



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:05 AM UTC

PDB ID : 1D6N / pdb_00001d6n
Title : TERNARY COMPLEX STRUCTURE OF HUMAN HGPRTASE, PRPP, MG2+, AND THE INHIBITOR HPP REVEALS THE INVOLVEMENT OF THE FLEXIBLE LOOP IN SUBSTRATE BINDING
Authors : Balendiran, G.K.
Deposited on : 1999-10-14
Resolution : 2.70 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)
Xtrriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

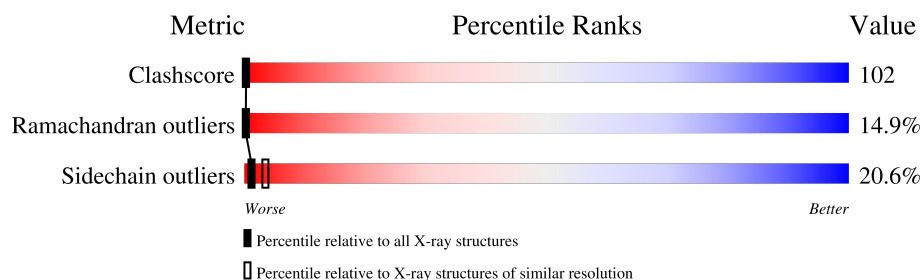
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	214	
1	B	214	

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
4	PRP	A	312	-	-	X	-
4	PRP	B	314	-	X	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3490 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 PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1686	1076	282	318	10			
1	B	214	Total	C	N	O	S	0	0	0
			1686	1076	282	318	10			

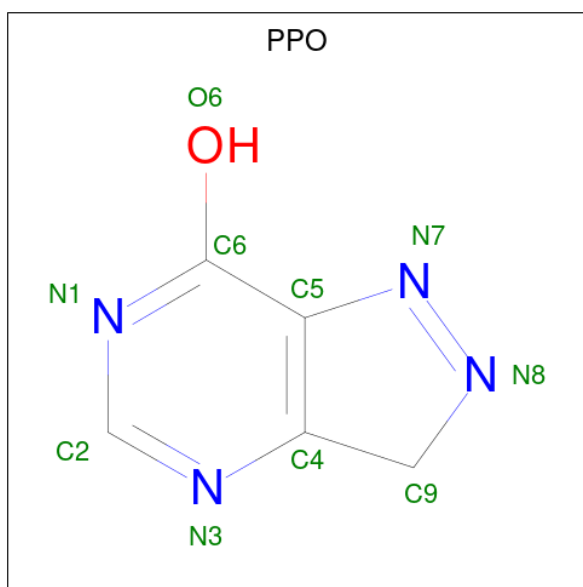
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	ALA	LYS	engineered mutation	UNP P00492
A	102	GLY	LYS	conflict	UNP P00492
B	68	ALA	LYS	engineered mutation	UNP P00492
B	102	GLY	LYS	conflict	UNP P00492

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

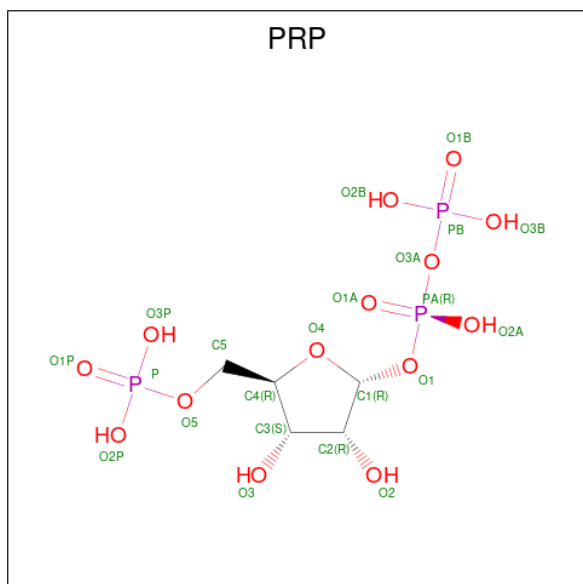
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 3H-PYRAZOLO[4,3-D]PYRIMIDIN-7-OL (CCD ID: PPO) (formula: C₅H₄N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	5	4	1		
3	B	1	Total	C	N	O	0	0
			10	5	4	1		

- Molecule 4 is 1-O-pyrophosphono-5-O-phosphono-alpha-D-ribofuranose (CCD ID: PRP) (formula: $C_5H_{13}O_{14}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			22	5	14	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	P	0	0
			22	5	14	3		

- Molecule 5 is water.

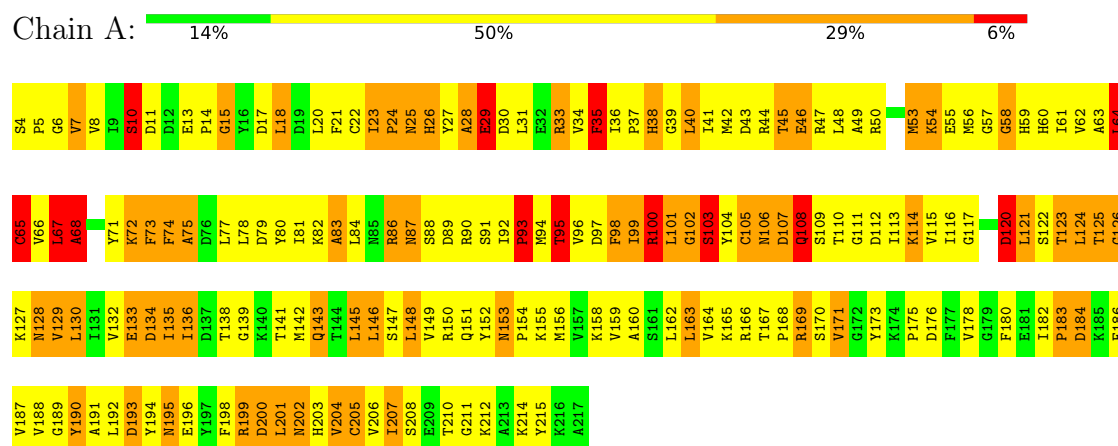
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	24	Total	O	0	0
			24	24		
5	B	28	Total	O	0	0
			28	28		

3 Residue-property plots

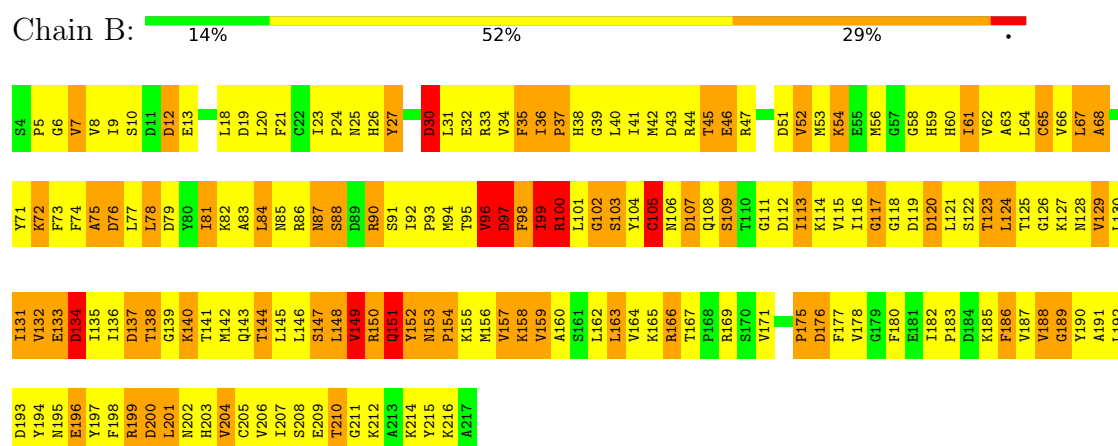
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

- Molecule 1: PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE)



- Molecule 1: PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	129.56Å 65.85Å 51.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.174 , 0.278	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3490	wwPDB-VP
Average B, all atoms (Å ²)	3.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.77	3/1719 (0.2%)	1.51	33/2324 (1.4%)
1	B	1.06	8/1719 (0.5%)	1.81	44/2324 (1.9%)
All	All	0.92	11/3438 (0.3%)	1.67	77/4648 (1.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	5
All	All	0	12

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	105	CYS	C-N	-22.01	1.02	1.33
1	B	109	SER	C-N	-13.47	1.15	1.33
1	B	105	CYS	CB-SG	-11.69	1.42	1.81
1	B	108	GLN	C-N	-10.90	1.19	1.33
1	A	105	CYS	C-N	10.16	1.48	1.33
1	B	151	GLN	CA-CB	-9.43	1.37	1.53
1	B	133	GLU	C-N	-8.54	1.21	1.33
1	A	65	CYS	CA-C	6.20	1.60	1.52
1	B	107	ASP	CA-CB	5.81	1.62	1.53
1	A	64	LEU	C-N	-5.55	1.25	1.33
1	B	132	VAL	C-N	5.08	1.39	1.33

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	105	CYS	O-C-N	-33.88	77.53	122.59
1	B	133	GLU	O-C-N	24.82	150.82	123.52
1	A	134	ASP	CA-CB-CG	23.70	136.30	112.60
1	A	108	GLN	CA-C-N	19.06	148.67	121.42
1	A	108	GLN	C-N-CA	19.06	148.67	121.42
1	B	109	SER	O-C-N	-18.31	101.92	122.79
1	B	133	GLU	CA-C-N	-17.27	88.56	121.54
1	B	133	GLU	C-N-CA	-17.27	88.56	121.54
1	B	134	ASP	CA-C-N	16.49	149.77	122.57
1	B	134	ASP	C-N-CA	16.49	149.77	122.57
1	B	134	ASP	CA-C-O	14.02	140.55	120.51
1	B	105	CYS	CA-C-N	12.72	152.67	123.16
1	B	105	CYS	C-N-CA	12.72	152.67	123.16
1	A	106	ASN	CA-CB-CG	12.54	125.14	112.60
1	B	109	SER	CA-C-N	10.91	138.38	122.99
1	B	109	SER	C-N-CA	10.91	138.38	122.99
1	A	108	GLN	N-CA-CB	-10.09	93.45	110.49
1	A	103	SER	O-C-N	-10.08	109.19	122.59
1	B	134	ASP	O-C-N	-9.96	109.35	122.59
1	A	190	TYR	CA-C-N	-9.93	108.44	122.74
1	A	190	TYR	C-N-CA	-9.93	108.44	122.74
1	A	190	TYR	O-C-N	8.96	134.51	122.59
1	A	108	GLN	O-C-N	-8.62	111.12	122.59
1	A	67	LEU	O-C-N	-8.36	114.04	122.99
1	B	134	ASP	CB-CA-C	-8.15	94.20	110.42
1	A	98	PHE	CA-C-N	8.13	133.19	120.34
1	A	98	PHE	C-N-CA	8.13	133.19	120.34
1	A	108	GLN	CB-CA-C	8.05	126.44	110.42
1	B	20	LEU	N-CA-C	-7.59	102.23	112.94
1	A	106	ASN	CB-CA-C	7.50	125.34	110.42
1	B	150	ARG	N-CA-CB	-7.35	97.29	111.11
1	A	103	SER	CA-C-N	7.26	135.41	121.54
1	A	103	SER	C-N-CA	7.26	135.41	121.54
1	B	97	ASP	CB-CG-OD2	6.95	134.39	118.40
1	B	97	ASP	CB-CG-OD1	-6.93	102.47	118.40
1	B	81	ILE	N-CA-C	-6.70	106.49	112.12
1	A	67	LEU	CB-CA-C	6.60	125.50	111.91
1	B	94	MET	N-CA-C	6.43	118.84	109.07
1	B	45	THR	N-CA-C	-6.41	104.21	111.07
1	B	12	ASP	N-CA-C	6.37	121.93	114.04
1	B	171	VAL	N-CA-C	-6.13	105.32	112.98
1	A	199	ARG	N-CA-C	-6.09	107.67	114.62
1	B	147	SER	N-CA-C	-6.08	104.34	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	VAL	CA-C-N	6.08	132.67	122.76
1	B	149	VAL	C-N-CA	6.08	132.67	122.76
1	A	109	SER	CB-CA-C	-6.02	99.35	109.53
1	B	129	VAL	N-CA-C	5.99	117.10	108.48
1	B	148	LEU	O-C-N	5.98	129.22	122.22
1	A	146	LEU	N-CA-C	-5.92	104.82	111.28
1	B	149	VAL	CA-C-O	-5.91	113.39	120.78
1	B	151	GLN	N-CA-CB	5.90	120.47	110.49
1	B	148	LEU	CA-C-O	-5.84	113.50	120.10
1	B	117	GLY	N-CA-C	5.77	117.97	111.85
1	B	100	ARG	N-CA-C	5.74	118.65	111.24
1	B	148	LEU	N-CA-C	-5.65	105.21	111.71
1	B	149	VAL	N-CA-C	-5.59	97.72	109.34
1	A	200	ASP	N-CA-C	-5.52	105.21	112.72
1	B	108	GLN	CA-C-N	5.48	130.95	120.97
1	B	108	GLN	C-N-CA	5.48	130.95	120.97
1	B	150	ARG	N-CA-C	5.43	118.61	107.37
1	B	61	ILE	N-CA-C	5.39	117.64	109.12
1	B	39	GLY	N-CA-C	-5.37	107.67	114.16
1	A	100	ARG	NE-CZ-NH2	5.36	124.02	119.20
1	B	109	SER	N-CA-CB	-5.33	102.74	110.36
1	A	33	ARG	NE-CZ-NH2	5.32	123.99	119.20
1	A	100	ARG	CB-CA-C	5.31	120.99	110.42
1	B	27	TYR	N-CA-C	-5.28	104.49	112.99
1	B	163	LEU	N-CA-C	5.27	117.32	108.73
1	A	38	HIS	N-CA-C	-5.26	105.45	111.07
1	A	123	THR	N-CA-C	5.26	122.00	110.80
1	A	67	LEU	CA-C-N	5.19	131.45	121.54
1	A	67	LEU	C-N-CA	5.19	131.45	121.54
1	A	65	CYS	CA-CB-SG	-5.14	102.58	114.40
1	A	95	THR	N-CA-C	-5.08	101.47	109.50
1	B	166	ARG	N-CA-C	-5.08	106.29	113.20
1	A	83	ALA	N-CA-C	5.07	117.20	111.02
1	A	15	GLY	N-CA-C	-5.01	102.67	111.80

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	101	LEU	Mainchain
1	A	103	SER	Mainchain
1	A	108	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	A	193	ASP	Mainchain
1	A	67	LEU	Peptide
1	A	68	ALA	Peptide
1	A	99	ILE	Mainchain
1	B	105	CYS	Peptide,Mainchain
1	B	109	SER	Peptide,Mainchain
1	B	149	VAL	Peptide

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	1686	0	1688	367	0
1	B	1686	0	1685	353	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	3	1	0
3	B	10	0	3	1	0
4	A	22	0	6	14	0
4	B	22	0	7	7	0
5	A	24	0	0	5	0
5	B	28	0	0	8	0
All	All	3490	0	3392	700	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 102.

All (700) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:LEU:CD2	1:A:124:LEU:HD21	1.50	1.41
1:A:65:CYS:SG	1:A:74:PHE:CD1	2.29	1.24
1:B:191:ALA:O	1:B:192:LEU:HD22	1.05	1.21
1:B:191:ALA:C	1:B:192:LEU:HD22	1.67	1.19
1:A:191:ALA:O	1:A:192:LEU:HD22	1.39	1.18
1:A:65:CYS:SG	1:A:132:VAL:HB	1.84	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:GLU:O	1:B:134:ASP:C	1.83	1.16
1:A:64:LEU:HD11	1:A:129:VAL:CG1	1.76	1.15
1:A:64:LEU:HD21	1:A:124:LEU:CD2	1.77	1.13
1:B:189:GLY:HA3	1:B:201:LEU:HD23	1.30	1.13
1:A:37:PRO:HD2	1:A:40:LEU:HD12	1.31	1.13
1:A:72:LYS:HZ2	1:B:82:LYS:HE2	1.16	1.11
1:A:64:LEU:HD22	1:A:124:LEU:HD21	1.33	1.11
1:A:129:VAL:HG12	1:A:130:LEU:H	1.16	1.10
1:B:191:ALA:O	1:B:192:LEU:CD2	1.99	1.09
1:A:64:LEU:HD21	1:A:124:LEU:HD21	1.13	1.09
1:A:63:ALA:HA	1:A:130:LEU:HB3	1.31	1.08
1:A:148:LEU:HA	1:A:151:GLN:HE21	1.10	1.08
1:B:160:ALA:HA	1:B:177:PHE:HB2	1.37	1.05
1:B:79:ASP:HA	1:B:82:LYS:HD3	1.35	1.04
1:B:67:LEU:HD23	1:B:68:ALA:H	1.15	1.04
1:B:64:LEU:CD1	1:B:97:ASP:HB3	1.89	1.03
1:A:27:TYR:CE2	1:A:198:PHE:HA	1.93	1.03
1:A:191:ALA:C	1:A:192:LEU:HD22	1.85	1.01
1:B:134:ASP:CG	1:B:135:ILE:H	1.62	1.01
1:A:72:LYS:NZ	1:B:82:LYS:HE2	1.76	1.00
1:B:64:LEU:HD12	1:B:97:ASP:HB3	1.44	1.00
1:B:97:ASP:C	1:B:98:PHE:HD1	1.71	0.98
1:A:27:TYR:HE2	1:A:198:PHE:HA	1.26	0.97
1:B:142:MET:SD	1:B:145:LEU:HD23	2.04	0.97
1:B:207:ILE:HD12	1:B:212:LYS:HG2	1.46	0.97
1:B:85:ASN:ND2	1:B:92:ILE:HB	1.78	0.97
1:A:195:ASN:HD21	1:A:215:TYR:HB3	1.30	0.96
1:B:131:ILE:HG21	1:B:142:MET:HE1	1.48	0.95
1:A:61:ILE:HG21	1:A:130:LEU:HD23	1.49	0.95
1:B:133:GLU:O	1:B:134:ASP:O	1.83	0.95
1:B:145:LEU:O	1:B:149:VAL:HG23	1.67	0.94
1:A:133:GLU:HG3	1:A:142:MET:CE	1.99	0.92
1:B:96:VAL:CG1	1:B:98:PHE:HE1	1.82	0.92
1:B:183:PRO:HB2	1:B:185:LYS:NZ	1.85	0.91
1:B:191:ALA:C	1:B:192:LEU:CD2	2.43	0.91
1:A:65:CYS:SG	1:A:74:PHE:CG	2.60	0.89
1:A:67:LEU:HG	1:A:99:ILE:O	1.73	0.89
1:A:68:ALA:O	4:A:312:PRP:PB	2.31	0.89
1:A:64:LEU:HD11	1:A:129:VAL:HG11	1.50	0.88
1:A:159:VAL:HB	1:A:176:ASP:H	1.37	0.88
1:A:65:CYS:O	1:A:99:ILE:HB	1.74	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:ALA:HA	1:B:86:ARG:NE	1.89	0.87
1:B:104:TYR:HB2	5:B:912:HOH:O	1.74	0.87
1:B:38:HIS:H	1:B:203:HIS:HD2	1.21	0.86
1:A:65:CYS:SG	1:A:74:PHE:CE1	2.68	0.86
1:A:64:LEU:CD2	1:A:124:LEU:CD2	2.41	0.85
1:A:129:VAL:HG12	1:A:130:LEU:N	1.92	0.84
1:B:67:LEU:CD2	1:B:68:ALA:H	1.90	0.84
1:B:126:GLY:O	1:B:127:LYS:HG3	1.78	0.84
1:A:100:ARG:HB3	1:A:117:GLY:O	1.78	0.84
1:B:100:ARG:HG3	1:B:102:GLY:H	1.43	0.83
1:A:67:LEU:HA	4:A:312:PRP:O3B	1.79	0.82
1:A:29:GLU:HB2	5:A:986:HOH:O	1.78	0.82
1:A:94:MET:O	1:B:196:GLU:HG3	1.79	0.82
1:B:35:PHE:HB3	1:B:36:ILE:HD12	1.59	0.82
1:B:97:ASP:C	1:B:98:PHE:CD1	2.58	0.82
1:B:100:ARG:HB3	1:B:117:GLY:C	2.05	0.82
1:B:96:VAL:HG11	1:B:98:PHE:HE1	1.42	0.81
1:B:183:PRO:HB2	1:B:185:LYS:HZ3	1.43	0.81
1:A:167:THR:OG1	1:A:168:PRO:HD2	1.80	0.81
1:B:149:VAL:HG12	1:B:149:VAL:O	1.79	0.81
1:A:133:GLU:HG3	1:A:142:MET:HE2	1.62	0.81
1:A:125:THR:O	1:A:127:LYS:HG3	1.81	0.80
1:A:110:THR:HG22	1:A:111:GLY:N	1.96	0.80
1:A:198:PHE:HE1	1:A:207:ILE:HG23	1.47	0.79
1:A:110:THR:HG22	1:A:111:GLY:H	1.48	0.79
1:B:119:ASP:HB3	5:B:920:HOH:O	1.83	0.79
1:B:146:LEU:HA	1:B:149:VAL:HB	1.64	0.79
1:A:86:ARG:HD2	1:A:87:ASN:OD1	1.83	0.79
1:A:147:SER:HA	1:A:150:ARG:NH2	1.97	0.78
1:B:38:HIS:H	1:B:203:HIS:CD2	2.02	0.78
1:A:100:ARG:HD2	1:A:116:ILE:HB	1.66	0.78
1:A:127:LYS:N	1:A:155:LYS:H	1.81	0.78
1:B:199:ARG:HB3	1:B:199:ARG:NH1	1.99	0.78
1:A:82:LYS:NZ	1:B:72:LYS:HD3	1.99	0.78
1:B:23:ILE:O	1:B:23:ILE:HD12	1.84	0.77
1:B:199:ARG:HB3	1:B:199:ARG:HH11	1.47	0.77
1:A:6:GLY:HA3	1:A:44:ARG:NH2	2.00	0.77
1:A:64:LEU:HD11	1:A:129:VAL:HG12	1.66	0.76
1:A:6:GLY:O	1:A:8:VAL:HG13	1.84	0.76
1:B:18:LEU:CD1	1:B:31:LEU:HB3	2.16	0.76
1:B:51:ASP:C	1:B:53:MET:H	1.93	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:ASN:N	1:A:128:ASN:HD22	1.84	0.76
1:B:64:LEU:HD13	1:B:97:ASP:HB3	1.66	0.76
1:B:85:ASN:CG	1:B:92:ILE:HB	2.11	0.76
1:B:146:LEU:O	1:B:150:ARG:HG3	1.86	0.76
1:B:100:ARG:HG2	1:B:116:ILE:C	2.11	0.75
1:A:148:LEU:HA	1:A:151:GLN:NE2	1.95	0.75
1:B:145:LEU:O	1:B:149:VAL:N	2.20	0.75
1:B:152:TYR:O	1:B:153:ASN:HB2	1.87	0.75
1:B:97:ASP:O	1:B:98:PHE:CD1	2.40	0.75
1:A:101:LEU:O	1:A:102:GLY:O	2.06	0.74
1:B:73:PHE:CE1	1:B:162:LEU:HB2	2.22	0.74
1:A:18:LEU:HD12	1:A:18:LEU:H	1.52	0.74
1:B:209:GLU:HA	1:B:212:LYS:HE3	1.68	0.74
1:A:100:ARG:HG2	1:A:102:GLY:H	1.53	0.74
1:B:96:VAL:HG11	1:B:98:PHE:CE1	2.22	0.74
1:A:60:HIS:C	1:A:61:ILE:HD12	2.13	0.74
1:A:129:VAL:CG1	1:A:130:LEU:H	1.98	0.74
1:B:123:THR:O	1:B:125:THR:N	2.20	0.73
1:A:202:ASN:H	1:A:202:ASN:ND2	1.86	0.73
1:B:72:LYS:HB3	1:B:191:ALA:HB2	1.69	0.73
1:B:147:SER:O	1:B:150:ARG:HB2	1.87	0.73
1:B:186:PHE:HD2	1:B:207:ILE:HD11	1.53	0.73
1:A:113:ILE:C	1:A:114:LYS:HD3	2.13	0.73
1:B:147:SER:HA	1:B:150:ARG:HD2	1.70	0.72
1:B:96:VAL:CG1	1:B:98:PHE:CE1	2.69	0.72
1:A:63:ALA:HA	1:A:130:LEU:CB	2.16	0.72
1:B:188:VAL:HG21	1:B:198:PHE:CD2	2.24	0.72
1:A:156:MET:HE2	1:A:158:LYS:NZ	2.05	0.72
1:A:196:GLU:OE1	1:B:95:THR:HA	1.89	0.72
1:B:34:VAL:HA	1:B:205:CYS:SG	2.29	0.72
1:B:36:ILE:HD12	1:B:36:ILE:N	2.05	0.72
1:B:190:TYR:O	1:B:192:LEU:HD23	1.90	0.72
1:B:85:ASN:HD21	1:B:92:ILE:HB	1.55	0.71
1:B:71:TYR:HE1	1:B:199:ARG:HH22	1.38	0.71
1:B:112:ASP:OD2	1:B:114:LYS:HG3	1.90	0.71
1:B:189:GLY:HA2	1:B:198:PHE:O	1.90	0.71
1:A:58:GLY:O	1:A:59:HIS:ND1	2.23	0.71
1:B:67:LEU:HD23	1:B:68:ALA:N	1.97	0.71
1:B:18:LEU:HD13	1:B:31:LEU:HB3	1.73	0.70
1:B:41:ILE:HG12	1:B:180:PHE:HE1	1.56	0.70
1:A:113:ILE:O	1:A:114:LYS:HD3	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:LYS:HD2	5:A:934:HOH:O	1.91	0.70
1:A:126:GLY:C	1:A:155:LYS:HB2	2.15	0.70
1:A:37:PRO:CD	1:A:40:LEU:HD12	2.18	0.70
1:B:142:MET:O	1:B:145:LEU:HB3	1.91	0.70
1:A:82:LYS:HE2	1:B:71:TYR:OH	1.90	0.69
1:A:6:GLY:HA3	1:A:44:ARG:HH21	1.56	0.69
1:A:30:ASP:HB3	1:A:198:PHE:HZ	1.57	0.69
1:B:38:HIS:CD2	1:B:202:ASN:HB3	2.28	0.69
1:B:99:ILE:HG13	1:B:118:GLY:O	1.93	0.69
1:A:66:VAL:HB	5:A:989:HOH:O	1.92	0.69
1:B:31:LEU:HD11	1:B:201:LEU:CD1	2.23	0.69
1:A:61:ILE:HG13	1:A:128:ASN:HB2	1.75	0.69
1:A:159:VAL:HG12	1:A:160:ALA:H	1.55	0.69
1:A:167:THR:HB	1:A:184:ASP:OD1	1.93	0.69
1:B:18:LEU:HD23	1:B:34:VAL:HG23	1.73	0.69
1:B:85:ASN:OD1	1:B:92:ILE:HD12	1.92	0.69
1:B:189:GLY:HA3	1:B:201:LEU:CD2	2.17	0.69
1:A:13:GLU:OE2	1:A:14:PRO:HD2	1.93	0.69
1:B:62:VAL:HG22	1:B:95:THR:HG23	1.75	0.69
1:B:36:ILE:HG21	1:B:180:PHE:CE1	2.29	0.68
1:B:52:VAL:HG12	1:B:52:VAL:O	1.91	0.68
1:A:121:LEU:HD22	1:A:148:LEU:HD23	1.75	0.68
1:B:35:PHE:HB3	1:B:36:ILE:CD1	2.23	0.68
1:B:200:ASP:OD2	1:B:200:ASP:N	2.26	0.68
1:A:39:GLY:O	1:A:41:ILE:N	2.26	0.68
1:A:31:LEU:C	1:A:208:SER:HB3	2.18	0.68
1:A:7:VAL:HB	1:A:180:PHE:CD2	2.28	0.68
1:A:214:LYS:HG3	1:A:215:TYR:CE1	2.28	0.68
1:B:135:ILE:HA	1:B:163:LEU:O	1.94	0.68
1:A:156:MET:HE2	1:A:158:LYS:HZ3	1.59	0.67
1:A:201:LEU:HD12	1:A:203:HIS:H	1.59	0.67
1:B:71:TYR:O	1:B:74:PHE:HB3	1.94	0.67
1:B:100:ARG:H	1:B:118:GLY:HA3	1.60	0.67
1:A:45:THR:HA	1:A:48:LEU:HD13	1.77	0.67
1:A:63:ALA:HB2	5:A:952:HOH:O	1.94	0.66
1:B:7:VAL:HG23	1:B:44:ARG:HH11	1.60	0.66
1:A:156:MET:CE	1:A:158:LYS:HZ3	2.08	0.66
1:A:53:MET:SD	1:A:92:ILE:HD11	2.35	0.66
1:A:159:VAL:HG12	1:A:160:ALA:N	2.08	0.66
1:A:186:PHE:HD2	1:A:207:ILE:CD1	2.06	0.66
1:B:131:ILE:HG22	1:B:132:VAL:N	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:GLU:HG3	1:B:95:THR:HB	1.76	0.66
1:B:62:VAL:HG22	1:B:95:THR:CG2	2.26	0.66
1:B:214:LYS:HD3	1:B:215:TYR:CZ	2.30	0.66
1:B:107:ASP:HA	1:B:186:PHE:CZ	2.31	0.66
4:B:314:PRP:O3B	4:B:314:PRP:O2A	2.14	0.66
1:B:74:PHE:CE1	1:B:78:LEU:HD22	2.31	0.65
1:A:162:LEU:HG	1:A:163:LEU:HD23	1.78	0.65
1:A:89:ASP:O	1:A:90:ARG:HD2	1.95	0.65
1:A:62:VAL:HA	1:A:95:THR:HG23	1.78	0.65
1:A:189:GLY:O	1:A:204:VAL:HG22	1.96	0.65
1:B:126:GLY:C	1:B:127:LYS:HG3	2.21	0.65
1:A:48:LEU:HD12	1:A:48:LEU:H	1.61	0.65
1:A:101:LEU:HA	1:A:115:VAL:HG22	1.78	0.65
1:B:7:VAL:HB	1:B:180:PHE:HA	1.79	0.65
1:B:41:ILE:HA	1:B:180:PHE:CZ	2.32	0.64
1:A:64:LEU:HD21	1:A:124:LEU:CG	2.27	0.64
1:A:124:LEU:O	1:A:154:PRO:HB3	1.97	0.64
1:A:74:PHE:CE1	1:A:78:LEU:HD11	2.33	0.64
1:B:113:ILE:HG21	1:B:144:THR:OG1	1.98	0.64
1:B:121:LEU:HD23	1:B:124:LEU:HD22	1.78	0.64
1:B:135:ILE:HG12	1:B:136:ILE:N	2.12	0.64
1:B:183:PRO:HB2	1:B:185:LYS:HZ1	1.62	0.64
1:A:190:TYR:O	1:A:191:ALA:HB3	1.96	0.64
1:B:77:LEU:O	1:B:81:ILE:HG13	1.96	0.63
1:A:110:THR:CG2	1:A:111:GLY:H	2.10	0.63
1:B:188:VAL:HG23	1:B:201:LEU:HD22	1.80	0.63
1:A:54:LYS:O	1:A:55:GLU:C	2.42	0.63
1:B:112:ASP:C	1:B:113:ILE:HD12	2.24	0.63
1:A:98:PHE:CG	1:B:67:LEU:HD11	2.33	0.63
1:A:104:TYR:CD2	1:A:105:CYS:N	2.67	0.63
1:A:191:ALA:C	1:A:192:LEU:CD2	2.68	0.63
1:A:101:LEU:O	1:A:101:LEU:HG	1.99	0.63
1:B:41:ILE:HA	1:B:180:PHE:HZ	1.63	0.63
1:B:53:MET:SD	1:B:84:LEU:HD22	2.39	0.62
1:B:96:VAL:HG12	1:B:98:PHE:HE1	1.63	0.62
1:B:113:ILE:HD12	1:B:113:ILE:N	2.13	0.62
1:A:41:ILE:O	1:A:42:MET:C	2.42	0.62
1:B:18:LEU:HD11	1:B:31:LEU:C	2.24	0.62
1:B:96:VAL:HG12	1:B:98:PHE:CE1	2.35	0.62
1:A:57:GLY:O	1:A:59:HIS:N	2.33	0.62
1:A:83:ALA:HB1	1:A:87:ASN:ND2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ILE:N	1:B:131:ILE:HD12	2.14	0.62
1:A:103:SER:OG	4:A:312:PRP:O2A	2.16	0.62
1:A:110:THR:CG2	1:A:111:GLY:N	2.62	0.62
1:B:113:ILE:HG21	1:B:144:THR:HG21	1.82	0.62
1:A:100:ARG:HD2	1:A:116:ILE:C	2.25	0.62
1:A:124:LEU:HD23	1:A:129:VAL:CG1	2.30	0.62
1:A:159:VAL:HG23	1:A:176:ASP:OD1	2.00	0.62
1:B:83:ALA:O	1:B:86:ARG:HG2	2.00	0.62
1:A:6:GLY:O	1:A:7:VAL:C	2.43	0.61
1:B:37:PRO:HB2	1:B:40:LEU:HB2	1.82	0.61
1:B:137:ASP:C	1:B:139:GLY:H	2.08	0.61
1:A:92:ILE:O	1:A:93:PRO:C	2.41	0.61
1:B:149:VAL:C	1:B:150:ARG:HG3	2.26	0.61
1:B:120:ASP:C	1:B:121:LEU:HD12	2.25	0.61
1:B:186:PHE:CD2	1:B:207:ILE:HD11	2.35	0.61
1:A:23:ILE:HD12	1:A:23:ILE:O	1.99	0.61
1:A:59:HIS:HB2	1:A:61:ILE:CD1	2.30	0.61
1:B:104:TYR:CD1	1:B:104:TYR:O	2.54	0.61
1:B:159:VAL:HG13	1:B:159:VAL:O	2.01	0.61
1:B:7:VAL:O	1:B:9:ILE:HG13	1.99	0.60
1:A:67:LEU:HD12	1:A:67:LEU:C	2.26	0.60
1:B:25:ASN:C	1:B:27:TYR:H	2.09	0.60
1:A:107:ASP:O	1:A:108:GLN:HB2	2.00	0.60
1:B:66:VAL:HB	1:B:133:GLU:HG3	1.83	0.60
1:B:119:ASP:OD1	1:B:119:ASP:O	2.18	0.60
1:B:144:THR:C	1:B:148:LEU:HD12	2.25	0.60
1:A:39:GLY:C	1:A:41:ILE:N	2.58	0.60
1:A:40:LEU:O	1:A:44:ARG:HB2	2.01	0.60
1:A:67:LEU:CA	4:A:312:PRP:O3B	2.50	0.60
1:B:51:ASP:C	1:B:53:MET:N	2.60	0.60
1:B:97:ASP:O	1:B:98:PHE:HD1	1.81	0.60
1:A:73:PHE:CE1	1:A:162:LEU:HD13	2.36	0.60
1:B:35:PHE:C	1:B:36:ILE:HD12	2.27	0.60
1:B:180:PHE:O	1:B:182:ILE:HG23	2.02	0.60
1:B:18:LEU:HD11	1:B:31:LEU:HB3	1.84	0.59
1:A:214:LYS:O	1:A:215:TYR:CD1	2.55	0.59
1:B:56:MET:HE1	1:B:130:LEU:HB3	1.84	0.59
1:B:159:VAL:HG12	1:B:176:ASP:OD1	2.02	0.59
1:B:66:VAL:HB	1:B:133:GLU:CG	2.32	0.59
1:A:120:ASP:O	1:A:122:SER:N	2.32	0.59
1:A:7:VAL:O	1:A:180:PHE:HA	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:THR:O	1:B:148:LEU:HD12	2.03	0.59
1:A:29:GLU:N	1:A:29:GLU:OE2	2.36	0.59
1:B:103:SER:HB2	4:B:314:PRP:O1A	2.02	0.59
1:A:193:ASP:O	3:A:300:PPO:HC2	2.03	0.59
1:A:58:GLY:C	1:A:59:HIS:ND1	2.61	0.58
1:A:122:SER:HA	1:A:152:TYR:CE2	2.38	0.58
1:A:67:LEU:C	4:A:312:PRP:O3B	2.46	0.58
1:A:135:ILE:HG23	4:A:312:PRP:H2	1.84	0.58
1:B:103:SER:C	1:B:105:CYS:H	2.11	0.58
1:B:148:LEU:C	1:B:150:ARG:H	2.10	0.58
1:A:18:LEU:CD2	1:A:31:LEU:HB2	2.34	0.58
1:B:127:LYS:C	1:B:155:LYS:HB3	2.28	0.58
1:B:72:LYS:CB	1:B:191:ALA:HB2	2.34	0.58
1:B:188:VAL:O	1:B:204:VAL:HA	2.03	0.58
1:B:197:TYR:CE1	5:B:908:HOH:O	2.52	0.58
1:A:46:GLU:HA	1:A:80:TYR:CD2	2.39	0.58
1:A:100:ARG:HD2	1:A:116:ILE:CB	2.33	0.58
1:A:210:THR:OG1	1:A:211:GLY:N	2.37	0.58
1:A:67:LEU:CG	1:A:99:ILE:O	2.50	0.57
1:A:83:ALA:O	1:A:86:ARG:HG3	2.03	0.57
1:B:137:ASP:CG	1:B:138:THR:H	2.11	0.57
1:A:47:ARG:O	1:A:50:ARG:N	2.37	0.57
1:A:25:ASN:O	1:A:28:ALA:N	2.35	0.57
1:A:74:PHE:O	1:A:75:ALA:C	2.47	0.57
1:A:82:LYS:HZ3	1:B:72:LYS:HD3	1.66	0.57
1:A:103:SER:HB3	4:A:312:PRP:O1A	2.04	0.57
1:A:72:LYS:O	1:A:73:PHE:C	2.47	0.57
1:A:133:GLU:OE2	4:A:312:PRP:H3	2.04	0.57
1:A:171:VAL:HG12	1:A:173:TYR:H	1.70	0.57
1:A:36:ILE:HD13	1:A:180:PHE:CE2	2.40	0.57
1:A:46:GLU:HB2	1:A:80:TYR:CZ	2.39	0.57
1:A:79:ASP:HA	1:A:82:LYS:HD2	1.85	0.57
1:A:186:PHE:HB3	1:A:207:ILE:HD12	1.86	0.57
1:A:86:ARG:CD	1:A:87:ASN:OD1	2.52	0.57
1:A:100:ARG:HG2	1:A:102:GLY:N	2.19	0.57
1:A:126:GLY:O	1:A:155:LYS:HE3	2.04	0.57
1:A:195:ASN:ND2	1:A:215:TYR:HB3	2.12	0.57
1:A:198:PHE:CE1	1:A:207:ILE:HG23	2.36	0.57
1:B:31:LEU:HD11	1:B:201:LEU:HD11	1.86	0.57
1:A:39:GLY:C	1:A:41:ILE:H	2.12	0.56
1:A:83:ALA:HB1	1:A:87:ASN:HD21	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:ILE:O	1:B:116:ILE:HG22	2.05	0.56
1:B:121:LEU:HD23	1:B:124:LEU:CD2	2.35	0.56
1:B:134:ASP:CG	1:B:135:ILE:N	2.45	0.56
1:A:169:ARG:HG3	1:A:169:ARG:HH11	1.70	0.56
1:A:59:HIS:HB2	1:A:61:ILE:HD11	1.87	0.56
1:A:101:LEU:HD22	1:A:145:LEU:HB2	1.86	0.56
1:A:165:LYS:HG3	1:A:183:PRO:O	2.05	0.56
1:A:208:SER:O	1:A:212:LYS:HB2	2.05	0.56
1:B:169:ARG:HG2	1:B:169:ARG:HH11	1.71	0.56
1:A:124:LEU:HB3	1:A:129:VAL:HG22	1.88	0.56
1:B:36:ILE:HG22	1:B:41:ILE:HG13	1.87	0.56
1:B:192:LEU:CD2	1:B:192:LEU:N	2.68	0.56
1:B:138:THR:N	4:B:314:PRP:O1P	2.38	0.56
1:A:100:ARG:CD	1:A:116:ILE:HB	2.35	0.56
1:B:100:ARG:HG2	1:B:116:ILE:O	2.06	0.56
1:A:29:GLU:OE2	1:A:30:ASP:OD1	2.24	0.56
1:B:129:VAL:O	1:B:157:VAL:HA	2.06	0.56
1:B:195:ASN:CG	1:B:195:ASN:O	2.49	0.56
1:B:113:ILE:HG21	1:B:144:THR:CB	2.36	0.55
1:A:18:LEU:HB3	1:A:23:ILE:HG12	1.88	0.55
1:B:67:LEU:O	1:B:68:ALA:HB3	2.05	0.55
1:B:131:ILE:HG22	1:B:132:VAL:H	1.71	0.55
1:B:175:PRO:O	1:B:176:ASP:CG	2.49	0.55
1:A:105:CYS:O	1:A:106:ASN:ND2	2.38	0.55
1:A:124:LEU:HD23	1:A:129:VAL:HG11	1.88	0.55
1:A:100:ARG:CZ	1:A:116:ILE:O	2.54	0.55
1:A:133:GLU:CD	4:A:312:PRP:O3	2.49	0.55
1:A:162:LEU:HG	1:A:163:LEU:CD2	2.36	0.55
1:B:65:CYS:O	1:B:99:ILE:HG23	2.06	0.55
1:A:72:LYS:NZ	1:B:82:LYS:CE	2.61	0.55
1:B:38:HIS:N	1:B:203:HIS:HD2	1.97	0.55
1:B:41:ILE:HG21	1:B:190:TYR:CE2	2.41	0.55
1:B:86:ARG:HG2	1:B:87:ASN:H	1.72	0.55
1:A:204:VAL:HG12	1:A:204:VAL:O	2.07	0.55
1:A:178:VAL:CG1	1:A:180:PHE:O	2.55	0.55
1:B:187:VAL:HB	1:B:204:VAL:HG12	1.89	0.55
1:A:147:SER:HA	1:A:150:ARG:HH22	1.71	0.54
1:B:75:ALA:O	1:B:76:ASP:C	2.50	0.54
1:B:23:ILE:HD12	1:B:23:ILE:C	2.31	0.54
1:B:32:GLU:HG3	1:B:33:ARG:HG3	1.89	0.54
1:B:103:SER:CB	4:B:314:PRP:O1A	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ILE:CG2	1:B:142:MET:HE1	2.28	0.54
1:A:167:THR:CG2	1:A:170:SER:HB3	2.37	0.54
1:B:164:VAL:HG21	1:B:178:VAL:CG2	2.37	0.54
1:A:159:VAL:HB	1:A:176:ASP:N	2.16	0.54
1:A:28:ALA:O	1:A:30:ASP:N	2.41	0.54
1:A:45:THR:O	1:A:48:LEU:N	2.40	0.54
1:B:10:SER:C	1:B:12:ASP:H	2.15	0.54
1:A:53:MET:O	1:A:56:MET:O	2.25	0.54
1:B:35:PHE:CD1	1:B:206:VAL:HG23	2.43	0.54
1:B:62:VAL:O	1:B:130:LEU:HD23	2.08	0.54
1:B:47:ARG:HG3	1:B:47:ARG:HH11	1.73	0.53
1:B:199:ARG:HH11	1:B:199:ARG:CB	2.21	0.53
1:A:82:LYS:HZ1	1:B:72:LYS:HD3	1.70	0.53
1:B:72:LYS:HB3	1:B:191:ALA:CB	2.37	0.53
1:A:78:LEU:O	1:A:81:ILE:HB	2.09	0.53
1:A:168:PRO:HG2	1:A:169:ARG:H	1.73	0.53
1:B:76:ASP:O	1:B:79:ASP:N	2.42	0.53
1:A:72:LYS:O	1:A:75:ALA:N	2.42	0.53
1:B:92:ILE:N	1:B:93:PRO:HD3	2.23	0.53
1:A:6:GLY:O	1:A:8:VAL:N	2.41	0.53
1:A:164:VAL:HG23	1:A:178:VAL:HG13	1.88	0.53
1:B:149:VAL:HG11	1:B:157:VAL:HG11	1.89	0.53
1:A:86:ARG:CZ	1:B:202:ASN:HD21	2.22	0.53
1:B:138:THR:OG1	1:B:140:LYS:HB2	2.09	0.53
1:A:125:THR:O	1:A:127:LYS:N	2.42	0.53
1:A:139:GLY:O	1:A:143:GLN:HB2	2.09	0.53
1:B:140:LYS:HE3	5:B:949:HOH:O	2.08	0.53
1:B:208:SER:C	1:B:210:THR:N	2.66	0.53
1:B:134:ASP:OD1	1:B:135:ILE:O	2.26	0.53
1:A:71:TYR:HB3	1:B:98:PHE:HZ	1.73	0.53
1:B:100:ARG:HD2	1:B:102:GLY:HA2	1.90	0.53
1:B:145:LEU:C	1:B:149:VAL:HG23	2.32	0.53
1:B:63:ALA:HA	1:B:130:LEU:CD2	2.39	0.52
1:B:127:LYS:O	1:B:155:LYS:HB3	2.09	0.52
1:A:201:LEU:HD11	1:A:203:HIS:HB2	1.90	0.52
1:B:36:ILE:N	1:B:36:ILE:CD1	2.72	0.52
1:B:71:TYR:CG	1:B:72:LYS:N	2.76	0.52
1:A:74:PHE:O	1:A:77:LEU:N	2.43	0.52
1:A:67:LEU:HD12	1:A:68:ALA:N	2.24	0.52
1:A:73:PHE:CE2	1:A:162:LEU:HB2	2.45	0.52
1:B:41:ILE:HD11	1:B:204:VAL:HG23	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:LEU:HG	1:B:129:VAL:HG21	1.92	0.52
1:A:37:PRO:HD2	1:A:40:LEU:CD1	2.22	0.52
1:A:128:ASN:N	1:A:128:ASN:ND2	2.55	0.52
1:B:63:ALA:HA	1:B:130:LEU:HD21	1.91	0.52
1:B:138:THR:HG22	1:B:169:ARG:HB2	1.92	0.52
1:A:61:ILE:HG23	1:A:128:ASN:O	2.10	0.52
1:A:201:LEU:HD11	1:A:205:CYS:SG	2.50	0.52
1:A:82:LYS:HZ1	1:B:71:TYR:HE2	1.58	0.52
1:A:141:THR:O	1:A:142:MET:C	2.53	0.52
1:A:188:VAL:CG2	1:A:207:ILE:HG12	2.39	0.52
1:B:75:ALA:O	1:B:78:LEU:N	2.43	0.52
1:A:156:MET:HE2	5:A:917:HOH:O	2.09	0.51
1:B:45:THR:O	1:B:47:ARG:N	2.44	0.51
1:B:41:ILE:HD11	1:B:204:VAL:CG2	2.40	0.51
1:B:101:LEU:HD22	1:B:145:LEU:HD13	1.92	0.51
1:A:11:ASP:C	1:A:13:GLU:H	2.18	0.51
1:B:134:ASP:OD1	1:B:135:ILE:C	2.54	0.51
1:A:56:MET:HE1	1:A:130:LEU:HD22	1.93	0.51
1:A:133:GLU:OE2	4:A:312:PRP:O3	2.28	0.51
1:A:188:VAL:HG13	1:A:207:ILE:HD11	1.91	0.51
1:A:24:PRO:HG3	1:B:86:ARG:CB	2.40	0.51
1:A:210:THR:C	1:A:212:LYS:H	2.19	0.51
1:B:25:ASN:O	1:B:27:TYR:N	2.44	0.51
1:B:54:LYS:HD3	5:B:903:HOH:O	2.11	0.51
1:B:165:LYS:C	1:B:167:THR:H	2.18	0.51
1:A:68:ALA:C	4:A:312:PRP:O3B	2.53	0.51
1:A:100:ARG:HD2	1:A:116:ILE:CA	2.41	0.51
1:B:27:TYR:HA	1:B:30:ASP:OD2	2.10	0.51
1:B:100:ARG:HG3	1:B:101:LEU:N	2.22	0.51
1:B:122:SER:HA	1:B:152:TYR:CE1	2.46	0.51
1:B:137:ASP:C	1:B:139:GLY:N	2.69	0.51
1:B:211:GLY:O	1:B:212:LYS:C	2.54	0.51
1:A:146:LEU:HG	1:A:150:ARG:NH1	2.26	0.51
1:A:64:LEU:HB2	1:A:99:ILE:CD1	2.41	0.50
1:B:113:ILE:HG21	1:B:144:THR:CG2	2.41	0.50
1:A:47:ARG:O	1:A:48:LEU:C	2.53	0.50
1:B:12:ASP:O	1:B:13:GLU:C	2.53	0.50
1:B:43:ASP:HA	1:B:46:GLU:HB3	1.93	0.50
1:B:127:LYS:O	1:B:155:LYS:N	2.43	0.50
1:B:140:LYS:O	1:B:143:GLN:HB2	2.11	0.50
3:B:301:PPO:C2	4:B:314:PRP:O2A	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:THR:O	1:A:47:ARG:N	2.45	0.50
1:A:210:THR:C	1:A:212:LYS:N	2.67	0.50
1:B:18:LEU:HD23	1:B:34:VAL:CG2	2.41	0.50
1:B:166:ARG:HH22	1:B:183:PRO:HG3	1.77	0.50
1:A:186:PHE:O	1:A:207:ILE:HG13	2.11	0.50
1:B:67:LEU:O	1:B:68:ALA:CB	2.59	0.50
1:B:125:THR:HA	1:B:153:ASN:O	2.11	0.50
1:A:71:TYR:CG	1:A:72:LYS:N	2.79	0.50
1:B:37:PRO:HD2	1:B:40:LEU:CD1	2.42	0.50
1:B:45:THR:C	1:B:47:ARG:N	2.67	0.50
1:B:158:LYS:O	1:B:159:VAL:HB	2.11	0.50
1:A:104:TYR:HD2	1:A:105:CYS:N	2.07	0.50
1:A:145:LEU:HD22	1:A:145:LEU:O	2.11	0.50
1:A:146:LEU:HD21	1:A:173:TYR:OH	2.11	0.50
1:A:194:TYR:O	1:A:195:ASN:C	2.55	0.50
1:A:126:GLY:O	1:A:155:LYS:HB2	2.12	0.50
1:A:190:TYR:O	1:A:190:TYR:CD2	2.65	0.50
1:B:130:LEU:HD23	1:B:130:LEU:H	1.77	0.50
1:B:135:ILE:HG12	1:B:136:ILE:H	1.77	0.50
1:B:144:THR:O	1:B:147:SER:HB3	2.12	0.49
1:B:166:ARG:NH2	1:B:183:PRO:HG3	2.27	0.49
1:A:27:TYR:CE2	1:A:198:PHE:HD2	2.30	0.49
1:A:63:ALA:O	1:A:96:VAL:HA	2.12	0.49
1:B:62:VAL:HB	1:B:129:VAL:HG22	1.94	0.49
1:A:29:GLU:OE2	1:A:30:ASP:N	2.44	0.49
1:B:41:ILE:HG21	1:B:190:TYR:HE2	1.78	0.49
1:B:131:ILE:CG2	1:B:132:VAL:N	2.76	0.49
1:B:146:LEU:CA	1:B:149:VAL:HB	2.38	0.49
1:B:18:LEU:HD23	1:B:34:VAL:N	2.27	0.49
1:A:186:PHE:HD2	1:A:207:ILE:HD12	1.74	0.49
1:B:35:PHE:HB2	1:B:204:VAL:O	2.13	0.49
1:B:61:ILE:HG22	1:B:62:VAL:N	2.27	0.49
1:B:100:ARG:CG	1:B:102:GLY:H	2.19	0.49
1:A:44:ARG:O	1:A:45:THR:C	2.54	0.49
1:B:83:ALA:HA	1:B:86:ARG:CZ	2.43	0.49
1:A:188:VAL:HG21	1:A:207:ILE:HG12	1.93	0.48
1:B:91:SER:C	1:B:92:ILE:HG13	2.37	0.48
1:B:100:ARG:HB3	1:B:117:GLY:O	2.13	0.48
1:B:113:ILE:HD11	1:B:140:LYS:HG2	1.94	0.48
1:B:73:PHE:CD1	1:B:162:LEU:HB2	2.48	0.48
1:B:115:VAL:C	1:B:116:ILE:HG12	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:LEU:C	1:B:150:ARG:N	2.71	0.48
1:A:124:LEU:CD1	1:A:124:LEU:N	2.76	0.48
1:A:133:GLU:OE2	4:A:312:PRP:C3	2.61	0.48
1:A:165:LYS:HA	1:A:182:ILE:O	2.13	0.48
1:A:35:PHE:HE2	1:A:182:ILE:HB	1.77	0.48
1:B:132:VAL:O	1:B:133:GLU:HG3	2.13	0.48
1:B:137:ASP:O	1:B:139:GLY:N	2.46	0.48
1:B:164:VAL:HG21	1:B:178:VAL:HG21	1.93	0.48
1:A:92:ILE:O	1:A:93:PRO:O	2.30	0.48
1:A:192:LEU:HD22	1:A:192:LEU:N	2.27	0.48
1:B:138:THR:OG1	1:B:140:LYS:HE2	2.13	0.48
1:B:206:VAL:HG12	1:B:207:ILE:O	2.13	0.48
1:A:38:HIS:ND1	1:A:202:ASN:HB3	2.29	0.48
1:A:41:ILE:O	1:A:44:ARG:N	2.47	0.48
1:A:45:THR:O	1:A:46:GLU:C	2.57	0.48
1:A:75:ALA:O	1:A:78:LEU:HB2	2.14	0.48
1:A:63:ALA:HB3	1:A:96:VAL:HG12	1.95	0.47
1:A:116:ILE:O	1:A:116:ILE:HG22	2.15	0.47
1:A:146:LEU:O	1:A:150:ARG:NH1	2.47	0.47
1:A:208:SER:C	1:A:210:THR:H	2.21	0.47
1:B:7:VAL:HG21	1:B:180:PHE:CD2	2.49	0.47
1:A:26:HIS:C	1:A:28:ALA:H	2.20	0.47
1:B:51:ASP:O	1:B:53:MET:N	2.47	0.47
1:B:62:VAL:HG21	1:B:127:LYS:HE3	1.96	0.47
1:A:60:HIS:ND1	1:A:60:HIS:N	2.61	0.47
1:A:159:VAL:CG1	1:A:160:ALA:H	2.25	0.47
1:A:195:ASN:HD21	1:A:215:TYR:CB	2.13	0.47
1:B:147:SER:O	1:B:150:ARG:N	2.46	0.47
1:A:166:ARG:HG3	1:A:166:ARG:HH11	1.79	0.47
1:A:26:HIS:O	1:A:29:GLU:OE2	2.33	0.47
1:A:57:GLY:N	1:A:59:HIS:NE2	2.62	0.47
1:B:119:ASP:C	1:B:121:LEU:HD12	2.39	0.47
1:B:58:GLY:HA2	1:B:90:ARG:CZ	2.45	0.47
1:B:101:LEU:CD2	1:B:145:LEU:HB2	2.45	0.47
1:B:149:VAL:O	1:B:149:VAL:CG1	2.47	0.47
1:A:147:SER:HA	1:A:150:ARG:CZ	2.43	0.47
1:B:21:PHE:HD1	1:B:34:VAL:HG21	1.78	0.47
1:B:45:THR:C	1:B:47:ARG:H	2.22	0.47
1:A:186:PHE:HB2	1:A:212:LYS:HZ3	1.80	0.47
1:B:107:ASP:CG	1:B:186:PHE:CE2	2.93	0.47
1:A:74:PHE:HD1	1:A:132:VAL:HG21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:LEU:HG	1:A:150:ARG:HH11	1.79	0.46
1:A:25:ASN:O	1:A:26:HIS:C	2.58	0.46
1:A:40:LEU:O	1:A:44:ARG:CB	2.63	0.46
1:A:101:LEU:O	1:A:102:GLY:C	2.59	0.46
1:B:43:ASP:O	1:B:46:GLU:HB3	2.14	0.46
1:A:18:LEU:O	1:A:23:ILE:HD11	2.16	0.46
1:A:66:VAL:HG13	1:A:100:ARG:O	2.15	0.46
1:A:128:ASN:HD22	1:A:155:LYS:HB3	1.79	0.46
1:B:56:MET:HE2	1:B:61:ILE:HG23	1.97	0.46
1:B:76:ASP:O	1:B:77:LEU:C	2.57	0.46
1:A:159:VAL:CG1	1:A:160:ALA:N	2.78	0.46
1:A:199:ARG:C	1:A:201:LEU:H	2.24	0.46
1:A:199:ARG:HG3	1:A:200:ASP:N	2.29	0.46
1:B:137:ASP:CG	1:B:138:THR:N	2.73	0.46
1:B:208:SER:HB3	1:B:210:THR:HG23	1.96	0.46
1:A:68:ALA:O	4:A:312:PRP:O3A	2.34	0.46
1:A:64:LEU:HB2	1:A:99:ILE:HD12	1.97	0.46
1:B:81:ILE:O	1:B:85:ASN:OD1	2.34	0.46
1:B:82:LYS:O	1:B:85:ASN:HB2	2.16	0.46
1:B:96:VAL:HG12	1:B:97:ASP:H	1.81	0.46
1:A:24:PRO:HG3	1:B:86:ARG:HB3	1.97	0.46
1:A:149:VAL:O	1:A:154:PRO:HD3	2.16	0.46
1:B:101:LEU:HG	1:B:101:LEU:O	2.16	0.46
1:A:125:THR:O	1:A:126:GLY:C	2.59	0.46
1:B:146:LEU:O	1:B:149:VAL:C	2.59	0.46
1:A:44:ARG:O	1:A:47:ARG:HB3	2.16	0.46
1:A:45:THR:HG22	1:A:46:GLU:N	2.30	0.46
1:A:91:SER:C	1:A:92:ILE:HG13	2.41	0.46
1:A:29:GLU:N	1:A:29:GLU:CD	2.74	0.45
1:B:52:VAL:O	1:B:52:VAL:CG1	2.63	0.45
1:A:62:VAL:HG12	1:A:64:LEU:HD23	1.98	0.45
1:B:121:LEU:O	1:B:124:LEU:HB2	2.16	0.45
1:A:41:ILE:O	1:A:43:ASP:N	2.50	0.45
1:A:192:LEU:CD2	1:A:192:LEU:N	2.80	0.45
1:A:211:GLY:HA2	1:A:214:LYS:CB	2.47	0.45
1:B:123:THR:C	1:B:125:THR:N	2.74	0.45
1:B:140:LYS:HB3	4:B:314:PRP:O3P	2.16	0.45
1:A:30:ASP:HB3	1:A:198:PHE:CZ	2.45	0.45
1:B:59:HIS:O	1:B:61:ILE:HG12	2.17	0.45
1:A:61:ILE:HG13	1:A:128:ASN:O	2.16	0.45
1:A:79:ASP:HA	1:A:82:LYS:CD	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:LYS:NZ	1:B:72:LYS:CD	2.76	0.45
1:A:128:ASN:HA	1:A:156:MET:O	2.16	0.45
1:B:194:TYR:O	1:B:195:ASN:OD1	2.35	0.45
1:B:208:SER:C	1:B:210:THR:H	2.24	0.45
1:A:38:HIS:HB2	1:A:203:HIS:HD2	1.81	0.45
1:A:186:PHE:CD2	1:A:207:ILE:HD12	2.52	0.45
1:B:131:ILE:N	1:B:131:ILE:CD1	2.79	0.45
1:A:77:LEU:O	1:A:81:ILE:HG13	2.17	0.45
1:B:113:ILE:HA	1:B:141:THR:HG22	1.99	0.45
1:A:169:ARG:HG3	1:A:169:ARG:NH1	2.31	0.45
1:A:206:VAL:HG12	1:A:207:ILE:N	2.32	0.45
1:B:131:ILE:HD11	1:B:157:VAL:HG13	1.98	0.45
1:A:26:HIS:CD2	1:A:27:TYR:HD1	2.35	0.45
1:A:167:THR:OG1	1:A:168:PRO:CD	2.58	0.45
1:A:187:VAL:HB	1:A:204:VAL:HG12	1.98	0.45
1:B:24:PRO:O	1:B:25:ASN:C	2.60	0.45
1:B:123:THR:O	1:B:124:LEU:C	2.58	0.45
1:B:197:TYR:O	1:B:198:PHE:HB2	2.17	0.45
1:A:10:SER:HB3	1:A:11:ASP:H	1.54	0.44
1:A:57:GLY:N	1:A:59:HIS:CD2	2.86	0.44
1:A:98:PHE:CD1	1:B:67:LEU:HD11	2.51	0.44
1:A:121:LEU:O	1:A:152:TYR:CD1	2.70	0.44
1:A:203:HIS:O	1:A:205:CYS:N	2.44	0.44
1:A:176:ASP:OD1	1:A:176:ASP:N	2.50	0.44
1:B:157:VAL:O	1:B:157:VAL:HG12	2.17	0.44
1:A:62:VAL:HG22	1:A:95:THR:HG21	1.98	0.44
1:A:156:MET:HE2	1:A:158:LYS:HZ1	1.81	0.44
1:A:201:LEU:HD21	1:A:205:CYS:SG	2.58	0.44
1:B:6:GLY:O	1:B:8:VAL:N	2.50	0.44
1:B:37:PRO:O	1:B:40:LEU:HB3	2.17	0.44
1:A:24:PRO:HB2	1:A:27:TYR:HB2	1.99	0.44
1:B:147:SER:O	1:B:150:ARG:CB	2.61	0.44
1:A:20:LEU:C	1:A:21:PHE:CD1	2.96	0.44
1:A:99:ILE:HG22	1:A:100:ARG:N	2.32	0.44
1:B:156:MET:CE	1:B:158:LYS:HE2	2.48	0.44
1:A:41:ILE:HG21	1:A:190:TYR:CE2	2.53	0.44
1:A:107:ASP:HB3	1:A:108:GLN:OE1	2.18	0.44
1:B:10:SER:C	1:B:12:ASP:N	2.76	0.44
1:B:36:ILE:O	1:B:37:PRO:C	2.60	0.44
1:B:83:ALA:HA	1:B:86:ARG:CD	2.45	0.44
1:B:158:LYS:HB3	1:B:159:VAL:H	1.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ARG:NH1	1:B:202:ASN:HD21	2.16	0.43
1:A:124:LEU:HD23	1:A:129:VAL:HG13	2.01	0.43
1:B:131:ILE:CG2	1:B:132:VAL:H	2.29	0.43
1:B:169:ARG:HG2	1:B:169:ARG:NH1	2.32	0.43
1:A:73:PHE:CD2	1:A:162:LEU:HB2	2.53	0.43
1:A:4:SER:OG	1:A:5:PRO:HD2	2.18	0.43
1:A:72:LYS:O	1:A:75:ALA:HB3	2.18	0.43
1:A:58:GLY:C	1:A:59:HIS:CG	2.96	0.43
1:A:74:PHE:CD1	1:A:78:LEU:HD11	2.54	0.43
1:B:59:HIS:HE1	5:B:905:HOH:O	2.00	0.43
1:B:72:LYS:NZ	1:B:76:ASP:OD2	2.51	0.43
1:B:98:PHE:CD1	1:B:98:PHE:N	2.87	0.43
1:B:105:CYS:O	1:B:106:ASN:CG	2.61	0.43
1:B:135:ILE:CG1	1:B:136:ILE:N	2.81	0.43
1:B:201:LEU:HD21	1:B:203:HIS:O	2.18	0.43
1:B:37:PRO:HD2	1:B:40:LEU:HD12	1.99	0.43
1:B:72:LYS:O	1:B:73:PHE:C	2.62	0.43
1:B:103:SER:C	1:B:105:CYS:N	2.76	0.43
1:B:137:ASP:HB3	4:B:314:PRP:O1P	2.18	0.43
1:A:138:THR:O	1:A:171:VAL:HG23	2.18	0.43
1:B:61:ILE:CG2	1:B:62:VAL:N	2.81	0.43
1:B:160:ALA:CA	1:B:177:PHE:HB2	2.26	0.43
1:A:120:ASP:C	1:A:122:SER:H	2.24	0.43
1:B:189:GLY:O	1:B:190:TYR:HB3	2.19	0.43
1:A:41:ILE:C	1:A:43:ASP:N	2.74	0.43
1:A:46:GLU:HA	1:A:80:TYR:CG	2.54	0.43
1:B:72:LYS:C	1:B:74:PHE:N	2.76	0.43
1:B:210:THR:HA	5:B:911:HOH:O	2.18	0.43
1:A:11:ASP:C	1:A:13:GLU:N	2.77	0.42
1:A:136:ILE:HD13	1:A:136:ILE:HA	1.92	0.42
1:B:167:THR:O	1:B:167:THR:HG23	2.18	0.42
1:A:23:ILE:HA	1:A:24:PRO:HD3	1.93	0.42
1:A:39:GLY:O	1:A:40:LEU:C	2.62	0.42
1:A:198:PHE:HE1	1:A:207:ILE:CG2	2.26	0.42
1:A:7:VAL:HG11	1:A:180:PHE:HE2	1.85	0.42
1:A:78:LEU:O	1:A:82:LYS:HG3	2.18	0.42
1:A:124:LEU:N	1:A:124:LEU:HD12	2.35	0.42
1:A:67:LEU:O	1:A:68:ALA:CB	2.67	0.42
1:A:145:LEU:HD13	1:A:145:LEU:C	2.44	0.42
1:B:139:GLY:O	1:B:143:GLN:HG3	2.19	0.42
1:A:73:PHE:CD1	1:A:162:LEU:HD13	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:VAL:CG1	1:A:175:PRO:HB3	2.50	0.42
1:B:72:LYS:O	1:B:74:PHE:N	2.52	0.42
1:B:72:LYS:HG2	1:B:190:TYR:CD1	2.55	0.42
1:A:7:VAL:HG23	1:A:44:ARG:NE	2.35	0.42
1:A:134:ASP:OD2	4:A:312:PRP:O2B	2.38	0.42
1:A:202:ASN:H	1:A:202:ASN:HD22	1.61	0.42
1:A:26:HIS:CD2	1:A:26:HIS:N	2.86	0.42
1:A:74:PHE:CD1	1:A:132:VAL:HG21	2.55	0.42
1:A:83:ALA:HA	1:A:86:ARG:CG	2.49	0.42
1:B:99:ILE:HA	1:B:118:GLY:HA3	2.01	0.42
1:B:104:TYR:O	1:B:105:CYS:C	2.62	0.42
1:A:20:LEU:HD23	1:A:20:LEU:HA	1.91	0.42
1:A:45:THR:CA	1:A:48:LEU:HD13	2.45	0.42
1:A:64:LEU:HB3	1:A:97:ASP:HB2	2.02	0.42
1:A:182:ILE:O	1:A:183:PRO:O	2.37	0.42
1:B:138:THR:C	1:B:140:LYS:N	2.77	0.42
1:B:164:VAL:CG1	1:B:165:LYS:N	2.83	0.42
1:A:28:ALA:C	1:A:30:ASP:N	2.78	0.42
1:B:77:LEU:O	1:B:77:LEU:HD12	2.20	0.42
1:A:14:PRO:O	1:A:15:GLY:C	2.62	0.42
1:A:26:HIS:CD2	1:A:27:TYR:CD1	3.08	0.42
1:A:27:TYR:CE2	1:A:198:PHE:CD2	3.08	0.42
1:A:46:GLU:O	1:A:49:ALA:HB3	2.20	0.42
1:A:107:ASP:O	1:A:108:GLN:CB	2.65	0.42
1:A:133:GLU:HG3	1:A:142:MET:HE3	1.94	0.42
1:A:190:TYR:HB2	1:A:202:ASN:O	2.20	0.42
1:B:64:LEU:HD12	1:B:97:ASP:CB	2.32	0.42
1:A:48:LEU:H	1:A:48:LEU:CD1	2.29	0.41
1:A:211:GLY:HA2	1:A:214:LYS:HB3	2.02	0.41
1:B:158:LYS:HB3	1:B:177:PHE:HE2	1.84	0.41
1:B:203:HIS:O	1:B:205:CYS:N	2.53	0.41
1:B:216:LYS:C	1:B:216:LYS:HD3	2.45	0.41
1:A:64:LEU:CD1	1:A:129:VAL:HG12	2.43	0.41
1:A:127:LYS:H	1:A:155:LYS:H	1.63	0.41
1:A:167:THR:OG1	1:A:169:ARG:NH1	2.54	0.41
1:B:81:ILE:O	1:B:82:LYS:C	2.62	0.41
1:A:7:VAL:HG11	1:A:180:PHE:CE2	2.55	0.41
1:A:61:ILE:CG2	1:A:130:LEU:HB2	2.50	0.41
1:A:168:PRO:HG2	1:A:169:ARG:N	2.36	0.41
1:A:17:ASP:OD2	1:A:17:ASP:N	2.52	0.41
1:B:59:HIS:HB3	1:B:128:ASN:ND2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:PRO:HA	5:B:945:HOH:O	2.21	0.41
1:A:186:PHE:HB2	1:A:212:LYS:NZ	2.36	0.41
1:B:36:ILE:HG22	1:B:41:ILE:CG1	2.50	0.41
1:B:37:PRO:O	1:B:40:LEU:CB	2.69	0.41
1:B:101:LEU:O	1:B:101:LEU:CG	2.68	0.41
1:B:104:TYR:O	1:B:106:ASN:N	2.54	0.41
1:A:151:GLN:C	1:A:153:ASN:N	2.76	0.41
1:B:41:ILE:O	1:B:42:MET:C	2.63	0.41
1:A:15:GLY:CA	1:A:34:VAL:O	2.68	0.41
1:A:81:ILE:O	1:A:82:LYS:C	2.63	0.41
1:A:146:LEU:HD22	1:A:173:TYR:CE2	2.55	0.41
1:A:167:THR:HG22	1:A:170:SER:HB3	2.01	0.41
1:B:36:ILE:HG21	1:B:41:ILE:HG12	2.03	0.41
1:B:104:TYR:O	1:B:104:TYR:HD1	2.02	0.41
1:B:146:LEU:HA	1:B:149:VAL:CB	2.43	0.41
1:A:26:HIS:CD2	1:A:27:TYR:H	2.39	0.41
1:A:190:TYR:HB3	1:A:204:VAL:HG22	2.03	0.41
1:B:21:PHE:HB3	1:B:203:HIS:CE1	2.56	0.41
1:B:25:ASN:C	1:B:27:TYR:N	2.75	0.41
1:B:134:ASP:OD2	1:B:134:ASP:N	2.54	0.41
1:A:72:LYS:CE	1:B:79:ASP:OD1	2.69	0.41
1:B:7:VAL:HG21	1:B:180:PHE:HD2	1.85	0.41
1:A:129:VAL:HG23	1:A:154:PRO:HB2	2.04	0.40
1:B:107:ASP:CG	1:B:186:PHE:CD2	3.00	0.40
1:A:125:THR:C	1:A:127:LYS:N	2.77	0.40
1:A:200:ASP:HA	1:B:82:LYS:HB3	2.02	0.40
1:B:7:VAL:O	1:B:7:VAL:HG12	2.19	0.40
1:B:143:GLN:O	1:B:147:SER:N	2.42	0.40
1:B:86:ARG:C	1:B:88:SER:H	2.29	0.40
1:A:48:LEU:HD12	1:A:48:LEU:N	2.33	0.40
1:A:72:LYS:HZ3	1:B:82:LYS:CE	2.32	0.40
1:A:122:SER:HA	1:A:152:TYR:CD2	2.56	0.40
1:A:128:ASN:ND2	1:A:155:LYS:HB3	2.37	0.40
1:B:90:ARG:NH1	1:B:90:ARG:HG2	2.36	0.40
1:B:101:LEU:CD2	1:B:145:LEU:HD22	2.52	0.40
1:B:119:ASP:OD1	1:B:119:ASP:C	2.64	0.40
1:B:136:ILE:N	1:B:163:LEU:O	2.54	0.40
1:B:183:PRO:CB	1:B:185:LYS:HZ1	2.32	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	212/214 (99%)	131 (62%)	53 (25%)	28 (13%)	0	0
1	B	212/214 (99%)	130 (61%)	47 (22%)	35 (16%)	0	0
All	All	424/428 (99%)	261 (62%)	100 (24%)	63 (15%)	0	0

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	10	SER
1	A	29	GLU
1	A	40	LEU
1	A	46	GLU
1	A	54	LYS
1	A	58	GLY
1	A	72	LYS
1	A	121	LEU
1	A	183	PRO
1	B	5	PRO
1	B	75	ALA
1	B	105	CYS
1	B	124	LEU
1	B	152	TYR
1	B	158	LYS
1	B	159	VAL
1	B	175	PRO
1	A	35	PHE
1	A	120	ASP
1	A	126	GLY
1	A	204	VAL
1	B	26	HIS
1	B	52	VAL
1	B	72	LYS

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Mol	Chain	Res	Type
1	B	76	ASP
1	B	87	ASN
1	B	134	ASP
1	B	137	ASP
1	B	138	THR
1	B	154	PRO
1	B	189	GLY
1	B	204	VAL
1	A	28	ALA
1	A	93	PRO
1	A	102	GLY
1	B	30	ASP
1	B	151	GLN
1	B	153	ASN
1	A	25	ASN
1	A	68	ALA
1	A	73	PHE
1	A	75	ALA
1	A	129	VAL
1	A	195	ASN
1	B	7	VAL
1	B	46	GLU
1	B	103	SER
1	A	24	PRO
1	A	45	THR
1	A	74	PHE
1	A	84	LEU
1	B	68	ALA
1	B	157	VAL
1	B	176	ASP
1	A	108	GLN
1	B	140	LYS
1	B	149	VAL
1	B	188	VAL
1	B	96	VAL
1	B	99	ILE
1	B	111	GLY
1	B	102	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	187/187 (100%)	144 (77%)	43 (23%)	1	2
1	B	187/187 (100%)	153 (82%)	34 (18%)	2	5
All	All	374/374 (100%)	297 (79%)	77 (21%)	1	3

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	18	LEU
1	A	22	CYS
1	A	23	ILE
1	A	26	HIS
1	A	29	GLU
1	A	33	ARG
1	A	35	PHE
1	A	53	MET
1	A	64	LEU
1	A	65	CYS
1	A	67	LEU
1	A	86	ARG
1	A	87	ASN
1	A	88	SER
1	A	93	PRO
1	A	95	THR
1	A	100	ARG
1	A	107	ASP
1	A	108	GLN
1	A	112	ASP
1	A	114	LYS
1	A	120	ASP
1	A	123	THR
1	A	124	LEU
1	A	125	THR
1	A	128	ASN

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Mol	Chain	Res	Type
1	A	130	LEU
1	A	133	GLU
1	A	135	ILE
1	A	136	ILE
1	A	143	GLN
1	A	145	LEU
1	A	148	LEU
1	A	153	ASN
1	A	163	LEU
1	A	169	ARG
1	A	171	VAL
1	A	184	ASP
1	A	201	LEU
1	A	202	ASN
1	A	205	CYS
1	A	207	ILE
1	B	19	ASP
1	B	30	ASP
1	B	35	PHE
1	B	36	ILE
1	B	37	PRO
1	B	54	LYS
1	B	60	HIS
1	B	65	CYS
1	B	67	LEU
1	B	78	LEU
1	B	84	LEU
1	B	88	SER
1	B	90	ARG
1	B	96	VAL
1	B	97	ASP
1	B	98	PHE
1	B	99	ILE
1	B	100	ARG
1	B	105	CYS
1	B	113	ILE
1	B	120	ASP
1	B	123	THR
1	B	131	ILE
1	B	134	ASP
1	B	144	THR
1	B	151	GLN

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Mol	Chain	Res	Type
1	B	154	PRO
1	B	186	PHE
1	B	193	ASP
1	B	196	GLU
1	B	199	ARG
1	B	200	ASP
1	B	201	LEU
1	B	210	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	85	ASN
1	A	106	ASN
1	A	128	ASN
1	A	151	GLN
1	A	195	ASN
1	B	26	HIS
1	B	38	HIS
1	B	59	HIS
1	B	128	ASN
1	B	202	ASN
1	B	203	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
4	PRP	B	314	2	20,22,22	4.79	10 (50%)	32,35,35	4.19	18 (56%)
4	PRP	A	312	2	20,22,22	3.28	11 (55%)	32,35,35	3.39	17 (53%)
3	PPO	B	301	-	11,11,11	3.79	7 (63%)	6,15,15	2.97	3 (50%)
3	PPO	A	300	-	11,11,11	3.58	6 (54%)	6,15,15	2.77	3 (50%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PRP	B	314	2	-	9/16/33/33	0/1/1/1
4	PRP	A	312	2	-	6/16/33/33	0/1/1/1
3	PPO	B	301	-	-	-	0/2/2/2
3	PPO	A	300	-	-	-	0/2/2/2

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	314	PRP	PA-O3A	-19.01	1.39	1.59
4	A	312	PRP	PA-O3A	-11.23	1.47	1.59
3	A	300	PPO	C9-C4	-7.92	1.37	1.50
3	B	301	PPO	C9-C4	-7.80	1.37	1.50
3	A	300	PPO	C9-N8	-5.74	1.38	1.46
3	B	301	PPO	C9-N8	-5.21	1.38	1.46
3	B	301	PPO	C2-N1	4.76	1.42	1.33
4	B	314	PRP	C5-C4	-4.66	1.37	1.51
3	B	301	PPO	C4-N3	4.25	1.40	1.34
4	A	312	PRP	PA-O1	4.02	1.71	1.59
4	B	314	PRP	PB-O3B	-3.90	1.40	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	300	PPO	C2-N1	3.76	1.40	1.33
4	A	312	PRP	C5-C4	-3.66	1.40	1.51
3	A	300	PPO	N7-N8	3.57	1.30	1.25
3	B	301	PPO	N7-N8	3.33	1.29	1.25
4	A	312	PRP	C3-C4	-3.19	1.44	1.53
3	B	301	PPO	C6-N1	3.12	1.45	1.35
4	B	314	PRP	PB-O1B	3.00	1.59	1.50
3	A	300	PPO	C4-N3	2.99	1.38	1.34
4	B	314	PRP	O5-C5	-2.82	1.33	1.44
4	B	314	PRP	C3-C4	-2.81	1.45	1.53
4	A	312	PRP	C1-C2	-2.55	1.49	1.52
4	A	312	PRP	P-O2P	-2.54	1.45	1.54
3	B	301	PPO	C2-N3	2.49	1.38	1.33
3	A	300	PPO	C6-N1	2.40	1.42	1.35
4	A	312	PRP	P-O5	2.36	1.67	1.60
4	B	314	PRP	P-O2P	-2.35	1.46	1.54
4	B	314	PRP	PA-O1A	2.28	1.58	1.50
4	A	312	PRP	PB-O1B	2.23	1.57	1.50
4	A	312	PRP	O5-C5	-2.15	1.36	1.44
4	A	312	PRP	C3-C2	-2.13	1.47	1.53
4	B	314	PRP	C3-C2	-2.12	1.47	1.53
4	B	314	PRP	P-O5	2.04	1.66	1.60
4	A	312	PRP	PB-O3B	-2.03	1.47	1.54

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	312	PRP	O3B-PB-O3A	11.62	143.60	104.64
4	B	314	PRP	O3A-PB-O1B	9.93	163.28	111.04
4	B	314	PRP	O1-PA-O1A	-9.07	80.83	109.81
4	B	314	PRP	O2A-PA-O3A	-8.23	85.04	107.27
4	A	312	PRP	O3A-PA-O1A	-7.60	87.83	110.70
4	B	314	PRP	O3B-PB-O1B	-7.35	82.19	110.83
4	B	314	PRP	O3B-PB-O2B	6.72	133.01	107.80
4	B	314	PRP	PA-O1-C1	5.81	144.87	121.21
4	B	314	PRP	O2A-PA-O1	-5.46	84.48	106.70
4	B	314	PRP	O1-C1-C2	5.19	115.08	106.65
3	B	301	PPO	C9-C4-C5	-5.08	104.32	109.75
4	A	312	PRP	O3A-PB-O1B	-4.89	85.33	111.04
4	B	314	PRP	O2B-PB-O3A	-4.78	88.62	104.64
4	B	314	PRP	O3A-PA-O1A	4.55	124.40	110.70
3	B	301	PPO	N1-C2-N3	-4.47	121.82	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	300	PPO	C9-C4-C5	-4.42	105.02	109.75
3	A	300	PPO	N1-C2-N3	-4.40	121.92	128.58
4	A	312	PRP	O1-C1-C2	4.38	113.76	106.65
4	A	312	PRP	O4-C1-C2	4.22	110.35	104.98
4	A	312	PRP	PA-O1-C1	3.77	136.55	121.21
4	B	314	PRP	O4-C1-C2	3.54	109.48	104.98
4	A	312	PRP	O1-PA-O1A	-3.27	99.36	109.81
4	A	312	PRP	C5-C4-C3	-3.20	103.68	115.21
4	B	314	PRP	C5-C4-C3	-3.04	104.29	115.21
4	A	312	PRP	C2-C3-C4	2.95	108.30	102.61
4	A	312	PRP	O2B-PB-O1B	-2.92	99.44	110.83
4	A	312	PRP	O5-C5-C4	2.88	118.81	108.99
4	B	314	PRP	C2-C3-C4	2.79	108.01	102.61
4	A	312	PRP	O3B-PB-O2B	-2.74	97.54	107.80
4	A	312	PRP	O2A-PA-O1A	-2.56	100.54	112.44
4	B	314	PRP	C1-C2-C3	2.53	105.44	102.29
4	B	314	PRP	O2B-PB-O1B	-2.52	101.03	110.83
3	A	300	PPO	C2-N1-C6	2.51	125.23	116.58
4	A	312	PRP	O3B-PB-O1B	2.51	120.61	110.83
4	B	314	PRP	O5-C5-C4	2.48	117.44	108.99
3	B	301	PPO	C2-N1-C6	2.40	124.86	116.58
4	B	314	PRP	O4-C4-C3	2.35	109.82	105.15
4	A	312	PRP	O4-C4-C3	2.24	109.60	105.15
4	B	314	PRP	O2P-P-O5	2.21	112.42	106.67
4	A	312	PRP	C1-C2-C3	2.14	104.96	102.29
4	A	312	PRP	O2P-P-O5	2.13	112.22	106.67

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	312	PRP	C2-C1-O1-PA
4	A	312	PRP	C5-O5-P-O2P
4	A	312	PRP	C5-O5-P-O3P
4	B	314	PRP	C2-C1-O1-PA
4	B	314	PRP	C1-O1-PA-O3A
4	B	314	PRP	C5-O5-P-O1P
4	B	314	PRP	C5-O5-P-O2P
4	B	314	PRP	C5-O5-P-O3P
4	B	314	PRP	PB-O3A-PA-O1
4	A	312	PRP	C5-O5-P-O1P
4	B	314	PRP	PB-O3A-PA-O1A

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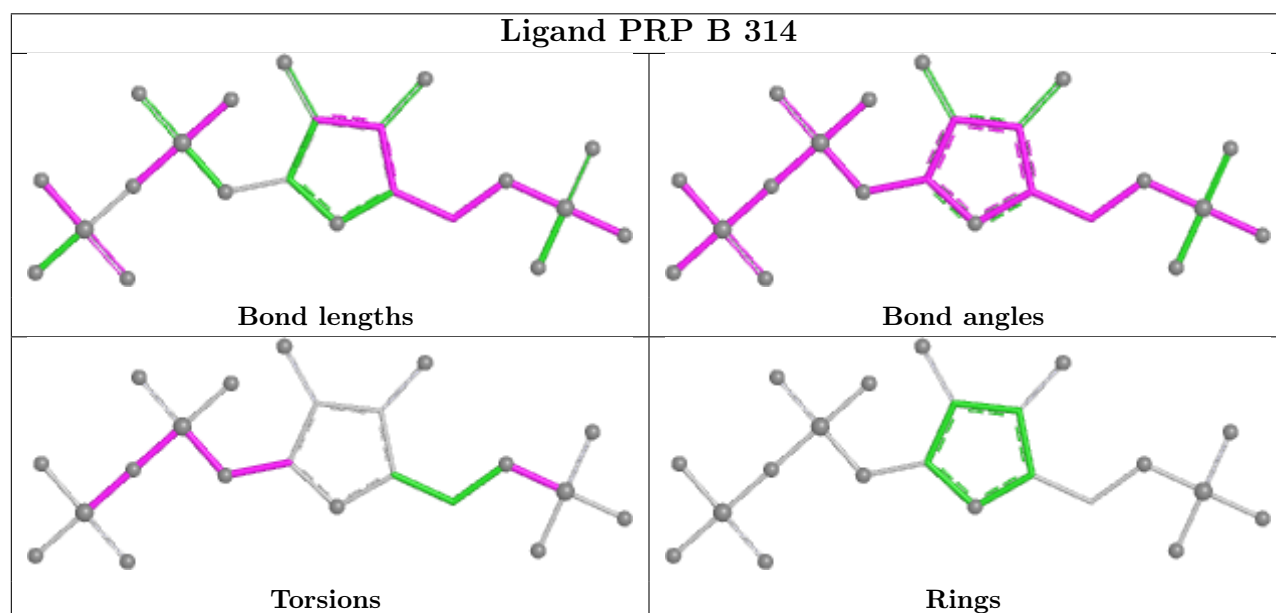
Mol	Chain	Res	Type	Atoms
4	B	314	PRP	PA-O3A-PB-O1B
4	A	312	PRP	PB-O3A-PA-O1A
4	A	312	PRP	C1-O1-PA-O2A
4	B	314	PRP	PB-O3A-PA-O2A

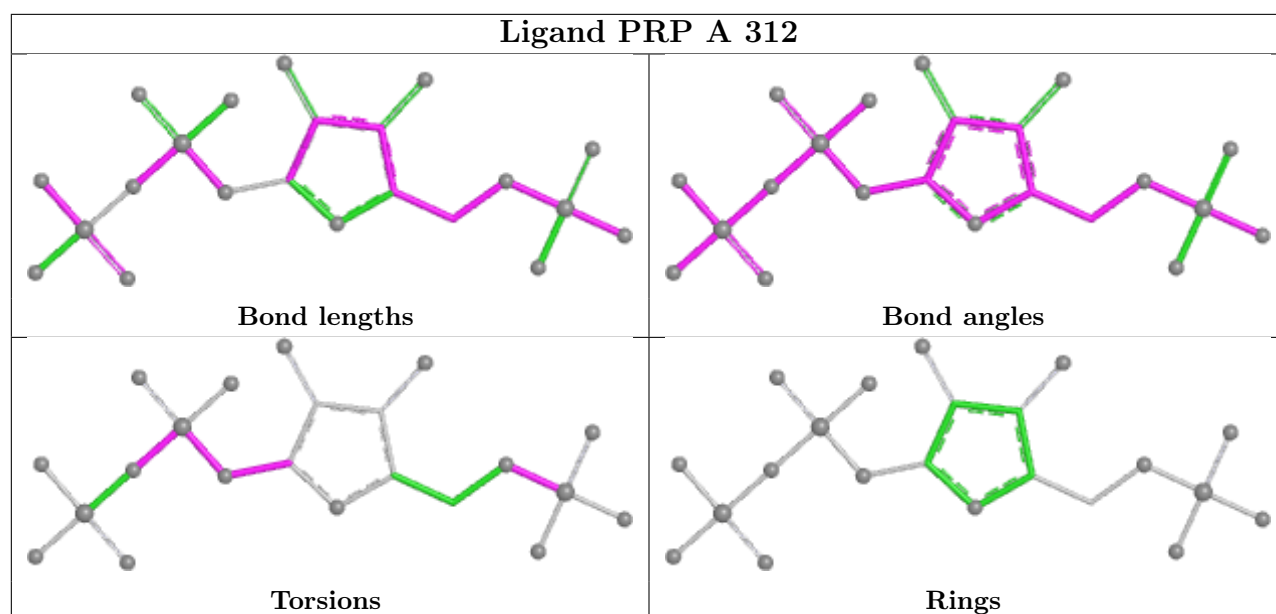
There are no ring outliers.

4 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	314	PRP	7	0
4	A	312	PRP	14	0
3	B	301	PPO	1	0
3	A	300	PPO	1	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	108:GLN	C	109:SER	N	1.19
1	B	109:SER	C	110:THR	N	1.15
1	B	105:CYS	C	106:ASN	N	1.02

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.