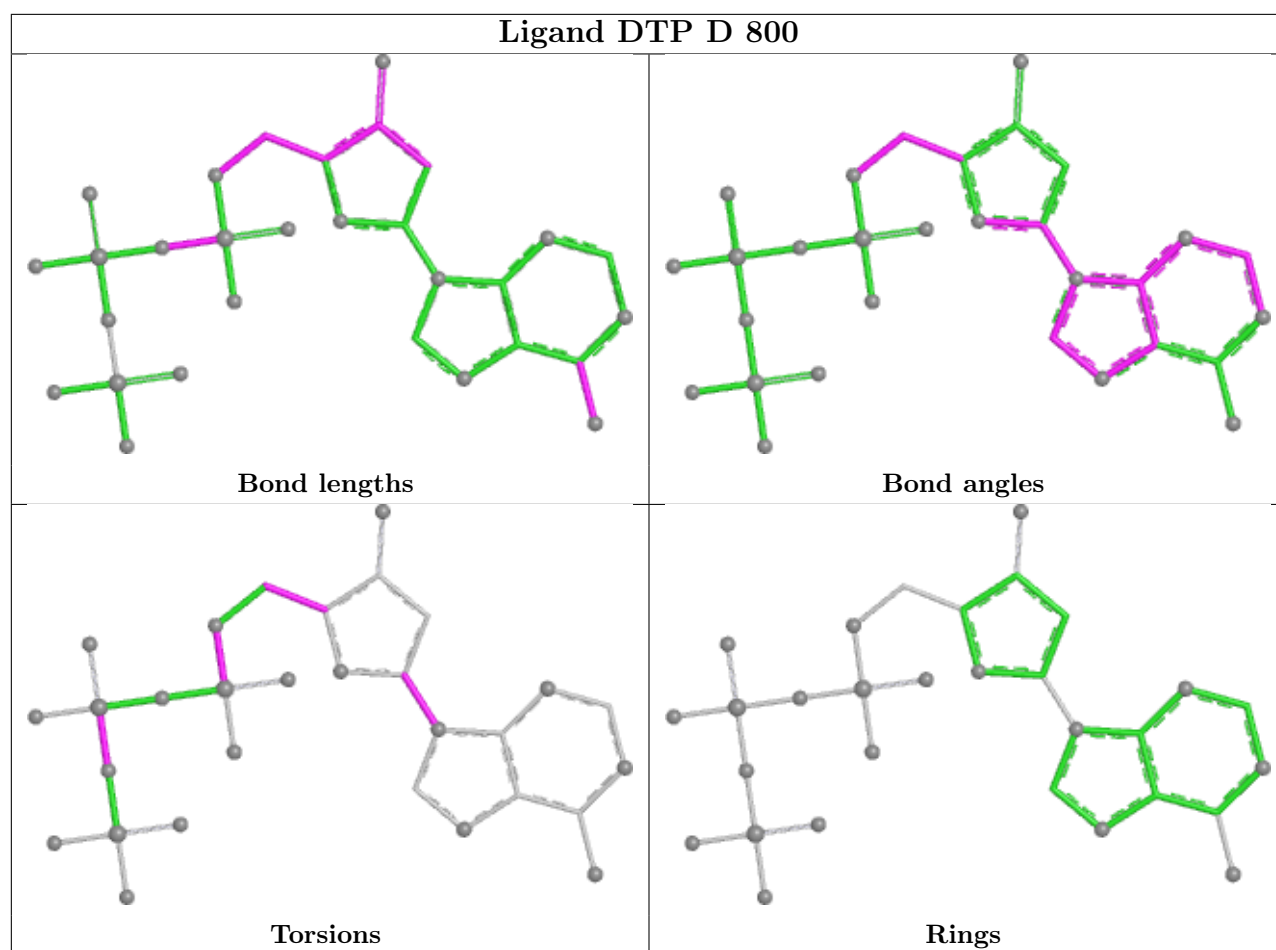












5.7 Other polymers [i](#)

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	732/761 (96%)	0.17	23 (3%)	51	45	157, 231, 260, 283	0
1	B	732/761 (96%)	0.18	19 (2%)	57	48	161, 232, 262, 279	0
1	C	732/761 (96%)	0.19	20 (2%)	56	48	197, 289, 342, 359	0
1	D	732/761 (96%)	0.26	18 (2%)	58	49	194, 290, 343, 359	0
2	E	348/375 (92%)	0.00	3 (0%)	81	69	145, 207, 237, 289	0
2	F	348/375 (92%)	0.05	4 (1%)	78	66	147, 206, 235, 285	0
2	G	352/375 (93%)	0.04	5 (1%)	73	62	147, 207, 237, 293	0
2	H	350/375 (93%)	0.15	5 (1%)	73	62	141, 203, 235, 286	0
All	All	4326/4544 (95%)	0.15	97 (2%)	62	53	141, 235, 312, 359	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	515	ILE	7.0
1	C	465	SER	6.3
1	B	489	LEU	5.1
1	A	467	PHE	4.9
1	B	467	PHE	4.6
1	B	243	ALA	4.6
1	C	258	ALA	4.3
1	B	246	LYS	4.1
1	C	485	ALA	4.0
2	G	140	ILE	4.0
1	A	143	PHE	4.0
1	A	685	MET	4.0
1	C	467	PHE	3.8
1	D	443	ALA	3.7
1	A	414	ILE	3.6
1	A	205	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	212	MET	3.5
1	A	415	GLN	3.5
1	B	308	MET	3.4
2	G	137	PHE	3.4
1	C	443	ALA	3.3
1	C	128	PHE	3.3
1	A	441	GLU	3.2
1	D	520	PHE	3.2
1	D	467	PHE	3.1
1	D	523	TYR	3.1
1	D	244	ILE	3.1
1	D	241	SER	3.1
1	C	245	VAL	3.1
1	D	243	ALA	3.0
1	A	300	GLY	3.0
1	D	62	ILE	3.0
1	B	517	VAL	2.9
1	B	443	ALA	2.9
1	C	259	GLY	2.9
1	D	285	PHE	2.8
1	A	436	SER	2.8
1	B	247	TYR	2.7
1	C	618	ALA	2.7
1	B	463	THR	2.7
1	D	207	LEU	2.7
2	F	167	TRP	2.7
1	B	313	VAL	2.7
1	D	500	ILE	2.7
2	E	329	SER	2.7
1	C	424	SER	2.6
1	A	439	CYS	2.6
1	B	107	VAL	2.6
2	H	307	TYR	2.5
2	F	56	SER	2.5
1	D	420	CYS	2.5
2	E	214	CYS	2.5
2	G	214	CYS	2.5
1	A	643	SER	2.5
1	B	306	TYR	2.5
1	C	442	ILE	2.5
1	C	143	PHE	2.4
1	B	682	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	485	ALA	2.4
1	D	692	SER	2.4
1	A	292	CYS	2.3
1	C	211	ILE	2.3
1	D	469	LEU	2.3
1	C	466	ALA	2.3
2	H	206	ILE	2.3
1	B	19	LEU	2.3
1	A	207	LEU	2.3
1	C	422	THR	2.3
1	B	424	SER	2.3
2	E	9	LYS	2.3
2	H	324	PRO	2.3
1	A	310	HIS	2.3
1	B	485	ALA	2.2
1	D	246	LYS	2.2
1	C	62	ILE	2.2
1	A	621	PRO	2.2
2	G	2	TYR	2.2
1	B	239	ALA	2.2
2	F	95	LEU	2.2
1	A	695	ALA	2.2
1	C	489	LEU	2.2
1	A	440	LEU	2.1
1	A	635	ILE	2.1
2	F	126	ILE	2.1
1	D	39	SER	2.1
1	B	259	GLY	2.1
1	A	261	ILE	2.1
1	C	401	LEU	2.1
1	A	332	HIS	2.1
1	A	307	PRO	2.1
2	G	97	PRO	2.1
1	A	49	PHE	2.0
1	D	363	GLY	2.0
1	B	452	VAL	2.0
2	H	93	VAL	2.0
2	H	150	ALA	2.0
1	C	49	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

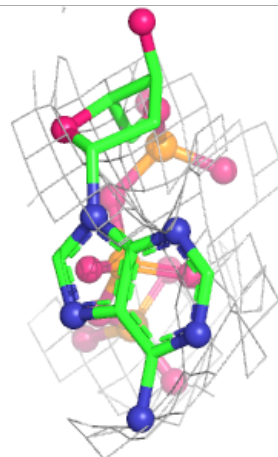
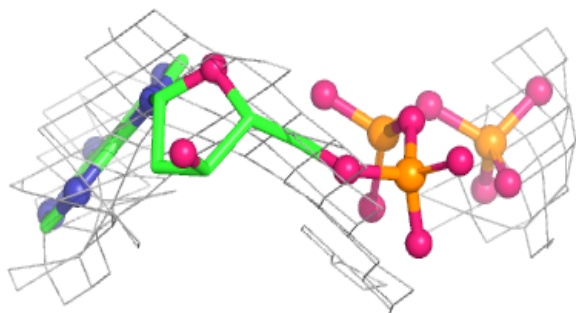
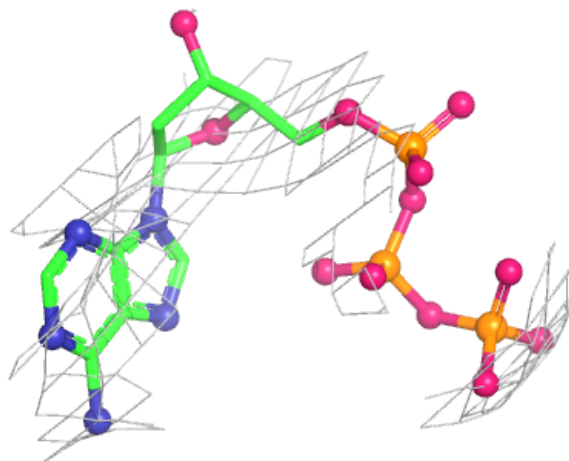
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	DTP	C	800	30/30	0.69	0.12	326,326,326,326	0
3	DTP	D	900	30/30	0.71	0.12	308,308,308,308	0
3	DTP	D	800	30/30	0.72	0.10	318,318,318,318	0
3	DTP	A	800	30/30	0.78	0.10	306,306,306,306	0
3	DTP	C	900	30/30	0.81	0.10	284,284,284,284	0
3	DTP	B	800	30/30	0.83	0.09	279,279,279,279	0
3	DTP	A	900	30/30	0.86	0.09	267,267,267,267	0
3	DTP	B	900	30/30	0.86	0.08	232,232,232,232	0
4	FE	E	1003	1/1	0.98	0.10	168,168,168,168	0
4	FE	E	1004	1/1	0.99	0.04	133,133,133,133	0
4	FE	F	1001	1/1	1.00	0.09	94,94,94,94	0
4	FE	F	1002	1/1	1.00	0.08	125,125,125,125	0
4	FE	G	1003	1/1	1.00	0.08	89,89,89,89	0
4	FE	G	1004	1/1	1.00	0.10	122,122,122,122	0
4	FE	H	1001	1/1	1.00	0.08	110,110,110,110	0
4	FE	H	1002	1/1	1.00	0.10	114,114,114,114	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

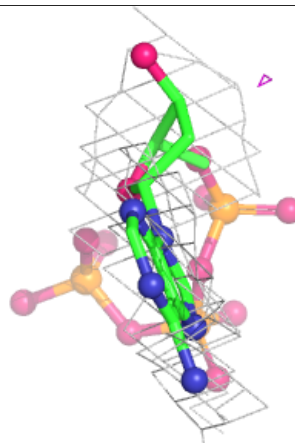
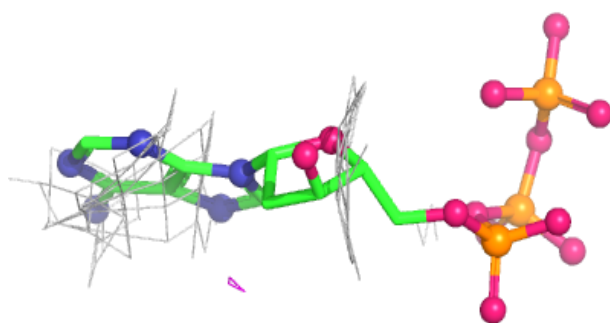
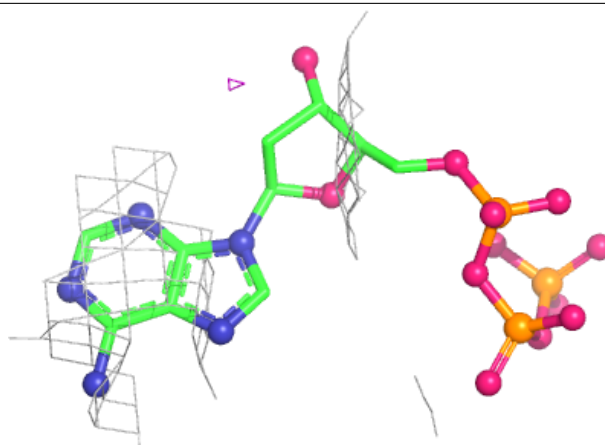
Electron density around DTP C 800:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



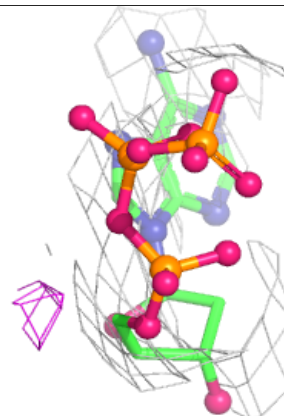
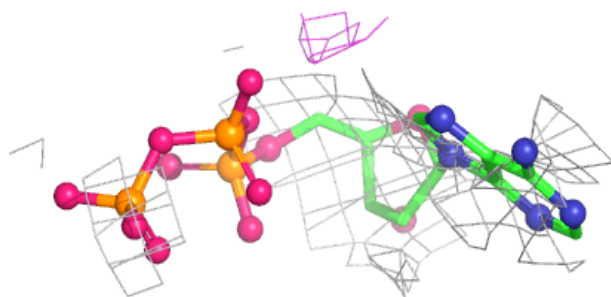
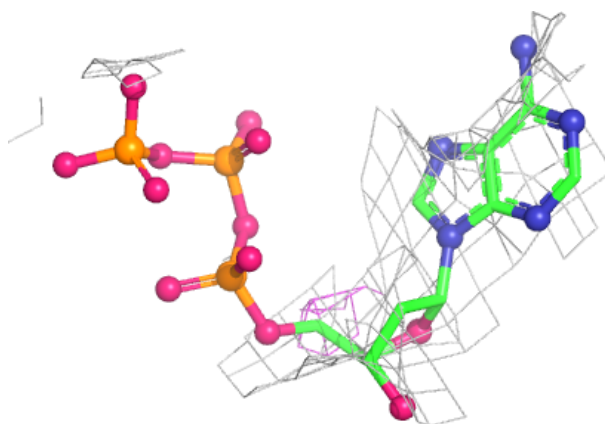
Electron density around DTP D 900:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



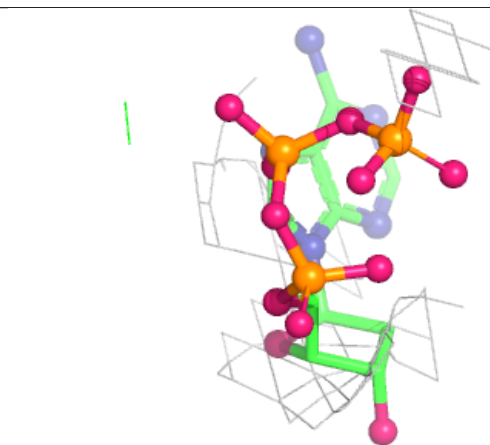
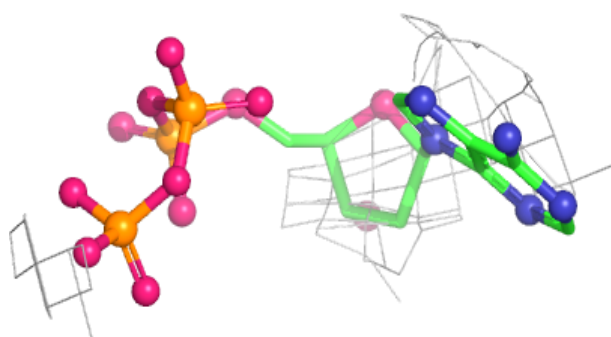
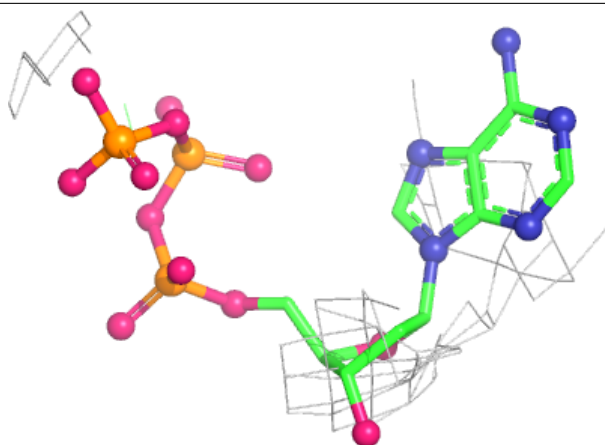
Electron density around DTP D 800:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

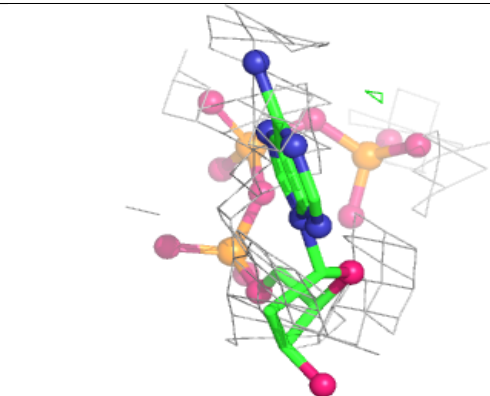
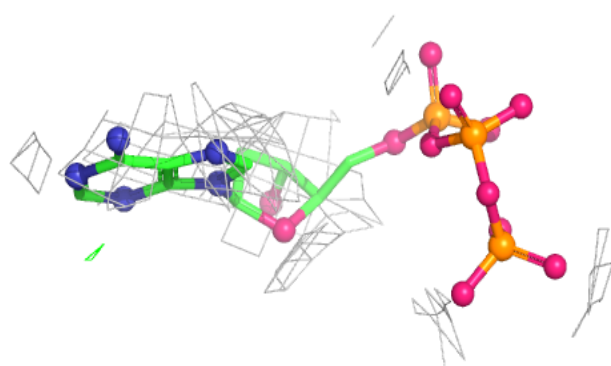
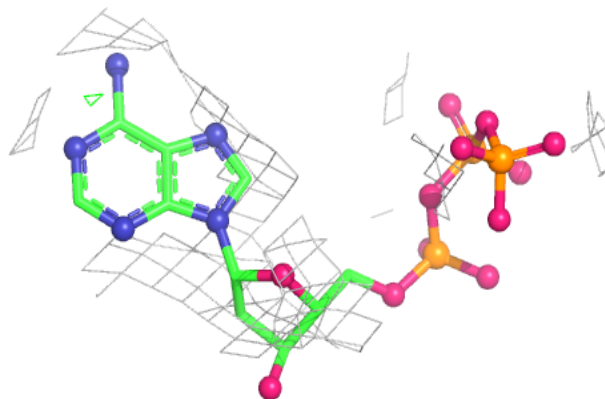


Electron density around DTP A 800:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

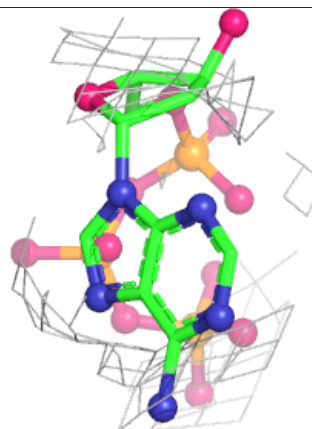
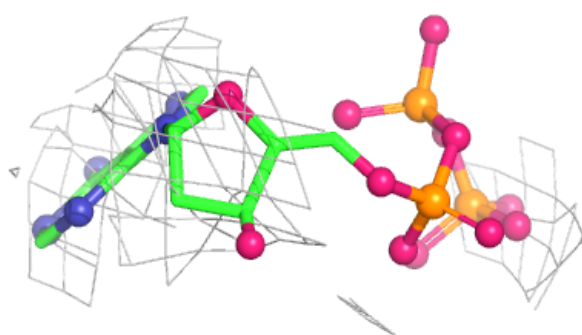
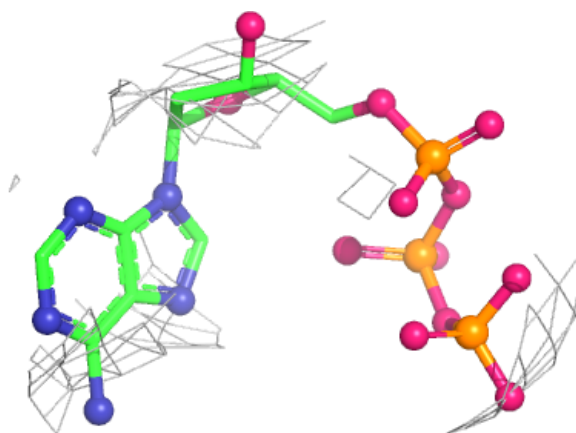
**Electron density around DTP C 900:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



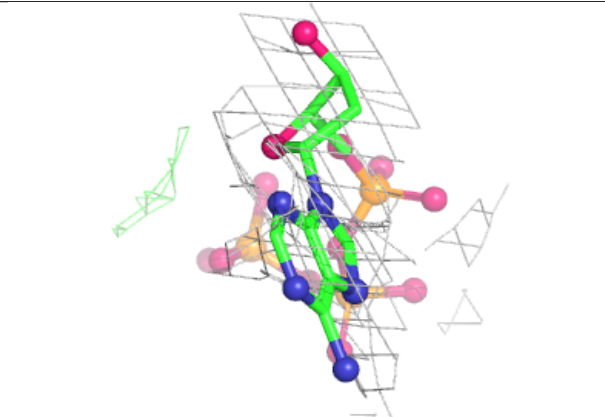
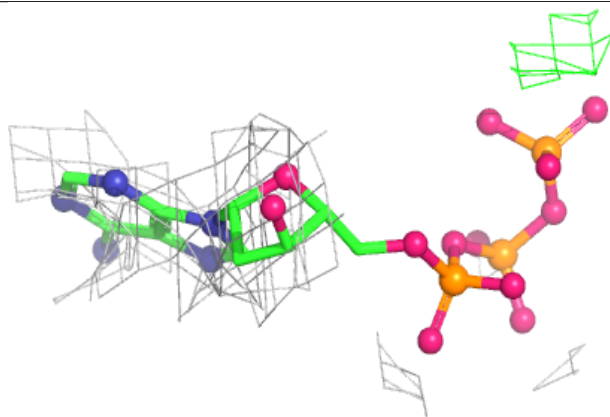
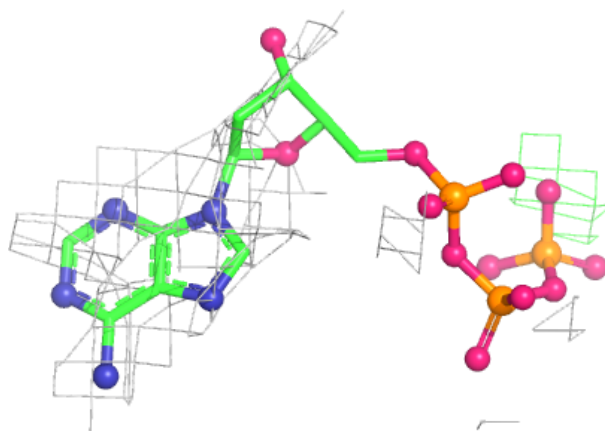
Electron density around DTP B 800:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

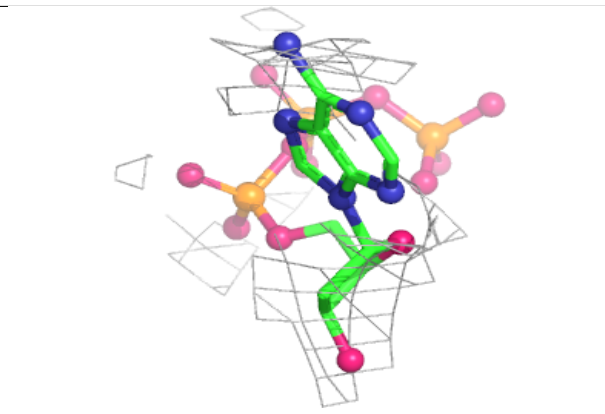
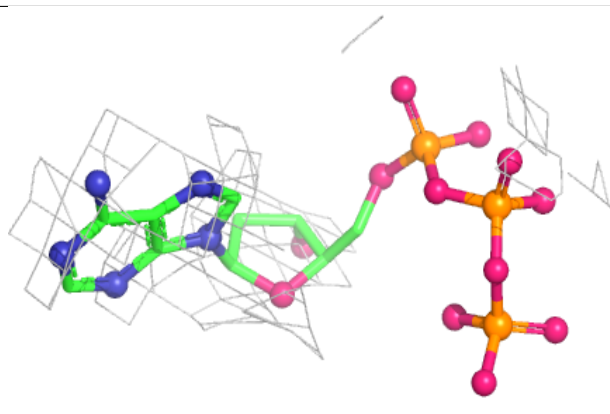
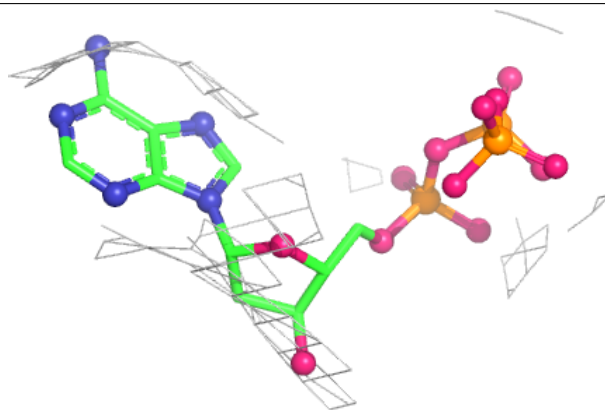


Electron density around DTP A 900:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around DTP B 900:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.