



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:12 AM UTC

PDB ID : 5D4W / pdb_00005d4w
Title : Crystal structure of Hsp104
Authors : Heuck, A.; Schitter-Sollner, S.; Clausen, T.
Deposited on : 2015-08-09
Resolution : 3.70 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)
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

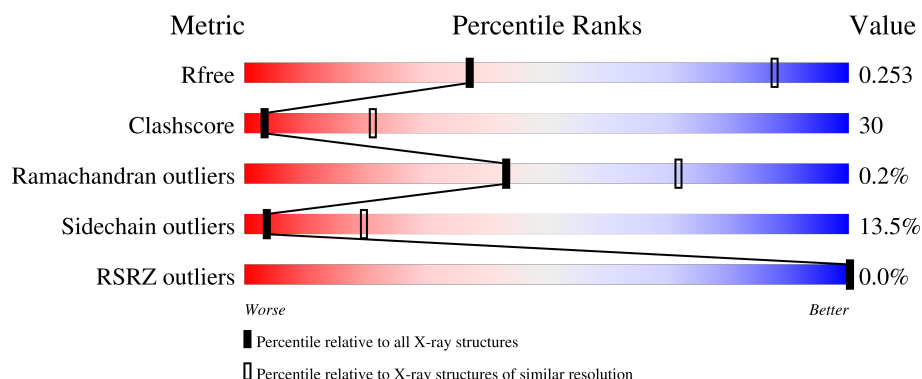
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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))
R_{free}	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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	926	
1	B	926	
1	C	926	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ADP	A	1001	-	-	X	-
2	ADP	B	1001	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16269 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Putative heat shock protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	688	Total	C	N	O	S	Se	0	0	0
			5369	3354	985	1009	5	16			
1	B	688	Total	C	N	O	S	Se	0	0	0
			5369	3354	985	1009	5	16			
1	C	688	Total	C	N	O	S	Se	0	0	0
			5369	3354	985	1009	5	16			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP G0S4G4
A	296	ALA	GLU	engineered mutation	UNP G0S4G4
A	707	ALA	GLU	engineered mutation	UNP G0S4G4
B	1	MSE	-	initiating methionine	UNP G0S4G4
B	296	ALA	GLU	engineered mutation	UNP G0S4G4
B	707	ALA	GLU	engineered mutation	UNP G0S4G4
C	1	MSE	-	initiating methionine	UNP G0S4G4
C	296	ALA	GLU	engineered mutation	UNP G0S4G4
C	707	ALA	GLU	engineered mutation	UNP G0S4G4

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

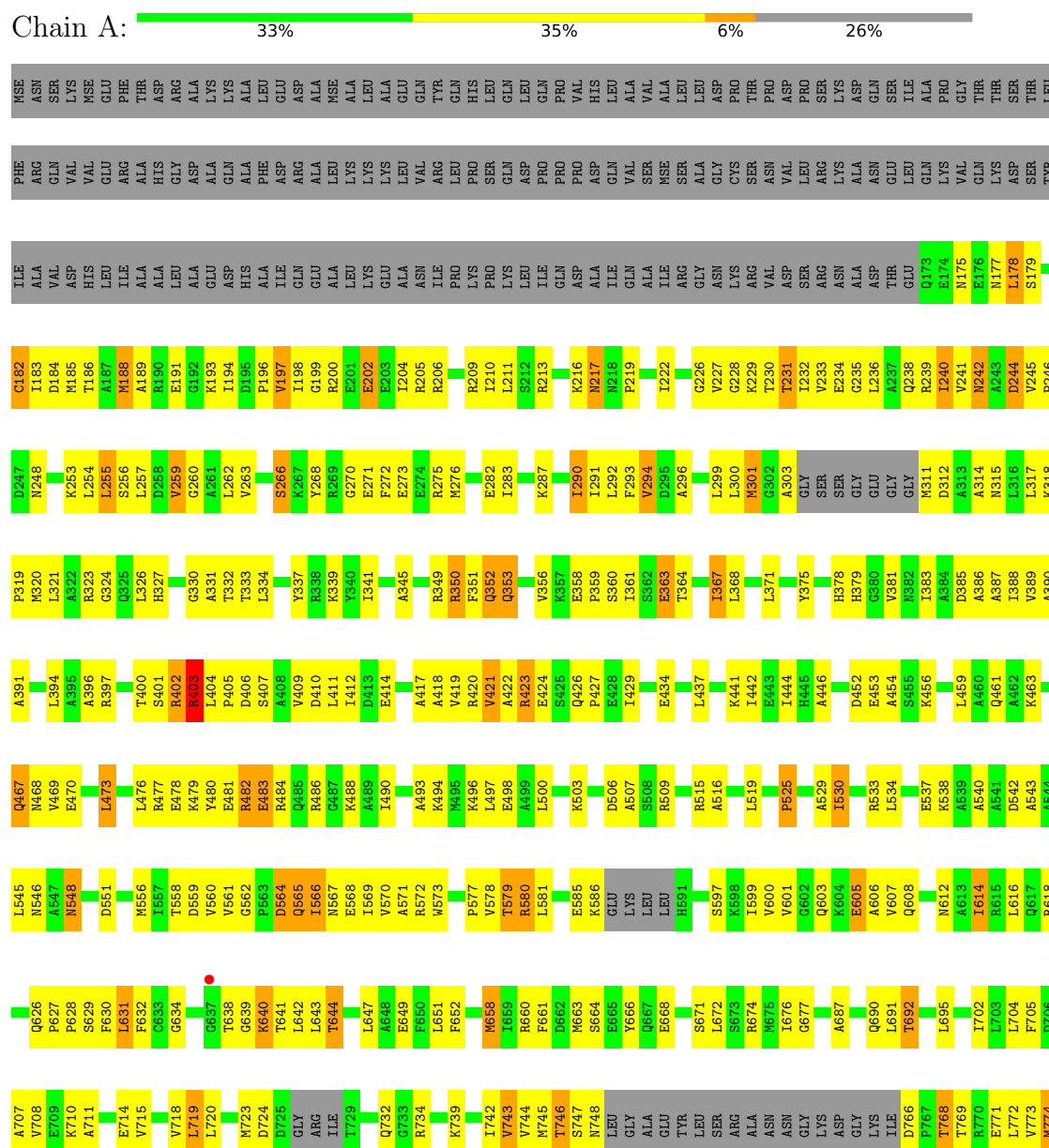


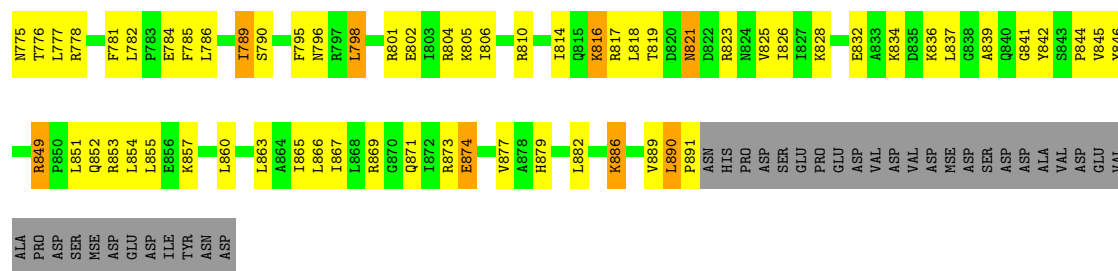
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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.

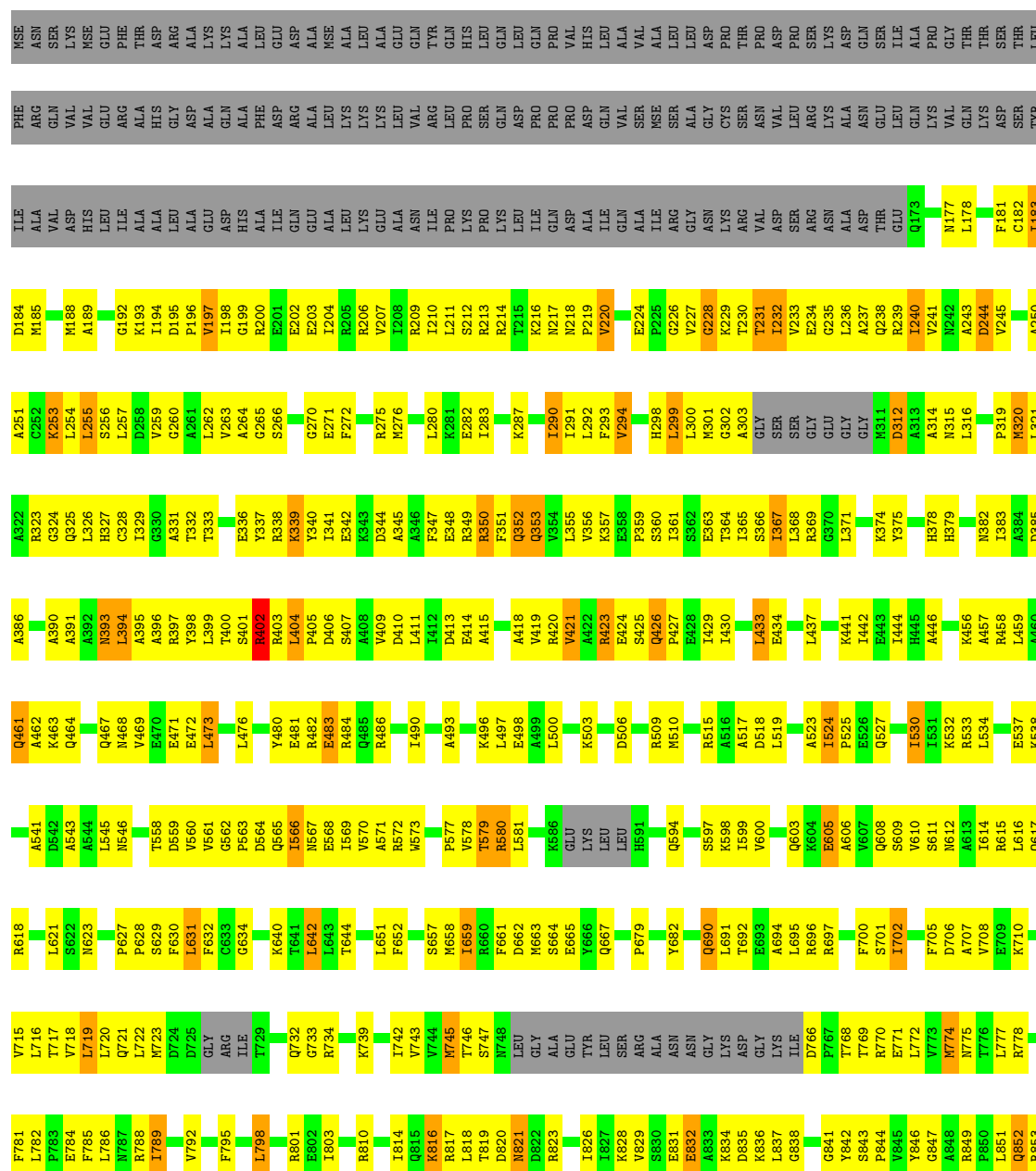
• Molecule 1: Putative heat shock protein

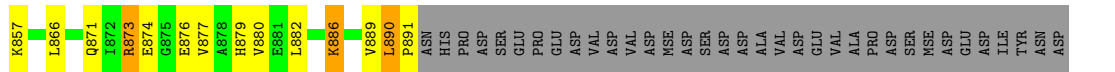
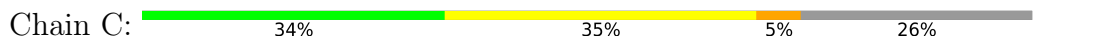
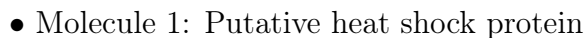




● Molecule 1: Putative heat shock protein

Chain B: 31% 37% 6% 26%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	144.92Å 93.17Å 144.42Å 90.00° 119.72° 90.00°	Depositor
Resolution (Å)	47.58 – 3.70 47.58 – 3.70	Depositor EDS
% Data completeness (in resolution range)	98.7 (47.58-3.70) 97.0 (47.58-3.70)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 3.57Å)	Xtriage
Refinement program	PHENIX (dev_2356: ???)	Depositor
R, R_{free}	0.237 , 0.277 0.222 , 0.253	Depositor DCC
R_{free} test set	1929 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	116.6	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 398.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	0.259 for l,k,-h-l 0.259 for -h-l,k,h 0.167 for -h-l,-k,l 0.157 for h,-k,-h-l 0.166 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	16269	wwPDB-VP
Average B, all atoms (Å ²)	210.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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: ADP

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	0.25	0/5414	0.55	0/7262
1	B	0.34	0/5414	0.63	2/7262 (0.0%)
1	C	0.26	0/5414	0.55	0/7262
All	All	0.29	0/16242	0.58	2/21786 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
1	C	0	1
All	All	0	6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	228	GLY	N-CA-C	5.21	125.52	113.18
1	B	320	MSE	N-CA-C	5.04	116.58	111.14

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	266	SER	Peptide
1	A	402	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	B	243	ALA	Peptide
1	B	385	ASP	Peptide
1	B	402	ARG	Peptide
1	C	402	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5369	0	5537	324	0
1	B	5369	0	5537	402	0
1	C	5369	0	5537	333	0
2	A	54	0	24	11	0
2	B	54	0	24	18	0
2	C	54	0	24	4	0
All	All	16269	0	16683	1002	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 30.

All (1002) 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:216:LYS:HB3	1:C:352:GLN:HB3	1.46	0.97
1:A:216:LYS:HB3	1:A:352:GLN:HB3	1.46	0.97
1:B:562:GLY:H	1:B:565:GLN:HB2	1.29	0.96
1:B:379:HIS:HA	1:B:420:ARG:HH12	1.31	0.91
1:B:200:ARG:HG3	1:B:232:ILE:HD11	1.55	0.89
1:A:836:LYS:HD3	1:A:886:LYS:HE2	1.56	0.88
1:C:618:ARG:HG3	1:C:651:LEU:HD11	1.56	0.86
1:B:200:ARG:HG2	2:B:1001:ADP:HN61	1.36	0.85
1:C:397:ARG:HH12	1:C:652:PHE:HA	1.44	0.82
1:B:836:LYS:HD3	1:B:886:LYS:HE2	1.59	0.82
1:B:524:ILE:HG12	1:B:525:PRO:HD3	1.63	0.81
1:A:628:PRO:HB2	1:A:742:ILE:HG13	1.62	0.81
1:A:257:LEU:HB2	1:A:292:LEU:HD11	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:634:GLY:HA3	1:B:795:PHE:HB2	1.64	0.80
1:A:185:MSE:HE1	1:A:194:ILE:HG13	1.63	0.80
1:C:571:ALA:HB2	1:C:578:VAL:HG13	1.62	0.80
1:A:603:GLN:HB3	1:A:606:ALA:HB3	1.64	0.80
1:A:493:ALA:HB1	1:A:530:ILE:HG13	1.64	0.79
1:B:568:GLU:O	1:B:572:ARG:N	2.10	0.79
1:A:182:CYS:HB2	1:A:257:LEU:HA	1.65	0.79
1:B:227:VAL:O	2:B:1001:ADP:H8	1.65	0.78
1:B:829:VAL:HG12	1:B:880:VAL:HB	1.63	0.78
1:B:240:ILE:HG12	1:B:245:VAL:HB	1.64	0.78
1:B:396:ALA:O	1:B:400:THR:OG1	2.01	0.77
1:C:614:ILE:HD11	1:C:651:LEU:HD22	1.67	0.77
1:A:663:MSE:HB2	1:A:707:ALA:HB3	1.66	0.77
1:B:611:SER:OG	1:B:615:ARG:NH2	2.16	0.77
1:C:640:LYS:NZ	1:C:747:SER:O	2.16	0.77
1:C:490:ILE:HD11	1:C:533:ARG:HB2	1.66	0.77
1:A:364:THR:HG21	1:A:404:LEU:HB3	1.65	0.76
1:B:814:ILE:HG13	1:B:817:ARG:HE	1.50	0.76
1:A:543:ALA:HA	1:A:546:ASN:HB3	1.67	0.76
1:C:578:VAL:HG12	1:C:581:LEU:HD22	1.65	0.76
1:A:427:PRO:HG3	1:A:556:MSE:HG3	1.67	0.76
1:B:293:PHE:CE2	1:B:331:ALA:HB2	2.20	0.76
1:A:814:ILE:HG13	1:A:817:ARG:HE	1.51	0.76
1:B:578:VAL:HG12	1:B:581:LEU:HD22	1.66	0.75
1:B:628:PRO:HG2	1:B:742:ILE:HG13	1.68	0.75
1:C:182:CYS:HB2	1:C:257:LEU:HA	1.68	0.75
1:B:614:ILE:HD11	1:B:651:LEU:HD22	1.68	0.75
1:C:836:LYS:HD3	1:C:886:LYS:HE2	1.70	0.74
1:A:534:LEU:HA	1:A:537:GLU:HG2	1.70	0.74
1:C:493:ALA:HA	1:C:496:LYS:HD2	1.69	0.74
1:B:188:MSE:O	1:B:192:GLY:N	2.21	0.74
1:B:430:ILE:HA	1:B:433:LEU:HD23	1.70	0.73
1:A:629:SER:HA	1:A:743:VAL:HG13	1.70	0.73
1:C:507:ALA:HB1	1:C:516:ALA:HA	1.69	0.73
1:B:211:LEU:HG	1:B:219:PRO:HD3	1.70	0.73
1:B:197:VAL:HA	2:B:1001:ADP:C2	2.23	0.73
1:B:603:GLN:HB3	1:B:606:ALA:HB3	1.71	0.73
1:A:497:LEU:HA	1:A:500:LEU:HD23	1.70	0.72
1:B:397:ARG:HH21	1:B:580:ARG:HH21	1.33	0.72
1:B:442:ILE:HB	1:C:517:ALA:HB2	1.71	0.72
1:A:200:ARG:HG2	2:A:1001:ADP:HN61	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:407:SER:OG	1:C:734:ARG:NH2	2.22	0.72
1:A:483:GLU:HA	1:A:486:ARG:HD2	1.72	0.72
1:C:628:PRO:HB2	1:C:742:ILE:HG13	1.69	0.72
1:A:798:LEU:HD21	1:A:844:PRO:HG3	1.70	0.72
1:A:630:PHE:O	1:A:745:MSE:N	2.23	0.72
1:C:579:THR:HG23	1:C:580:ARG:HG3	1.71	0.72
1:A:419:VAL:HG22	1:A:423:ARG:HG3	1.72	0.72
1:B:618:ARG:HG3	1:B:651:LEU:HD11	1.72	0.71
1:A:578:VAL:HG12	1:A:581:LEU:HD22	1.72	0.71
1:B:200:ARG:CG	2:B:1001:ADP:HN61	2.04	0.71
1:B:198:ILE:HG23	1:B:199:GLY:H	1.54	0.71
1:B:200:ARG:HD2	1:B:203:GLU:OE1	1.90	0.71
1:A:402:ARG:NH1	1:B:733:GLY:O	2.24	0.71
1:B:233:VAL:HG11	1:B:293:PHE:CD2	2.26	0.71
1:B:497:LEU:HA	1:B:500:LEU:HD23	1.73	0.71
1:A:640:LYS:NZ	1:A:747:SER:O	2.19	0.70
1:B:810:ARG:HD3	1:B:855:LEU:HD22	1.72	0.70
1:C:543:ALA:HA	1:C:546:ASN:HB3	1.72	0.70
1:A:423:ARG:HB3	1:A:558:THR:HA	1.74	0.70
1:A:211:LEU:HG	1:A:219:PRO:HD3	1.73	0.69
1:B:224:GLU:OE1	1:B:696:ARG:NH2	2.25	0.69
1:B:534:LEU:HA	1:B:537:GLU:HG2	1.74	0.69
1:C:483:GLU:HA	1:C:486:ARG:HD2	1.74	0.69
1:A:506:ASP:HA	1:A:509:ARG:HB2	1.74	0.69
1:C:321:LEU:HD13	1:C:350:ARG:HG2	1.74	0.69
1:C:634:GLY:HA3	1:C:795:PHE:HB2	1.75	0.69
1:C:394:LEU:HD23	1:C:570:VAL:HG21	1.74	0.69
1:B:433:LEU:HD21	1:B:473:LEU:HD21	1.75	0.68
1:C:771:GLU:O	1:C:775:ASN:ND2	2.26	0.68
1:A:628:PRO:HD2	1:A:742:ILE:HA	1.75	0.68
1:C:200:ARG:NH2	1:C:357:LYS:O	2.24	0.68
1:C:317:LEU:HD13	1:C:321:LEU:HD12	1.75	0.68
1:A:364:THR:O	1:A:368:LEU:N	2.24	0.68
1:B:220:VAL:HG13	1:B:353:GLN:HA	1.75	0.68
1:C:211:LEU:HD22	1:C:327:HIS:HB3	1.74	0.68
1:C:409:VAL:HA	1:C:412:ILE:HG22	1.75	0.68
1:A:213:ARG:HB2	1:A:217:ASN:HB3	1.74	0.68
1:C:420:ARG:HA	1:C:423:ARG:HD2	1.75	0.68
1:A:545:LEU:HA	1:A:548:ASN:HB2	1.75	0.68
1:B:568:GLU:OE1	1:B:568:GLU:N	2.24	0.68
1:C:506:ASP:HA	1:C:509:ARG:HB2	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:715:VAL:HA	1:B:718:VAL:HG22	1.75	0.68
1:A:233:VAL:HA	1:A:236:LEU:HB3	1.76	0.68
1:A:185:MSE:HG2	1:A:256:SER:HB3	1.75	0.67
1:A:634:GLY:HA3	1:A:795:PHE:HB2	1.75	0.67
1:A:397:ARG:HH21	1:A:580:ARG:HH21	1.39	0.67
1:B:571:ALA:HB2	1:B:578:VAL:HG13	1.77	0.67
1:B:810:ARG:NH2	1:B:852:GLN:HB2	2.09	0.67
1:B:405:PRO:O	1:B:409:VAL:HG13	1.94	0.67
1:A:578:VAL:HA	1:A:581:LEU:HD13	1.76	0.67
1:A:410:ASP:OD1	1:B:213:ARG:NH2	2.28	0.67
1:B:663:MSE:HB2	1:B:707:ALA:HB3	1.75	0.67
1:A:632:PHE:N	1:A:745:MSE:O	2.27	0.67
1:B:182:CYS:HB2	1:B:257:LEU:HA	1.74	0.67
1:C:630:PHE:HB2	1:C:744:VAL:HG12	1.77	0.67
1:C:690:GLN:O	1:C:690:GLN:NE2	2.27	0.67
1:C:773:VAL:O	1:C:777:LEU:N	2.22	0.67
1:C:599:ILE:HG23	1:C:600:VAL:HG23	1.77	0.66
1:C:639:GLY:N	2:C:1002:ADP:O1A	2.28	0.66
1:A:417:ALA:HA	1:A:420:ARG:HD2	1.76	0.66
1:A:486:ARG:HD3	1:A:537:GLU:HB3	1.76	0.66
1:C:434:GLU:OE2	1:C:477:ARG:NH1	2.28	0.66
1:A:402:ARG:O	1:A:407:SER:HB2	1.96	0.66
1:C:603:GLN:HB3	1:C:606:ALA:HB3	1.77	0.66
1:B:226:GLY:C	1:B:406:ASP:HB2	2.21	0.66
1:B:506:ASP:HA	1:B:509:ARG:HB2	1.78	0.66
1:C:829:VAL:HG12	1:C:880:VAL:HB	1.77	0.66
1:A:630:PHE:HB2	1:A:744:VAL:HG12	1.76	0.65
1:A:319:PRO:O	1:A:323:ARG:N	2.22	0.65
1:B:368:LEU:HD13	1:B:409:VAL:HG12	1.78	0.65
1:C:396:ALA:O	1:C:400:THR:OG1	2.13	0.65
1:C:695:LEU:O	1:C:739:LYS:NZ	2.21	0.65
1:C:578:VAL:HA	1:C:581:LEU:HD13	1.79	0.65
1:A:515:ARG:HD2	1:A:519:LEU:HD11	1.78	0.65
1:B:406:ASP:HA	1:B:409:VAL:HG22	1.79	0.65
1:B:777:LEU:HD22	1:B:781:PHE:HE2	1.62	0.65
1:C:882:LEU:HD12	1:C:886:LYS:HB3	1.77	0.65
1:A:228:GLY:O	1:A:232:ILE:N	2.29	0.65
1:A:420:ARG:HA	1:A:423:ARG:HD2	1.78	0.65
1:B:360:SER:N	1:B:363:GLU:HB2	2.12	0.65
1:B:213:ARG:HB2	1:B:217:ASN:HB3	1.80	0.64
1:B:458:ARG:O	1:B:462:ALA:HB3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ARG:HH11	1:B:734:ARG:HB2	1.63	0.64
1:C:732:GLN:O	1:C:734:ARG:NE	2.27	0.64
1:C:871:GLN:HE22	1:C:890:LEU:HD11	1.61	0.64
1:A:175:ASN:O	1:A:179:SER:N	2.24	0.64
1:B:770:ARG:O	1:B:774:MSE:HG2	1.98	0.64
1:B:200:ARG:NH2	1:B:359:PRO:HD3	2.12	0.64
1:A:769:THR:HG23	1:A:772:LEU:HD13	1.79	0.64
1:B:237:ALA:HA	1:B:240:ILE:HB	1.79	0.64
1:B:364:THR:O	1:B:368:LEU:N	2.23	0.64
1:A:423:ARG:HD3	1:A:424:GLU:N	2.12	0.64
1:B:446:ALA:HB2	1:C:518:ASP:HA	1.79	0.64
1:C:695:LEU:HB3	1:C:739:LYS:HD3	1.78	0.64
1:C:200:ARG:O	1:C:204:ILE:HG12	1.98	0.63
1:A:186:THR:HA	1:A:189:ALA:HB3	1.79	0.63
1:B:254:LEU:HA	1:B:291:ILE:O	1.99	0.63
1:B:260:GLY:HA3	1:C:343:LYS:HB3	1.80	0.63
1:A:889:VAL:HG13	1:A:891:PRO:HD3	1.81	0.63
1:C:417:ALA:HA	1:C:420:ARG:HD2	1.80	0.63
1:B:280:LEU:HD23	1:B:320:MSE:HE3	1.78	0.63
1:B:298:HIS:HB3	1:B:332:THR:HG21	1.80	0.63
1:C:345:ALA:O	1:C:349:ARG:HB2	1.98	0.63
1:C:408:ALA:O	1:C:412:ILE:N	2.30	0.63
1:C:426:GLN:HG2	1:C:480:TYR:HE1	1.63	0.63
1:A:618:ARG:HG3	1:A:651:LEU:HD11	1.79	0.63
1:B:332:THR:OG1	1:B:336:GLU:HG3	1.98	0.63
1:C:672:LEU:HD21	1:C:711:ALA:HA	1.79	0.63
1:A:823:ARG:HB2	1:A:874:GLU:HG3	1.80	0.63
1:A:708:VAL:HB	1:A:747:SER:HA	1.81	0.63
1:B:640:LYS:NZ	1:B:747:SER:O	2.28	0.63
1:B:662:ASP:HB3	1:B:665:GLU:HG2	1.81	0.63
1:C:419:VAL:HG22	1:C:423:ARG:HG3	1.81	0.63
1:A:882:LEU:HD12	1:A:886:LYS:HB3	1.81	0.62
1:B:219:PRO:HD2	1:B:328:CYS:O	1.99	0.62
1:B:419:VAL:HB	1:B:561:VAL:HG23	1.82	0.62
1:B:379:HIS:CA	1:B:420:ARG:HH12	2.06	0.62
1:A:599:ILE:HG23	1:A:600:VAL:HG23	1.82	0.62
1:A:789:ILE:HG12	1:A:790:SER:N	2.14	0.62
1:C:497:LEU:HA	1:C:500:LEU:HD23	1.82	0.62
1:C:784:GLU:HG3	1:C:788:ARG:HE	1.64	0.62
1:A:240:ILE:HG12	1:A:245:VAL:HB	1.81	0.62
1:A:825:VAL:HG22	1:A:874:GLU:HA	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:629:SER:HA	1:B:743:VAL:HG13	1.81	0.62
1:B:889:VAL:HG13	1:B:891:PRO:HD3	1.82	0.62
1:A:816:LYS:HA	1:A:819:THR:HG22	1.82	0.62
1:B:188:MSE:HB3	1:B:193:LYS:HB3	1.82	0.62
1:B:194:ILE:HG21	1:B:234:GLU:HB3	1.82	0.62
1:B:229:LYS:HE2	1:B:331:ALA:HB1	1.81	0.62
1:C:188:MSE:O	1:C:192:GLY:N	2.30	0.62
1:B:359:PRO:HD2	1:B:405:PRO:HG2	1.82	0.61
1:A:320:MSE:SE	1:A:324:GLY:HA3	2.50	0.61
1:B:375:TYR:CD2	1:C:214:ARG:HD3	2.35	0.61
1:B:434:GLU:HA	1:B:437:LEU:HG	1.80	0.61
1:C:426:GLN:OE1	1:C:477:ARG:NH1	2.32	0.61
1:C:569:ILE:HG12	1:C:572:ARG:HH21	1.64	0.61
1:C:889:VAL:HG13	1:C:891:PRO:HD3	1.82	0.61
1:A:798:LEU:HB2	1:A:842:TYR:HB2	1.81	0.61
1:C:257:LEU:HB2	1:C:292:LEU:HD11	1.82	0.61
1:C:826:ILE:HG23	1:C:877:VAL:HA	1.82	0.61
1:B:211:LEU:HA	1:B:217:ASN:O	1.99	0.61
1:B:569:ILE:O	1:B:573:TRP:HB2	2.01	0.61
1:A:666:TYR:HE2	1:A:674:ARG:HD2	1.65	0.61
1:C:227:VAL:HA	1:C:405:PRO:HG2	1.83	0.61
1:C:611:SER:OG	1:C:615:ARG:NH2	2.21	0.61
1:B:608:GLN:O	1:B:612:ASN:N	2.32	0.61
1:C:628:PRO:HD2	1:C:742:ILE:HA	1.82	0.61
1:B:423:ARG:HB3	1:B:558:THR:HA	1.82	0.60
1:C:294:VAL:HG21	1:C:300:LEU:HD11	1.83	0.60
1:B:599:ILE:HG23	1:B:600:VAL:HG23	1.82	0.60
1:C:273:GLU:HA	1:C:276:MSE:HB2	1.82	0.60
1:B:426:GLN:HG2	1:B:480:TYR:HE1	1.66	0.60
1:B:197:VAL:HA	2:B:1001:ADP:N1	2.16	0.60
1:B:652:PHE:HZ	1:B:702:ILE:HG23	1.66	0.60
1:B:866:LEU:HD12	1:B:871:GLN:HB2	1.84	0.60
1:C:358:GLU:HB2	1:C:403:ARG:NE	2.15	0.60
1:C:437:LEU:HD22	1:C:469:VAL:HG21	1.84	0.60
1:C:836:LYS:HD2	1:C:882:LEU:HD11	1.84	0.60
1:A:259:VAL:O	1:A:263:VAL:HG23	2.02	0.60
1:A:851:LEU:O	1:A:855:LEU:HB2	2.01	0.60
1:C:486:ARG:HD3	1:C:537:GLU:HB3	1.82	0.60
1:B:784:GLU:HG3	1:B:788:ARG:HE	1.67	0.59
1:C:184:ASP:HA	1:C:255:LEU:HA	1.83	0.59
1:C:457:ALA:O	1:C:461:GLN:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:509:ARG:HB3	1:C:510:MSE:SE	2.52	0.59
1:A:732:GLN:O	1:A:734:ARG:NE	2.29	0.59
1:B:567:ASN:HB3	1:B:578:VAL:HG11	1.83	0.59
1:B:871:GLN:HE22	1:B:890:LEU:HD11	1.67	0.59
1:A:798:LEU:HD23	1:A:842:TYR:HD1	1.68	0.59
1:B:720:LEU:HA	1:B:723:MSE:SE	2.53	0.59
1:C:601:VAL:HG11	1:C:805:LYS:HD3	1.85	0.59
1:C:798:LEU:HD21	1:C:844:PRO:HG3	1.84	0.59
1:A:774:MSE:HE2	1:A:786:LEU:HD23	1.85	0.59
1:B:402:ARG:HG2	1:C:733:GLY:O	2.02	0.59
1:A:677:GLY:O	1:A:692:THR:HA	2.03	0.59
1:B:420:ARG:HE	1:C:212:SER:HB2	1.67	0.59
1:B:490:ILE:HD11	1:B:533:ARG:HB2	1.84	0.59
1:C:497:LEU:HD13	1:C:526:GLU:HG2	1.83	0.59
1:C:715:VAL:HA	1:C:718:VAL:HG22	1.84	0.59
1:B:404:LEU:HB3	1:B:405:PRO:HD3	1.85	0.59
1:B:415:ALA:O	1:B:561:VAL:HG21	2.02	0.59
1:B:578:VAL:HA	1:B:581:LEU:HD13	1.83	0.59
1:A:863:LEU:HD23	1:B:621:LEU:HD11	1.85	0.59
1:B:319:PRO:O	1:B:323:ARG:N	2.32	0.59
1:C:403:ARG:HH12	1:C:696:ARG:HH12	1.51	0.59
1:A:211:LEU:HA	1:A:217:ASN:O	2.03	0.58
1:A:300:LEU:HB3	1:A:314:ALA:HB2	1.85	0.58
1:B:207:VAL:HA	1:B:210:ILE:HD12	1.84	0.58
1:A:231:THR:HA	1:A:234:GLU:HB2	1.83	0.58
1:B:777:LEU:HB3	1:B:781:PHE:HD2	1.67	0.58
1:A:853:ARG:NH2	1:B:792:VAL:HG22	2.19	0.58
1:B:379:HIS:NE2	1:B:413:ASP:OD1	2.34	0.58
1:A:441:LYS:O	1:A:444:ILE:HG12	2.02	0.58
1:A:579:THR:HG23	1:A:580:ARG:HG3	1.84	0.58
1:A:715:VAL:HA	1:A:718:VAL:HG22	1.85	0.58
1:B:414:GLU:OE1	1:C:732:GLN:NE2	2.37	0.58
1:A:178:LEU:N	1:A:282:GLU:OE1	2.35	0.58
1:C:568:GLU:HA	1:C:571:ALA:HB3	1.86	0.58
1:B:219:PRO:HG2	1:B:329:ILE:HG23	1.86	0.58
1:B:399:LEU:HD11	1:C:732:GLN:HB2	1.85	0.58
1:C:666:TYR:HE2	1:C:674:ARG:HD2	1.69	0.58
1:C:270:GLY:C	1:C:272:PHE:H	2.11	0.58
1:C:400:THR:HA	1:C:403:ARG:HA	1.84	0.58
1:A:781:PHE:HB2	1:A:786:LEU:HD11	1.86	0.58
1:B:216:LYS:HB3	1:B:352:GLN:HB3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:LEU:HD22	1:B:469:VAL:HG21	1.85	0.58
1:B:444:ILE:HB	1:B:459:LEU:HD22	1.86	0.58
1:C:608:GLN:O	1:C:612:ASN:N	2.34	0.58
1:B:816:LYS:HA	1:B:819:THR:HG22	1.84	0.57
1:C:579:THR:O	1:C:583:THR:OG1	2.15	0.57
1:A:771:GLU:O	1:A:775:ASN:ND2	2.37	0.57
1:B:183:ILE:O	1:B:256:SER:N	2.32	0.57
1:B:224:GLU:OE1	1:B:357:LYS:HG3	2.04	0.57
1:B:359:PRO:O	1:B:364:THR:HG23	2.04	0.57
1:B:831:GLU:O	1:B:835:ASP:N	2.36	0.57
1:C:280:LEU:HD23	1:C:320:MSE:HE3	1.85	0.57
1:C:823:ARG:HB2	1:C:874:GLU:HG3	1.85	0.57
1:B:196:PRO:HA	1:B:238:GLN:HE22	1.70	0.57
1:B:717:THR:O	1:B:721:GLN:N	2.29	0.57
1:C:843:SER:HB3	1:C:847:GLY:O	2.04	0.57
1:A:810:ARG:NH2	1:A:852:GLN:HB2	2.20	0.57
1:A:817:ARG:O	1:A:821:ASN:ND2	2.26	0.57
1:B:206:ARG:O	1:B:209:ARG:N	2.37	0.57
1:B:667:GLN:HA	1:B:710:LYS:HD2	1.85	0.57
1:B:854:LEU:HD13	1:B:857:LYS:HB3	1.85	0.57
1:A:379:HIS:HE1	1:B:214:ARG:HB2	1.69	0.57
1:A:490:ILE:HD11	1:A:533:ARG:HB2	1.85	0.57
1:B:347:PHE:O	1:B:351:PHE:HB2	2.05	0.57
1:B:420:ARG:NE	1:C:212:SER:HB2	2.20	0.57
1:B:426:GLN:HG2	1:B:480:TYR:CE1	2.39	0.57
1:C:397:ARG:HH22	1:C:652:PHE:C	2.13	0.57
1:A:773:VAL:O	1:A:777:LEU:N	2.21	0.57
1:B:378:HIS:CG	1:C:214:ARG:HG3	2.40	0.57
1:B:379:HIS:HE2	1:C:214:ARG:HB2	1.70	0.57
1:B:777:LEU:HB2	1:B:786:LEU:HD21	1.87	0.57
1:C:185:MSE:HE1	1:C:194:ILE:HG13	1.85	0.57
1:B:216:LYS:HD3	1:B:352:GLN:HB3	1.87	0.57
1:C:568:GLU:O	1:C:572:ARG:N	2.27	0.57
1:A:719:LEU:HD21	1:A:745:MSE:HE2	1.87	0.57
1:B:228:GLY:O	1:B:231:THR:OG1	2.17	0.57
1:B:228:GLY:HA2	2:B:1001:ADP:O2A	2.05	0.57
1:B:413:ASP:HB3	1:C:213:ARG:HE	1.68	0.57
1:A:459:LEU:HD13	1:A:463:LYS:HG3	1.87	0.56
1:A:568:GLU:O	1:A:572:ARG:N	2.25	0.56
1:B:292:LEU:HD23	1:B:294:VAL:HG12	1.87	0.56
1:B:270:GLY:C	1:B:272:PHE:H	2.11	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:MSE:HE2	1:A:234:GLU:HG2	1.87	0.56
1:A:229:LYS:HG3	1:A:331:ALA:HB1	1.85	0.56
1:A:484:ARG:HH12	1:A:488:LYS:HE2	1.70	0.56
1:A:854:LEU:HD13	1:A:857:LYS:HB3	1.85	0.56
1:B:227:VAL:O	2:B:1001:ADP:C8	2.56	0.56
1:B:239:ARG:HB3	1:B:244:ASP:OD2	2.05	0.56
1:B:395:ALA:HB2	1:B:411:LEU:HD22	1.88	0.56
1:C:774:MSE:HE1	1:C:792:VAL:HG11	1.86	0.56
1:C:777:LEU:HB3	1:C:781:PHE:HD2	1.70	0.56
1:C:837:LEU:O	1:C:841:GLY:N	2.39	0.56
1:A:317:LEU:HD13	1:A:321:LEU:HD12	1.86	0.56
1:A:866:LEU:HD12	1:A:871:GLN:HB2	1.86	0.56
1:C:638:THR:HG23	1:C:848:ALA:HB2	1.87	0.56
1:B:798:LEU:HD21	1:B:844:PRO:HG3	1.87	0.56
1:A:853:ARG:HH21	1:B:792:VAL:H	1.52	0.56
1:B:383:ILE:HG12	1:B:561:VAL:O	2.05	0.56
1:B:627:PRO:O	1:B:629:SER:N	2.38	0.56
1:C:358:GLU:HB2	1:C:403:ARG:HE	1.71	0.56
1:C:423:ARG:HB3	1:C:558:THR:HA	1.88	0.56
1:A:421:VAL:HG11	1:B:209:ARG:HE	1.71	0.56
1:B:421:VAL:HG22	1:C:209:ARG:HH21	1.71	0.56
1:C:220:VAL:HG11	1:C:337:TYR:HE1	1.71	0.56
1:C:402:ARG:O	1:C:407:SER:HB2	2.05	0.56
1:B:231:THR:HA	1:B:234:GLU:HB2	1.87	0.56
1:A:229:LYS:HA	1:A:232:ILE:HD12	1.88	0.56
1:A:321:LEU:HD22	1:A:350:ARG:HG2	1.88	0.56
1:C:219:PRO:HG2	1:C:329:ILE:HG12	1.87	0.56
1:C:228:GLY:HA3	2:C:1001:ADP:H8	1.71	0.56
1:A:479:LYS:HA	1:A:482:ARG:HB2	1.88	0.55
1:C:318:LYS:HB2	1:C:319:PRO:HD3	1.88	0.55
1:C:526:GLU:CD	1:C:526:GLU:H	2.14	0.55
1:B:200:ARG:O	1:B:204:ILE:HG12	2.07	0.55
1:B:293:PHE:HE2	1:B:331:ALA:HB2	1.65	0.55
1:C:199:GLY:HA3	1:C:367:ILE:HD11	1.88	0.55
1:C:679:PRO:HG2	1:C:682:TYR:CE1	2.42	0.55
1:A:228:GLY:HA3	2:A:1001:ADP:H8	1.70	0.55
1:B:321:LEU:HD22	1:B:350:ARG:HG2	1.88	0.55
1:C:406:ASP:HA	1:C:409:VAL:HG22	1.88	0.55
1:B:798:LEU:HD23	1:B:842:TYR:HD1	1.71	0.55
1:C:629:SER:HA	1:C:743:VAL:HG13	1.89	0.55
1:C:359:PRO:HB2	1:C:363:GLU:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:458:ARG:O	1:C:462:ALA:HB3	2.07	0.55
1:C:851:LEU:O	1:C:855:LEU:HB2	2.06	0.55
1:A:177:ASN:N	1:A:282:GLU:OE2	2.38	0.55
1:B:820:ASP:OD1	1:B:821:ASN:ND2	2.39	0.55
1:A:493:ALA:HA	1:A:496:LYS:HD2	1.89	0.55
1:B:419:VAL:HG22	1:B:423:ARG:HG3	1.88	0.55
1:C:817:ARG:O	1:C:821:ASN:ND2	2.37	0.55
1:B:718:VAL:O	1:B:722:LEU:HB2	2.07	0.55
1:C:814:ILE:O	1:C:818:LEU:HB2	2.06	0.55
1:B:371:LEU:HD12	2:B:1001:ADP:H2'	1.89	0.55
1:B:769:THR:HG23	1:B:772:LEU:HD13	1.90	0.54
1:A:294:VAL:HG13	1:A:330:GLY:HA2	1.88	0.54
1:B:695:LEU:HD22	1:B:739:LYS:HG2	1.90	0.54
1:B:493:ALA:HA	1:B:496:LYS:HD2	1.87	0.54
1:C:593:GLU:OE2	1:C:611:SER:HB2	2.07	0.54
1:C:233:VAL:HA	1:C:236:LEU:HB3	1.89	0.54
1:C:854:LEU:HD13	1:C:857:LYS:HB3	1.89	0.54
1:A:321:LEU:HD11	1:A:351:PHE:HE1	1.72	0.54
1:B:851:LEU:O	1:B:855:LEU:HB2	2.08	0.54
1:B:853:ARG:NH2	1:C:792:VAL:HG22	2.23	0.54
1:A:199:GLY:HA3	1:A:367:ILE:HD11	1.89	0.54
1:A:814:ILE:HA	1:A:817:ARG:HE	1.73	0.54
1:B:652:PHE:CZ	1:B:702:ILE:HG23	2.42	0.54
1:B:691:LEU:HD11	1:B:705:PHE:HZ	1.72	0.54
1:B:843:SER:HB3	1:B:847:GLY:O	2.08	0.54
1:C:231:THR:HA	1:C:234:GLU:HB2	1.90	0.54
1:C:531:ILE:O	1:C:535:GLU:HG2	2.07	0.54
1:A:562:GLY:H	1:A:565:GLN:HB2	1.72	0.54
1:A:641:THR:HG23	1:A:704:LEU:HD13	1.88	0.54
1:B:594:GLN:O	1:B:598:LYS:HB2	2.07	0.54
1:C:360:SER:N	1:C:363:GLU:HB2	2.23	0.54
1:C:846:TYR:O	1:C:849:ARG:NH1	2.39	0.54
1:A:631:LEU:HD22	1:A:745:MSE:SE	2.57	0.54
1:C:441:LYS:O	1:C:441:LYS:NZ	2.31	0.54
1:C:774:MSE:HE2	1:C:786:LEU:HD23	1.90	0.54
1:B:617:GLN:HG2	1:B:628:PRO:HD3	1.90	0.53
1:A:478:GLU:O	1:A:482:ARG:N	2.41	0.53
1:B:418:ALA:HA	1:C:209:ARG:CZ	2.39	0.53
1:B:568:GLU:H	1:B:568:GLU:CD	2.16	0.53
1:C:403:ARG:HH22	1:C:696:ARG:HH22	1.55	0.53
1:B:543:ALA:HA	1:B:546:ASN:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:605:GLU:HA	1:A:608:GLN:HB2	1.90	0.53
1:A:434:GLU:HA	1:A:437:LEU:HG	1.91	0.53
1:B:300:LEU:HB3	1:B:314:ALA:HB2	1.91	0.53
1:B:378:HIS:CB	1:C:214:ARG:HG3	2.38	0.53
1:C:577:PRO:O	1:C:579:THR:HG22	2.09	0.53
1:C:691:LEU:HD11	1:C:705:PHE:HZ	1.74	0.53
1:C:769:THR:HG23	1:C:772:LEU:HD13	1.90	0.53
1:A:660:ARG:NH1	1:B:784:GLU:OE1	2.42	0.53
1:C:478:GLU:O	1:C:482:ARG:N	2.42	0.53
1:A:663:MSE:SE	1:A:705:PHE:HB3	2.58	0.53
1:B:291:ILE:HA	1:B:327:HIS:O	2.08	0.53
1:A:705:PHE:O	1:A:746:THR:OG1	2.20	0.53
1:B:864:ALA:HB2	1:C:621:LEU:HG	1.90	0.53
1:C:652:PHE:HB3	1:C:700:PHE:HB3	1.91	0.53
1:A:476:LEU:O	1:A:480:TYR:HB3	2.08	0.53
1:B:184:ASP:HA	1:B:255:LEU:HA	1.89	0.53
1:B:254:LEU:HD21	1:B:293:PHE:HB3	1.90	0.53
1:B:339:LYS:HD3	1:B:340:TYR:CZ	2.44	0.53
1:A:421:VAL:HG11	1:B:209:ARG:NE	2.24	0.53
1:C:537:GLU:HA	1:C:540:ALA:HB3	1.89	0.53
1:C:652:PHE:HZ	1:C:702:ILE:HG12	1.74	0.53
1:C:866:LEU:HB3	1:C:871:GLN:HB3	1.91	0.53
1:A:270:GLY:C	1:A:272:PHE:H	2.17	0.52
1:A:381:VAL:HG13	1:A:419:VAL:HG11	1.91	0.52
1:B:264:ALA:O	1:B:275:ARG:NH2	2.36	0.52
1:B:437:LEU:O	1:B:441:LYS:N	2.41	0.52
1:B:716:LEU:HD22	1:B:719:LEU:HD23	1.92	0.52
1:A:383:ILE:HG21	1:A:387:ALA:HB3	1.90	0.52
1:A:640:LYS:HZ2	1:A:748:ASN:HA	1.74	0.52
1:B:420:ARG:HA	1:B:423:ARG:HH11	1.74	0.52
1:B:420:ARG:HG2	1:B:421:VAL:N	2.24	0.52
1:C:476:LEU:O	1:C:480:TYR:HB3	2.09	0.52
1:A:406:ASP:HA	1:A:409:VAL:HG22	1.91	0.52
1:B:198:ILE:HG21	1:B:367:ILE:HA	1.91	0.52
1:B:228:GLY:HA2	2:B:1001:ADP:PA	2.49	0.52
1:B:262:LEU:HD13	1:B:276:MSE:SE	2.60	0.52
1:B:490:ILE:HA	1:B:493:ALA:HB3	1.89	0.52
1:B:617:GLN:O	1:B:623:ASN:ND2	2.41	0.52
1:A:828:LYS:HG2	1:A:879:HIS:NE2	2.24	0.52
1:B:337:TYR:CE1	1:B:353:GLN:HB3	2.45	0.52
1:C:594:GLN:O	1:C:598:LYS:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:THR:N	2:A:1001:ADP:O3B	2.43	0.52
1:B:280:LEU:HD21	1:B:316:LEU:HB3	1.92	0.52
1:A:301:MSE:H	1:A:301:MSE:SE	2.43	0.52
1:A:400:THR:HA	1:A:403:ARG:HA	1.92	0.52
1:A:571:ALA:HB1	1:A:577:PRO:HA	1.90	0.52
1:B:228:GLY:HA2	2:B:1001:ADP:O5'	2.09	0.52
1:B:394:LEU:HD23	1:B:570:VAL:HG21	1.92	0.52
1:B:568:GLU:HA	1:B:571:ALA:HB3	1.90	0.52
2:B:1001:ADP:H2'	2:B:1001:ADP:N3	2.23	0.52
1:A:379:HIS:HA	1:A:420:ARG:HH22	1.74	0.52
1:A:577:PRO:O	1:A:579:THR:HG22	2.10	0.52
1:A:652:PHE:HZ	1:A:702:ILE:HG12	1.73	0.52
1:A:695:LEU:O	1:A:739:LYS:NZ	2.34	0.52
1:B:657:SER:HB3	1:B:701:SER:HA	1.91	0.52
1:A:525:PRO:O	1:A:529:ALA:N	2.38	0.52
1:A:828:LYS:HG2	1:A:879:HIS:CE1	2.45	0.52
1:B:570:VAL:HB	1:B:581:LEU:HD21	1.91	0.52
1:B:611:SER:O	1:B:615:ARG:NE	2.43	0.52
1:B:262:LEU:O	1:B:275:ARG:NH2	2.42	0.52
1:C:234:GLU:O	1:C:238:GLN:HB2	2.10	0.52
1:C:423:ARG:HD3	1:C:424:GLU:N	2.24	0.52
1:A:360:SER:H	1:A:363:GLU:HB2	1.75	0.52
1:C:493:ALA:O	1:C:496:LYS:HB2	2.10	0.52
1:A:196:PRO:HB3	1:A:238:GLN:HE22	1.76	0.51
1:A:627:PRO:O	1:A:629:SER:N	2.44	0.51
1:B:197:VAL:HG11	1:B:231:THR:O	2.10	0.51
1:B:441:LYS:O	1:B:444:ILE:HG12	2.09	0.51
1:B:481:GLU:HA	1:B:484:ARG:HB2	1.92	0.51
1:A:639:GLY:HA2	1:A:642:LEU:HB3	1.92	0.51
1:A:666:TYR:CE2	1:A:674:ARG:HD2	2.46	0.51
1:A:414:GLU:HB3	1:A:569:ILE:HD13	1.93	0.51
1:A:568:GLU:OE1	1:A:568:GLU:N	2.28	0.51
1:A:426:GLN:HG2	1:A:480:TYR:HE1	1.76	0.51
1:A:442:ILE:HG22	1:B:517:ALA:HB2	1.91	0.51
1:A:573:TRP:HA	1:A:573:TRP:CE3	2.46	0.51
1:B:562:GLY:N	1:B:565:GLN:HB2	2.12	0.51
1:C:220:VAL:HG13	1:C:353:GLN:HA	1.91	0.51
1:A:414:GLU:O	1:A:418:ALA:N	2.44	0.51
1:B:220:VAL:HG11	1:B:337:TYR:HE1	1.76	0.51
1:B:421:VAL:CG2	1:C:209:ARG:HH21	2.23	0.51
1:C:789:ILE:HG12	1:C:791:SER:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:ASN:OD1	1:A:469:VAL:N	2.41	0.51
1:B:375:TYR:CE2	1:C:214:ARG:HD3	2.45	0.51
1:B:605:GLU:O	1:B:609:SER:N	2.27	0.51
1:C:708:VAL:HG13	1:C:746:THR:O	2.10	0.51
1:A:360:SER:N	1:A:363:GLU:HB2	2.25	0.51
1:C:229:LYS:HG3	1:C:331:ALA:HB1	1.92	0.51
1:C:436:ARG:HG3	1:C:437:LEU:HD23	1.91	0.51
1:B:253:LYS:O	1:B:290:ILE:HG12	2.11	0.51
1:A:296:ALA:HA	1:A:332:THR:HB	1.93	0.51
1:A:481:GLU:HA	1:A:484:ARG:HB2	1.93	0.51
1:B:537:GLU:HG3	1:B:538:LYS:N	2.25	0.51
1:C:211:LEU:HG	1:C:219:PRO:CD	2.40	0.51
1:A:361:ILE:HG12	1:A:396:ALA:HB2	1.91	0.51
1:B:228:GLY:HA3	2:B:1001:ADP:C8	2.46	0.51
1:B:573:TRP:HA	1:B:573:TRP:CE3	2.46	0.51
1:B:871:GLN:HE22	1:B:890:LEU:HD21	1.76	0.51
1:A:567:ASN:HB3	1:A:578:VAL:HG11	1.92	0.50
1:A:886:LYS:HB3	1:A:886:LYS:HZ3	1.75	0.50
1:B:353:GLN:N	1:B:353:GLN:OE1	2.44	0.50
1:A:453:GLU:O	1:A:456:LYS:NZ	2.36	0.50
1:A:559:ASP:N	1:A:559:ASP:OD1	2.44	0.50
1:A:719:LEU:O	1:A:723:MSE:HG2	2.12	0.50
1:B:397:ARG:HH12	1:B:652:PHE:HA	1.74	0.50
1:B:706:ASP:HA	1:B:746:THR:OG1	2.11	0.50
1:C:339:LYS:HD3	1:C:340:TYR:CZ	2.47	0.50
1:C:573:TRP:HA	1:C:573:TRP:CE3	2.46	0.50
1:A:394:LEU:HD23	1:A:570:VAL:HG21	1.92	0.50
1:B:782:LEU:HD12	1:B:784:GLU:HB3	1.92	0.50
1:B:789:ILE:HG12	1:B:789:ILE:O	2.11	0.50
1:B:817:ARG:O	1:B:821:ASN:ND2	2.27	0.50
1:C:568:GLU:N	1:C:568:GLU:OE1	2.44	0.50
1:B:628:PRO:HG2	1:B:742:ILE:CG1	2.41	0.50
1:C:228:GLY:O	1:C:232:ILE:HG12	2.11	0.50
1:C:641:THR:HG23	1:C:704:LEU:HD13	1.93	0.50
1:C:777:LEU:HD22	1:C:781:PHE:HE2	1.75	0.50
1:A:318:LYS:HB2	1:A:319:PRO:HD3	1.92	0.50
1:B:301:MSE:HG3	1:B:314:ALA:HB3	1.92	0.50
1:B:486:ARG:HD3	1:B:537:GLU:HB3	1.94	0.50
1:C:211:LEU:HG	1:C:219:PRO:HD3	1.93	0.50
1:A:291:ILE:HA	1:A:327:HIS:O	2.12	0.50
1:C:299:LEU:O	1:C:312:ASP:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:567:ASN:HB3	1:C:578:VAL:HG11	1.92	0.50
1:C:677:GLY:O	1:C:692:THR:HA	2.11	0.50
1:C:825:VAL:HG22	1:C:874:GLU:HA	1.94	0.50
1:C:403:ARG:NH2	1:C:696:ARG:HH22	2.10	0.50
1:C:464:GLN:HA	1:C:467:GLN:HB2	1.92	0.50
1:A:271:GLU:O	1:A:275:ARG:HD3	2.11	0.50
1:A:397:ARG:HH12	1:A:652:PHE:HA	1.75	0.50
1:B:618:ARG:NH2	1:B:651:LEU:HG	2.27	0.50
1:C:224:GLU:HG3	1:C:225:PRO:N	2.27	0.50
1:A:651:LEU:HD23	1:A:742:ILE:HG21	1.93	0.50
1:C:627:PRO:O	1:C:629:SER:N	2.45	0.50
1:A:561:VAL:HA	1:A:565:GLN:HG3	1.94	0.49
1:B:299:LEU:HG	1:B:303:ALA:HA	1.95	0.49
1:B:464:GLN:HA	1:B:467:GLN:HB2	1.95	0.49
1:B:708:VAL:HG13	1:B:746:THR:O	2.12	0.49
1:A:197:VAL:HG22	1:A:235:GLY:HA3	1.93	0.49
1:C:262:LEU:HA	1:C:275:ARG:HH21	1.76	0.49
1:C:294:VAL:HG13	1:C:330:GLY:HA2	1.95	0.49
1:C:773:VAL:HG12	1:C:777:LEU:HG	1.95	0.49
1:A:268:TYR:HB2	1:A:271:GLU:OE1	2.12	0.49
1:B:379:HIS:NE2	1:C:214:ARG:HB2	2.28	0.49
1:B:515:ARG:HD2	1:B:519:LEU:HD11	1.93	0.49
1:C:379:HIS:CA	1:C:420:ARG:HH12	2.26	0.49
1:C:652:PHE:CZ	1:C:702:ILE:HG23	2.47	0.49
1:A:239:ARG:HB3	1:A:244:ASP:CG	2.38	0.49
1:A:301:MSE:SE	1:A:301:MSE:N	2.95	0.49
1:A:420:ARG:HA	1:A:423:ARG:HH11	1.77	0.49
1:A:773:VAL:HA	1:A:776:THR:OG1	2.12	0.49
1:A:810:ARG:HD3	1:A:855:LEU:HD22	1.95	0.49
1:A:814:ILE:HG13	1:A:817:ARG:NE	2.25	0.49
1:B:691:LEU:O	1:B:695:LEU:N	2.46	0.49
1:C:219:PRO:HD2	1:C:328:CYS:O	2.12	0.49
1:C:419:VAL:HG13	1:C:423:ARG:NH1	2.26	0.49
1:C:580:ARG:HA	1:C:583:THR:HB	1.95	0.49
1:B:237:ALA:O	1:B:241:VAL:HG22	2.13	0.49
1:B:338:ARG:HA	1:B:342:GLU:OE1	2.13	0.49
1:B:632:PHE:N	1:B:745:MSE:O	2.44	0.49
1:C:386:ALA:HA	1:C:389:VAL:HG22	1.95	0.49
1:C:581:LEU:H	1:C:581:LEU:HD12	1.78	0.49
1:C:592:MSE:HG2	1:C:593:GLU:OE1	2.12	0.49
1:C:651:LEU:HD23	1:C:742:ILE:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:691:LEU:HD11	1:A:705:PHE:HZ	1.78	0.49
1:B:425:SER:O	1:B:426:GLN:HG3	2.13	0.49
1:C:205:ARG:HB3	1:C:205:ARG:CZ	2.41	0.49
1:C:662:ASP:HB3	1:C:665:GLU:HG2	1.95	0.49
1:A:409:VAL:HA	1:A:412:ILE:HG22	1.93	0.49
1:A:608:GLN:OE1	1:A:612:ASN:ND2	2.42	0.49
1:B:245:VAL:HG21	1:B:250:ALA:HA	1.93	0.49
1:B:321:LEU:HD13	1:B:350:ARG:HG2	1.95	0.49
1:B:397:ARG:HG3	1:B:398:TYR:CE2	2.48	0.49
1:B:524:ILE:HD13	1:B:524:ILE:H	1.77	0.49
1:C:500:LEU:HD21	1:C:526:GLU:HG3	1.94	0.49
1:C:611:SER:HG	1:C:615:ARG:HH21	1.54	0.49
1:A:262:LEU:HB3	1:A:272:PHE:CE1	2.48	0.49
1:A:367:ILE:HG23	2:A:1001:ADP:C2	2.48	0.49
1:A:826:ILE:HG23	1:A:877:VAL:HA	1.94	0.49
1:B:213:ARG:HH12	1:B:352:GLN:NE2	2.10	0.49
1:B:337:TYR:HA	1:B:341:ILE:HG13	1.93	0.49
1:B:399:LEU:HD22	1:C:734:ARG:HH21	1.78	0.49
1:A:437:LEU:HD22	1:A:469:VAL:HG21	1.94	0.48
1:B:198:ILE:N	2:B:1001:ADP:N1	2.55	0.48
1:B:365:ILE:O	1:B:369:ARG:N	2.44	0.48
1:C:271:GLU:O	1:C:275:ARG:HD3	2.13	0.48
1:C:663:MSE:HB2	1:C:707:ALA:HB3	1.95	0.48
1:B:337:TYR:CD2	1:B:341:ILE:HB	2.48	0.48
1:B:651:LEU:HD23	1:B:742:ILE:HG21	1.94	0.48
1:C:775:ASN:O	1:C:778:ARG:HB2	2.13	0.48
1:C:403:ARG:HH12	1:C:696:ARG:NH1	2.11	0.48
1:C:668:GLU:O	1:C:672:LEU:HB2	2.12	0.48
1:C:810:ARG:HD3	1:C:855:LEU:HD22	1.95	0.48
1:A:227:VAL:HA	1:A:405:PRO:HG2	1.95	0.48
1:B:860:LEU:O	1:B:863:LEU:HB3	2.13	0.48
1:C:341:ILE:O	1:C:347:PHE:HB3	2.13	0.48
1:B:854:LEU:HA	1:B:857:LYS:HB2	1.95	0.48
1:C:365:ILE:HD13	1:C:389:VAL:HG12	1.95	0.48
1:C:390:ALA:O	1:C:394:LEU:HB2	2.14	0.48
1:C:695:LEU:HD22	1:C:739:LYS:HG2	1.95	0.48
1:A:197:VAL:HG11	1:A:231:THR:O	2.14	0.48
1:B:265:GLY:HA3	1:B:275:ARG:HH12	1.78	0.48
1:C:197:VAL:HG23	2:C:1001:ADP:N6	2.28	0.48
1:C:667:GLN:HA	1:C:710:LYS:HD2	1.95	0.48
1:C:866:LEU:HD12	1:C:871:GLN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:ARG:NH1	1:A:867:ILE:HG21	2.29	0.48
1:C:230:THR:N	2:C:1001:ADP:O3B	2.47	0.48
1:C:420:ARG:HG2	1:C:421:VAL:H	1.78	0.48
1:C:630:PHE:O	1:C:745:MSE:N	2.38	0.48
1:A:378:HIS:CG	1:B:214:ARG:HG3	2.48	0.48
1:A:853:ARG:NH2	1:B:792:VAL:H	2.12	0.48
1:B:559:ASP:OD1	1:B:559:ASP:N	2.47	0.48
1:B:828:LYS:HG2	1:B:879:HIS:NE2	2.29	0.48
1:C:781:PHE:HB2	1:C:786:LEU:HD11	1.95	0.48
1:A:200:ARG:O	1:A:204:ILE:HG12	2.14	0.48
1:B:231:THR:O	1:B:235:GLY:N	2.33	0.48
1:C:358:GLU:OE2	1:C:403:ARG:HG3	2.14	0.48
1:C:379:HIS:O	1:C:420:ARG:NH1	2.43	0.48
1:C:559:ASP:N	1:C:559:ASP:OD1	2.47	0.48
1:C:569:ILE:HG12	1:C:572:ARG:NH2	2.29	0.48
1:A:407:SER:O	1:A:411:LEU:HB2	2.13	0.47
1:C:237:ALA:HA	1:C:240:ILE:HB	1.96	0.47
1:C:379:HIS:C	1:C:420:ARG:HH12	2.21	0.47
1:A:226:GLY:O	1:A:405:PRO:HB2	2.13	0.47
1:A:229:LYS:HG2	2:A:1001:ADP:O3B	2.14	0.47
1:A:371:LEU:HA	1:A:371:LEU:HD23	1.71	0.47
1:B:581:LEU:HD12	1:B:581:LEU:H	1.78	0.47
1:C:219:PRO:O	1:C:329:ILE:HA	2.14	0.47
1:A:446:ALA:HB2	1:B:518:ASP:HA	1.96	0.47
1:B:493:ALA:HB1	1:B:530:ILE:HG22	1.96	0.47
1:C:423:ARG:NH2	1:C:559:ASP:OD2	2.47	0.47
1:A:283:ILE:HG23	1:A:290:ILE:HD12	1.96	0.47
1:A:444:ILE:HD12	1:A:463:LYS:HE3	1.97	0.47
1:A:467:GLN:O	1:A:470:GLU:HB3	2.14	0.47
1:B:220:VAL:HG21	1:B:337:TYR:CD1	2.49	0.47
1:B:263:VAL:HG11	1:C:343:LYS:HE3	1.95	0.47
1:A:345:ALA:O	1:A:349:ARG:HB2	2.15	0.47
1:A:490:ILE:HA	1:A:493:ALA:HB3	1.96	0.47
1:B:298:HIS:O	1:B:302:GLY:N	2.44	0.47
1:B:823:ARG:HB2	1:B:874:GLU:CG	2.45	0.47
1:A:178:LEU:HD13	1:A:282:GLU:OE1	2.15	0.47
1:A:353:GLN:OE1	1:A:353:GLN:N	2.47	0.47
1:A:710:LYS:HA	1:A:710:LYS:HD3	1.51	0.47
1:A:777:LEU:HB3	1:A:781:PHE:HD2	1.79	0.47
1:B:402:ARG:O	1:B:403:ARG:NE	2.48	0.47
1:C:198:ILE:HG23	1:C:199:GLY:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:652:PHE:HZ	1:C:702:ILE:HG23	1.79	0.47
1:A:198:ILE:HG23	1:A:199:GLY:H	1.80	0.47
1:A:585:GLU:HG3	1:A:586:LYS:HG2	1.96	0.47
1:B:210:ILE:O	1:B:217:ASN:HA	2.15	0.47
1:C:359:PRO:HD2	1:C:405:PRO:HG3	1.96	0.47
1:C:468:ASN:OD1	1:C:469:VAL:N	2.46	0.47
1:A:385:ASP:O	1:A:388:ILE:HG22	2.14	0.47
1:B:391:ALA:HB2	1:B:566:ILE:HG13	1.96	0.47
1:B:468:ASN:OD1	1:B:469:VAL:N	2.48	0.47
1:B:781:PHE:HB2	1:B:786:LEU:HD11	1.96	0.47
1:B:866:LEU:HB3	1:B:871:GLN:HB3	1.97	0.47
1:C:802:GLU:O	1:C:806:ILE:HG12	2.15	0.47
1:A:200:ARG:HG2	2:A:1001:ADP:N6	2.26	0.47
1:A:427:PRO:HB2	1:A:429:ILE:HG12	1.96	0.47
1:A:638:THR:HA	2:A:1002:ADP:C8	2.50	0.47
1:B:409:VAL:HG11	2:B:1001:ADP:O2'	2.15	0.47
1:B:564:ASP:O	1:B:567:ASN:N	2.48	0.47
1:B:694:ALA:HA	1:B:697:ARG:HB3	1.97	0.47
1:A:775:ASN:O	1:A:778:ARG:HB2	2.15	0.46
1:B:332:THR:CG2	1:B:336:GLU:HB2	2.44	0.46
1:B:664:SER:HA	1:B:710:LYS:HG3	1.96	0.46
1:C:387:ALA:O	1:C:391:ALA:N	2.48	0.46
1:C:383:ILE:HG21	1:C:387:ALA:HB3	1.96	0.46
1:C:419:VAL:HG23	1:C:557:ILE:HG22	1.97	0.46
1:C:666:TYR:HD2	1:C:671:SER:HG	1.63	0.46
1:A:375:TYR:CD2	1:B:214:ARG:HD3	2.50	0.46
1:A:581:LEU:HD12	1:A:581:LEU:H	1.80	0.46
1:B:608:GLN:OE1	1:B:612:ASN:ND2	2.48	0.46
1:C:438:ARG:O	1:C:442:ILE:HB	2.15	0.46
1:A:337:TYR:HA	1:A:341:ILE:HG13	1.97	0.46
1:B:420:ARG:HG2	1:B:421:VAL:H	1.80	0.46
1:B:457:ALA:O	1:B:461:GLN:HB3	2.15	0.46
1:B:515:ARG:HH11	1:B:519:LEU:HD11	1.81	0.46
1:B:708:VAL:HB	1:B:781:PHE:HZ	1.79	0.46
1:C:241:VAL:HG23	1:C:242:ASN:OD1	2.15	0.46
1:A:287:LYS:HA	1:A:287:LYS:HD3	1.60	0.46
1:A:410:ASP:OD2	1:B:732:GLN:NE2	2.48	0.46
1:A:871:GLN:HE22	1:A:890:LEU:HD21	1.81	0.46
1:B:777:LEU:HD22	1:B:781:PHE:CE2	2.45	0.46
1:B:828:LYS:HG2	1:B:879:HIS:CE1	2.50	0.46
1:B:837:LEU:O	1:B:841:GLY:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:420:ARG:HG2	1:C:421:VAL:N	2.30	0.46
1:C:714:GLU:O	1:C:718:VAL:HG13	2.16	0.46
1:C:798:LEU:HD23	1:C:842:TYR:HD1	1.80	0.46
1:A:421:VAL:HG21	1:B:209:ARG:HH21	1.81	0.46
1:A:537:GLU:HA	1:A:540:ALA:HB3	1.96	0.46
1:A:839:ALA:HA	1:A:842:TYR:CE2	2.51	0.46
1:B:257:LEU:HB2	1:B:292:LEU:HD21	1.97	0.46
1:B:293:PHE:CZ	1:B:331:ALA:HB2	2.49	0.46
1:B:782:LEU:HG	1:B:785:PHE:H	1.81	0.46
1:B:784:GLU:O	1:B:788:ARG:HG2	2.16	0.46
1:C:366:SER:HA	1:C:369:ARG:HD2	1.97	0.46
1:C:396:ALA:HA	1:C:404:LEU:HD21	1.98	0.46
1:B:360:SER:O	1:B:364:THR:N	2.35	0.46
1:B:519:LEU:O	1:B:523:ALA:HB2	2.15	0.46
1:B:605:GLU:HA	1:B:608:GLN:HB2	1.97	0.46
1:B:863:LEU:HD23	1:C:621:LEU:HD11	1.97	0.46
1:C:777:LEU:HD22	1:C:781:PHE:CE2	2.50	0.46
1:C:848:ALA:O	1:C:851:LEU:HB3	2.16	0.46
1:B:403:ARG:HA	1:B:403:ARG:HD3	1.73	0.46
1:C:299:LEU:HG	1:C:303:ALA:HA	1.97	0.46
1:C:475:PRO:O	1:C:479:LYS:N	2.28	0.46
1:C:705:PHE:O	1:C:746:THR:OG1	2.26	0.46
1:C:476:LEU:HG	1:C:480:TYR:HB3	1.97	0.46
1:A:804:ARG:HG2	1:A:834:LYS:HE2	1.98	0.45
1:B:216:LYS:HE3	1:B:348:GLU:HG2	1.98	0.45
1:C:490:ILE:HD12	1:C:530:ILE:HG23	1.96	0.45
1:C:567:ASN:HB3	1:C:578:VAL:CG1	2.46	0.45
1:A:228:GLY:HA3	2:A:1001:ADP:C8	2.51	0.45
1:A:402:ARG:HG3	1:B:734:ARG:NE	2.32	0.45
1:A:434:GLU:HB3	1:A:473:LEU:HD12	1.97	0.45
1:B:219:PRO:HG2	1:B:329:ILE:HG12	1.98	0.45
1:C:854:LEU:HA	1:C:857:LYS:HB2	1.98	0.45
1:A:379:HIS:CE1	1:B:214:ARG:HB2	2.51	0.45
1:A:537:GLU:HG3	1:A:538:LYS:N	2.32	0.45
1:B:218:ASN:O	1:B:351:PHE:HA	2.16	0.45
1:A:632:PHE:O	1:A:746:THR:HA	2.16	0.45
1:C:292:LEU:O	1:C:329:ILE:N	2.40	0.45
1:B:425:SER:HA	1:C:246:PRO:HA	1.99	0.45
1:C:206:ARG:O	1:C:209:ARG:N	2.49	0.45
1:C:444:ILE:HD12	1:C:463:LYS:HG3	1.98	0.45
1:C:463:LYS:O	1:C:467:GLN:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LEU:HG	1:A:219:PRO:CD	2.45	0.45
1:A:394:LEU:HD21	1:A:581:LEU:HD23	1.99	0.45
1:A:644:THR:HG23	1:A:702:ILE:HD12	1.99	0.45
1:A:386:ALA:HA	1:A:389:VAL:HG22	1.99	0.45
1:A:837:LEU:O	1:A:841:GLY:N	2.49	0.45
1:B:230:THR:HG22	1:B:234:GLU:OE1	2.16	0.45
1:B:345:ALA:O	1:B:349:ARG:HB2	2.17	0.45
1:B:708:VAL:HB	1:B:781:PHE:CZ	2.52	0.45
1:C:229:LYS:HE2	1:C:331:ALA:HB1	1.99	0.45
1:A:668:GLU:O	1:A:672:LEU:HB2	2.17	0.45
1:A:695:LEU:HB3	1:A:739:LYS:HD3	1.98	0.45
1:A:723:MSE:HE1	1:A:789:ILE:HA	1.99	0.45
1:B:216:LYS:O	1:B:352:GLN:HG2	2.16	0.45
1:B:283:ILE:HG23	1:B:290:ILE:HG23	1.98	0.45
1:C:197:VAL:HG22	1:C:235:GLY:HA3	1.99	0.45
1:C:608:GLN:OE1	1:C:612:ASN:ND2	2.49	0.45
1:A:239:ARG:HB3	1:A:244:ASP:OD2	2.17	0.44
1:A:402:ARG:HG2	1:B:733:GLY:HA2	2.00	0.44
1:B:690:GLN:O	1:B:690:GLN:NE2	2.49	0.44
1:C:361:ILE:HG12	1:C:396:ALA:CB	2.46	0.44
1:B:321:LEU:HB3	1:B:350:ARG:HD3	1.98	0.44
1:C:205:ARG:HB3	1:C:205:ARG:NH1	2.31	0.44
1:C:430:ILE:HG13	1:C:476:LEU:HD22	1.99	0.44
1:C:558:THR:O	1:C:560:VAL:N	2.48	0.44
1:A:266:SER:HB2	1:A:271:GLU:HG2	1.99	0.44
1:A:420:ARG:HG2	1:A:421:VAL:N	2.32	0.44
1:C:197:VAL:CG1	1:C:231:THR:HG22	2.48	0.44
1:C:784:GLU:O	1:C:788:ARG:HG2	2.18	0.44
1:C:873:ARG:N	1:C:876:GLU:OE1	2.50	0.44
1:A:185:MSE:CG	1:A:256:SER:HB3	2.45	0.44
1:A:222:ILE:HD12	1:A:334:LEU:HB3	2.00	0.44
1:A:260:GLY:HA3	1:B:344:ASP:OD1	2.17	0.44
1:A:614:ILE:HD12	1:A:614:ILE:HA	1.74	0.44
1:A:658:MSE:HG3	1:A:702:ILE:HD12	2.00	0.44
1:A:836:LYS:HD2	1:A:882:LEU:HD11	2.00	0.44
1:A:423:ARG:HD3	1:A:424:GLU:H	1.80	0.44
1:A:597:SER:HA	1:A:600:VAL:O	2.18	0.44
1:A:768:THR:HG23	1:A:769:THR:H	1.82	0.44
1:A:849:ARG:H	1:A:849:ARG:HG2	1.43	0.44
1:B:320:MSE:SE	1:B:324:GLY:HA3	2.67	0.44
1:B:361:ILE:HG12	1:B:396:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:476:LEU:O	1:B:480:TYR:HB3	2.18	0.44
1:A:568:GLU:HA	1:A:571:ALA:HB3	1.99	0.44
1:B:189:ALA:HB1	1:B:241:VAL:HG21	1.99	0.44
1:B:720:LEU:HD11	1:B:785:PHE:HD1	1.82	0.44
1:B:723:MSE:HE1	1:B:745:MSE:SE	2.68	0.44
1:B:798:LEU:HD23	1:B:842:TYR:CD1	2.52	0.44
1:C:666:TYR:O	1:C:672:LEU:HD13	2.18	0.44
1:C:828:LYS:HG2	1:C:879:HIS:NE2	2.33	0.44
1:A:178:LEU:O	1:A:182:CYS:N	2.46	0.44
1:B:188:MSE:HB2	1:B:194:ILE:HG12	2.00	0.44
1:B:300:LEU:O	1:B:314:ALA:N	2.51	0.44
1:B:413:ASP:CB	1:C:213:ARG:HE	2.31	0.44
1:C:178:LEU:HD11	1:C:283:ILE:HG13	1.99	0.44
1:C:321:LEU:HD22	1:C:350:ARG:HG2	2.00	0.44
1:C:337:TYR:CD2	1:C:341:ILE:HB	2.53	0.44
1:C:393:ASN:OD1	1:C:393:ASN:N	2.49	0.44
1:C:419:VAL:O	1:C:423:ARG:HG3	2.17	0.44
1:C:719:LEU:O	1:C:723:MSE:HG2	2.17	0.44
1:A:420:ARG:HE	1:B:212:SER:HB2	1.82	0.44
1:A:676:ILE:HD12	1:A:687:ALA:HB3	1.99	0.44
1:A:782:LEU:HD12	1:A:784:GLU:HB3	1.99	0.44
1:C:183:ILE:HD12	1:C:183:ILE:HA	1.89	0.44
1:C:359:PRO:HB2	1:C:363:GLU:CB	2.47	0.44
1:C:543:ALA:O	1:C:547:ALA:N	2.48	0.44
1:C:567:ASN:O	1:C:571:ALA:N	2.45	0.44
1:A:241:VAL:HG23	1:A:242:ASN:OD1	2.18	0.44
1:B:717:THR:HA	1:B:720:LEU:HB2	1.99	0.44
1:C:426:GLN:HA	1:C:480:TYR:OH	2.18	0.44
1:C:833:ALA:HA	1:C:882:LEU:HD13	1.99	0.44
1:A:371:LEU:O	1:A:375:TYR:HD1	2.01	0.43
1:A:446:ALA:CB	1:B:518:ASP:HA	2.48	0.43
1:A:453:GLU:HB3	1:A:456:LYS:HZ2	1.82	0.43
1:A:463:LYS:O	1:A:467:GLN:HB2	2.18	0.43
1:B:245:VAL:HG13	1:B:250:ALA:HB1	1.99	0.43
1:B:406:ASP:OD2	2:B:1001:ADP:H4'	2.18	0.43
1:B:803:ILE:HG13	1:B:842:TYR:HB3	2.00	0.43
1:A:273:GLU:HA	1:A:276:MSE:HB2	1.99	0.43
1:A:666:TYR:O	1:A:672:LEU:HD13	2.19	0.43
1:A:262:LEU:HB3	1:A:272:PHE:CD1	2.53	0.43
1:A:299:LEU:O	1:A:312:ASP:HB2	2.18	0.43
1:A:359:PRO:CG	1:A:405:PRO:HG3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:600:VAL:HG13	2:B:1002:ADP:N6	2.33	0.43
1:C:706:ASP:HA	1:C:746:THR:OG1	2.18	0.43
1:A:200:ARG:CG	2:A:1001:ADP:HN61	2.29	0.43
1:A:773:VAL:HG12	1:A:777:LEU:HG	2.00	0.43
1:B:266:SER:HA	1:B:271:GLU:HG2	2.01	0.43
1:A:503:LYS:NZ	1:A:519:LEU:HD13	2.33	0.43
1:B:198:ILE:HG22	2:B:1001:ADP:N1	2.33	0.43
1:B:832:GLU:CD	1:B:832:GLU:H	2.22	0.43
1:C:209:ARG:HA	1:C:212:SER:OG	2.19	0.43
1:C:246:PRO:O	1:C:250:ALA:HB2	2.17	0.43
1:C:426:GLN:NE2	1:C:481:GLU:OE1	2.51	0.43
1:B:287:LYS:HA	1:B:287:LYS:HD3	1.70	0.43
1:B:419:VAL:HG21	1:B:559:ASP:HA	2.01	0.43
1:B:846:TYR:OH	1:C:771:GLU:OE2	2.34	0.43
1:C:338:ARG:HA	1:C:342:GLU:OE1	2.18	0.43
1:C:401:SER:O	1:C:402:ARG:NE	2.49	0.43
1:A:419:VAL:HA	1:A:422:ALA:HB3	2.00	0.43
1:B:402:ARG:NE	1:B:402:ARG:HA	2.33	0.43
1:B:503:LYS:NZ	1:B:519:LEU:HD13	2.34	0.43
1:C:420:ARG:HG2	1:C:421:VAL:HG12	1.99	0.43
1:C:632:PHE:O	1:C:746:THR:HA	2.19	0.43
1:A:197:VAL:CG1	1:A:231:THR:HG22	2.48	0.43
1:A:202:GLU:H	1:A:202:GLU:HG2	1.62	0.43
1:A:257:LEU:HD22	1:A:259:VAL:HG22	2.00	0.43
1:A:477:ARG:O	1:A:481:GLU:HB2	2.19	0.43
1:A:626:GLN:HA	1:A:723:MSE:O	2.17	0.43
1:B:177:ASN:HB2	1:B:282:GLU:CD	2.44	0.43
1:B:211:LEU:HD23	1:B:217:ASN:O	2.18	0.43
1:B:216:LYS:HB3	1:B:352:GLN:HG2	2.01	0.43
1:B:298:HIS:CG	1:B:336:GLU:HB3	2.54	0.43
1:B:379:HIS:HA	1:B:420:ARG:NH1	2.15	0.43
1:B:421:VAL:HG21	1:C:205:ARG:HH22	1.84	0.43
1:B:427:PRO:HB2	1:B:429:ILE:HG12	1.99	0.43
1:C:287:LYS:HA	1:C:287:LYS:HD3	1.65	0.43
1:C:558:THR:C	1:C:560:VAL:H	2.24	0.43
1:A:184:ASP:HA	1:A:255:LEU:HA	2.01	0.43
1:A:378:HIS:CB	1:B:214:ARG:HG3	2.49	0.43
1:B:341:ILE:O	1:B:347:PHE:HB3	2.19	0.43
1:B:719:LEU:HD21	1:B:745:MSE:HE3	2.00	0.43
1:B:814:ILE:HA	1:B:817:ARG:HG2	2.00	0.43
1:B:271:GLU:O	1:B:275:ARG:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:TYR:HA	1:B:341:ILE:CG1	2.48	0.43
1:B:345:ALA:HB1	1:B:349:ARG:HD3	2.01	0.43
1:B:421:VAL:CG2	1:C:205:ARG:HH22	2.32	0.43
1:C:493:ALA:HA	1:C:496:LYS:CD	2.46	0.43
1:C:685:HIS:CG	1:C:686:ASP:H	2.36	0.43
1:A:246:PRO:C	1:A:248:ASN:N	2.77	0.42
1:A:567:ASN:HB3	1:A:578:VAL:CG1	2.49	0.42
1:A:666:TYR:HB3	1:A:671:SER:O	2.19	0.42
1:B:834:LYS:O	1:B:838:GLY:N	2.46	0.42
1:C:711:ALA:HB1	1:C:716:LEU:HB2	2.01	0.42
1:A:846:TYR:OH	1:B:771:GLU:OE2	2.26	0.42
1:B:226:GLY:O	1:B:406:ASP:HB2	2.19	0.42
1:B:407:SER:CB	1:C:734:ARG:HH22	2.32	0.42
1:B:456:LYS:HE3	1:B:456:LYS:HB2	1.93	0.42
1:C:301:MSE:HG3	1:C:314:ALA:HB3	2.01	0.42
1:C:365:ILE:HD11	1:C:389:VAL:HA	2.00	0.42
1:C:381:VAL:HG13	1:C:419:VAL:HG11	2.00	0.42
1:A:188:MSE:HA	1:A:191:GLU:HB3	2.00	0.42
1:A:205:ARG:CZ	1:A:205:ARG:HB3	2.50	0.42
1:A:691:LEU:O	1:A:695:LEU:N	2.50	0.42
1:B:312:ASP:OD1	1:B:312:ASP:N	2.52	0.42
1:B:386:ALA:HB3	1:B:563:PRO:HD3	2.00	0.42
1:C:635:PRO:HG3	1:C:797:ARG:HA	2.01	0.42
1:A:337:TYR:HA	1:A:341:ILE:CG1	2.50	0.42
1:A:391:ALA:HB2	1:A:566:ILE:HG13	2.01	0.42
1:A:601:VAL:HG11	1:A:805:LYS:HD3	2.02	0.42
1:A:798:LEU:H	1:A:798:LEU:HD22	1.84	0.42
1:A:865:ILE:O	1:A:869:ARG:N	2.50	0.42
1:B:471:GLU:HB3	1:B:472:GLU:OE2	2.19	0.42
1:B:658:MSE:HB2	1:B:702:ILE:HD11	2.00	0.42
1:A:188:MSE:HB3	1:A:193:LYS:HB3	2.01	0.42
1:A:206:ARG:O	1:A:209:ARG:N	2.52	0.42
1:A:420:ARG:HB3	1:A:420:ARG:NH1	2.34	0.42
1:B:270:GLY:C	1:B:272:PHE:N	2.77	0.42
1:C:652:PHE:CZ	1:C:702:ILE:HG12	2.55	0.42
1:A:561:VAL:HG13	1:A:565:GLN:HB2	2.00	0.42
1:A:789:ILE:HG12	1:A:790:SER:H	1.81	0.42
1:B:393:ASN:OD1	1:B:393:ASN:N	2.53	0.42
1:B:577:PRO:O	1:B:579:THR:HG22	2.19	0.42
1:B:679:PRO:HG2	1:B:682:TYR:CE1	2.55	0.42
1:C:532:LYS:HB3	1:C:532:LYS:HE3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ILE:HD12	1:A:183:ILE:HA	1.84	0.42
1:A:186:THR:HA	1:A:189:ALA:CB	2.48	0.42
1:A:229:LYS:HG2	2:A:1001:ADP:PB	2.60	0.42
1:B:597:SER:HA	1:B:600:VAL:O	2.19	0.42
1:C:341:ILE:HA	1:C:347:PHE:HD2	1.84	0.42
1:A:798:LEU:HD23	1:A:842:TYR:CD1	2.52	0.42
1:C:420:ARG:O	1:C:424:GLU:HB2	2.19	0.42
1:A:714:GLU:O	1:A:718:VAL:HG13	2.20	0.42
1:A:720:LEU:HD21	1:A:785:PHE:HD1	1.85	0.42
1:B:181:PHE:CZ	1:B:275:ARG:HG2	2.54	0.42
1:B:299:LEU:HG	1:B:312:ASP:OD2	2.20	0.42
1:B:320:MSE:O	1:B:325:GLN:N	2.53	0.42
1:B:831:GLU:OE1	1:B:834:LYS:HD2	2.20	0.42
1:A:420:ARG:HG2	1:A:421:VAL:H	1.84	0.42
1:B:230:THR:O	1:B:233:VAL:HG22	2.20	0.42
1:B:239:ARG:HB3	1:B:244:ASP:CG	2.44	0.42
1:B:420:ARG:O	1:B:424:GLU:HB2	2.20	0.42
1:B:483:GLU:OE2	1:B:541:ALA:HA	2.19	0.42
1:B:610:VAL:HA	1:B:630:PHE:CE2	2.55	0.42
1:B:695:LEU:HB3	1:B:739:LYS:HD3	2.02	0.42
1:C:419:VAL:HG13	1:C:423:ARG:HH11	1.84	0.42
1:A:494:LYS:O	1:A:497:LEU:N	2.52	0.41
1:A:607:VAL:HG22	1:A:643:LEU:HD11	2.02	0.41
1:B:419:VAL:HG22	1:B:423:ARG:CG	2.50	0.41
1:C:388:ILE:HA	1:C:391:ALA:HB3	2.02	0.41
1:C:459:LEU:O	1:C:463:LYS:N	2.39	0.41
1:A:233:VAL:HG21	1:A:293:PHE:CD2	2.56	0.41
1:A:401:SER:O	1:A:402:ARG:NE	2.53	0.41
1:A:603:GLN:OE1	1:A:796:ASN:N	2.43	0.41
1:B:390:ALA:O	1:B:394:LEU:HD13	2.20	0.41
1:B:429:ILE:O	1:B:433:LEU:HB3	2.20	0.41
1:B:642:LEU:HG	2:B:1002:ADP:C4	2.55	0.41
1:C:228:GLY:O	1:C:232:ILE:N	2.50	0.41
1:A:379:HIS:HA	1:A:420:ARG:NH2	2.35	0.41
1:B:652:PHE:HB3	1:B:700:PHE:HB3	2.02	0.41
1:C:420:ARG:NH1	1:C:420:ARG:HB3	2.35	0.41
1:A:197:VAL:HG23	2:A:1001:ADP:N6	2.36	0.41
1:A:299:LEU:HG	1:A:303:ALA:HA	2.02	0.41
1:A:564:ASP:O	1:A:567:ASN:N	2.53	0.41
1:B:188:MSE:SE	1:B:194:ILE:HG12	2.70	0.41
1:B:227:VAL:HG12	1:B:405:PRO:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:407:SER:O	1:B:411:LEU:HB2	2.20	0.41
1:C:176:GLU:OE1	1:C:180:LYS:HD2	2.20	0.41
1:C:239:ARG:HB3	1:C:244:ASP:CG	2.45	0.41
1:C:282:GLU:O	1:C:286:SER:HB3	2.20	0.41
1:C:386:ALA:HB3	1:C:563:PRO:HD3	2.03	0.41
1:A:452:ASP:O	1:A:454:ALA:N	2.53	0.41
1:A:507:ALA:HB1	1:A:516:ALA:HA	2.02	0.41
1:B:226:GLY:HA3	1:B:406:ASP:CB	2.50	0.41
1:C:849:ARG:H	1:C:849:ARG:HG2	1.63	0.41
1:B:197:VAL:CG2	1:B:235:GLY:HA3	2.51	0.41
1:C:518:ASP:OD1	1:C:518:ASP:N	2.54	0.41
1:A:542:ASP:HA	1:A:545:LEU:HB2	2.02	0.41
1:B:194:ILE:CG2	1:B:234:GLU:HB3	2.49	0.41
1:B:216:LYS:HE2	1:B:734:ARG:HD3	2.01	0.41
1:B:240:ILE:HG23	1:B:251:ALA:HA	2.03	0.41
1:B:403:ARG:O	1:B:407:SER:HB2	2.21	0.41
1:B:631:LEU:HD22	1:B:745:MSE:HB2	2.02	0.41
1:B:826:ILE:HG23	1:B:877:VAL:HA	2.02	0.41
1:C:224:GLU:OE1	1:C:403:ARG:HB3	2.20	0.41
1:A:204:ILE:HD13	1:A:232:ILE:HG23	2.02	0.41
1:A:254:LEU:HG	1:A:291:ILE:HB	2.02	0.41
1:A:390:ALA:O	1:A:394:LEU:HB2	2.21	0.41
1:A:530:ILE:HD13	1:A:530:ILE:HA	1.76	0.41
1:B:195:ASP:CG	1:B:374:LYS:HG2	2.46	0.41
1:B:196:PRO:HD2	1:B:374:LYS:HD3	2.03	0.41
1:B:254:LEU:HD21	1:B:293:PHE:H	1.86	0.41
1:C:196:PRO:HA	1:C:238:GLN:HE22	1.86	0.41
1:C:444:ILE:HD13	1:C:463:LYS:HA	2.02	0.41
1:A:210:ILE:O	1:A:217:ASN:HA	2.21	0.41
1:A:378:HIS:HB2	1:B:214:ARG:HG3	2.02	0.41
1:A:644:THR:HG23	1:A:702:ILE:CD1	2.50	0.41
1:A:672:LEU:HD21	1:A:711:ALA:HA	2.02	0.41
1:A:769:THR:O	1:A:772:LEU:HB3	2.21	0.41
1:B:219:PRO:O	1:B:329:ILE:HA	2.21	0.41
1:B:378:HIS:HB2	1:C:214:ARG:HG3	2.01	0.41
1:B:510:MSE:HE2	1:B:510:MSE:HB2	1.98	0.41
1:B:527:GLN:O	1:B:530:ILE:HG12	2.20	0.41
1:B:810:ARG:HD2	1:B:851:LEU:HD21	2.03	0.41
1:C:186:THR:HG21	1:C:253:LYS:HE3	2.03	0.41
1:C:426:GLN:HG2	1:C:480:TYR:CE1	2.51	0.41
1:C:666:TYR:CE2	1:C:674:ARG:HD2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:823:ARG:HB2	1:C:874:GLU:CG	2.50	0.41
1:A:444:ILE:HD12	1:A:463:LYS:HG2	2.02	0.41
1:A:664:SER:HA	1:A:710:LYS:HG3	2.03	0.41
1:A:802:GLU:O	1:A:806:ILE:HG12	2.20	0.41
1:B:257:LEU:HD12	1:B:292:LEU:HD11	2.03	0.41
1:B:371:LEU:HD23	1:B:371:LEU:HA	1.83	0.41
1:B:463:LYS:O	1:B:467:GLN:N	2.54	0.41
1:B:463:LYS:O	1:B:467:GLN:HB2	2.21	0.41
1:B:774:MSE:O	1:B:778:ARG:HG2	2.21	0.41
1:C:255:LEU:HD21	1:C:290:ILE:HG13	2.02	0.41
1:C:360:SER:OG	1:C:363:GLU:N	2.47	0.41
1:C:368:LEU:HD21	1:C:412:ILE:HD12	2.03	0.41
1:C:371:LEU:HD23	1:C:371:LEU:HA	1.94	0.41
1:C:661:PHE:HD2	1:C:662:ASP:H	1.68	0.41
1:C:745:MSE:HE1	1:C:789:ILE:HG21	2.03	0.41
1:A:191:GLU:OE1	1:A:193:LYS:N	2.54	0.40
1:A:400:THR:O	1:A:403:ARG:HD3	2.21	0.40
1:B:228:GLY:O	1:B:232:ILE:HD13	2.21	0.40
1:B:659:ILE:HG21	1:B:690:GLN:HE22	1.85	0.40
1:B:720:LEU:O	1:B:723:MSE:HG2	2.21	0.40
1:C:178:LEU:N	1:C:282:GLU:OE1	2.53	0.40
1:C:188:MSE:HB2	1:C:194:ILE:HG12	2.02	0.40
1:A:211:LEU:HD23	1:A:217:ASN:O	2.21	0.40
1:A:723:MSE:HG3	1:A:724:ASP:H	1.87	0.40
1:A:860:LEU:O	1:A:863:LEU:HB3	2.22	0.40
1:B:198:ILE:HG23	1:B:199:GLY:N	2.29	0.40
1:B:355:LEU:HD23	1:B:357:LYS:NZ	2.36	0.40
1:C:222:ILE:H	1:C:222:ILE:HD13	1.86	0.40
1:C:544:ALA:HB3	1:C:556:MSE:HE1	2.03	0.40
1:C:592:MSE:HE2	1:C:592:MSE:HB3	1.98	0.40
1:A:419:VAL:HG21	1:A:559:ASP:HA	2.03	0.40
1:A:845:VAL:HG13	1:A:846:TYR:CD2	2.56	0.40
1:B:366:SER:HA	1:B:369:ARG:HD2	2.03	0.40
1:B:401:SER:OG	1:B:402:ARG:N	2.54	0.40
1:B:446:ALA:HB3	1:C:521:TYR:HB3	2.04	0.40
1:B:691:LEU:HD11	1:B:705:PHE:CZ	2.56	0.40
1:B:777:LEU:CB	1:B:786:LEU:HD21	2.50	0.40
1:C:632:PHE:N	1:C:745:MSE:O	2.52	0.40
1:A:723:MSE:HG3	1:A:724:ASP:N	2.36	0.40
1:C:420:ARG:HA	1:C:423:ARG:HH11	1.86	0.40
1:C:433:LEU:O	1:C:437:LEU:HG	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:739:LYS:HD2	1:C:740:ASN:H	1.86	0.40
1:B:341:ILE:HA	1:B:347:PHE:CD2	2.57	0.40
1:C:436:ARG:NH2	1:C:469:VAL:HG11	2.36	0.40
1:C:456:LYS:HE3	1:C:456:LYS:HB2	1.97	0.40
1:C:669:ARG:O	1:C:673:SER:N	2.47	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	678/926 (73%)	585 (86%)	91 (13%)	2 (0%)	36	65
1	B	678/926 (73%)	594 (88%)	83 (12%)	1 (0%)	48	78
1	C	678/926 (73%)	587 (87%)	89 (13%)	2 (0%)	36	65
All	All	2034/2778 (73%)	1766 (87%)	263 (13%)	5 (0%)	43	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	403	ARG
1	A	403	ARG
1	A	525	PRO
1	C	359	PRO
1	B	426	GLN

5.3.2 Protein sidechains [i](#)

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	571/751 (76%)	495 (87%)	76 (13%)	4	20
1	B	571/751 (76%)	494 (86%)	77 (14%)	4	20
1	C	571/751 (76%)	493 (86%)	78 (14%)	3	19
All	All	1713/2253 (76%)	1482 (86%)	231 (14%)	4	20

All (231) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	178	LEU
1	A	182	CYS
1	A	188	MSE
1	A	197	VAL
1	A	202	GLU
1	A	217	ASN
1	A	231	THR
1	A	240	ILE
1	A	242	ASN
1	A	244	ASP
1	A	253	LYS
1	A	255	LEU
1	A	259	VAL
1	A	290	ILE
1	A	294	VAL
1	A	301	MSE
1	A	311	MSE
1	A	315	ASN
1	A	326	LEU
1	A	333	THR
1	A	339	LYS
1	A	350	ARG
1	A	352	GLN
1	A	353	GLN
1	A	356	VAL
1	A	358	GLU
1	A	363	GLU
1	A	367	ILE
1	A	403	ARG
1	A	421	VAL
1	A	423	ARG

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Mol	Chain	Res	Type
1	A	461	GLN
1	A	467	GLN
1	A	473	LEU
1	A	482	ARG
1	A	483	GLU
1	A	498	GLU
1	A	530	ILE
1	A	548	ASN
1	A	551	ASP
1	A	560	VAL
1	A	564	ASP
1	A	565	GLN
1	A	566	ILE
1	A	579	THR
1	A	580	ARG
1	A	605	GLU
1	A	614	ILE
1	A	616	LEU
1	A	631	LEU
1	A	640	LYS
1	A	644	THR
1	A	647	LEU
1	A	649	GLU
1	A	658	MSE
1	A	661	PHE
1	A	690	GLN
1	A	692	THR
1	A	719	LEU
1	A	743	VAL
1	A	746	THR
1	A	766	ASP
1	A	768	THR
1	A	774	MSE
1	A	789	ILE
1	A	798	LEU
1	A	801	ARG
1	A	816	LYS
1	A	818	LEU
1	A	821	ASN
1	A	832	GLU
1	A	849	ARG
1	A	873	ARG

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Mol	Chain	Res	Type
1	A	874	GLU
1	A	886	LYS
1	A	890	LEU
1	B	178	LEU
1	B	183	ILE
1	B	185	MSE
1	B	197	VAL
1	B	202	GLU
1	B	220	VAL
1	B	231	THR
1	B	232	ILE
1	B	236	LEU
1	B	240	ILE
1	B	244	ASP
1	B	253	LYS
1	B	255	LEU
1	B	259	VAL
1	B	290	ILE
1	B	294	VAL
1	B	299	LEU
1	B	312	ASP
1	B	315	ASN
1	B	326	LEU
1	B	333	THR
1	B	339	LYS
1	B	350	ARG
1	B	352	GLN
1	B	353	GLN
1	B	356	VAL
1	B	367	ILE
1	B	382	ASN
1	B	393	ASN
1	B	394	LEU
1	B	402	ARG
1	B	404	LEU
1	B	410	ASP
1	B	421	VAL
1	B	423	ARG
1	B	433	LEU
1	B	461	GLN
1	B	473	LEU
1	B	482	ARG

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Mol	Chain	Res	Type
1	B	483	GLU
1	B	498	GLU
1	B	524	ILE
1	B	530	ILE
1	B	532	LYS
1	B	545	LEU
1	B	560	VAL
1	B	566	ILE
1	B	579	THR
1	B	580	ARG
1	B	605	GLU
1	B	616	LEU
1	B	631	LEU
1	B	642	LEU
1	B	644	THR
1	B	659	ILE
1	B	661	PHE
1	B	690	GLN
1	B	692	THR
1	B	702	ILE
1	B	719	LEU
1	B	745	MSE
1	B	766	ASP
1	B	768	THR
1	B	774	MSE
1	B	775	ASN
1	B	789	ILE
1	B	798	LEU
1	B	801	ARG
1	B	816	LYS
1	B	818	LEU
1	B	821	ASN
1	B	832	GLU
1	B	849	ARG
1	B	852	GLN
1	B	873	ARG
1	B	886	LYS
1	B	890	LEU
1	C	178	LEU
1	C	197	VAL
1	C	222	ILE
1	C	224	GLU

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Mol	Chain	Res	Type
1	C	231	THR
1	C	232	ILE
1	C	240	ILE
1	C	244	ASP
1	C	253	LYS
1	C	255	LEU
1	C	259	VAL
1	C	290	ILE
1	C	294	VAL
1	C	301	MSE
1	C	315	ASN
1	C	326	LEU
1	C	333	THR
1	C	339	LYS
1	C	350	ARG
1	C	352	GLN
1	C	356	VAL
1	C	367	ILE
1	C	393	ASN
1	C	397	ARG
1	C	402	ARG
1	C	403	ARG
1	C	421	VAL
1	C	423	ARG
1	C	436	ARG
1	C	441	LYS
1	C	442	ILE
1	C	447	LEU
1	C	482	ARG
1	C	483	GLU
1	C	498	GLU
1	C	515	ARG
1	C	518	ASP
1	C	522	TYR
1	C	524	ILE
1	C	530	ILE
1	C	537	GLU
1	C	545	LEU
1	C	556	MSE
1	C	560	VAL
1	C	564	ASP
1	C	565	GLN

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Mol	Chain	Res	Type
1	C	566	ILE
1	C	573	TRP
1	C	579	THR
1	C	580	ARG
1	C	586	LYS
1	C	592	MSE
1	C	605	GLU
1	C	616	LEU
1	C	631	LEU
1	C	642	LEU
1	C	644	THR
1	C	659	ILE
1	C	661	PHE
1	C	670	HIS
1	C	690	GLN
1	C	692	THR
1	C	719	LEU
1	C	745	MSE
1	C	768	THR
1	C	774	MSE
1	C	789	ILE
1	C	796	ASN
1	C	798	LEU
1	C	801	ARG
1	C	816	LYS
1	C	818	LEU
1	C	821	ASN
1	C	832	GLU
1	C	849	ARG
1	C	873	ARG
1	C	886	LYS
1	C	890	LEU

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	298	HIS
1	A	379	HIS
1	A	467	GLN
1	A	565	GLN
1	A	567	ASN
1	A	775	ASN

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Mol	Chain	Res	Type
1	B	690	GLN
1	B	815	GLN
1	B	852	GLN
1	B	871	GLN
1	C	690	GLN
1	C	871	GLN

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 ⓘ

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ADP	C	1001	-	28,29,29	1.51	4 (14%)	43,45,45	1.88	7 (16%)
2	ADP	B	1002	-	28,29,29	1.46	5 (17%)	43,45,45	1.94	7 (16%)
2	ADP	C	1002	-	28,29,29	1.48	5 (17%)	43,45,45	1.91	7 (16%)
2	ADP	A	1001	-	28,29,29	1.49	4 (14%)	43,45,45	1.87	8 (18%)
2	ADP	B	1001	-	28,29,29	2.54	8 (28%)	43,45,45	2.58	19 (44%)
2	ADP	A	1002	-	28,29,29	1.46	5 (17%)	43,45,45	1.84	8 (18%)

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
2	ADP	C	1001	-	-	1/16/32/32	0/3/3/3
2	ADP	B	1002	-	-	4/16/32/32	0/3/3/3
2	ADP	C	1002	-	-	5/16/32/32	0/3/3/3
2	ADP	A	1001	-	-	2/16/32/32	0/3/3/3
2	ADP	B	1001	-	-	8/16/32/32	0/3/3/3
2	ADP	A	1002	-	-	4/16/32/32	0/3/3/3

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	ADP	PA-O3A	9.51	1.69	1.59
2	B	1001	ADP	C5-C4	5.55	1.49	1.39
2	C	1001	ADP	C5-C4	5.24	1.48	1.39
2	A	1001	ADP	C5-C4	5.13	1.48	1.39
2	C	1002	ADP	C5-C4	4.97	1.48	1.39
2	B	1002	ADP	C5-C4	4.89	1.47	1.39
2	A	1002	ADP	C5-C4	4.86	1.47	1.39
2	B	1001	ADP	C5-C6	3.48	1.50	1.41
2	C	1001	ADP	C5-C6	2.93	1.49	1.41
2	A	1001	ADP	C5-C6	2.88	1.49	1.41
2	A	1002	ADP	C5-C6	2.86	1.49	1.41
2	B	1002	ADP	C5-C6	2.80	1.48	1.41
2	C	1002	ADP	C5-C6	2.72	1.48	1.41
2	B	1001	ADP	C5-N7	-2.60	1.34	1.39
2	B	1001	ADP	C8-N7	2.55	1.36	1.31
2	B	1001	ADP	C1'-N9	2.51	1.53	1.46
2	C	1001	ADP	C8-N7	2.51	1.36	1.31
2	C	1002	ADP	C5-N7	-2.44	1.34	1.39
2	C	1002	ADP	PA-O3A	2.41	1.62	1.59
2	A	1001	ADP	C8-N7	2.40	1.36	1.31
2	B	1002	ADP	C5-N7	-2.39	1.34	1.39
2	B	1001	ADP	C8-N9	-2.39	1.33	1.37
2	A	1002	ADP	C5-N7	-2.34	1.34	1.39
2	A	1002	ADP	C8-N7	2.30	1.36	1.31
2	A	1001	ADP	C5-N7	-2.29	1.34	1.39
2	C	1002	ADP	C8-N7	2.26	1.36	1.31
2	B	1002	ADP	C8-N7	2.24	1.36	1.31
2	C	1001	ADP	C5-N7	-2.23	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	ADP	O4'-C1'	2.21	1.47	1.42
2	B	1002	ADP	PA-O3A	2.19	1.61	1.59
2	A	1002	ADP	PA-O3A	2.15	1.61	1.59

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	ADP	C5-C4-N3	-7.65	116.19	126.72
2	B	1002	ADP	C5-C4-N3	-6.88	117.24	126.72
2	C	1002	ADP	C5-C4-N3	-6.71	117.47	126.72
2	A	1001	ADP	C5-C4-N3	-6.70	117.49	126.72
2	C	1001	ADP	C5-C4-N3	-6.67	117.53	126.72
2	A	1002	ADP	C5-C4-N3	-6.23	118.13	126.72
2	B	1002	ADP	N3-C4-N9	5.39	136.34	127.17
2	B	1001	ADP	C4-C5-N7	-5.31	104.51	110.58
2	C	1002	ADP	N3-C4-N9	5.18	135.98	127.17
2	C	1001	ADP	N3-C4-N9	4.97	135.62	127.17
2	A	1001	ADP	N3-C4-N9	4.87	135.45	127.17
2	B	1001	ADP	N3-C4-N9	4.83	135.38	127.17
2	B	1001	ADP	C2-N3-C4	4.77	123.48	111.83
2	A	1002	ADP	N3-C4-N9	4.73	135.21	127.17
2	B	1001	ADP	N3-C2-N1	-4.67	121.51	128.58
2	B	1002	ADP	C2-N3-C4	4.00	121.59	111.83
2	C	1001	ADP	C2-N3-C4	3.97	121.53	111.83
2	A	1001	ADP	C2-N3-C4	3.93	121.42	111.83
2	C	1002	ADP	C2-N3-C4	3.85	121.23	111.83
2	B	1001	ADP	O2'-C2'-C3'	-3.79	99.67	111.82
2	A	1002	ADP	C2-N3-C4	3.77	121.05	111.83
2	A	1002	ADP	C4-C5-N7	-3.67	106.39	110.58
2	A	1001	ADP	C4-C5-N7	-3.66	106.40	110.58
2	C	1002	ADP	C4-C5-N7	-3.54	106.54	110.58
2	C	1001	ADP	C4-C5-N7	-3.52	106.55	110.58
2	B	1001	ADP	C2-N1-C6	3.45	124.40	118.73
2	B	1002	ADP	C4-C5-N7	-3.45	106.64	110.58
2	B	1001	ADP	O2A-PA-O3A	3.18	115.88	107.27
2	C	1001	ADP	N3-C2-N1	-3.16	123.81	128.58
2	B	1001	ADP	C5-N7-C8	3.11	108.33	103.45
2	A	1001	ADP	N3-C2-N1	-3.04	123.97	128.58
2	A	1002	ADP	N3-C2-N1	-3.00	124.04	128.58
2	B	1002	ADP	N3-C2-N1	-2.92	124.16	128.58
2	C	1002	ADP	N3-C2-N1	-2.89	124.21	128.58
2	B	1001	ADP	O3B-PB-O2B	2.84	118.46	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	ADP	O3'-C3'-C2'	-2.65	103.31	111.82
2	A	1002	ADP	C5-N7-C8	2.58	107.50	103.45
2	C	1002	ADP	C5-N7-C8	2.56	107.48	103.45
2	B	1001	ADP	O4'-C1'-N9	2.52	112.93	108.09
2	B	1002	ADP	C5-N7-C8	2.52	107.40	103.45
2	B	1001	ADP	C6-C5-N7	2.51	136.94	132.09
2	B	1002	ADP	C3'-C2'-C1'	2.50	106.20	101.46
2	C	1002	ADP	C3'-C2'-C1'	2.46	106.11	101.46
2	B	1001	ADP	O2A-PA-O5'	-2.44	96.50	107.57
2	A	1002	ADP	C3'-C2'-C1'	2.43	106.07	101.46
2	B	1001	ADP	C5-C4-N9	2.41	108.43	105.81
2	C	1001	ADP	C5-N7-C8	2.39	107.20	103.45
2	B	1001	ADP	O3B-PB-O1B	-2.35	101.66	110.83
2	A	1001	ADP	C5-N7-C8	2.35	107.14	103.45
2	B	1001	ADP	C3'-C2'-C1'	2.33	105.88	101.46
2	A	1001	ADP	C3'-C2'-C1'	2.32	105.85	101.46
2	B	1001	ADP	O3A-PA-O1A	2.24	117.44	110.70
2	B	1001	ADP	O2'-C2'-C1'	2.16	117.53	110.10
2	C	1001	ADP	C3'-C2'-C1'	2.11	105.46	101.46
2	A	1001	ADP	O4'-C1'-N9	2.05	112.03	108.09
2	A	1002	ADP	C6-C5-N7	2.01	135.97	132.09

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	ADP	C5'-O5'-PA-O1A
2	A	1002	ADP	C5'-O5'-PA-O2A
2	A	1002	ADP	C5'-O5'-PA-O3A
2	B	1001	ADP	C5'-O5'-PA-O1A
2	B	1001	ADP	C5'-O5'-PA-O2A
2	B	1001	ADP	C5'-O5'-PA-O3A
2	B	1001	ADP	O4'-C4'-C5'-O5'
2	B	1002	ADP	C5'-O5'-PA-O3A
2	C	1002	ADP	C5'-O5'-PA-O1A
2	C	1002	ADP	C5'-O5'-PA-O2A
2	C	1002	ADP	C5'-O5'-PA-O3A
2	B	1001	ADP	C2'-C1'-N9-C4
2	B	1001	ADP	C3'-C4'-C5'-O5'
2	B	1001	ADP	C2'-C1'-N9-C8
2	A	1002	ADP	C3'-C4'-C5'-O5'
2	A	1002	ADP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	B	1002	ADP	C2'-C1'-N9-C8
2	B	1002	ADP	C5'-O5'-PA-O1A
2	B	1002	ADP	C2'-C1'-N9-C4
2	C	1002	ADP	C2'-C1'-N9-C8
2	A	1001	ADP	C2'-C1'-N9-C8
2	C	1001	ADP	C2'-C1'-N9-C8
2	C	1002	ADP	C2'-C1'-N9-C4
2	B	1001	ADP	PB-O3A-PA-O2A

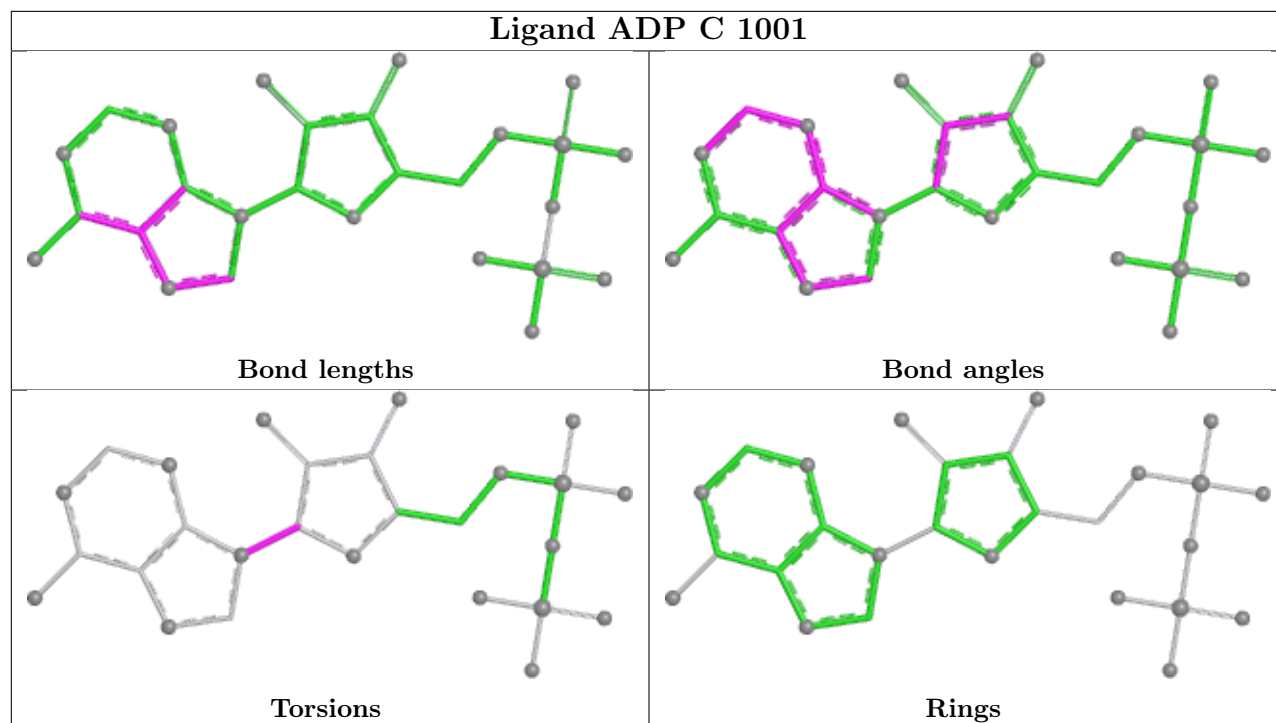
There are no ring outliers.

6 monomers are involved in 33 short contacts:

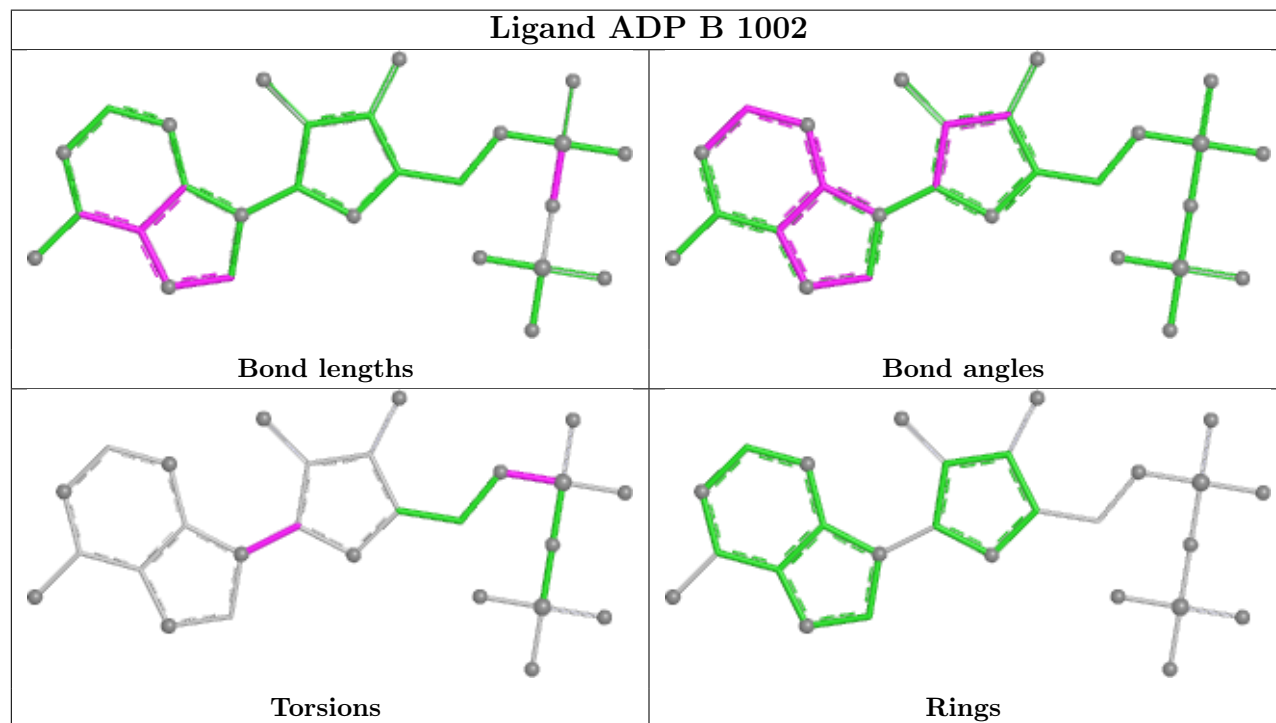
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1001	ADP	3	0
2	B	1002	ADP	2	0
2	C	1002	ADP	1	0
2	A	1001	ADP	10	0
2	B	1001	ADP	16	0
2	A	1002	ADP	1	0

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.

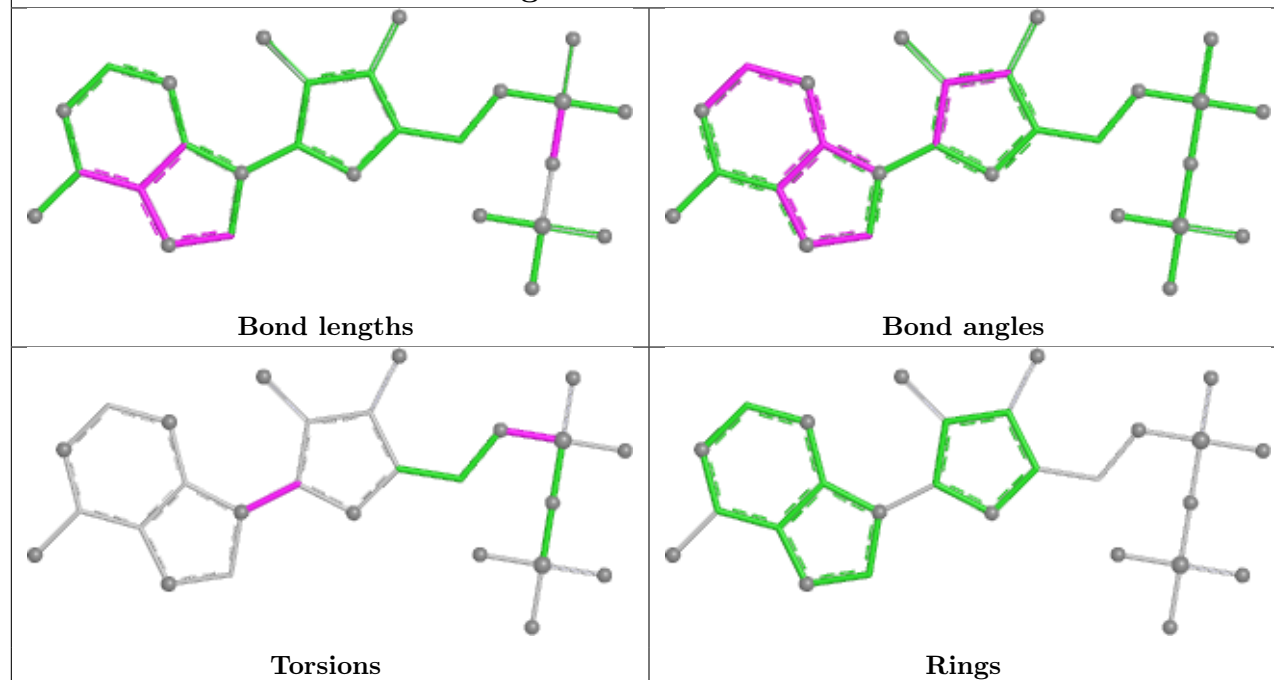
Ligand ADP C 1001



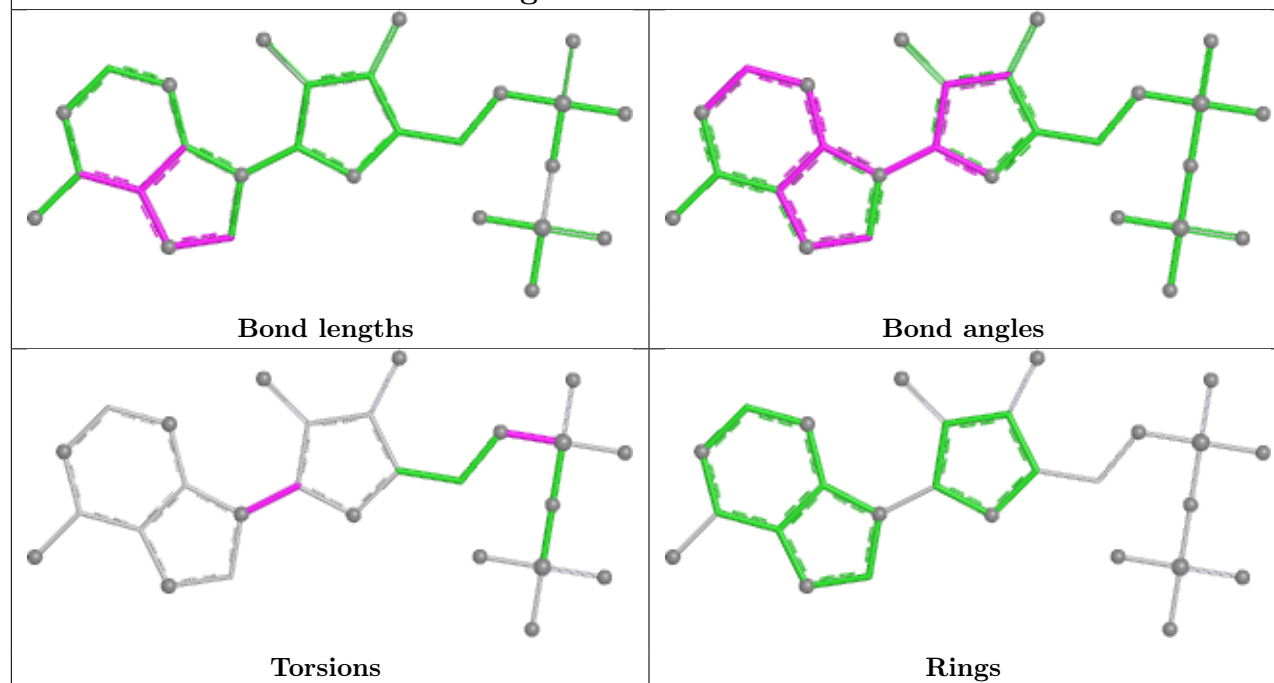
Ligand ADP B 1002

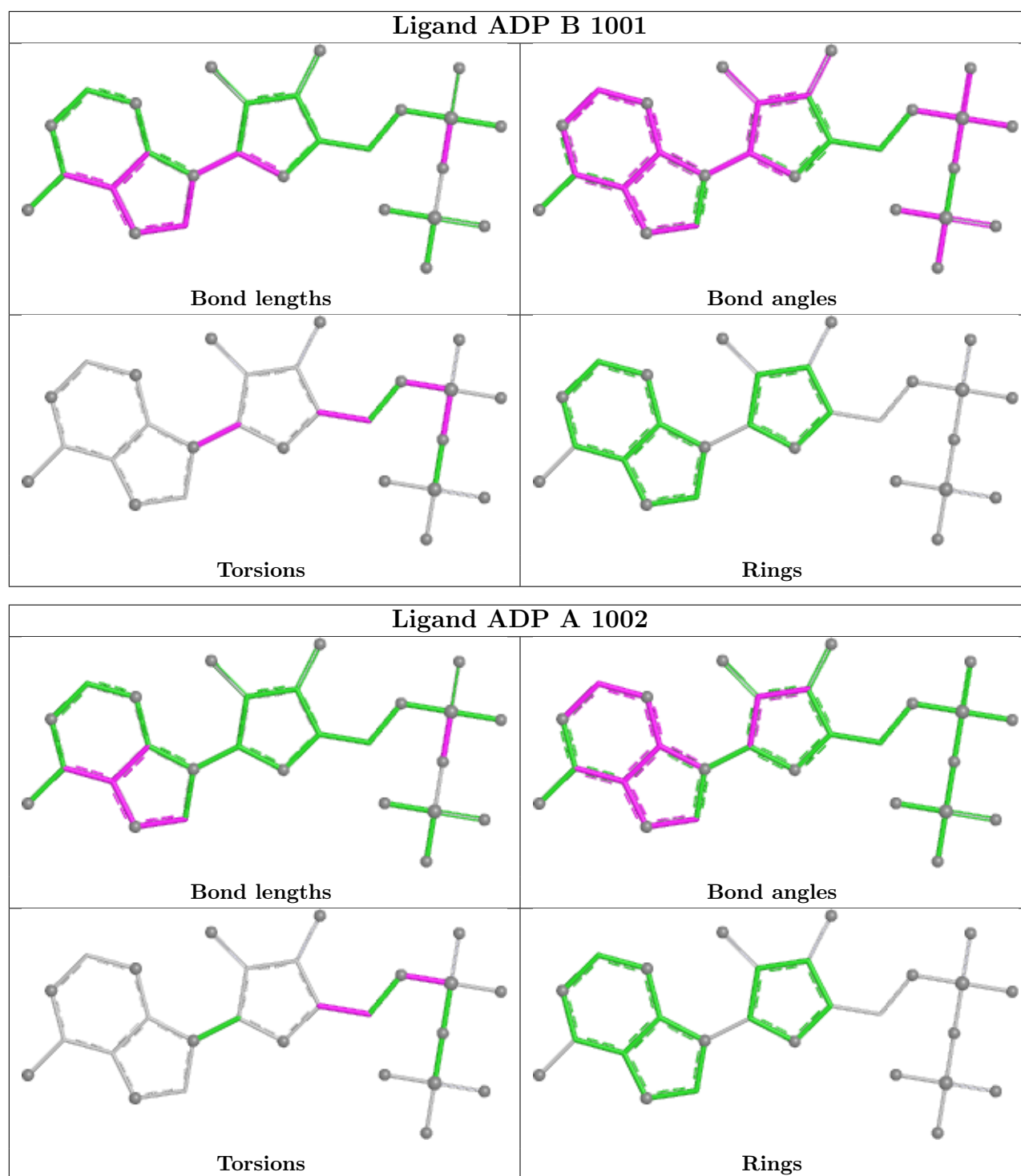


Ligand ADP C 1002



Ligand ADP A 1001





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	672/926 (72%)	-1.04	1 (0%) 92 86	102, 224, 282, 313	10 (1%)
1	B	672/926 (72%)	-1.12	0 100 100	1, 203, 268, 309	10 (1%)
1	C	672/926 (72%)	-1.11	0 100 100	38, 217, 272, 294	10 (1%)
All	All	2016/2778 (72%)	-1.09	1 (0%) 100 100	1, 217, 275, 313	30 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	637	GLY	2.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ADP	A	1001	27/27	0.99	0.04	173,225,244,252	0
2	ADP	A	1002	27/27	0.99	0.03	197,248,253,257	0

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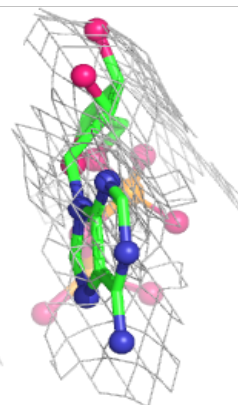
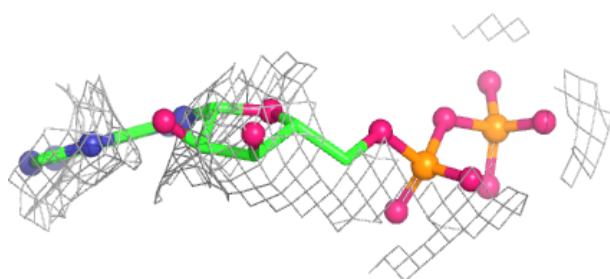
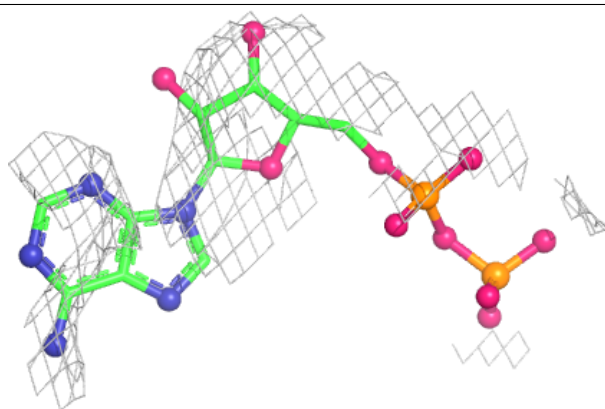
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ADP	B	1002	27/27	0.99	0.04	214,240,243,245	0
2	ADP	C	1001	27/27	0.99	0.04	169,220,243,244	0
2	ADP	C	1002	27/27	0.99	0.04	198,227,236,239	0
2	ADP	B	1001	27/27	1.00	0.02	2,6,13,16	0

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.

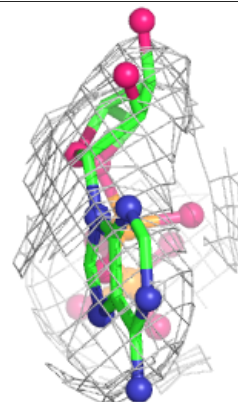
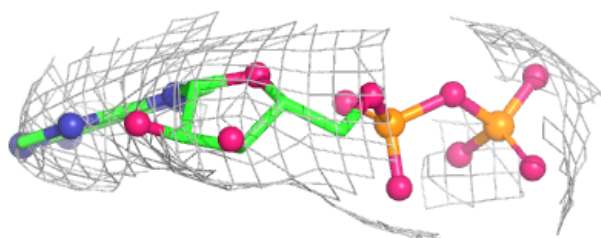
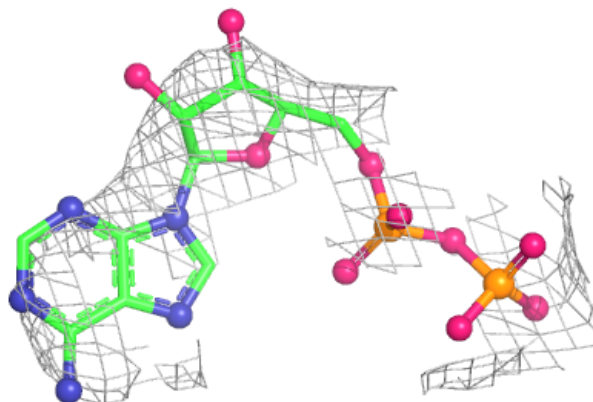
Electron density around ADP A 1001:

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

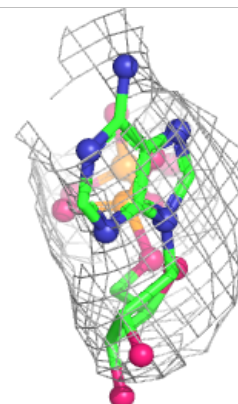
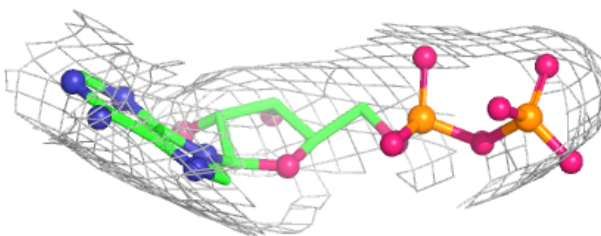
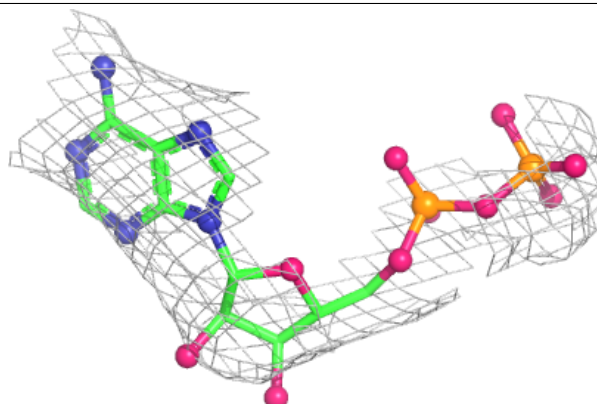


Electron density around ADP A 1002:

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

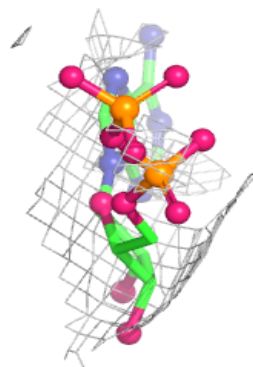
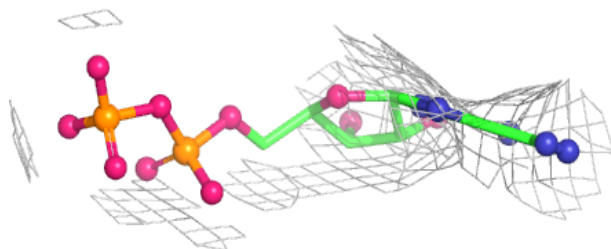
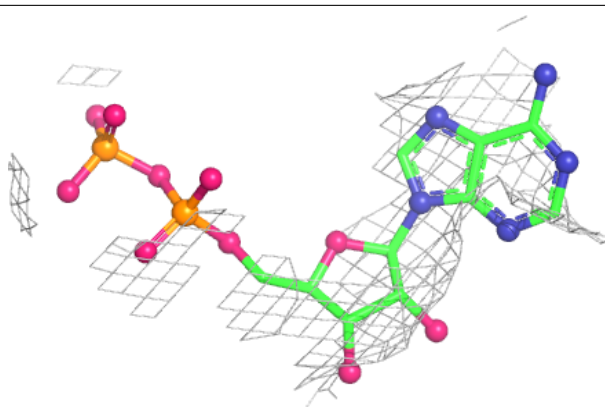
**Electron density around ADP B 1002:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

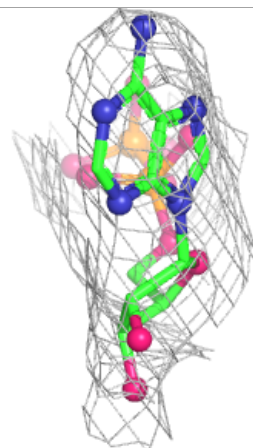
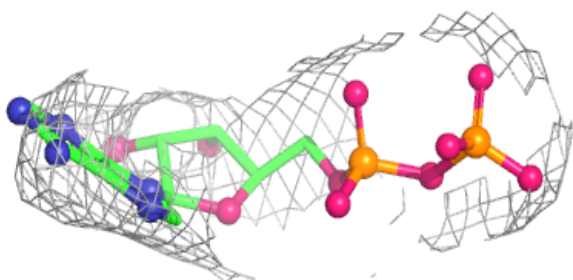
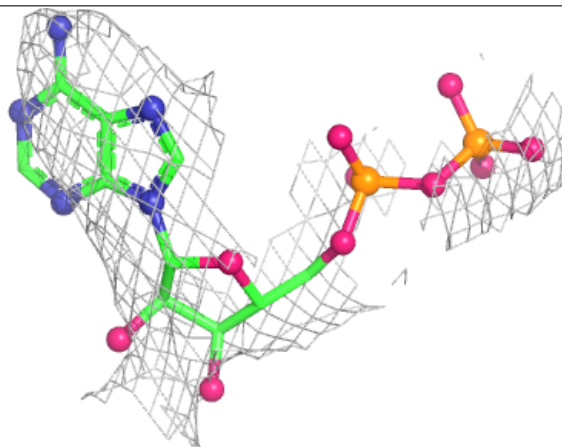


Electron density around ADP C 1001:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

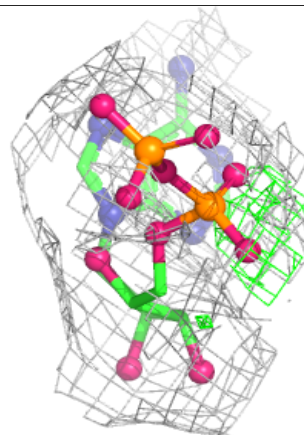
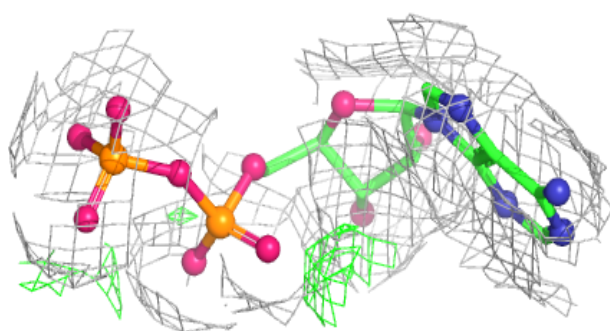
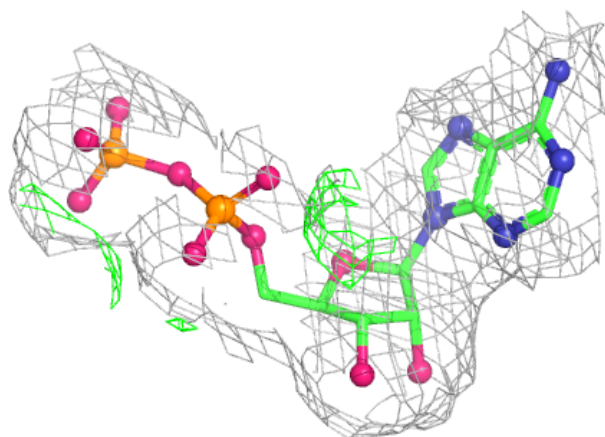
**Electron density around ADP C 1002:**

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



Electron density around ADP B 1001:

$2mF_o-DF_c$ (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.