



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 07:14 pm BST

PDB ID : 2Y8I  
Title : Structural basis for the allosteric interference of myosin function by mutants G680A and G680V of Dictyostelium myosin-2  
Authors : Preller, M.; Bauer, S.; Adamek, N.; Fujita-Becker, S.; Fedorov, R.; Geeves, M.A.; Manstein, D.J.  
Deposited on : 2011-02-07  
Resolution : 3.13 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

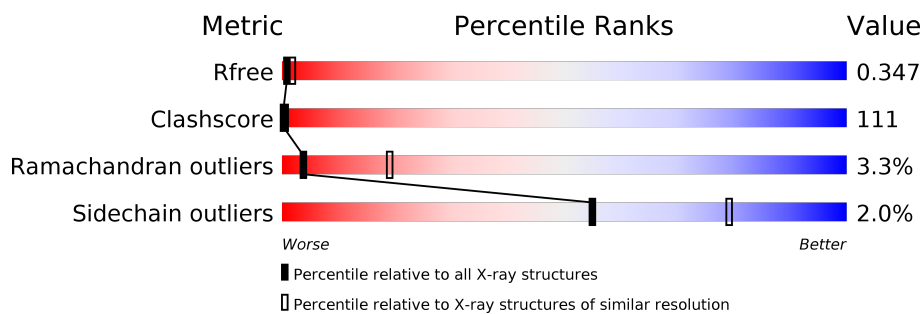
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.13 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))
$R_{free}$	130704	1626 (3.18-3.10)
Clashscore	141614	1735 (3.18-3.10)
Ramachandran outliers	138981	1677 (3.18-3.10)
Sidechain outliers	138945	1677 (3.18-3.10)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	X	758	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6376 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 MYOSIN-2 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	X	758	6090	3868	1053	1153	16	18	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	680	ALA	GLY	engineered mutation	UNP P08799

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	1	Total	Mg	0	0
			1	1		

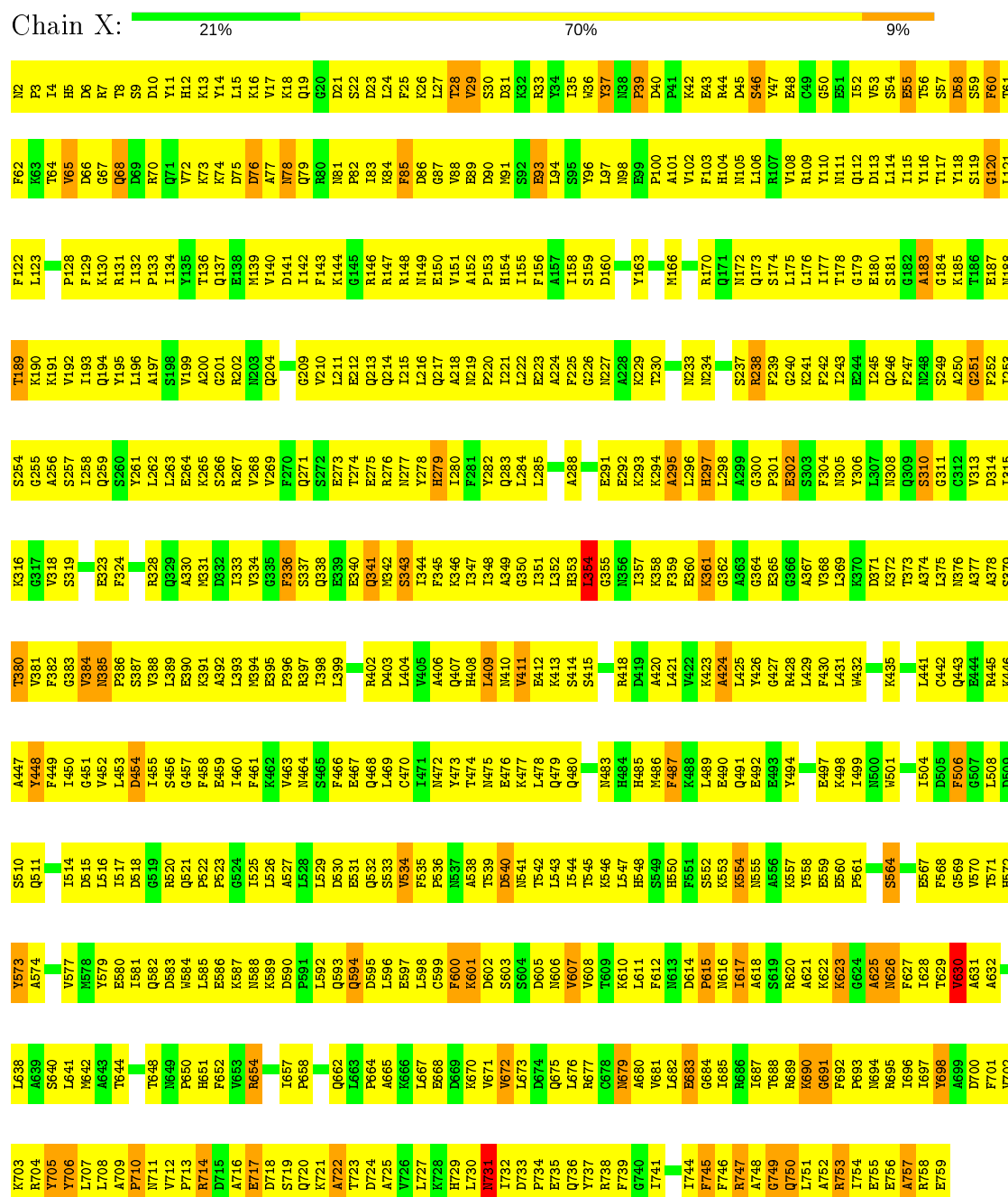
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	X	258	Total	O	0	0
			258	258		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

#### • Molecule 1: MYOSIN-2 HEAVY CHAIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.00Å 105.80Å 180.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.21 – 3.13 20.22 – 3.13	Depositor EDS
% Data completeness (in resolution range)	96.3 (20.21-3.13) 96.4 (20.22-3.13)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 3.16Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.245 , 0.337 0.315 , 0.347	Depositor DCC
$R_{free}$ test set	942 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.18 , 43.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.71	EDS
Total number of atoms	6376	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	X	0.54	0/6210	0.99	48/8379 (0.6%)

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	705	TYR	N-CA-C	8.37	133.59	111.00
1	X	28	THR	N-CA-C	-7.76	90.05	111.00
1	X	364	GLY	N-CA-C	-7.31	94.83	113.10
1	X	534	VAL	CB-CA-C	-7.29	97.55	111.40
1	X	251	GLY	N-CA-C	7.25	131.22	113.10
1	X	706	TYR	N-CA-CB	-7.09	97.84	110.60
1	X	594	GLN	N-CA-C	7.06	130.07	111.00
1	X	617	ILE	N-CA-C	7.04	130.01	111.00
1	X	58	ASP	CB-CA-C	-6.95	96.51	110.40
1	X	683	GLU	CB-CA-C	-6.74	96.91	110.40
1	X	749	GLY	N-CA-C	6.58	129.56	113.10
1	X	731	ASN	N-CA-C	6.38	128.22	111.00
1	X	78	ASN	N-CA-C	-6.35	93.86	111.00
1	X	698	TYR	CB-CA-C	-6.22	97.97	110.40
1	X	120	GLY	N-CA-C	-6.18	97.66	113.10
1	X	705	TYR	CB-CA-C	-6.18	98.05	110.40
1	X	343	SER	CB-CA-C	-6.03	98.64	110.10
1	X	55	GLU	N-CA-C	-6.01	94.77	111.00
1	X	354	LEU	CB-CA-C	5.98	121.56	110.20
1	X	59	SER	N-CA-CB	5.93	119.39	110.50
1	X	564	SER	CB-CA-C	-5.92	98.85	110.10
1	X	384	VAL	CB-CA-C	-5.89	100.20	111.40
1	X	553	LYS	N-CA-C	5.84	126.77	111.00
1	X	630	VAL	CB-CA-C	-5.80	100.37	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	722	ALA	CB-CA-C	-5.78	101.43	110.10
1	X	39	PRO	CB-CA-C	-5.75	97.64	112.00
1	X	607	VAL	CB-CA-C	-5.64	100.69	111.40
1	X	68	GLN	CB-CA-C	-5.62	99.16	110.40
1	X	654	ARG	NE-CZ-NH1	-5.62	117.49	120.30
1	X	424	ALA	CB-CA-C	-5.57	101.75	110.10
1	X	76	ASP	N-CA-CB	-5.54	100.63	110.60
1	X	679	ASN	CB-CA-C	-5.53	99.34	110.40
1	X	683	GLU	N-CA-C	5.50	125.84	111.00
1	X	85	PHE	N-CA-C	5.49	125.83	111.00
1	X	385	ASN	N-CA-C	5.49	125.82	111.00
1	X	310	SER	CB-CA-C	-5.48	99.69	110.10
1	X	627	PHE	N-CA-CB	-5.43	100.82	110.60
1	X	626	ASN	CB-CA-C	-5.41	99.58	110.40
1	X	627	PHE	N-CA-C	5.33	125.40	111.00
1	X	750	GLN	N-CA-C	-5.32	96.65	111.00
1	X	341	GLN	CB-CA-C	-5.26	99.88	110.40
1	X	29	VAL	N-CA-C	5.23	125.13	111.00
1	X	192	VAL	CB-CA-C	-5.22	101.49	111.40
1	X	672	VAL	CB-CA-C	-5.17	101.59	111.40
1	X	714	ARG	NE-CZ-NH1	-5.13	117.73	120.30
1	X	279	HIS	CB-CA-C	-5.11	100.18	110.40
1	X	380	THR	CB-CA-C	-5.10	97.82	111.60
1	X	717	GLU	N-CA-C	5.09	124.75	111.00

There are no chirality outliers.

There are no planarity outliers.

## 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	X	6090	0	6045	1344	3
2	X	27	0	12	5	0
3	X	1	0	0	0	0
4	X	258	0	0	233	2
All	All	6376	0	6057	1345	4



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 111.

All (1345) 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:X:27:LEU:HD12	1:X:28:THR:N	1.25	1.51
1:X:27:LEU:CD1	1:X:28:THR:H	1.26	1.48
1:X:35:ILE:CD1	1:X:77:ALA:HB1	1.42	1.47
1:X:35:ILE:HD11	1:X:77:ALA:CB	1.45	1.46
1:X:172:ASN:ND2	1:X:449:PHE:CD2	1.84	1.44
1:X:458:PHE:CE1	1:X:574:ALA:HB2	1.58	1.38
1:X:172:ASN:OD1	1:X:448:TYR:HA	1.23	1.35
1:X:85:PHE:O	1:X:88:VAL:HG13	1.26	1.31
1:X:432:TRP:CD1	1:X:610:LYS:NZ	2.00	1.28
1:X:623:LYS:HB3	1:X:628:ILE:CD1	1.64	1.27
1:X:284:LEU:CD2	1:X:348:ILE:HD11	1.61	1.27
1:X:345:PHE:O	1:X:348:ILE:HG13	1.17	1.27
1:X:222:LEU:C	4:X:2082:HOH:O	1.65	1.27
1:X:654:ARG:HG3	1:X:681:VAL:CG1	1.64	1.26
1:X:577:VAL:HG13	1:X:579:TYR:CE1	1.70	1.26
1:X:85:PHE:O	1:X:88:VAL:CG1	1.82	1.26
1:X:251:GLY:O	1:X:252:PHE:HD1	1.13	1.26
1:X:446:LYS:NZ	1:X:449:PHE:HB3	1.50	1.25
1:X:746:PHE:HB3	4:X:2248:HOH:O	1.35	1.25
1:X:544:ILE:HD13	1:X:581:ILE:CG1	1.66	1.25
1:X:172:ASN:ND2	1:X:449:PHE:HD2	1.24	1.24
1:X:117:THR:HG21	4:X:2046:HOH:O	1.26	1.24
1:X:247:PHE:CD1	1:X:253:ILE:HA	1.71	1.24
1:X:24:LEU:O	1:X:27:LEU:HD23	1.33	1.24
1:X:751:LEU:HA	4:X:2252:HOH:O	1.32	1.23
1:X:577:VAL:CG1	1:X:579:TYR:HE1	1.52	1.23
1:X:40:ASP:HB3	4:X:2022:HOH:O	1.07	1.22
1:X:449:PHE:CZ	1:X:648:THR:HG21	1.74	1.22
1:X:251:GLY:O	1:X:252:PHE:CD1	1.93	1.22
1:X:219:ASN:O	1:X:223:GLU:OE1	1.54	1.22
1:X:213:GLN:HB3	4:X:2078:HOH:O	1.34	1.21
1:X:357:ILE:CD1	1:X:375:LEU:HD12	1.70	1.21
1:X:222:LEU:O	4:X:2082:HOH:O	1.55	1.20
1:X:458:PHE:CE1	1:X:574:ALA:CB	2.25	1.20
1:X:702:VAL:HG13	4:X:2233:HOH:O	1.38	1.19
1:X:610:LYS:HB2	4:X:2198:HOH:O	1.43	1.18
1:X:548:HIS:HA	4:X:2180:HOH:O	1.44	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:736:GLN:O	1:X:747:ARG:HB2	1.41	1.17
1:X:458:PHE:HE1	1:X:574:ALA:CB	1.56	1.16
1:X:273:GLU:O	1:X:274:THR:HG22	1.45	1.16
1:X:432:TRP:HD1	1:X:610:LYS:NZ	1.39	1.15
1:X:147:ARG:HB2	1:X:150:GLU:HG2	1.18	1.15
1:X:122:PHE:CD1	1:X:654:ARG:HG2	1.80	1.15
1:X:166:MET:HA	1:X:173:GLN:NE2	1.61	1.14
1:X:593:GLN:O	4:X:2193:HOH:O	1.65	1.14
1:X:654:ARG:HG3	1:X:681:VAL:HG12	1.14	1.13
1:X:296:LEU:HD23	4:X:2104:HOH:O	1.49	1.13
1:X:58:ASP:CA	4:X:2029:HOH:O	1.96	1.13
1:X:14:TYR:CZ	1:X:133:PRO:HG2	1.83	1.13
1:X:85:PHE:C	4:X:2039:HOH:O	1.84	1.13
1:X:172:ASN:OD1	1:X:448:TYR:CA	1.96	1.13
1:X:725:ALA:HB1	4:X:2087:HOH:O	1.45	1.13
1:X:385:ASN:HB3	1:X:388:VAL:HG22	1.31	1.12
1:X:296:LEU:O	1:X:296:LEU:HD12	1.45	1.12
1:X:202:ARG:HB2	4:X:2077:HOH:O	1.47	1.12
1:X:733:ASP:OD1	1:X:734:PRO:HD2	1.46	1.12
1:X:692:PHE:CD1	4:X:2243:HOH:O	1.98	1.12
1:X:196:LEU:HD12	1:X:245:ILE:HD12	1.24	1.12
1:X:723:THR:HG21	4:X:2234:HOH:O	1.46	1.11
1:X:747:ARG:HB3	4:X:2250:HOH:O	1.51	1.11
1:X:679:ASN:ND2	4:X:2214:HOH:O	1.78	1.11
1:X:178:THR:HG22	4:X:2147:HOH:O	1.48	1.11
1:X:296:LEU:HB3	4:X:2104:HOH:O	1.48	1.11
1:X:25:PHE:HZ	4:X:2254:HOH:O	1.31	1.10
1:X:702:VAL:O	1:X:706:TYR:CD2	2.04	1.10
1:X:703:LYS:C	4:X:2219:HOH:O	1.89	1.10
1:X:172:ASN:CG	1:X:449:PHE:CD2	2.26	1.09
1:X:357:ILE:HD11	1:X:375:LEU:HD12	1.32	1.09
1:X:621:ALA:O	1:X:628:ILE:HG12	1.52	1.09
1:X:343:SER:O	1:X:347:ILE:HG12	1.51	1.09
1:X:238:ARG:HG2	1:X:278:TYR:HE1	0.95	1.09
1:X:689:ARG:HG3	1:X:693:PRO:HD3	1.24	1.09
1:X:313:VAL:HG23	1:X:314:ASP:H	1.13	1.09
1:X:623:LYS:HB3	1:X:628:ILE:HD11	1.28	1.09
1:X:719:SER:HB3	1:X:723:THR:HB	1.24	1.08
1:X:606:ASN:HB2	4:X:2197:HOH:O	1.51	1.08
1:X:398:ILE:CD1	1:X:407:GLN:HE21	1.65	1.08
1:X:238:ARG:HG2	1:X:278:TYR:CE1	1.87	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:357:ILE:CD1	1:X:375:LEU:CD1	2.32	1.08
1:X:724:ASP:HB3	4:X:2235:HOH:O	1.50	1.08
1:X:486:MET:O	1:X:490:GLU:HG2	1.53	1.07
1:X:166:MET:CA	1:X:173:GLN:HE22	1.68	1.07
1:X:121:LEU:C	4:X:2048:HOH:O	1.92	1.07
1:X:692:PHE:CG	4:X:2243:HOH:O	2.06	1.07
1:X:431:LEU:HD23	1:X:617:ILE:HG12	1.10	1.06
1:X:27:LEU:HD13	1:X:28:THR:HG23	1.36	1.06
1:X:594:GLN:HA	4:X:2193:HOH:O	1.56	1.06
1:X:695:ARG:HG2	1:X:745:PHE:HB3	1.31	1.05
1:X:84:LYS:NZ	1:X:704:ARG:HD2	1.71	1.05
1:X:257:SER:HB3	4:X:2095:HOH:O	1.56	1.05
1:X:14:TYR:CD2	4:X:2004:HOH:O	2.08	1.05
1:X:238:ARG:HG3	1:X:264:GLU:HB3	1.38	1.05
1:X:27:LEU:HB2	4:X:2016:HOH:O	1.57	1.04
1:X:689:ARG:HG3	1:X:693:PRO:CD	1.86	1.04
1:X:707:LEU:HD12	4:X:2221:HOH:O	1.56	1.04
1:X:296:LEU:HD11	1:X:298:LEU:CD1	1.88	1.03
1:X:424:ALA:O	1:X:428:ARG:HD2	1.57	1.03
1:X:544:ILE:CD1	1:X:581:ILE:HG13	1.88	1.03
1:X:130:LYS:HG3	1:X:132:ILE:HD11	1.37	1.03
1:X:296:LEU:HD11	1:X:298:LEU:HD11	1.39	1.03
1:X:196:LEU:CD1	1:X:245:ILE:HD12	1.89	1.03
1:X:27:LEU:HD13	4:X:2017:HOH:O	1.55	1.03
1:X:14:TYR:HD2	4:X:2004:HOH:O	1.38	1.02
1:X:577:VAL:CG1	1:X:579:TYR:CE1	2.34	1.02
1:X:431:LEU:CD2	1:X:617:ILE:HG12	1.90	1.02
1:X:692:PHE:CE1	4:X:2243:HOH:O	2.08	1.02
1:X:64:THR:O	1:X:67:GLY:N	1.91	1.01
1:X:736:GLN:O	1:X:747:ARG:CB	2.08	1.01
1:X:229:LYS:HE2	1:X:234:ASN:ND2	1.75	1.01
1:X:284:LEU:CD2	1:X:348:ILE:CD1	2.39	1.01
1:X:45:ASP:O	1:X:46:SER:HB2	1.59	1.01
1:X:276:ARG:HG3	1:X:282:TYR:CZ	1.94	1.01
1:X:337:SER:HA	4:X:2121:HOH:O	1.59	1.01
1:X:623:LYS:CB	1:X:628:ILE:HD11	1.90	1.01
1:X:706:TYR:CD2	4:X:2219:HOH:O	2.13	1.01
1:X:249:SER:HB2	4:X:2063:HOH:O	1.60	1.00
1:X:449:PHE:HZ	1:X:648:THR:CG2	1.74	1.00
1:X:628:ILE:HD13	4:X:2202:HOH:O	1.59	1.00
1:X:257:SER:CB	4:X:2095:HOH:O	2.08	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:25:PHE:CZ	4:X:2254:HOH:O	2.09	1.00
1:X:24:LEU:O	1:X:27:LEU:CD2	2.09	1.00
1:X:449:PHE:HZ	1:X:648:THR:HG21	1.05	1.00
1:X:431:LEU:HD23	1:X:617:ILE:CG1	1.92	1.00
1:X:238:ARG:NE	1:X:238:ARG:HA	1.76	0.99
1:X:672:VAL:O	1:X:676:LEU:HD23	1.62	0.99
1:X:747:ARG:CB	4:X:2250:HOH:O	2.09	0.99
1:X:247:PHE:CE1	1:X:253:ILE:HG12	1.97	0.99
1:X:704:ARG:O	1:X:705:TYR:CD2	2.15	0.99
1:X:246:GLN:HG2	1:X:446:LYS:HE2	1.42	0.99
1:X:372:LYS:CA	4:X:2129:HOH:O	2.10	0.99
1:X:746:PHE:CD1	4:X:2250:HOH:O	2.15	0.99
1:X:14:TYR:HB2	4:X:2004:HOH:O	1.60	0.99
1:X:341:GLN:CG	4:X:2122:HOH:O	2.11	0.99
1:X:313:VAL:HG23	1:X:314:ASP:N	1.74	0.98
1:X:544:ILE:HD13	1:X:581:ILE:HG13	1.01	0.98
1:X:706:TYR:CE2	4:X:2219:HOH:O	2.16	0.98
1:X:458:PHE:CZ	1:X:574:ALA:HB2	1.97	0.98
1:X:296:LEU:HD12	1:X:298:LEU:HG	1.42	0.97
1:X:398:ILE:HG12	1:X:407:GLN:NE2	1.79	0.97
1:X:577:VAL:HG13	1:X:579:TYR:HE1	0.84	0.97
1:X:118:TYR:HD2	1:X:148:ARG:HH21	1.05	0.97
1:X:172:ASN:CG	4:X:2067:HOH:O	1.99	0.97
1:X:284:LEU:HD23	1:X:348:ILE:HD11	1.45	0.97
1:X:345:PHE:O	1:X:348:ILE:CG1	2.12	0.97
1:X:702:VAL:HA	4:X:2233:HOH:O	1.63	0.97
1:X:166:MET:SD	1:X:448:TYR:HB3	2.05	0.96
1:X:623:LYS:HB3	1:X:628:ILE:HD12	1.47	0.96
1:X:446:LYS:HZ1	1:X:449:PHE:HB3	1.26	0.96
1:X:498:LYS:O	1:X:499:ILE:HG13	1.66	0.96
1:X:398:ILE:HD13	1:X:407:GLN:HE21	1.27	0.96
1:X:590:ASP:O	1:X:590:ASP:OD1	1.84	0.96
1:X:706:TYR:CZ	1:X:714:ARG:HA	2.00	0.96
1:X:247:PHE:HD1	1:X:253:ILE:HA	1.29	0.95
1:X:398:ILE:CG1	1:X:407:GLN:NE2	2.29	0.95
1:X:360:GLU:C	4:X:2127:HOH:O	2.03	0.95
1:X:146:ARG:HA	4:X:2055:HOH:O	1.66	0.95
1:X:118:TYR:HD2	1:X:148:ARG:NH2	1.65	0.95
1:X:703:LYS:CA	4:X:2219:HOH:O	2.13	0.95
1:X:87:GLY:N	1:X:105:ASN:OD1	2.00	0.95
1:X:172:ASN:CB	1:X:449:PHE:CE2	2.49	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:284:LEU:HD21	1:X:348:ILE:HD11	1.46	0.95
1:X:485:HIS:NE2	1:X:489:LEU:HD11	1.82	0.95
1:X:170:ARG:HA	1:X:448:TYR:HE2	1.30	0.95
1:X:746:PHE:CE1	4:X:2252:HOH:O	2.19	0.94
1:X:695:ARG:HG2	1:X:745:PHE:CB	1.97	0.94
1:X:747:ARG:HE	1:X:748:ALA:H	1.09	0.94
1:X:58:ASP:C	4:X:2029:HOH:O	2.04	0.94
1:X:210:VAL:O	1:X:214:GLN:HG3	1.68	0.94
1:X:276:ARG:HD2	1:X:282:TYR:CG	2.02	0.94
1:X:251:GLY:C	1:X:252:PHE:HD1	1.72	0.93
1:X:84:LYS:HD3	1:X:755:GLU:OE2	1.66	0.93
1:X:397:ARG:HA	1:X:406:ALA:HA	1.48	0.93
1:X:219:ASN:C	1:X:223:GLU:OE1	2.07	0.93
1:X:296:LEU:CB	4:X:2104:HOH:O	2.08	0.93
1:X:172:ASN:CB	1:X:449:PHE:CD2	2.52	0.92
1:X:166:MET:HA	1:X:173:GLN:HE22	0.80	0.92
1:X:372:LYS:C	4:X:2129:HOH:O	2.06	0.92
1:X:196:LEU:HD12	1:X:245:ILE:CD1	1.98	0.91
1:X:753:ARG:H	1:X:753:ARG:HD2	1.33	0.91
1:X:238:ARG:CG	1:X:278:TYR:HE1	1.83	0.91
1:X:357:ILE:HD12	1:X:375:LEU:CD1	2.00	0.91
1:X:746:PHE:CB	4:X:2248:HOH:O	1.98	0.91
1:X:177:ILE:HD12	1:X:189:THR:OG1	1.69	0.91
1:X:180:GLU:O	1:X:183:ALA:CB	2.19	0.90
1:X:449:PHE:CZ	1:X:648:THR:CG2	2.48	0.90
1:X:361:LYS:O	1:X:361:LYS:HD2	1.70	0.90
1:X:672:VAL:O	1:X:676:LEU:CD2	2.20	0.90
1:X:738:ARG:HD2	4:X:2244:HOH:O	1.72	0.90
1:X:202:ARG:HH11	1:X:252:PHE:HB3	1.35	0.89
1:X:284:LEU:HD23	1:X:348:ILE:CD1	2.01	0.89
1:X:122:PHE:CD1	1:X:654:ARG:CG	2.56	0.89
1:X:733:ASP:OD1	1:X:734:PRO:CD	2.20	0.89
1:X:558:TYR:CE2	4:X:2180:HOH:O	2.25	0.89
1:X:605:ASP:HB3	1:X:608:VAL:HB	1.53	0.89
1:X:14:TYR:HE2	4:X:2005:HOH:O	1.55	0.89
1:X:172:ASN:OD1	1:X:449:PHE:N	2.06	0.89
1:X:35:ILE:HD13	1:X:77:ALA:HB1	1.54	0.89
1:X:349:ALA:HA	1:X:352:LEU:HD23	1.53	0.89
1:X:213:GLN:NE2	1:X:333:ILE:HD12	1.88	0.88
1:X:498:LYS:C	1:X:499:ILE:HG13	1.94	0.88
1:X:170:ARG:NH2	4:X:2063:HOH:O	2.02	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:668:GLU:HB3	1:X:670:LYS:HG2	1.55	0.88
1:X:479:GLN:HE22	1:X:680:ALA:HB2	1.39	0.88
1:X:706:TYR:OH	1:X:714:ARG:CB	2.21	0.88
1:X:218:ALA:O	1:X:221:ILE:HB	1.73	0.88
1:X:296:LEU:CG	4:X:2104:HOH:O	2.20	0.88
1:X:123:LEU:HD22	1:X:158:ILE:HG12	1.54	0.88
1:X:242:PHE:HB3	1:X:259:GLN:HB3	1.53	0.88
1:X:110:TYR:CE2	1:X:667:LEU:HD13	2.09	0.88
1:X:384:VAL:HG12	1:X:385:ASN:N	1.89	0.88
1:X:410:ASN:ND2	1:X:413:LYS:CE	2.37	0.88
1:X:421:LEU:O	1:X:425:LEU:CD2	2.21	0.88
1:X:446:LYS:HZ2	1:X:449:PHE:HB3	1.36	0.87
1:X:692:PHE:CD2	4:X:2243:HOH:O	2.20	0.87
1:X:409:LEU:H	1:X:409:LEU:HD22	1.39	0.87
1:X:628:ILE:HG22	1:X:629:THR:H	1.40	0.87
1:X:580:GLU:HB3	1:X:582:GLN:OE1	1.73	0.87
1:X:692:PHE:CZ	4:X:2243:HOH:O	2.23	0.87
1:X:158:ILE:HG22	1:X:175:LEU:HD21	1.57	0.87
1:X:28:THR:HG23	4:X:2017:HOH:O	1.74	0.87
1:X:385:ASN:HB3	1:X:388:VAL:CG2	2.04	0.86
1:X:4:ILE:H	1:X:4:ILE:HD12	1.38	0.86
1:X:753:ARG:N	1:X:753:ARG:HD2	1.90	0.86
1:X:247:PHE:CE1	1:X:253:ILE:HA	2.10	0.86
1:X:385:ASN:ND2	1:X:388:VAL:HG13	1.89	0.86
1:X:410:ASN:OD1	1:X:412:GLU:HG2	1.75	0.86
1:X:558:TYR:HE2	4:X:2180:HOH:O	1.56	0.86
1:X:421:LEU:O	1:X:425:LEU:HD23	1.76	0.86
1:X:255:GLY:HA3	1:X:441:LEU:O	1.76	0.85
1:X:14:TYR:CE1	1:X:133:PRO:HG2	2.09	0.85
1:X:213:GLN:O	4:X:2079:HOH:O	1.94	0.85
1:X:217:GLN:HG3	4:X:2079:HOH:O	1.76	0.85
1:X:276:ARG:HD2	1:X:282:TYR:CD2	2.10	0.85
1:X:57:SER:C	4:X:2029:HOH:O	2.14	0.85
1:X:695:ARG:NH2	4:X:2218:HOH:O	2.09	0.85
1:X:211:LEU:CD2	1:X:254:SER:O	2.25	0.85
1:X:117:THR:CG2	4:X:2046:HOH:O	1.97	0.85
1:X:180:GLU:O	1:X:183:ALA:HB3	1.76	0.85
1:X:725:ALA:CB	4:X:2087:HOH:O	2.12	0.85
1:X:457:GLY:C	4:X:2148:HOH:O	2.14	0.85
1:X:654:ARG:CG	1:X:681:VAL:CG1	2.51	0.85
1:X:746:PHE:HE1	4:X:2252:HOH:O	1.53	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:27:LEU:HD12	1:X:28:THR:CA	2.06	0.85
1:X:455:ILE:CG2	4:X:2147:HOH:O	2.25	0.85
1:X:175:LEU:HD23	1:X:651:HIS:HB2	1.59	0.85
1:X:147:ARG:CB	1:X:150:GLU:HG2	2.03	0.85
1:X:82:PRO:HG3	1:X:756:GLU:OE2	1.76	0.84
1:X:10:ASP:CG	4:X:2005:HOH:O	2.15	0.84
1:X:343:SER:O	1:X:347:ILE:CG1	2.23	0.84
1:X:719:SER:HA	1:X:722:ALA:HB3	1.58	0.84
1:X:313:VAL:CG2	1:X:314:ASP:H	1.90	0.84
1:X:279:HIS:O	1:X:283:GLN:HG3	1.77	0.84
1:X:748:ALA:O	4:X:2251:HOH:O	1.95	0.84
1:X:736:GLN:O	1:X:747:ARG:HD2	1.76	0.84
1:X:24:LEU:HD12	1:X:26:LYS:HD2	1.58	0.84
1:X:747:ARG:NE	1:X:748:ALA:H	1.76	0.84
1:X:692:PHE:CE2	4:X:2243:HOH:O	2.28	0.84
1:X:388:VAL:HA	1:X:391:LYS:HB3	1.59	0.84
1:X:361:LYS:HG3	1:X:411:VAL:HG11	1.60	0.84
1:X:265:LYS:O	1:X:268:VAL:HG12	1.77	0.83
1:X:398:ILE:HD13	1:X:407:GLN:NE2	1.94	0.83
1:X:35:ILE:CD1	1:X:77:ALA:CB	2.24	0.83
1:X:174:SER:CB	4:X:2207:HOH:O	2.27	0.83
1:X:514:ILE:O	1:X:518:ASP:OD1	1.96	0.83
1:X:706:TYR:OH	1:X:714:ARG:HB2	1.77	0.83
1:X:526:LEU:HD22	1:X:631:ALA:HB1	1.60	0.83
1:X:695:ARG:HG2	1:X:745:PHE:CG	2.13	0.83
1:X:212:GLU:O	1:X:216:LEU:HG	1.79	0.82
1:X:732:ILE:HD12	1:X:732:ILE:H	1.44	0.82
1:X:166:MET:SD	1:X:448:TYR:CB	2.66	0.82
1:X:640:SER:O	1:X:644:THR:OG1	1.96	0.82
1:X:122:PHE:HD1	1:X:654:ARG:HG2	1.43	0.82
1:X:254:SER:HB2	1:X:443:GLN:OE1	1.78	0.82
1:X:345:PHE:HA	1:X:348:ILE:HG12	1.59	0.82
1:X:431:LEU:CD2	1:X:617:ILE:CG1	2.53	0.82
1:X:357:ILE:HD11	1:X:375:LEU:CD1	2.02	0.82
1:X:215:ILE:HG12	1:X:441:LEU:HD13	1.60	0.82
1:X:398:ILE:CG1	1:X:407:GLN:HE21	1.92	0.82
1:X:605:ASP:CB	1:X:608:VAL:HB	2.10	0.82
1:X:747:ARG:HE	1:X:748:ALA:N	1.77	0.82
1:X:702:VAL:O	1:X:706:TYR:HD2	1.64	0.81
1:X:195:TYR:CE2	1:X:199:VAL:HG11	2.16	0.81
1:X:58:ASP:N	4:X:2029:HOH:O	2.06	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:172:ASN:ND2	1:X:449:PHE:CE2	2.37	0.81
1:X:628:ILE:HG22	1:X:629:THR:N	1.95	0.81
1:X:130:LYS:CG	1:X:132:ILE:HD11	2.10	0.81
1:X:213:GLN:HB2	4:X:2079:HOH:O	1.80	0.81
1:X:263:LEU:HD21	1:X:430:PHE:CD2	2.16	0.80
1:X:132:ILE:CD1	4:X:2050:HOH:O	2.28	0.80
1:X:118:TYR:HE1	1:X:153:PRO:HA	1.43	0.80
1:X:736:GLN:O	1:X:747:ARG:CD	2.29	0.80
1:X:56:THR:HG22	1:X:57:SER:N	1.94	0.80
1:X:357:ILE:CG1	1:X:375:LEU:HD12	2.11	0.80
1:X:396:PRO:HG2	1:X:398:ILE:HD11	1.62	0.80
1:X:172:ASN:OD1	1:X:448:TYR:C	2.19	0.80
1:X:357:ILE:HD12	1:X:375:LEU:HD11	1.64	0.80
1:X:654:ARG:CG	1:X:681:VAL:HG12	2.06	0.80
1:X:141:ASP:OD2	4:X:2053:HOH:O	2.00	0.80
1:X:520:ARG:O	1:X:523:PRO:HG3	1.82	0.80
1:X:689:ARG:HG3	1:X:693:PRO:CG	2.11	0.79
1:X:662:GLN:CG	4:X:2208:HOH:O	2.29	0.79
1:X:458:PHE:CE2	4:X:2215:HOH:O	2.34	0.79
1:X:262:LEU:O	1:X:262:LEU:HD12	1.81	0.79
1:X:296:LEU:CD1	1:X:298:LEU:HG	2.12	0.79
1:X:385:ASN:CB	1:X:388:VAL:HG22	2.12	0.79
1:X:273:GLU:O	1:X:274:THR:CG2	2.30	0.79
1:X:84:LYS:CE	1:X:704:ARG:HD2	2.12	0.79
1:X:184:GLY:HA2	2:X:1001:ADP:PA	2.23	0.79
1:X:410:ASN:ND2	1:X:413:LYS:HE3	1.99	0.78
1:X:98:ASN:O	1:X:102:VAL:HG23	1.83	0.78
1:X:172:ASN:CB	4:X:2067:HOH:O	2.28	0.78
1:X:136:THR:O	1:X:139:MET:HB2	1.82	0.78
1:X:361:LYS:O	1:X:361:LYS:CD	2.30	0.78
1:X:276:ARG:CG	1:X:282:TYR:CZ	2.66	0.78
1:X:380:THR:O	4:X:2132:HOH:O	2.01	0.78
1:X:28:THR:CG2	4:X:2017:HOH:O	2.28	0.78
1:X:122:PHE:CE1	1:X:654:ARG:HG2	2.19	0.77
1:X:29:VAL:HG12	1:X:29:VAL:O	1.83	0.77
1:X:132:ILE:HD12	4:X:2050:HOH:O	1.82	0.77
1:X:35:ILE:HD11	1:X:77:ALA:HB1	0.78	0.77
1:X:695:ARG:CG	1:X:745:PHE:HB3	2.11	0.77
1:X:504:ILE:HA	4:X:2166:HOH:O	1.83	0.77
1:X:172:ASN:HB3	1:X:449:PHE:CD2	2.19	0.77
1:X:14:TYR:CZ	1:X:133:PRO:CG	2.68	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:361:LYS:HB3	1:X:367:ALA:HA	1.66	0.77
1:X:239:PHE:HD1	1:X:240:GLY:O	1.68	0.77
1:X:172:ASN:HB2	1:X:449:PHE:CE2	2.18	0.76
1:X:593:GLN:C	4:X:2193:HOH:O	2.17	0.76
1:X:19:GLN:HB2	4:X:2003:HOH:O	1.83	0.76
1:X:428:ARG:HB3	1:X:611:LEU:HD22	1.66	0.76
1:X:24:LEU:CD1	1:X:26:LYS:HD2	2.15	0.76
1:X:26:LYS:O	1:X:26:LYS:CG	2.30	0.76
1:X:45:ASP:O	1:X:46:SER:CB	2.34	0.76
1:X:626:ASN:C	4:X:2201:HOH:O	2.23	0.76
1:X:702:VAL:CG1	4:X:2233:HOH:O	2.08	0.76
1:X:594:GLN:HG3	1:X:594:GLN:O	1.85	0.76
1:X:689:ARG:CG	1:X:693:PRO:HD3	2.13	0.76
1:X:296:LEU:CD1	1:X:296:LEU:O	2.30	0.76
1:X:368:VAL:O	1:X:369:LEU:HD23	1.85	0.76
1:X:447:ALA:O	1:X:448:TYR:O	2.04	0.76
1:X:118:TYR:CD2	1:X:148:ARG:NE	2.53	0.75
1:X:158:ILE:CG2	1:X:175:LEU:HD21	2.16	0.75
1:X:247:PHE:CD1	1:X:253:ILE:CA	2.63	0.75
1:X:620:ARG:HD2	1:X:628:ILE:O	1.85	0.75
1:X:428:ARG:CB	1:X:611:LEU:HD13	2.16	0.75
1:X:377:ALA:O	1:X:380:THR:HB	1.86	0.75
1:X:147:ARG:H	1:X:150:GLU:HG3	1.52	0.75
1:X:82:PRO:HA	1:X:756:GLU:OE1	1.86	0.74
1:X:337:SER:OG	1:X:340:GLU:HB2	1.87	0.74
1:X:147:ARG:H	1:X:150:GLU:CG	1.99	0.74
1:X:577:VAL:HG11	1:X:579:TYR:CE1	2.22	0.74
1:X:600:PHE:HB3	1:X:612:PHE:CD2	2.22	0.74
1:X:296:LEU:CD2	4:X:2104:HOH:O	2.12	0.74
1:X:331:MET:HG2	1:X:336:PHE:HD2	1.51	0.74
1:X:296:LEU:CD1	1:X:298:LEU:CD1	2.64	0.74
1:X:446:LYS:HZ1	1:X:449:PHE:CB	1.99	0.74
1:X:211:LEU:HD21	1:X:254:SER:O	1.86	0.74
1:X:108:VAL:O	1:X:111:ASN:HB2	1.87	0.74
1:X:727:LEU:HD23	1:X:737:TYR:OH	1.86	0.74
1:X:84:LYS:HZ1	1:X:704:ARG:HD2	1.52	0.74
1:X:341:GLN:HG3	4:X:2122:HOH:O	1.78	0.74
1:X:304:PHE:CE2	1:X:352:LEU:HB3	2.23	0.74
1:X:385:ASN:O	1:X:389:LEU:HB2	1.88	0.74
1:X:398:ILE:HD13	1:X:407:GLN:CG	2.18	0.74
1:X:455:ILE:HG23	4:X:2147:HOH:O	1.84	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:458:PHE:CE1	1:X:574:ALA:HB3	2.22	0.73
1:X:706:TYR:OH	1:X:714:ARG:HA	1.87	0.73
1:X:682:LEU:O	1:X:685:ILE:HG22	1.87	0.73
1:X:274:THR:HG22	4:X:2098:HOH:O	1.87	0.73
1:X:276:ARG:CG	1:X:282:TYR:CE1	2.71	0.73
1:X:213:GLN:CB	4:X:2078:HOH:O	2.06	0.73
1:X:275:GLU:N	4:X:2099:HOH:O	2.22	0.73
1:X:732:ILE:CG2	1:X:737:TYR:CD2	2.71	0.73
1:X:395:GLU:HA	1:X:407:GLN:O	1.89	0.73
1:X:426:TYR:CZ	4:X:2139:HOH:O	2.41	0.73
1:X:458:PHE:HE1	1:X:574:ALA:HB2	1.10	0.73
1:X:735:GLU:HA	1:X:738:ARG:HH22	1.54	0.73
1:X:110:TYR:HE2	1:X:667:LEU:HD13	1.52	0.73
1:X:276:ARG:HD2	1:X:282:TYR:CD1	2.24	0.73
1:X:230:THR:HA	1:X:275:GLU:HG2	1.69	0.73
1:X:177:ILE:HG22	1:X:185:LYS:HG2	1.70	0.72
1:X:27:LEU:CD1	4:X:2017:HOH:O	2.22	0.72
1:X:344:ILE:HG22	1:X:345:PHE:N	2.04	0.72
1:X:250:ALA:HB3	4:X:2094:HOH:O	1.89	0.72
1:X:265:LYS:HE2	1:X:423:LYS:HB3	1.71	0.72
1:X:559:GLU:OE1	1:X:559:GLU:O	2.08	0.72
1:X:98:ASN:OD1	1:X:100:PRO:HG2	1.88	0.72
1:X:360:GLU:O	4:X:2127:HOH:O	2.06	0.72
1:X:115:ILE:HG21	1:X:128:PRO:HG3	1.71	0.72
1:X:120:GLY:O	1:X:148:ARG:NH2	2.23	0.72
1:X:172:ASN:HB3	1:X:449:PHE:CE2	2.25	0.72
1:X:498:LYS:O	1:X:499:ILE:CG1	2.37	0.72
1:X:525:ILE:O	1:X:529:LEU:HB2	1.89	0.72
1:X:548:HIS:ND1	1:X:560:GLU:HG3	2.05	0.72
1:X:288:ALA:HB1	1:X:292:GLU:CD	2.10	0.72
1:X:35:ILE:HG13	1:X:79:GLN:HA	1.70	0.72
1:X:737:TYR:CD1	1:X:739:PHE:CE1	2.78	0.72
1:X:296:LEU:O	1:X:297:HIS:O	2.07	0.71
1:X:359:PHE:O	4:X:2127:HOH:O	2.08	0.71
1:X:546:LYS:NZ	1:X:550:HIS:HE1	1.89	0.71
1:X:146:ARG:HH11	1:X:151:VAL:HG11	1.54	0.71
1:X:211:LEU:HD22	1:X:254:SER:O	1.90	0.71
1:X:424:ALA:O	1:X:428:ARG:CD	2.37	0.71
1:X:623:LYS:CB	1:X:628:ILE:CD1	2.53	0.71
1:X:446:LYS:NZ	1:X:449:PHE:CB	2.43	0.71
1:X:175:LEU:HD23	1:X:651:HIS:CB	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:250:ALA:CB	4:X:2094:HOH:O	2.37	0.71
1:X:398:ILE:HD13	1:X:407:GLN:HG3	1.71	0.71
1:X:529:LEU:HD22	1:X:588:ASN:HD22	1.55	0.71
1:X:131:ARG:O	1:X:132:ILE:HD13	1.91	0.71
1:X:410:ASN:HD21	1:X:413:LYS:HE2	1.56	0.71
1:X:541:ASN:O	1:X:545:THR:OG1	2.04	0.71
1:X:367:ALA:HB2	1:X:411:VAL:HA	1.72	0.71
1:X:706:TYR:OH	1:X:714:ARG:CA	2.38	0.71
1:X:458:PHE:CZ	4:X:2215:HOH:O	2.44	0.70
1:X:305:ASN:HA	1:X:308:ASN:OD1	1.90	0.70
1:X:398:ILE:CD1	1:X:407:GLN:NE2	2.41	0.70
1:X:27:LEU:CD1	1:X:28:THR:HG23	2.17	0.70
1:X:485:HIS:NE2	1:X:489:LEU:CD1	2.55	0.70
1:X:118:TYR:HD1	1:X:153:PRO:HB3	1.57	0.70
1:X:458:PHE:N	4:X:2148:HOH:O	2.23	0.70
1:X:581:ILE:HG22	1:X:581:ILE:O	1.90	0.70
1:X:331:MET:O	1:X:336:PHE:HB2	1.91	0.70
1:X:104:HIS:O	1:X:108:VAL:HG23	1.89	0.70
1:X:56:THR:HG22	1:X:57:SER:H	1.55	0.70
1:X:707:LEU:O	4:X:2221:HOH:O	2.09	0.70
1:X:732:ILE:CG2	1:X:737:TYR:HD2	2.04	0.70
1:X:753:ARG:H	1:X:753:ARG:CD	2.04	0.70
1:X:184:GLY:HA2	2:X:1001:ADP:O3A	1.91	0.70
1:X:445:ARG:HG3	1:X:445:ARG:O	1.92	0.70
1:X:487:PHE:CZ	1:X:506:PHE:HB2	2.26	0.70
1:X:85:PHE:CA	4:X:2039:HOH:O	2.31	0.70
1:X:123:LEU:HD22	1:X:158:ILE:CG1	2.22	0.69
1:X:621:ALA:O	1:X:628:ILE:CG1	2.35	0.69
1:X:118:TYR:CE2	1:X:148:ARG:NE	2.60	0.69
1:X:625:ALA:O	1:X:626:ASN:OD1	2.10	0.69
1:X:76:ASP:CB	4:X:2032:HOH:O	2.38	0.69
1:X:249:SER:O	4:X:2063:HOH:O	2.11	0.69
1:X:54:SER:N	1:X:61:THR:OG1	2.25	0.69
1:X:142:ILE:HG22	1:X:143:PHE:N	2.07	0.69
1:X:687:ILE:O	1:X:690:LYS:HB2	1.93	0.69
1:X:703:LYS:HA	4:X:2219:HOH:O	1.84	0.69
1:X:202:ARG:NH1	1:X:252:PHE:HB3	2.08	0.69
1:X:133:PRO:C	4:X:2051:HOH:O	2.30	0.69
1:X:229:LYS:HE2	1:X:234:ASN:HD21	1.58	0.69
1:X:681:VAL:HG23	1:X:682:LEU:N	2.08	0.69
1:X:212:GLU:O	1:X:216:LEU:CG	2.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:241:LYS:HA	1:X:259:GLN:O	1.91	0.69
1:X:623:LYS:N	1:X:628:ILE:HD11	2.07	0.69
1:X:29:VAL:CG1	1:X:29:VAL:O	2.40	0.69
1:X:595:ASP:OD1	1:X:598:LEU:HD23	1.93	0.69
1:X:217:GLN:O	1:X:330:ALA:HB1	1.93	0.68
1:X:732:ILE:HG22	1:X:737:TYR:CD2	2.28	0.68
1:X:118:TYR:CD2	1:X:148:ARG:NH2	2.56	0.68
1:X:187:GLU:CB	4:X:2068:HOH:O	2.40	0.68
1:X:473:TYR:O	1:X:477:LYS:HG2	1.93	0.68
1:X:6:ASP:O	1:X:12:HIS:NE2	2.26	0.68
1:X:160:ASP:O	1:X:163:TYR:HB3	1.92	0.68
1:X:196:LEU:CD1	1:X:245:ILE:CD1	2.64	0.68
1:X:432:TRP:HD1	1:X:610:LYS:HZ3	1.04	0.68
1:X:594:GLN:CG	1:X:594:GLN:O	2.41	0.68
1:X:747:ARG:HG3	1:X:749:GLY:H	1.59	0.68
1:X:385:ASN:OD1	1:X:385:ASN:C	2.30	0.68
1:X:428:ARG:HB2	1:X:611:LEU:HD13	1.74	0.68
1:X:144:LYS:HE3	1:X:199:VAL:HG12	1.74	0.68
1:X:213:GLN:C	4:X:2079:HOH:O	2.31	0.68
1:X:359:PHE:CE1	1:X:415:SER:HA	2.29	0.68
1:X:172:ASN:ND2	4:X:2067:HOH:O	2.22	0.68
1:X:342:MET:SD	1:X:346:LYS:HB2	2.34	0.68
1:X:628:ILE:CG2	1:X:629:THR:H	2.07	0.68
1:X:121:LEU:CB	4:X:2048:HOH:O	2.41	0.68
1:X:341:GLN:O	1:X:345:PHE:CD2	2.47	0.68
1:X:131:ARG:NH1	1:X:132:ILE:O	2.26	0.67
1:X:319:SER:HA	4:X:2116:HOH:O	1.93	0.67
1:X:464:ASN:HD22	1:X:577:VAL:CG2	2.07	0.67
1:X:654:ARG:HG3	1:X:681:VAL:HG13	1.74	0.67
1:X:91:MET:HA	4:X:2041:HOH:O	1.94	0.67
1:X:271:GLN:HB3	1:X:275:GLU:O	1.94	0.67
1:X:255:GLY:CA	1:X:441:LEU:O	2.42	0.67
1:X:345:PHE:C	1:X:348:ILE:HG13	2.10	0.67
1:X:593:GLN:O	1:X:596:LEU:HD12	1.93	0.67
1:X:64:THR:O	1:X:66:ASP:N	2.27	0.67
1:X:341:GLN:HG2	4:X:2122:HOH:O	1.84	0.67
1:X:681:VAL:HG23	1:X:682:LEU:H	1.59	0.67
1:X:504:ILE:N	4:X:2169:HOH:O	2.26	0.67
1:X:564:SER:HB3	4:X:2186:HOH:O	1.94	0.67
1:X:455:ILE:HG22	4:X:2147:HOH:O	1.89	0.67
1:X:185:LYS:NZ	2:X:1001:ADP:O2B	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:53:VAL:HB	1:X:61:THR:HB	1.76	0.67
1:X:225:PHE:HD1	1:X:280:ILE:HG21	1.59	0.67
1:X:319:SER:O	1:X:323:GLU:HB2	1.94	0.67
1:X:84:LYS:HZ2	1:X:704:ARG:HD2	1.58	0.67
1:X:178:THR:CG2	4:X:2147:HOH:O	2.22	0.67
1:X:731:ASN:O	1:X:731:ASN:CG	2.33	0.67
1:X:257:SER:O	1:X:258:ILE:HG13	1.94	0.66
1:X:27:LEU:CD1	1:X:28:THR:N	2.09	0.66
1:X:641:LEU:O	1:X:644:THR:HB	1.94	0.66
1:X:410:ASN:HD21	1:X:413:LYS:CE	2.08	0.66
1:X:193:ILE:O	1:X:196:LEU:HB2	1.96	0.66
1:X:26:LYS:O	1:X:26:LYS:HG2	1.95	0.66
1:X:296:LEU:O	1:X:297:HIS:C	2.32	0.66
1:X:672:VAL:HA	1:X:675:GLN:HE21	1.59	0.66
1:X:479:GLN:NE2	1:X:680:ALA:HB2	2.10	0.66
1:X:48:GLU:HG2	1:X:65:VAL:HG21	1.77	0.66
1:X:27:LEU:HD13	1:X:28:THR:CG2	2.21	0.66
1:X:662:GLN:HG2	4:X:2208:HOH:O	1.90	0.66
1:X:689:ARG:HB2	1:X:693:PRO:HB3	1.78	0.66
1:X:88:VAL:HG23	4:X:2041:HOH:O	1.96	0.66
1:X:476:GLU:OE2	1:X:510:SER:HB2	1.96	0.65
1:X:56:THR:CG2	1:X:57:SER:N	2.59	0.65
1:X:242:PHE:HD1	1:X:453:LEU:HB2	1.60	0.65
1:X:315:ILE:HB	4:X:2114:HOH:O	1.95	0.65
1:X:719:SER:CB	1:X:723:THR:HB	2.15	0.65
1:X:72:VAL:HG11	1:X:77:ALA:HB2	1.78	0.65
1:X:230:THR:HG22	1:X:275:GLU:OE1	1.95	0.65
1:X:546:LYS:HZ3	1:X:550:HIS:HE1	1.42	0.65
1:X:420:ALA:CB	1:X:592:LEU:HD13	2.27	0.65
1:X:371:ASP:O	4:X:2129:HOH:O	2.14	0.65
1:X:409:LEU:N	1:X:409:LEU:HD22	2.11	0.65
1:X:103:PHE:CZ	1:X:667:LEU:HD23	2.32	0.65
1:X:174:SER:HB3	4:X:2207:HOH:O	1.93	0.65
1:X:594:GLN:OE1	1:X:597:GLU:HB2	1.97	0.65
1:X:82:PRO:HB3	1:X:756:GLU:OE1	1.97	0.65
1:X:180:GLU:O	1:X:183:ALA:HB2	1.95	0.65
1:X:390:GLU:HA	1:X:393:LEU:HB2	1.78	0.65
1:X:122:PHE:CE1	1:X:654:ARG:CG	2.79	0.65
1:X:410:ASN:CG	1:X:412:GLU:HG2	2.16	0.64
1:X:226:GLY:HA3	1:X:239:PHE:HE2	1.62	0.64
1:X:261:TYR:HD1	4:X:2097:HOH:O	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:54:SER:HB2	1:X:61:THR:HG21	1.80	0.64
1:X:87:GLY:HA2	1:X:109:ARG:HG3	1.78	0.64
1:X:118:TYR:CE1	1:X:153:PRO:HA	2.30	0.64
1:X:166:MET:CA	1:X:173:GLN:NE2	2.40	0.64
1:X:497:GLU:O	1:X:498:LYS:HB3	1.97	0.64
1:X:56:THR:CG2	1:X:57:SER:H	2.10	0.64
1:X:154:HIS:CE1	1:X:155:ILE:HG22	2.33	0.64
1:X:19:GLN:CB	4:X:2003:HOH:O	2.41	0.64
1:X:361:LYS:HG3	1:X:411:VAL:CG1	2.27	0.64
1:X:384:VAL:CG1	1:X:385:ASN:N	2.60	0.64
1:X:174:SER:N	4:X:2207:HOH:O	2.30	0.64
1:X:174:SER:O	1:X:651:HIS:N	2.29	0.64
1:X:226:GLY:O	1:X:238:ARG:HB2	1.97	0.64
1:X:229:LYS:HG3	1:X:234:ASN:HA	1.78	0.64
1:X:293:LYS:HA	1:X:298:LEU:HB2	1.79	0.64
1:X:703:LYS:HA	4:X:2224:HOH:O	1.97	0.64
1:X:747:ARG:HG3	1:X:749:GLY:N	2.11	0.64
1:X:662:GLN:HG3	4:X:2208:HOH:O	1.96	0.64
1:X:657:ILE:HG12	1:X:658:PRO:HD2	1.79	0.64
1:X:130:LYS:HG3	1:X:132:ILE:CD1	2.22	0.64
1:X:139:MET:HA	1:X:139:MET:CE	2.28	0.64
1:X:275:GLU:C	4:X:2099:HOH:O	2.35	0.64
1:X:202:ARG:HH11	1:X:252:PHE:CB	2.10	0.64
1:X:331:MET:HG2	1:X:336:PHE:CD2	2.31	0.64
1:X:373:THR:O	1:X:376:ASN:HB2	1.98	0.64
1:X:548:HIS:CE1	1:X:560:GLU:HG3	2.33	0.64
1:X:388:VAL:O	1:X:392:ALA:N	2.28	0.63
1:X:710:PRO:HG3	4:X:2221:HOH:O	1.97	0.63
1:X:142:ILE:C	1:X:144:LYS:H	2.02	0.63
1:X:420:ALA:HB3	1:X:592:LEU:HD13	1.81	0.63
1:X:564:SER:CB	4:X:2186:HOH:O	2.46	0.63
1:X:7:ARG:HA	1:X:12:HIS:CE1	2.33	0.63
1:X:694:ASN:HD22	1:X:751:LEU:HD13	1.63	0.63
1:X:746:PHE:N	4:X:2248:HOH:O	2.31	0.63
1:X:137:GLN:O	1:X:140:VAL:HB	1.99	0.63
1:X:238:ARG:HG3	1:X:264:GLU:CB	2.22	0.63
1:X:58:ASP:OD1	1:X:73:LYS:HG3	1.98	0.63
1:X:695:ARG:HG2	1:X:745:PHE:CD1	2.33	0.63
1:X:175:LEU:C	1:X:176:LEU:HD12	2.18	0.63
1:X:385:ASN:OD1	1:X:386:PRO:N	2.32	0.63
1:X:479:GLN:HE22	1:X:680:ALA:CB	2.11	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:47:TYR:HE1	1:X:673:LEU:CD2	2.12	0.63
1:X:360:GLU:CA	4:X:2127:HOH:O	2.43	0.63
1:X:703:LYS:HA	1:X:706:TYR:HE2	1.64	0.63
1:X:732:ILE:HG21	1:X:737:TYR:CD2	2.34	0.63
1:X:296:LEU:CD1	1:X:298:LEU:CG	2.76	0.63
1:X:385:ASN:OD1	1:X:387:SER:N	2.32	0.63
1:X:121:LEU:HB3	4:X:2048:HOH:O	1.98	0.62
1:X:256:ALA:O	1:X:442:CYS:HB2	1.99	0.62
1:X:30:SER:C	1:X:31:ASP:OD1	2.37	0.62
1:X:37:TYR:O	1:X:48:GLU:N	2.32	0.62
1:X:723:THR:CG2	4:X:2234:HOH:O	2.21	0.62
1:X:706:TYR:CZ	1:X:714:ARG:CA	2.79	0.62
1:X:734:PRO:HD3	4:X:2241:HOH:O	1.98	0.62
1:X:144:LYS:NZ	1:X:144:LYS:HB2	2.12	0.62
1:X:249:SER:CB	4:X:2063:HOH:O	2.33	0.62
1:X:361:LYS:N	1:X:361:LYS:HD2	2.14	0.62
1:X:225:PHE:CD1	1:X:280:ILE:HG21	2.35	0.62
1:X:62:PHE:HB2	1:X:70:ARG:O	2.00	0.62
1:X:97:LEU:HD13	1:X:689:ARG:HD2	1.81	0.62
1:X:338:GLN:NE2	4:X:2123:HOH:O	2.31	0.62
1:X:357:ILE:HG13	1:X:375:LEU:HD12	1.80	0.62
1:X:526:LEU:HD22	1:X:631:ALA:CB	2.28	0.62
1:X:735:GLU:HA	1:X:738:ARG:NH2	2.14	0.62
1:X:90:ASP:C	4:X:2041:HOH:O	2.36	0.62
1:X:14:TYR:CE1	1:X:133:PRO:CG	2.82	0.62
1:X:457:GLY:HA2	1:X:475:ASN:OD1	1.99	0.62
1:X:431:LEU:HD21	1:X:617:ILE:HG13	1.81	0.62
1:X:668:GLU:CD	1:X:670:LYS:HE2	2.19	0.62
1:X:685:ILE:HG21	4:X:2047:HOH:O	2.00	0.62
1:X:85:PHE:O	1:X:88:VAL:HG12	1.90	0.62
1:X:459:GLU:HB3	1:X:461:PHE:CZ	2.35	0.61
1:X:628:ILE:CG2	1:X:629:THR:N	2.63	0.61
1:X:689:ARG:CD	1:X:693:PRO:HG3	2.30	0.61
1:X:337:SER:N	1:X:340:GLU:OE1	2.30	0.61
1:X:708:LEU:HD23	1:X:708:LEU:O	2.00	0.61
1:X:238:ARG:NE	1:X:238:ARG:CA	2.59	0.61
1:X:664:PRO:O	1:X:665:ALA:HB3	2.01	0.61
1:X:357:ILE:CD1	1:X:374:ALA:HB3	2.29	0.61
1:X:243:ILE:HG23	1:X:257:SER:O	2.01	0.61
1:X:238:ARG:HE	1:X:264:GLU:HB2	1.65	0.61
1:X:247:PHE:CZ	1:X:253:ILE:HG12	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:27:LEU:HD12	1:X:28:THR:H	0.48	0.61
1:X:35:ILE:HG13	1:X:78:ASN:O	2.00	0.61
1:X:3:PRO:O	1:X:6:ASP:O	2.19	0.61
1:X:732:ILE:N	1:X:732:ILE:HD12	2.14	0.61
1:X:19:GLN:HG3	4:X:2003:HOH:O	1.99	0.61
1:X:247:PHE:CE1	1:X:253:ILE:CG1	2.81	0.61
1:X:91:MET:N	4:X:2041:HOH:O	2.33	0.61
1:X:8:THR:HG23	1:X:9:SER:N	2.16	0.61
1:X:180:GLU:OE1	1:X:675:GLN:HG2	2.00	0.61
1:X:172:ASN:HB3	1:X:449:PHE:CG	2.36	0.60
1:X:409:LEU:HD13	1:X:409:LEU:N	2.15	0.60
1:X:698:TYR:CG	1:X:698:TYR:O	2.52	0.60
1:X:82:PRO:CA	1:X:756:GLU:OE1	2.49	0.60
1:X:241:LYS:HG2	1:X:454:ASP:OD1	2.01	0.60
1:X:586:GLU:HG3	1:X:586:GLU:O	2.02	0.60
1:X:606:ASN:CB	4:X:2197:HOH:O	2.25	0.60
1:X:711:ASN:ND2	1:X:729:HIS:CG	2.70	0.60
1:X:82:PRO:HB3	1:X:756:GLU:CD	2.22	0.60
1:X:540:ASP:HB3	1:X:581:ILE:HG22	1.82	0.60
1:X:672:VAL:HA	1:X:675:GLN:NE2	2.17	0.60
1:X:691:GLY:O	1:X:748:ALA:HB2	2.01	0.60
1:X:730:LEU:HD13	1:X:754:ILE:HG21	1.83	0.60
1:X:213:GLN:CB	4:X:2079:HOH:O	2.45	0.60
1:X:739:PHE:CD2	1:X:744:ILE:HD11	2.36	0.60
1:X:670:LYS:HG3	1:X:671:VAL:HG23	1.84	0.60
1:X:238:ARG:HE	1:X:238:ARG:HA	1.62	0.60
1:X:704:ARG:O	1:X:705:TYR:CG	2.53	0.60
1:X:275:GLU:CA	4:X:2099:HOH:O	2.50	0.59
1:X:468:GLN:C	1:X:470:CYS:N	2.54	0.59
1:X:487:PHE:CE2	1:X:506:PHE:HB2	2.37	0.59
1:X:121:LEU:O	4:X:2048:HOH:O	2.11	0.59
1:X:330:ALA:O	1:X:334:VAL:HG22	2.02	0.59
1:X:35:ILE:HD11	1:X:77:ALA:HB3	1.69	0.59
1:X:458:PHE:O	1:X:458:PHE:CD1	2.55	0.59
1:X:269:VAL:HG12	1:X:306:TYR:CZ	2.38	0.59
1:X:44:ARG:CB	4:X:2023:HOH:O	2.50	0.59
1:X:432:TRP:NE1	1:X:610:LYS:NZ	2.48	0.59
1:X:15:LEU:HD13	1:X:143:PHE:HZ	1.67	0.59
1:X:538:ALA:HB1	1:X:542:THR:HG21	1.84	0.59
1:X:170:ARG:HA	1:X:448:TYR:CE2	2.23	0.59
1:X:249:SER:CA	4:X:2063:HOH:O	2.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:251:GLY:C	1:X:252:PHE:CD1	2.61	0.59
1:X:396:PRO:O	1:X:398:ILE:HD12	2.03	0.59
1:X:706:TYR:HD1	1:X:712:VAL:O	1.85	0.59
1:X:390:GLU:HG2	1:X:394:MET:HG2	1.83	0.59
1:X:410:ASN:OD1	1:X:412:GLU:CG	2.49	0.59
1:X:657:ILE:CG1	1:X:658:PRO:HD2	2.33	0.59
1:X:371:ASP:C	4:X:2129:HOH:O	2.40	0.58
1:X:586:GLU:OE1	4:X:2192:HOH:O	2.17	0.58
1:X:158:ILE:CG2	1:X:175:LEU:CD2	2.81	0.58
1:X:720:GLN:HE22	1:X:741:ILE:HG13	1.67	0.58
1:X:276:ARG:HG2	1:X:282:TYR:CE1	2.39	0.58
1:X:432:TRP:HE1	1:X:610:LYS:HE2	1.68	0.58
1:X:195:TYR:O	1:X:199:VAL:HG22	2.03	0.58
1:X:477:LYS:CD	1:X:514:ILE:HD12	2.32	0.58
1:X:744:ILE:C	1:X:745:PHE:CD1	2.76	0.58
1:X:24:LEU:HD12	1:X:26:LYS:CD	2.31	0.58
1:X:380:THR:C	4:X:2132:HOH:O	2.40	0.58
1:X:337:SER:O	4:X:2122:HOH:O	2.16	0.58
1:X:667:LEU:HD11	1:X:672:VAL:HG21	1.85	0.58
1:X:727:LEU:HD21	1:X:739:PHE:HE2	1.68	0.58
1:X:477:LYS:HD3	1:X:514:ILE:HD12	1.86	0.58
1:X:711:ASN:HD21	1:X:729:HIS:CG	2.22	0.58
1:X:118:TYR:CD1	1:X:153:PRO:HB3	2.39	0.58
1:X:428:ARG:HH12	1:X:618:ALA:HB2	1.69	0.58
1:X:263:LEU:HB2	1:X:265:LYS:HG3	1.86	0.58
1:X:514:ILE:O	1:X:518:ASP:CG	2.42	0.57
1:X:585:LEU:HD11	4:X:2175:HOH:O	2.04	0.57
1:X:384:VAL:HG12	1:X:385:ASN:H	1.68	0.57
1:X:474:THR:CG2	1:X:478:LEU:HD11	2.34	0.57
1:X:570:VAL:HG12	1:X:571:THR:N	2.19	0.57
1:X:170:ARG:CA	1:X:448:TYR:HE2	2.13	0.57
1:X:247:PHE:CE1	1:X:253:ILE:CA	2.84	0.57
1:X:292:GLU:O	1:X:296:LEU:HG	2.04	0.57
1:X:701:PHE:HA	1:X:704:ARG:HB3	1.85	0.57
1:X:27:LEU:CD1	1:X:28:THR:OG1	2.53	0.57
1:X:617:ILE:CG2	1:X:617:ILE:O	2.49	0.57
1:X:268:VAL:HG13	1:X:269:VAL:HG13	1.86	0.57
1:X:580:GLU:O	1:X:581:ILE:HD13	2.04	0.57
1:X:241:LYS:O	1:X:453:LEU:HD12	2.05	0.57
1:X:60:PHE:HE1	1:X:74:LYS:HZ2	1.49	0.57
1:X:623:LYS:CA	1:X:628:ILE:HD11	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:737:TYR:O	1:X:738:ARG:HD3	2.05	0.57
1:X:82:PRO:CB	1:X:756:GLU:OE1	2.51	0.57
1:X:118:TYR:CD2	1:X:148:ARG:CZ	2.88	0.57
1:X:119:SER:O	1:X:120:GLY:C	2.42	0.57
1:X:266:SER:CA	1:X:423:LYS:HE2	2.35	0.57
1:X:550:HIS:O	1:X:554:LYS:HE3	2.05	0.57
1:X:732:ILE:HG22	1:X:737:TYR:HD2	1.67	0.57
1:X:342:MET:SD	1:X:346:LYS:HD3	2.44	0.57
1:X:583:ASP:O	1:X:587:LYS:HG2	2.04	0.57
1:X:110:TYR:HA	1:X:114:LEU:O	2.05	0.57
1:X:102:VAL:O	1:X:106:LEU:CD2	2.53	0.56
1:X:209:GLY:HA2	4:X:2072:HOH:O	2.05	0.56
1:X:474:THR:O	1:X:478:LEU:HG	2.05	0.56
1:X:571:THR:OG1	4:X:2187:HOH:O	2.18	0.56
1:X:739:PHE:CG	1:X:744:ILE:HD11	2.39	0.56
1:X:27:LEU:CG	1:X:28:THR:H	2.03	0.56
1:X:657:ILE:HG22	1:X:675:GLN:NE2	2.20	0.56
1:X:727:LEU:HD21	1:X:739:PHE:CE2	2.40	0.56
1:X:58:ASP:HA	1:X:74:LYS:HB2	1.86	0.56
1:X:149:ASN:OD1	1:X:150:GLU:N	2.38	0.56
1:X:35:ILE:HD11	1:X:77:ALA:CA	2.30	0.56
1:X:668:GLU:C	1:X:670:LYS:H	2.08	0.56
1:X:732:ILE:H	1:X:732:ILE:CD1	2.16	0.56
1:X:242:PHE:CD1	1:X:453:LEU:HB2	2.39	0.56
1:X:668:GLU:OE1	1:X:670:LYS:HE3	2.05	0.56
1:X:431:LEU:HD21	1:X:617:ILE:CG1	2.33	0.56
1:X:723:THR:CB	4:X:2234:HOH:O	2.53	0.56
1:X:154:HIS:ND1	1:X:155:ILE:N	2.53	0.56
1:X:331:MET:CG	1:X:336:PHE:HD2	2.19	0.56
1:X:345:PHE:HA	1:X:348:ILE:CG1	2.33	0.56
1:X:682:LEU:O	1:X:685:ILE:CG2	2.53	0.56
1:X:747:ARG:NE	1:X:748:ALA:N	2.45	0.56
1:X:691:GLY:O	1:X:692:PHE:CG	2.59	0.56
1:X:87:GLY:HA2	1:X:109:ARG:CG	2.35	0.56
1:X:178:THR:HA	1:X:185:LYS:HD3	1.88	0.56
1:X:247:PHE:HE1	1:X:253:ILE:HG23	1.70	0.56
1:X:584:TRP:HD1	4:X:2190:HOH:O	1.88	0.56
1:X:285:LEU:HD13	1:X:301:PRO:HB3	1.88	0.56
1:X:426:TYR:CE1	4:X:2139:HOH:O	2.59	0.56
1:X:590:ASP:C	1:X:590:ASP:OD1	2.42	0.56
1:X:706:TYR:CE1	1:X:713:PRO:C	2.79	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:134:ILE:C	1:X:139:MET:HG3	2.26	0.56
1:X:426:TYR:HB2	4:X:2140:HOH:O	2.05	0.56
1:X:64:THR:C	1:X:66:ASP:N	2.58	0.56
1:X:736:GLN:C	1:X:747:ARG:HD2	2.26	0.56
1:X:62:PHE:CE1	1:X:72:VAL:HG12	2.40	0.55
1:X:72:VAL:HG22	1:X:73:LYS:N	2.21	0.55
1:X:72:VAL:CG1	1:X:77:ALA:HB2	2.35	0.55
1:X:354:LEU:O	1:X:418:ARG:NH1	2.39	0.55
1:X:709:ALA:O	1:X:711:ASN:N	2.39	0.55
1:X:54:SER:H	1:X:61:THR:HG1	1.52	0.55
1:X:170:ARG:NH2	4:X:2065:HOH:O	2.40	0.55
1:X:227:ASN:OD1	1:X:237:SER:HA	2.06	0.55
1:X:266:SER:HA	1:X:423:LYS:HE2	1.88	0.55
1:X:4:ILE:H	1:X:4:ILE:CD1	2.14	0.55
1:X:670:LYS:HG3	1:X:671:VAL:N	2.22	0.55
1:X:212:GLU:HG2	4:X:2077:HOH:O	2.06	0.55
1:X:377:ALA:HA	1:X:380:THR:HB	1.87	0.55
1:X:410:ASN:CG	1:X:413:LYS:HE3	2.26	0.55
1:X:91:MET:HG2	1:X:118:TYR:O	2.06	0.55
1:X:30:SER:O	1:X:31:ASP:OD1	2.25	0.55
1:X:540:ASP:O	1:X:543:LEU:N	2.40	0.55
1:X:737:TYR:CB	1:X:747:ARG:H	2.19	0.55
1:X:118:TYR:HD2	1:X:148:ARG:CZ	2.20	0.55
1:X:238:ARG:CG	1:X:278:TYR:CE1	2.69	0.55
1:X:539:THR:O	1:X:540:ASP:C	2.44	0.55
1:X:681:VAL:CG2	1:X:682:LEU:H	2.19	0.55
1:X:353:HIS:C	1:X:355:GLY:N	2.58	0.55
1:X:617:ILE:HG23	1:X:617:ILE:O	2.07	0.55
1:X:194:GLN:O	1:X:197:ALA:HB3	2.07	0.55
1:X:296:LEU:O	1:X:298:LEU:HG	2.06	0.55
1:X:390:GLU:HG2	1:X:394:MET:CG	2.36	0.55
1:X:44:ARG:HB2	4:X:2023:HOH:O	2.07	0.55
1:X:592:LEU:HD11	1:X:596:LEU:HD13	1.88	0.55
1:X:311:GLY:HA2	4:X:2109:HOH:O	2.07	0.55
1:X:159:SER:O	1:X:160:ASP:C	2.45	0.54
1:X:458:PHE:CB	1:X:472:ASN:HD22	2.19	0.54
1:X:570:VAL:HG12	1:X:571:THR:H	1.70	0.54
1:X:739:PHE:CE2	1:X:744:ILE:HD11	2.41	0.54
1:X:91:MET:CA	4:X:2041:HOH:O	2.55	0.54
1:X:276:ARG:HD2	1:X:282:TYR:CE2	2.40	0.54
1:X:331:MET:C	1:X:336:PHE:HB2	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:17:VAL:O	1:X:18:LYS:HB3	2.06	0.54
1:X:6:ASP:O	1:X:12:HIS:CE1	2.61	0.54
1:X:213:GLN:CA	4:X:2079:HOH:O	2.56	0.54
1:X:361:LYS:CB	1:X:367:ALA:HA	2.35	0.54
1:X:372:LYS:HA	4:X:2129:HOH:O	1.88	0.54
1:X:247:PHE:O	1:X:447:ALA:HB3	2.07	0.54
1:X:279:HIS:O	1:X:283:GLN:CG	2.52	0.54
1:X:459:GLU:HG2	1:X:461:PHE:HE1	1.73	0.54
1:X:703:LYS:HA	1:X:706:TYR:CE2	2.42	0.54
1:X:705:TYR:CE2	1:X:755:GLU:HA	2.43	0.54
1:X:142:ILE:HG23	1:X:146:ARG:NH1	2.22	0.54
1:X:10:ASP:HB3	1:X:14:TYR:CD2	2.42	0.54
1:X:498:LYS:O	1:X:498:LYS:HG3	2.08	0.54
1:X:702:VAL:HG22	1:X:723:THR:OG1	2.08	0.54
1:X:222:LEU:CB	4:X:2082:HOH:O	2.54	0.54
1:X:238:ARG:HB3	1:X:264:GLU:H	1.72	0.54
1:X:428:ARG:HB3	1:X:611:LEU:HD13	1.87	0.54
1:X:501:TRP:CH2	1:X:738:ARG:HG3	2.43	0.54
1:X:534:VAL:O	1:X:536:PRO:HD3	2.07	0.54
1:X:561:PRO:HG2	1:X:564:SER:O	2.08	0.54
1:X:581:ILE:O	1:X:581:ILE:CG2	2.55	0.54
1:X:734:PRO:O	1:X:738:ARG:NH1	2.41	0.54
1:X:480:GLN:O	1:X:483:ASN:HB2	2.08	0.53
1:X:607:VAL:O	1:X:607:VAL:HG12	2.08	0.53
1:X:700:ASP:O	1:X:703:LYS:HG2	2.08	0.53
1:X:296:LEU:HD12	1:X:298:LEU:CG	2.27	0.53
1:X:588:ASN:OD1	1:X:629:THR:HB	2.08	0.53
1:X:533:SER:O	1:X:589:LYS:HD2	2.08	0.53
1:X:48:GLU:HG2	1:X:65:VAL:CG2	2.38	0.53
1:X:48:GLU:CG	1:X:65:VAL:HG21	2.37	0.53
1:X:154:HIS:CE1	1:X:155:ILE:CG2	2.91	0.53
1:X:539:THR:O	1:X:542:THR:HG22	2.07	0.53
1:X:33:ARG:CZ	1:X:753:ARG:NH1	2.71	0.53
1:X:10:ASP:HB3	1:X:14:TYR:CE2	2.43	0.53
1:X:543:LEU:O	1:X:547:LEU:HG	2.08	0.53
1:X:692:PHE:HD2	1:X:748:ALA:N	2.06	0.53
1:X:746:PHE:CE1	4:X:2250:HOH:O	2.49	0.53
1:X:106:LEU:H	1:X:106:LEU:HD23	1.73	0.53
1:X:130:LYS:CD	1:X:132:ILE:HD11	2.38	0.53
1:X:155:ILE:HG23	1:X:156:PHE:N	2.23	0.53
1:X:246:GLN:O	1:X:254:SER:N	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:27:LEU:HD12	1:X:28:THR:CB	2.39	0.53
1:X:58:ASP:HA	4:X:2029:HOH:O	1.85	0.53
1:X:596:LEU:HA	1:X:599:CYS:SG	2.49	0.53
1:X:736:GLN:CA	1:X:747:ARG:HD2	2.39	0.53
1:X:620:ARG:NH1	1:X:629:THR:HA	2.24	0.53
1:X:668:GLU:OE1	1:X:670:LYS:CE	2.57	0.53
1:X:73:LYS:HG2	1:X:74:LYS:N	2.23	0.53
1:X:398:ILE:HG12	1:X:407:GLN:HE22	1.70	0.53
1:X:739:PHE:CG	1:X:744:ILE:CD1	2.91	0.53
1:X:172:ASN:HB2	4:X:2067:HOH:O	2.02	0.53
1:X:369:LEU:HD12	1:X:390:GLU:OE1	2.09	0.53
1:X:486:MET:O	1:X:490:GLU:CG	2.43	0.53
1:X:573:TYR:OH	1:X:683:GLU:HG2	2.09	0.53
1:X:284:LEU:HD22	1:X:348:ILE:CD1	2.36	0.52
1:X:630:VAL:O	1:X:630:VAL:CG1	2.53	0.52
1:X:756:GLU:O	1:X:757:ALA:HB2	2.08	0.52
1:X:122:PHE:CE1	1:X:654:ARG:NE	2.76	0.52
1:X:27:LEU:CD1	1:X:28:THR:CB	2.86	0.52
1:X:53:VAL:HB	1:X:61:THR:CB	2.38	0.52
1:X:758:ARG:NE	4:X:2019:HOH:O	2.43	0.52
1:X:397:ARG:HA	1:X:406:ALA:CA	2.31	0.52
1:X:596:LEU:HA	1:X:599:CYS:HG	1.73	0.52
1:X:120:GLY:HA3	4:X:2049:HOH:O	2.09	0.52
1:X:172:ASN:HD22	1:X:449:PHE:HE2	1.47	0.52
1:X:176:LEU:N	1:X:651:HIS:O	2.39	0.52
1:X:202:ARG:HD3	1:X:252:PHE:HB3	1.89	0.52
1:X:26:LYS:O	1:X:26:LYS:HG3	2.09	0.52
1:X:458:PHE:CB	1:X:472:ASN:ND2	2.72	0.52
1:X:530:ASP:OD1	1:X:588:ASN:ND2	2.42	0.52
1:X:263:LEU:HD21	1:X:430:PHE:CE2	2.44	0.52
1:X:410:ASN:OD1	1:X:410:ASN:C	2.46	0.52
1:X:492:GLU:C	1:X:494:TYR:N	2.63	0.52
1:X:603:SER:OG	1:X:608:VAL:HG11	2.09	0.52
1:X:628:ILE:HG22	1:X:632:ALA:HB3	1.91	0.52
1:X:700:ASP:O	1:X:704:ARG:N	2.43	0.52
1:X:90:ASP:O	1:X:93:GLU:HG3	2.10	0.52
1:X:142:ILE:C	1:X:144:LYS:N	2.63	0.52
1:X:202:ARG:NH1	1:X:252:PHE:CB	2.71	0.52
1:X:324:PHE:HE2	1:X:328:ARG:HH21	1.54	0.52
1:X:681:VAL:CG2	1:X:682:LEU:N	2.72	0.52
1:X:712:VAL:HG13	1:X:713:PRO:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:694:ASN:HD22	1:X:751:LEU:CD1	2.22	0.52
1:X:293:LYS:CA	1:X:298:LEU:HB2	2.39	0.52
1:X:410:ASN:O	1:X:412:GLU:N	2.43	0.52
1:X:736:GLN:O	1:X:747:ARG:CG	2.56	0.52
1:X:732:ILE:HG21	1:X:737:TYR:HD2	1.68	0.52
1:X:746:PHE:C	4:X:2250:HOH:O	2.47	0.52
1:X:377:ALA:HA	1:X:380:THR:CB	2.39	0.52
1:X:428:ARG:NH1	1:X:618:ALA:HB2	2.25	0.52
1:X:534:VAL:HG12	1:X:534:VAL:O	2.09	0.52
1:X:546:LYS:C	1:X:548:HIS:H	2.12	0.52
1:X:116:TYR:HE2	1:X:134:ILE:CD1	2.23	0.52
1:X:595:ASP:HA	1:X:598:LEU:CB	2.40	0.52
1:X:712:VAL:CG2	1:X:725:ALA:HB3	2.40	0.52
1:X:759:GLU:HG2	1:X:759:GLU:OXT	2.10	0.52
1:X:88:VAL:CG2	4:X:2041:HOH:O	2.56	0.52
1:X:224:ALA:O	1:X:280:ILE:N	2.42	0.51
1:X:304:PHE:CD2	1:X:352:LEU:HB3	2.43	0.51
1:X:544:ILE:O	1:X:548:HIS:CD2	2.63	0.51
1:X:110:TYR:CD2	1:X:667:LEU:HD13	2.43	0.51
1:X:288:ALA:CB	1:X:292:GLU:OE2	2.59	0.51
1:X:147:ARG:O	1:X:150:GLU:HB2	2.10	0.51
1:X:552:SER:HB2	4:X:2180:HOH:O	2.10	0.51
1:X:644:THR:HG22	1:X:644:THR:O	2.11	0.51
1:X:103:PHE:HA	1:X:106:LEU:HD21	1.91	0.51
1:X:213:GLN:HA	1:X:216:LEU:HB2	1.92	0.51
1:X:464:ASN:ND2	1:X:577:VAL:CG2	2.72	0.51
1:X:732:ILE:CG2	1:X:737:TYR:CE2	2.93	0.51
1:X:142:ILE:O	1:X:144:LYS:N	2.43	0.51
1:X:361:LYS:CG	1:X:411:VAL:HG11	2.35	0.51
1:X:446:LYS:HG2	1:X:447:ALA:N	2.25	0.51
1:X:14:TYR:OH	1:X:133:PRO:CG	2.58	0.51
1:X:483:ASN:HB3	1:X:508:LEU:HD21	1.93	0.51
1:X:689:ARG:CB	1:X:693:PRO:HB3	2.41	0.51
1:X:739:PHE:CD1	1:X:744:ILE:HD11	2.45	0.51
1:X:233:ASN:OD1	1:X:234:ASN:N	2.36	0.51
1:X:383:GLY:HA2	4:X:2132:HOH:O	2.09	0.51
1:X:620:ARG:NH2	1:X:630:VAL:HG23	2.25	0.51
1:X:691:GLY:C	1:X:692:PHE:CD1	2.84	0.51
1:X:706:TYR:CD1	1:X:712:VAL:O	2.61	0.51
1:X:737:TYR:HA	1:X:747:ARG:HA	1.93	0.51
1:X:735:GLU:CA	1:X:738:ARG:HH12	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:605:ASP:OD1	1:X:608:VAL:N	2.44	0.51
1:X:719:SER:O	1:X:723:THR:HG22	2.10	0.51
1:X:284:LEU:HD23	1:X:348:ILE:HD13	1.92	0.51
1:X:485:HIS:CD2	1:X:489:LEU:CD1	2.94	0.51
1:X:4:ILE:N	1:X:4:ILE:HD12	2.16	0.51
1:X:662:GLN:N	4:X:2208:HOH:O	2.43	0.51
1:X:706:TYR:OH	1:X:714:ARG:CG	2.58	0.51
1:X:731:ASN:O	1:X:731:ASN:ND2	2.44	0.51
1:X:735:GLU:C	1:X:738:ARG:HH12	2.13	0.51
1:X:10:ASP:O	1:X:13:LYS:HG2	2.11	0.50
1:X:703:LYS:CA	4:X:2224:HOH:O	2.56	0.50
1:X:172:ASN:HB3	1:X:449:PHE:CZ	2.45	0.50
1:X:347:ILE:HD12	1:X:608:VAL:CG2	2.42	0.50
1:X:61:THR:C	1:X:62:PHE:HD1	2.15	0.50
1:X:133:PRO:CA	4:X:2051:HOH:O	2.59	0.50
1:X:18:LYS:O	1:X:18:LYS:HG3	2.10	0.50
1:X:40:ASP:C	1:X:42:LYS:H	2.15	0.50
1:X:409:LEU:HD23	1:X:414:SER:CB	2.42	0.50
1:X:445:ARG:O	1:X:445:ARG:CG	2.58	0.50
1:X:467:GLU:O	1:X:470:CYS:HB2	2.12	0.50
1:X:577:VAL:HG11	1:X:579:TYR:CZ	2.46	0.50
1:X:657:ILE:HG22	1:X:675:GLN:CD	2.32	0.50
1:X:82:PRO:HG3	1:X:756:GLU:CD	2.31	0.50
1:X:89:GLU:O	1:X:118:TYR:O	2.29	0.50
1:X:19:GLN:CG	4:X:2003:HOH:O	2.58	0.50
1:X:266:SER:N	1:X:423:LYS:HE2	2.27	0.50
1:X:614:ASP:O	1:X:616:ASN:N	2.44	0.50
1:X:202:ARG:HG2	1:X:253:ILE:HB	1.94	0.50
1:X:79:GLN:HB2	4:X:2036:HOH:O	2.10	0.50
1:X:732:ILE:HG22	1:X:737:TYR:CE2	2.47	0.50
1:X:97:LEU:HD12	1:X:689:ARG:NH1	2.26	0.50
1:X:246:GLN:CG	1:X:446:LYS:HE2	2.27	0.50
1:X:450:ILE:HG22	1:X:450:ILE:O	2.12	0.50
1:X:199:VAL:HG23	1:X:200:ALA:N	2.25	0.50
1:X:399:LEU:HD12	1:X:403:ASP:O	2.12	0.50
1:X:458:PHE:HB3	1:X:472:ASN:HD22	1.77	0.50
1:X:47:TYR:CE1	1:X:673:LEU:CD2	2.94	0.50
1:X:702:VAL:O	1:X:706:TYR:CE2	2.61	0.50
1:X:224:ALA:O	1:X:280:ILE:HB	2.11	0.49
1:X:269:VAL:HG12	1:X:306:TYR:CE1	2.47	0.49
1:X:594:GLN:O	1:X:594:GLN:OE1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:735:GLU:HA	1:X:738:ARG:HH12	1.76	0.49
1:X:377:ALA:O	1:X:381:VAL:N	2.41	0.49
1:X:409:LEU:CD2	1:X:409:LEU:H	2.09	0.49
1:X:526:LEU:O	1:X:530:ASP:HB2	2.11	0.49
1:X:141:ASP:HA	1:X:144:LYS:NZ	2.26	0.49
1:X:189:THR:O	1:X:193:ILE:HG12	2.12	0.49
1:X:27:LEU:CD1	1:X:28:THR:CG2	2.88	0.49
1:X:458:PHE:HB2	1:X:472:ASN:ND2	2.27	0.49
1:X:73:LYS:HG2	1:X:74:LYS:H	1.77	0.49
1:X:247:PHE:HE1	1:X:253:ILE:HG12	1.70	0.49
1:X:315:ILE:O	1:X:316:LYS:C	2.50	0.49
1:X:361:LYS:CD	1:X:361:LYS:C	2.78	0.49
1:X:459:GLU:HG2	1:X:461:PHE:CE1	2.48	0.49
1:X:546:LYS:C	1:X:548:HIS:N	2.66	0.49
1:X:166:MET:CG	1:X:448:TYR:CD2	2.96	0.49
1:X:485:HIS:CD2	1:X:489:LEU:HD12	2.47	0.49
1:X:2:ASN:HB3	1:X:4:ILE:HD13	1.94	0.49
1:X:739:PHE:CZ	1:X:744:ILE:HD11	2.48	0.49
1:X:173:GLN:C	4:X:2207:HOH:O	2.50	0.49
1:X:173:GLN:HB2	1:X:450:ILE:HD13	1.95	0.49
1:X:353:HIS:O	1:X:355:GLY:N	2.46	0.49
1:X:409:LEU:HD13	1:X:409:LEU:H	1.78	0.49
1:X:361:LYS:HG2	1:X:411:VAL:HG21	1.95	0.49
1:X:561:PRO:HD3	1:X:568:PHE:HA	1.94	0.49
1:X:696:ILE:HG13	1:X:698:TYR:H	1.78	0.48
1:X:713:PRO:HG2	1:X:716:ALA:HB2	1.94	0.48
1:X:172:ASN:O	1:X:648:THR:HB	2.13	0.48
1:X:397:ARG:HD2	1:X:404:LEU:HG	1.94	0.48
1:X:738:ARG:O	1:X:745:PHE:CE2	2.66	0.48
1:X:45:ASP:OD1	1:X:677:ARG:NH2	2.36	0.48
1:X:530:ASP:CG	1:X:588:ASN:HD21	2.16	0.48
1:X:582:GLN:O	4:X:2190:HOH:O	2.20	0.48
1:X:11:TYR:CD1	1:X:15:LEU:HD12	2.48	0.48
1:X:213:GLN:CG	4:X:2078:HOH:O	2.52	0.48
1:X:529:LEU:O	1:X:529:LEU:HD23	2.14	0.48
1:X:577:VAL:HG11	1:X:579:TYR:OH	2.13	0.48
1:X:684:GLY:C	1:X:687:ILE:HG22	2.34	0.48
1:X:8:THR:CG2	1:X:9:SER:N	2.77	0.48
1:X:468:GLN:C	1:X:470:CYS:H	2.17	0.48
1:X:708:LEU:HD22	1:X:730:LEU:HD21	1.96	0.48
1:X:23:ASP:N	1:X:23:ASP:OD1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:131:ARG:C	1:X:132:ILE:HD13	2.34	0.48
1:X:181:SER:C	1:X:183:ALA:H	2.16	0.48
1:X:736:GLN:O	1:X:747:ARG:CA	2.62	0.48
1:X:82:PRO:CB	1:X:756:GLU:CD	2.82	0.48
1:X:389:LEU:O	1:X:393:LEU:HB2	2.13	0.48
1:X:515:ASP:HA	1:X:518:ASP:OD1	2.14	0.48
1:X:625:ALA:C	1:X:626:ASN:OD1	2.52	0.48
1:X:385:ASN:HA	1:X:386:PRO:HD3	1.70	0.48
1:X:547:LEU:O	1:X:558:TYR:OH	2.32	0.48
1:X:706:TYR:HD2	4:X:2219:HOH:O	1.74	0.47
1:X:737:TYR:HB2	1:X:747:ARG:H	1.78	0.47
1:X:89:GLU:HG3	1:X:109:ARG:HH12	1.78	0.47
1:X:132:ILE:HD13	4:X:2050:HOH:O	2.03	0.47
1:X:187:GLU:HB3	4:X:2068:HOH:O	2.08	0.47
1:X:265:LYS:O	1:X:268:VAL:CG1	2.58	0.47
1:X:375:LEU:C	1:X:377:ALA:H	2.17	0.47
1:X:692:PHE:CD2	1:X:748:ALA:N	2.82	0.47
1:X:727:LEU:O	1:X:731:ASN:HA	2.14	0.47
1:X:734:PRO:CD	4:X:2241:HOH:O	2.59	0.47
1:X:22:SER:N	4:X:2012:HOH:O	2.41	0.47
1:X:569:GLY:HA2	1:X:577:VAL:O	2.13	0.47
1:X:66:ASP:HB2	1:X:68:GLN:OE1	2.14	0.47
1:X:18:LYS:O	1:X:19:GLN:C	2.53	0.47
1:X:689:ARG:HG3	1:X:693:PRO:HG3	1.92	0.47
1:X:736:GLN:HA	1:X:747:ARG:HD2	1.95	0.47
1:X:377:ALA:HA	1:X:380:THR:OG1	2.15	0.47
1:X:85:PHE:CD1	1:X:85:PHE:N	2.81	0.47
1:X:395:GLU:HG3	1:X:408:HIS:CG	2.49	0.47
1:X:739:PHE:CE1	1:X:744:ILE:HD11	2.50	0.47
1:X:84:LYS:HB3	1:X:755:GLU:OE2	2.14	0.47
2:X:1001:ADP:C2	4:X:2256:HOH:O	2.55	0.47
1:X:254:SER:OG	1:X:255:GLY:N	2.41	0.47
1:X:276:ARG:HG2	1:X:277:ASN:N	2.30	0.47
1:X:14:TYR:CB	4:X:2004:HOH:O	2.32	0.47
1:X:544:ILE:HD13	1:X:581:ILE:CD1	2.41	0.47
1:X:564:SER:OG	1:X:567:GLU:HG3	2.15	0.47
1:X:85:PHE:O	4:X:2039:HOH:O	2.15	0.47
1:X:347:ILE:HD12	1:X:608:VAL:HG23	1.96	0.47
1:X:85:PHE:HA	4:X:2039:HOH:O	2.09	0.47
1:X:388:VAL:O	1:X:389:LEU:C	2.53	0.47
1:X:390:GLU:O	1:X:393:LEU:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:47:TYR:CD1	1:X:47:TYR:N	2.82	0.47
1:X:550:HIS:O	1:X:554:LYS:HG3	2.15	0.47
1:X:559:GLU:OE2	1:X:560:GLU:O	2.33	0.47
1:X:74:LYS:HD3	4:X:2029:HOH:O	2.15	0.47
1:X:756:GLU:O	1:X:756:GLU:HG3	2.15	0.47
1:X:16:LYS:C	1:X:18:LYS:H	2.18	0.47
1:X:219:ASN:O	1:X:220:PRO:C	2.53	0.47
1:X:328:ARG:HG2	1:X:341:GLN:OE1	2.15	0.47
1:X:523:PRO:HB3	1:X:527:ALA:HB1	1.97	0.47
1:X:544:ILE:HD13	1:X:581:ILE:HG12	1.79	0.47
1:X:735:GLU:HA	1:X:738:ARG:NH1	2.30	0.47
1:X:81:ASN:ND2	1:X:101:ALA:HB1	2.29	0.47
1:X:432:TRP:NE1	1:X:610:LYS:CE	2.78	0.46
1:X:689:ARG:CG	1:X:693:PRO:CG	2.90	0.46
1:X:223:GLU:HG3	1:X:227:ASN:HD22	1.80	0.46
1:X:64:THR:O	1:X:65:VAL:C	2.53	0.46
1:X:703:LYS:O	4:X:2219:HOH:O	2.15	0.46
1:X:706:TYR:CE1	1:X:714:ARG:N	2.83	0.46
1:X:21:ASP:CG	4:X:2011:HOH:O	2.52	0.46
1:X:33:ARG:HH22	1:X:753:ARG:HA	1.80	0.46
1:X:368:VAL:C	1:X:369:LEU:HD23	2.36	0.46
1:X:420:ALA:HB1	1:X:592:LEU:HD13	1.97	0.46
1:X:477:LYS:HG3	1:X:638:LEU:HD21	1.98	0.46
1:X:671:VAL:O	1:X:675:GLN:HG3	2.16	0.46
1:X:696:ILE:HD11	1:X:701:PHE:HB2	1.97	0.46
1:X:706:TYR:OH	1:X:714:ARG:HG3	2.16	0.46
1:X:733:ASP:OD1	1:X:734:PRO:N	2.48	0.46
1:X:736:GLN:OE1	1:X:747:ARG:HD3	2.15	0.46
1:X:42:LYS:HG3	1:X:43:GLU:N	2.31	0.46
1:X:745:PHE:HE1	4:X:2157:HOH:O	1.95	0.46
1:X:116:TYR:HE2	1:X:134:ILE:HD12	1.80	0.46
1:X:353:HIS:O	1:X:354:LEU:C	2.53	0.46
1:X:372:LYS:N	4:X:2129:HOH:O	2.37	0.46
1:X:530:ASP:OD1	1:X:629:THR:OG1	2.33	0.46
1:X:341:GLN:O	1:X:345:PHE:HD2	1.97	0.46
1:X:398:ILE:HD12	1:X:398:ILE:N	2.31	0.46
1:X:425:LEU:O	1:X:429:LEU:CB	2.64	0.46
1:X:120:GLY:CA	4:X:2049:HOH:O	2.64	0.46
1:X:11:TYR:HD1	1:X:15:LEU:HD12	1.81	0.46
1:X:515:ASP:O	1:X:516:LEU:C	2.52	0.46
1:X:347:ILE:HD11	1:X:605:ASP:OD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:747:ARG:HG2	1:X:750:GLN:H	1.81	0.46
1:X:712:VAL:HG22	1:X:722:ALA:O	2.16	0.46
1:X:83:ILE:HD13	1:X:86:ASP:OD2	2.16	0.46
1:X:136:THR:HG23	4:X:2051:HOH:O	2.15	0.46
1:X:159:SER:O	1:X:163:TYR:N	2.49	0.46
1:X:389:LEU:HD23	1:X:389:LEU:O	2.16	0.46
1:X:52:ILE:CG2	1:X:55:GLU:OE2	2.63	0.46
1:X:710:PRO:CG	4:X:2221:HOH:O	2.61	0.46
1:X:752:ALA:HB1	1:X:756:GLU:HG2	1.98	0.46
1:X:219:ASN:C	1:X:221:ILE:N	2.68	0.46
1:X:313:VAL:CG2	1:X:314:ASP:N	2.48	0.46
1:X:348:ILE:HG13	1:X:349:ALA:H	1.80	0.46
1:X:148:ARG:HA	4:X:2058:HOH:O	2.16	0.45
1:X:724:ASP:CB	4:X:2235:HOH:O	2.31	0.45
1:X:188:ASN:O	1:X:191:LYS:N	2.47	0.45
1:X:345:PHE:CA	1:X:348:ILE:HG12	2.38	0.45
1:X:22:SER:HB2	4:X:2012:HOH:O	2.16	0.45
1:X:274:THR:C	4:X:2099:HOH:O	2.54	0.45
1:X:276:ARG:HG3	1:X:282:TYR:OH	2.14	0.45
1:X:396:PRO:O	1:X:398:ILE:CD1	2.65	0.45
1:X:572:HIS:C	1:X:574:ALA:H	2.19	0.45
1:X:600:PHE:C	1:X:602:ASP:N	2.69	0.45
1:X:428:ARG:O	1:X:611:LEU:HD21	2.16	0.45
1:X:739:PHE:CD1	1:X:744:ILE:HG13	2.51	0.45
1:X:15:LEU:HD21	1:X:134:ILE:HB	1.97	0.45
1:X:187:GLU:HB2	4:X:2068:HOH:O	2.11	0.45
1:X:300:GLY:O	1:X:302:GLU:N	2.49	0.45
1:X:361:LYS:H	1:X:361:LYS:HD2	1.82	0.45
1:X:215:ILE:HA	1:X:441:LEU:HD11	1.98	0.45
1:X:720:GLN:NE2	1:X:741:ILE:HG13	2.31	0.45
1:X:84:LYS:HZ1	1:X:704:ARG:CD	2.25	0.45
1:X:546:LYS:NZ	1:X:550:HIS:CE1	2.77	0.45
1:X:64:THR:C	1:X:66:ASP:H	2.19	0.45
1:X:144:LYS:CB	1:X:144:LYS:NZ	2.80	0.45
1:X:193:ILE:HG23	1:X:245:ILE:HD11	1.98	0.45
1:X:233:ASN:CG	1:X:234:ASN:H	2.17	0.45
1:X:276:ARG:CD	1:X:282:TYR:CE2	3.00	0.45
1:X:752:ALA:HA	1:X:755:GLU:HB3	1.99	0.45
1:X:79:GLN:N	4:X:2036:HOH:O	2.28	0.45
1:X:288:ALA:CB	1:X:292:GLU:CD	2.84	0.45
1:X:36:TRP:N	1:X:78:ASN:O	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:423:LYS:O	1:X:427:GLY:N	2.43	0.45
1:X:615:PRO:C	1:X:617:ILE:N	2.70	0.45
1:X:650:PRO:HB2	1:X:652:PHE:CZ	2.52	0.45
1:X:211:LEU:HA	1:X:214:GLN:OE1	2.16	0.45
1:X:385:ASN:CG	1:X:388:VAL:HG13	2.37	0.45
1:X:7:ARG:NH1	4:X:2003:HOH:O	2.25	0.45
1:X:166:MET:SD	1:X:448:TYR:HB2	2.54	0.45
1:X:747:ARG:HG2	1:X:750:GLN:O	2.16	0.45
1:X:90:ASP:OD1	1:X:118:TYR:HB3	2.17	0.45
1:X:91:MET:SD	1:X:117:THR:HG21	2.57	0.45
1:X:264:GLU:HG3	1:X:267:ARG:CB	2.47	0.45
1:X:291:GLU:O	1:X:295:ALA:HB2	2.16	0.45
1:X:60:PHE:HD1	1:X:60:PHE:HA	1.65	0.45
1:X:641:LEU:O	1:X:644:THR:CB	2.63	0.45
1:X:654:ARG:CB	1:X:681:VAL:CG1	2.95	0.45
1:X:671:VAL:HG12	1:X:675:GLN:NE2	2.32	0.45
1:X:128:PRO:O	1:X:129:PHE:HB2	2.18	0.44
1:X:463:VAL:HG23	1:X:463:VAL:O	2.16	0.44
1:X:477:LYS:HD2	1:X:514:ILE:HD12	1.98	0.44
1:X:520:ARG:O	1:X:523:PRO:CG	2.59	0.44
1:X:64:THR:CG2	1:X:68:GLN:HB2	2.48	0.44
1:X:14:TYR:CE2	4:X:2005:HOH:O	2.42	0.44
1:X:365:GLU:OE1	1:X:365:GLU:HA	2.17	0.44
1:X:455:ILE:HG13	1:X:456:SER:N	2.33	0.44
1:X:702:VAL:HG11	1:X:719:SER:OG	2.17	0.44
1:X:702:VAL:HG21	1:X:719:SER:OG	2.17	0.44
1:X:132:ILE:HG22	1:X:133:PRO:HD2	1.97	0.44
1:X:379:SER:HB2	1:X:386:PRO:HG3	1.99	0.44
1:X:620:ARG:NH1	1:X:628:ILE:O	2.24	0.44
1:X:654:ARG:CB	1:X:681:VAL:HG11	2.47	0.44
1:X:14:TYR:OH	1:X:133:PRO:HG3	2.17	0.44
1:X:139:MET:O	1:X:140:VAL:C	2.55	0.44
1:X:15:LEU:CD1	1:X:143:PHE:HZ	2.29	0.44
1:X:4:ILE:HD11	1:X:146:ARG:HH12	1.82	0.44
1:X:223:GLU:O	1:X:227:ASN:HB2	2.17	0.44
1:X:246:GLN:O	1:X:247:PHE:HD1	2.00	0.44
1:X:746:PHE:O	1:X:747:ARG:O	2.35	0.44
1:X:189:THR:HG23	1:X:452:VAL:HG11	1.99	0.44
1:X:717:GLU:HG3	1:X:718:ASP:N	2.32	0.44
1:X:96:TYR:HE2	4:X:2042:HOH:O	1.99	0.44
1:X:184:GLY:HA2	2:X:1001:ADP:O1A	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:431:LEU:O	1:X:435:LYS:HG2	2.17	0.44
1:X:53:VAL:HG21	1:X:62:PHE:O	2.17	0.44
1:X:642:MET:C	1:X:644:THR:H	2.20	0.44
1:X:691:GLY:C	1:X:692:PHE:CG	2.91	0.44
1:X:239:PHE:CD1	1:X:240:GLY:O	2.59	0.44
1:X:336:PHE:HD1	1:X:340:GLU:CD	2.20	0.44
1:X:395:GLU:HG2	1:X:407:GLN:O	2.17	0.44
1:X:448:TYR:N	1:X:448:TYR:CD1	2.86	0.44
1:X:2:ASN:HB2	1:X:5:HIS:NE2	2.32	0.44
1:X:747:ARG:N	4:X:2250:HOH:O	2.51	0.44
1:X:294:LYS:O	1:X:296:LEU:N	2.50	0.44
1:X:344:ILE:O	1:X:348:ILE:HG23	2.18	0.44
1:X:122:PHE:CE2	1:X:681:VAL:HA	2.53	0.44
1:X:689:ARG:CG	1:X:693:PRO:HG3	2.48	0.44
1:X:703:LYS:CB	4:X:2224:HOH:O	2.65	0.44
1:X:747:ARG:HB2	4:X:2250:HOH:O	2.00	0.44
1:X:283:GLN:OE1	1:X:323:GLU:OE1	2.36	0.44
1:X:497:GLU:O	1:X:498:LYS:CB	2.64	0.44
1:X:516:LEU:O	1:X:525:ILE:HG12	2.18	0.44
1:X:572:HIS:C	1:X:574:ALA:N	2.71	0.44
1:X:737:TYR:CD1	1:X:739:PHE:CD1	3.05	0.44
1:X:129:PHE:CE2	1:X:662:GLN:HA	2.53	0.43
1:X:285:LEU:HD21	1:X:298:LEU:HD22	1.99	0.43
1:X:410:ASN:OD1	1:X:412:GLU:N	2.44	0.43
1:X:449:PHE:CZ	1:X:648:THR:HG22	2.48	0.43
1:X:708:LEU:N	1:X:759:GLU:OXT	2.50	0.43
1:X:750:GLN:O	1:X:750:GLN:HG3	2.17	0.43
1:X:35:ILE:CG1	1:X:78:ASN:O	2.66	0.43
1:X:109:ARG:HE	1:X:109:ARG:HB3	1.66	0.43
1:X:336:PHE:HD1	1:X:336:PHE:HA	1.58	0.43
1:X:375:LEU:C	1:X:377:ALA:N	2.71	0.43
1:X:37:TYR:CE1	1:X:39:PRO:HG3	2.54	0.43
1:X:172:ASN:CG	1:X:449:PHE:N	2.69	0.43
1:X:469:LEU:HD22	1:X:584:TRP:HH2	1.83	0.43
1:X:668:GLU:C	1:X:670:LYS:N	2.71	0.43
1:X:704:ARG:O	1:X:704:ARG:HG3	2.18	0.43
1:X:273:GLU:HA	1:X:310:SER:O	2.18	0.43
1:X:53:VAL:N	1:X:61:THR:OG1	2.46	0.43
1:X:102:VAL:O	1:X:106:LEU:HD22	2.19	0.43
1:X:274:THR:CG2	4:X:2098:HOH:O	2.54	0.43
1:X:614:ASP:HA	1:X:615:PRO:HD2	1.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:672:VAL:O	1:X:676:LEU:HD22	2.12	0.43
1:X:424:ALA:O	1:X:428:ARG:CG	2.67	0.43
1:X:491:GLN:HA	1:X:494:TYR:HB2	2.01	0.43
1:X:529:LEU:C	1:X:529:LEU:HD23	2.39	0.43
1:X:449:PHE:CE1	1:X:648:THR:HG21	2.44	0.43
1:X:697:ILE:O	1:X:698:TYR:HB3	2.19	0.43
1:X:11:TYR:CE1	1:X:152:ALA:HB2	2.54	0.43
1:X:217:GLN:HB3	1:X:330:ALA:CB	2.47	0.43
1:X:250:ALA:N	4:X:2094:HOH:O	2.51	0.43
1:X:315:ILE:HG21	1:X:318:VAL:HG21	2.01	0.43
1:X:522:PRO:HA	1:X:523:PRO:HD3	1.72	0.43
1:X:577:VAL:O	1:X:577:VAL:HG13	2.17	0.43
1:X:587:LYS:O	1:X:590:ASP:HB2	2.18	0.43
1:X:361:LYS:HD3	1:X:361:LYS:O	2.11	0.43
1:X:472:ASN:O	1:X:473:TYR:C	2.56	0.43
1:X:597:GLU:O	1:X:601:LYS:HG3	2.19	0.43
1:X:664:PRO:O	1:X:665:ALA:CB	2.66	0.43
1:X:689:ARG:HD2	1:X:693:PRO:HG3	1.99	0.43
1:X:501:TRP:CZ2	1:X:738:ARG:HG3	2.54	0.43
1:X:83:ILE:C	1:X:85:PHE:N	2.69	0.43
1:X:8:THR:O	1:X:9:SER:C	2.56	0.43
1:X:210:VAL:HG12	1:X:214:GLN:OE1	2.19	0.43
1:X:629:THR:O	1:X:632:ALA:HB3	2.19	0.43
1:X:62:PHE:CZ	1:X:72:VAL:HG12	2.54	0.43
1:X:72:VAL:HG22	1:X:73:LYS:H	1.84	0.43
1:X:108:VAL:O	1:X:111:ASN:CB	2.64	0.43
1:X:17:VAL:O	1:X:18:LYS:CB	2.66	0.43
1:X:197:ALA:O	1:X:201:GLY:HA3	2.19	0.43
1:X:247:PHE:O	1:X:447:ALA:O	2.37	0.43
1:X:25:PHE:O	1:X:25:PHE:CG	2.71	0.43
1:X:37:TYR:OH	1:X:64:THR:HB	2.19	0.43
1:X:687:ILE:O	1:X:690:LYS:CB	2.64	0.43
1:X:739:PHE:CD2	1:X:744:ILE:CD1	3.01	0.43
1:X:73:LYS:HE2	1:X:75:ASP:HB2	2.01	0.43
1:X:146:ARG:HD3	1:X:151:VAL:CG1	2.49	0.42
1:X:360:GLU:O	1:X:367:ALA:HB1	2.18	0.42
1:X:378:ALA:O	1:X:379:SER:C	2.57	0.42
1:X:35:ILE:CD1	1:X:77:ALA:HB3	2.36	0.42
1:X:421:LEU:O	1:X:425:LEU:HD22	2.13	0.42
1:X:458:PHE:C	4:X:2148:HOH:O	2.57	0.42
1:X:521:GLN:HA	1:X:522:PRO:HA	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:595:ASP:HA	1:X:598:LEU:HB3	2.00	0.42
1:X:122:PHE:CD1	1:X:654:ARG:HG3	2.50	0.42
1:X:276:ARG:HD2	1:X:282:TYR:CE1	2.54	0.42
1:X:516:LEU:HD23	1:X:555:ASN:HD22	1.84	0.42
1:X:692:PHE:CE2	1:X:747:ARG:NH2	2.80	0.42
1:X:2:ASN:O	1:X:5:HIS:CD2	2.73	0.42
1:X:351:ILE:HD11	1:X:425:LEU:HB2	2.00	0.42
1:X:529:LEU:HD22	1:X:588:ASN:ND2	2.29	0.42
1:X:540:ASP:O	1:X:541:ASN:C	2.58	0.42
1:X:664:PRO:HA	4:X:2044:HOH:O	2.19	0.42
1:X:667:LEU:CD1	1:X:672:VAL:HG21	2.47	0.42
1:X:683:GLU:O	1:X:683:GLU:HG3	2.19	0.42
1:X:698:TYR:OH	1:X:719:SER:C	2.57	0.42
1:X:702:VAL:HG21	1:X:719:SER:CB	2.49	0.42
1:X:544:ILE:CG1	1:X:581:ILE:HG13	2.47	0.42
1:X:600:PHE:C	1:X:602:ASP:H	2.23	0.42
1:X:622:LYS:C	1:X:628:ILE:HD11	2.40	0.42
1:X:692:PHE:CE2	1:X:737:TYR:HA	2.54	0.42
1:X:88:VAL:HG22	1:X:105:ASN:HD21	1.84	0.42
1:X:166:MET:HG3	1:X:448:TYR:HD2	1.84	0.42
1:X:697:ILE:O	1:X:697:ILE:HG12	2.20	0.42
1:X:188:ASN:C	1:X:190:LYS:N	2.73	0.42
1:X:35:ILE:O	1:X:50:GLY:N	2.43	0.42
1:X:479:GLN:HG3	4:X:2171:HOH:O	2.19	0.42
1:X:531:GLU:O	1:X:535:PHE:CE1	2.73	0.42
1:X:687:ILE:HD12	1:X:687:ILE:HA	1.91	0.42
1:X:172:ASN:N	4:X:2067:HOH:O	2.47	0.42
1:X:384:VAL:CG1	1:X:385:ASN:H	2.30	0.42
1:X:480:GLN:NE2	1:X:511:GLN:OE1	2.53	0.42
1:X:517:ILE:HA	1:X:525:ILE:HG12	2.01	0.42
1:X:548:HIS:CG	1:X:560:GLU:HG3	2.55	0.42
1:X:751:LEU:CA	4:X:2252:HOH:O	2.17	0.42
1:X:264:GLU:CG	1:X:267:ARG:HB2	2.50	0.42
1:X:454:ASP:OD1	1:X:454:ASP:O	2.38	0.42
1:X:47:TYR:CE1	1:X:673:LEU:HD21	2.55	0.42
1:X:712:VAL:HG23	1:X:725:ALA:HB3	2.02	0.42
1:X:695:ARG:CG	1:X:745:PHE:CD1	3.02	0.42
1:X:375:LEU:O	1:X:377:ALA:N	2.52	0.42
1:X:398:ILE:HD13	1:X:407:GLN:CD	2.39	0.42
1:X:732:ILE:N	1:X:732:ILE:CD1	2.78	0.41
1:X:219:ASN:O	1:X:221:ILE:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:296:LEU:HD11	1:X:298:LEU:HD12	1.90	0.41
1:X:361:LYS:HB3	1:X:411:VAL:HG13	2.01	0.41
1:X:476:GLU:HG3	1:X:514:ILE:HD11	2.02	0.41
1:X:745:PHE:CD1	1:X:745:PHE:N	2.88	0.41
1:X:112:GLN:O	1:X:113:ASP:CB	2.67	0.41
1:X:33:ARG:NH1	1:X:753:ARG:NH1	2.67	0.41
1:X:391:LYS:HB2	1:X:391:LYS:NZ	2.35	0.41
1:X:265:LYS:HB3	1:X:423:LYS:HD3	2.01	0.41
1:X:466:PHE:HB2	1:X:584:TRP:NE1	2.35	0.41
1:X:721:LYS:O	1:X:721:LYS:HD3	2.20	0.41
1:X:731:ASN:C	1:X:731:ASN:ND2	2.73	0.41
1:X:84:LYS:CB	1:X:755:GLU:OE2	2.69	0.41
1:X:144:LYS:HZ1	1:X:144:LYS:HB2	1.83	0.41
1:X:89:GLU:HG2	1:X:153:PRO:HD3	2.02	0.41
1:X:213:GLN:HE22	1:X:333:ILE:HD12	1.81	0.41
1:X:398:ILE:CB	1:X:407:GLN:NE2	2.82	0.41
1:X:91:MET:O	1:X:94:LEU:HG	2.19	0.41
1:X:358:LYS:HE3	1:X:359:PHE:O	2.20	0.41
1:X:52:ILE:HG22	1:X:55:GLU:OE2	2.21	0.41
1:X:58:ASP:O	1:X:58:ASP:OD1	2.38	0.41
1:X:387:SER:OG	1:X:388:VAL:N	2.54	0.41
1:X:172:ASN:HB3	1:X:449:PHE:CD1	2.55	0.41
1:X:460:ILE:C	1:X:461:PHE:CD1	2.94	0.41
1:X:466:PHE:O	1:X:468:GLN:N	2.54	0.41
1:X:6:ASP:OD1	1:X:8:THR:HG22	2.21	0.41
1:X:179:GLY:O	1:X:185:LYS:HE3	2.20	0.41
1:X:223:GLU:HG3	1:X:227:ASN:ND2	2.35	0.41
1:X:304:PHE:O	1:X:308:ASN:OD1	2.38	0.41
1:X:263:LEU:HD11	1:X:430:PHE:CB	2.50	0.41
1:X:560:GLU:HG2	1:X:561:PRO:HD2	2.02	0.41
1:X:132:ILE:CG2	1:X:133:PRO:HD2	2.50	0.41
1:X:147:ARG:HB2	1:X:150:GLU:CG	2.13	0.41
1:X:179:GLY:HA2	4:X:2213:HOH:O	2.20	0.41
1:X:197:ALA:O	1:X:201:GLY:CA	2.69	0.41
1:X:397:ARG:HG2	1:X:406:ALA:HB2	2.03	0.41
1:X:592:LEU:CD1	1:X:596:LEU:HD13	2.51	0.41
1:X:687:ILE:HG23	1:X:688:THR:N	2.36	0.41
1:X:245:ILE:HG22	1:X:247:PHE:CE1	2.55	0.41
1:X:239:PHE:CE2	1:X:430:PHE:CE2	3.08	0.41
1:X:532:GLN:OE1	1:X:543:LEU:HB2	2.21	0.41
1:X:590:ASP:O	1:X:590:ASP:CG	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:84:LYS:HE3	1:X:704:ARG:HD2	1.97	0.41
1:X:172:ASN:CB	1:X:449:PHE:CZ	2.99	0.41
1:X:331:MET:CG	1:X:336:PHE:CD2	3.00	0.41
1:X:474:THR:HG22	1:X:478:LEU:CD1	2.50	0.41
1:X:668:GLU:CD	1:X:670:LYS:CE	2.89	0.41
1:X:76:ASP:HB3	4:X:2032:HOH:O	2.15	0.41
1:X:10:ASP:CB	4:X:2005:HOH:O	2.65	0.41
1:X:196:LEU:HD13	1:X:245:ILE:CD1	2.50	0.41
1:X:345:PHE:CA	1:X:348:ILE:CG1	2.97	0.41
1:X:360:GLU:O	1:X:367:ALA:HA	2.20	0.41
1:X:595:ASP:HA	1:X:598:LEU:HB2	2.03	0.41
1:X:668:GLU:HB3	1:X:670:LYS:CG	2.39	0.41
1:X:399:LEU:HA	1:X:403:ASP:O	2.21	0.40
1:X:611:LEU:HA	1:X:611:LEU:HD23	1.93	0.40
1:X:6:ASP:OD2	1:X:9:SER:HB3	2.21	0.40
1:X:154:HIS:CE1	1:X:156:PHE:H	2.39	0.40
1:X:174:SER:HA	1:X:451:GLY:O	2.21	0.40
1:X:213:GLN:N	4:X:2078:HOH:O	2.54	0.40
1:X:294:LYS:C	1:X:296:LEU:N	2.74	0.40
1:X:331:MET:HB3	1:X:336:PHE:CB	2.51	0.40
1:X:410:ASN:ND2	1:X:412:GLU:HG2	2.36	0.40
1:X:701:PHE:O	1:X:704:ARG:N	2.54	0.40
1:X:735:GLU:HA	1:X:738:ARG:CZ	2.51	0.40
1:X:734:PRO:O	1:X:738:ARG:CZ	2.69	0.40
1:X:85:PHE:HE1	1:X:755:GLU:CD	2.25	0.40
1:X:212:GLU:O	1:X:216:LEU:CD1	2.70	0.40
1:X:348:ILE:O	1:X:351:ILE:N	2.48	0.40
1:X:361:LYS:CG	1:X:411:VAL:CG1	2.96	0.40
1:X:223:GLU:CG	1:X:227:ASN:HD22	2.34	0.40
1:X:249:SER:C	4:X:2063:HOH:O	2.56	0.40
1:X:336:PHE:HA	1:X:340:GLU:OE1	2.20	0.40
1:X:350:GLY:HA3	1:X:382:PHE:CZ	2.56	0.40
1:X:285:LEU:CD2	1:X:298:LEU:HD22	2.51	0.40
1:X:315:ILE:HB	1:X:318:VAL:HB	2.04	0.40
1:X:354:LEU:HD21	1:X:378:ALA:CB	2.51	0.40
1:X:557:LYS:O	1:X:558:TYR:HB2	2.22	0.40
1:X:747:ARG:HG2	1:X:750:GLN:N	2.35	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:397:ARG:NH1	1:X:402:ARG:O[2_556]	1.10	1.10
1:X:204:GLN:O	1:X:273:GLU:OE2[1_455]	1.56	0.64
1:X:402:ARG:CG	4:X:2255:HOH:O[3_645]	1.93	0.27
4:X:2065:HOH:O	4:X:2149:HOH:O[1_455]	2.02	0.18

## 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	X	756/758 (100%)	617 (82%)	114 (15%)	25 (3%)	<b>4</b> <b>19</b>

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	46	SER
1	X	297	HIS
1	X	448	TYR
1	X	540	ASP
1	X	623	LYS
1	X	625	ALA
1	X	690	LYS
1	X	295	ALA
1	X	747	ARG
1	X	757	ALA
1	X	93	GLU
1	X	189	THR
1	X	302	GLU
1	X	601	LYS
1	X	710	PRO
1	X	731	ASN
1	X	183	ALA
1	X	354	LEU
1	X	573	TYR
1	X	65	VAL

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Mol	Chain	Res	Type
1	X	691	GLY
1	X	411	VAL
1	X	615	PRO
1	X	362	GLY
1	X	630	VAL

### 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	X	662/662 (100%)	649 (98%)	13 (2%)	55 79

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	37	TYR
1	X	60	PHE
1	X	238	ARG
1	X	336	PHE
1	X	361	LYS
1	X	409	LEU
1	X	454	ASP
1	X	487	PHE
1	X	506	PHE
1	X	554	LYS
1	X	600	PHE
1	X	745	PHE
1	X	753	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	111	ASN
1	X	171	GLN
1	X	173	GLN

*Continued on next page...*

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Mol	Chain	Res	Type
1	X	213	GLN
1	X	227	ASN
1	X	234	ASN
1	X	259	GLN
1	X	305	ASN
1	X	376	ASN
1	X	407	GLN
1	X	439	ASN
1	X	464	ASN
1	X	472	ASN
1	X	479	GLN
1	X	550	HIS
1	X	576	GLN
1	X	588	ASN
1	X	679	ASN
1	X	711	ASN
1	X	720	GLN
1	X	729	HIS
1	X	731	ASN
1	X	750	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z  > 2$
2	ADP	X	1001	-	24,29,29	1.88	7 (29%)	29,45,45	1.60	5 (17%)

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	X	1001	-	-	0/12/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	1001	ADP	C2'-C1'	-5.39	1.45	1.53
2	X	1001	ADP	C2'-C3'	-4.07	1.42	1.53
2	X	1001	ADP	O4'-C4'	-2.71	1.38	1.45
2	X	1001	ADP	C3'-C4'	-2.64	1.46	1.53
2	X	1001	ADP	PA-O2A	-2.36	1.44	1.55
2	X	1001	ADP	O5'-C5'	-2.30	1.35	1.44
2	X	1001	ADP	C6-N6	2.25	1.42	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	1001	ADP	N3-C2-N1	-5.14	120.65	128.68
2	X	1001	ADP	C3'-C2'-C1'	3.11	105.66	100.98
2	X	1001	ADP	PA-O3A-PB	-2.15	125.44	132.83
2	X	1001	ADP	C5'-C4'-C3'	-2.14	107.16	115.18
2	X	1001	ADP	O3B-PB-O3A	2.09	111.65	104.64

There are no chirality outliers.

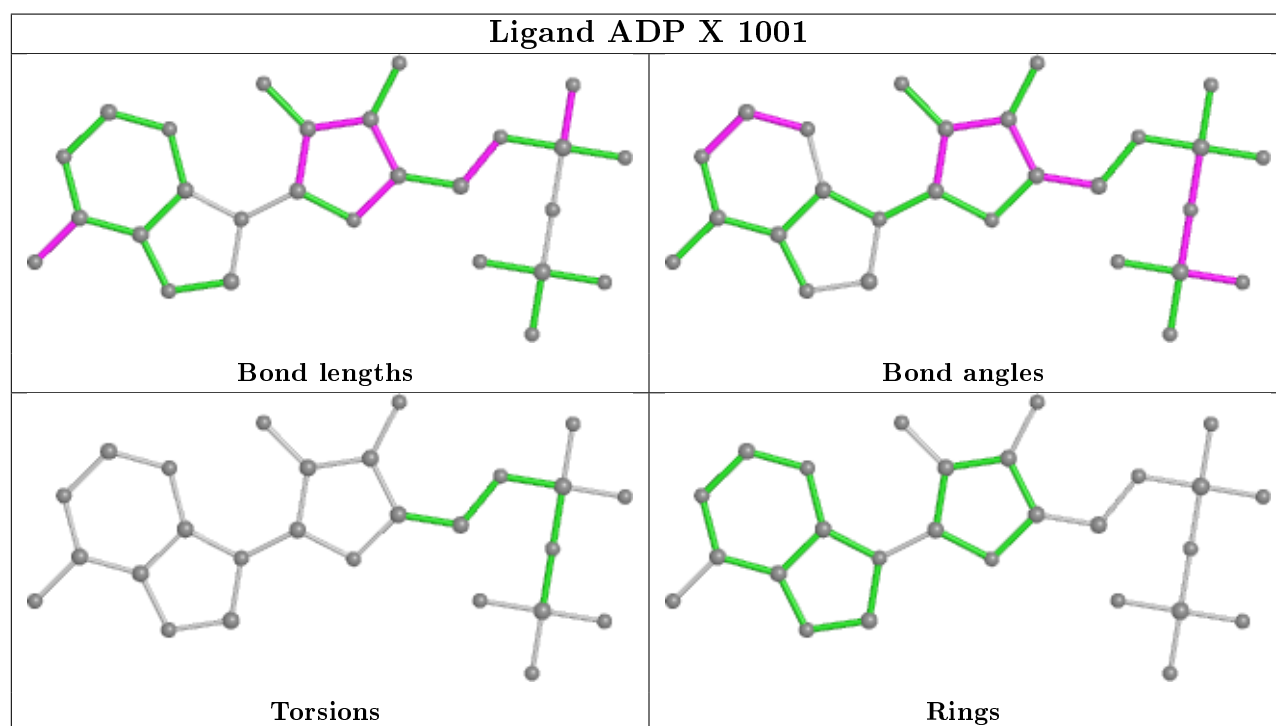
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	X	1001	ADP	5	0

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



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

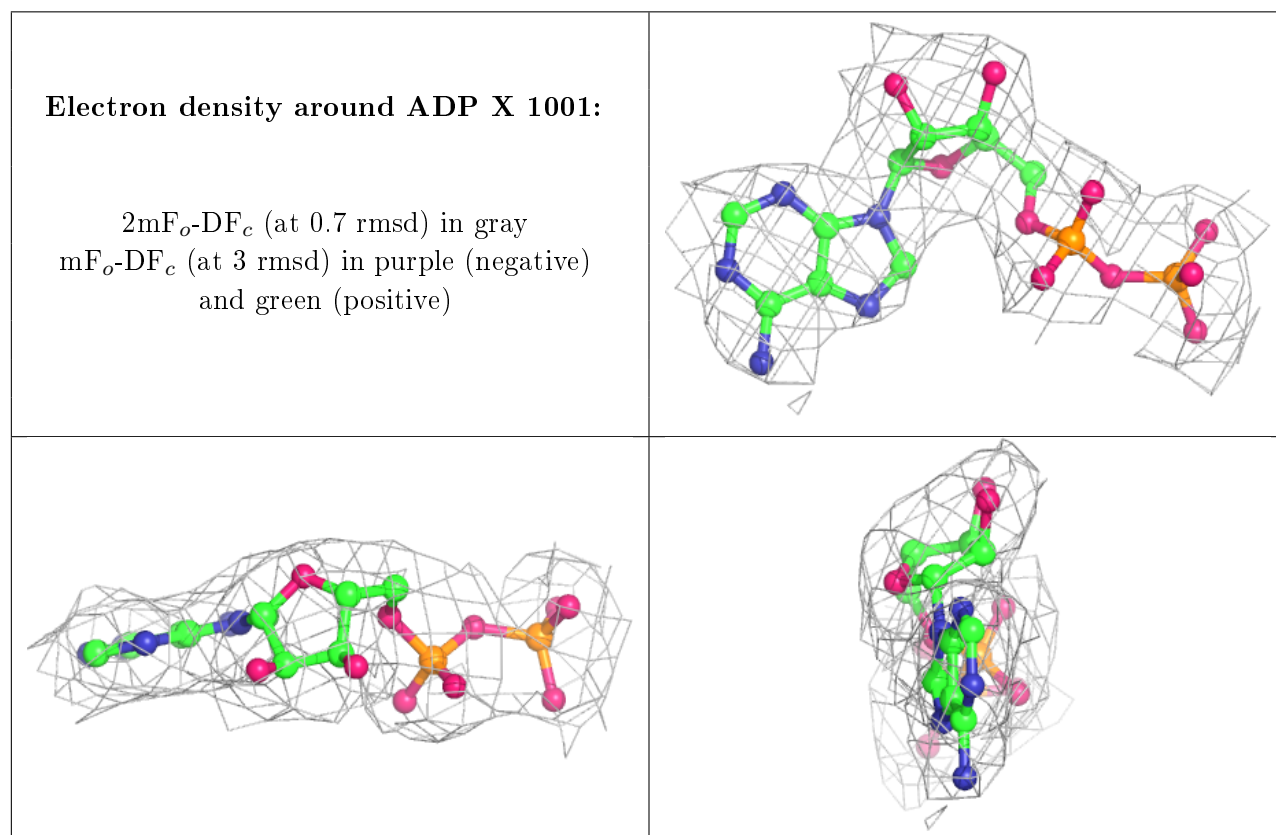
### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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.



## 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.