



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 06:18 am BST

PDB ID : 1G21  
Title : MGATP-BOUND AND NUCLEOTIDE-FREE STRUCTURES OF A NITROGENASE PROTEIN COMPLEX BETWEEN LEU127DEL-FE PROTEIN AND THE MOFE PROTEIN  
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Deposited on : 2000-10-16  
Resolution : 3.00 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

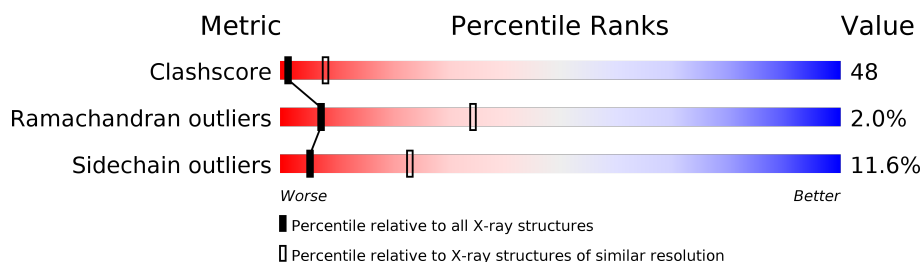
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	492	
1	C	492	
2	B	523	
2	D	523	
3	E	289	
3	F	289	
3	G	289	
3	H	289	

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
5	CFM	A	1496	-	-	X	-
5	CFM	C	3496	-	-	X	-
9	ATP	G	7292	-	-	X	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 24237 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 NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3776	2402	642	708	24			
1	C	476	Total	C	N	O	S	0	0	0
			3776	2402	642	708	24			

- Molecule 2 is a protein called NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total	C	N	O	S	0	0	0
			4170	2663	704	775	28			
2	D	522	Total	C	N	O	S	0	0	0
			4170	2663	704	775	28			

- Molecule 3 is a protein called NITROGENASE IRON PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	268	Total	C	N	O	S	109	0	0
			2029	1265	347	397	20			
3	F	267	Total	C	N	O	S	71	0	0
			2020	1260	346	394	20			
3	G	268	Total	C	N	O	S	130	0	0
			2029	1265	347	397	20			
3	H	268	Total	C	N	O	S	116	0	0
			2029	1265	347	397	20			

There are 4 discrepancies between the modelled and reference sequences:

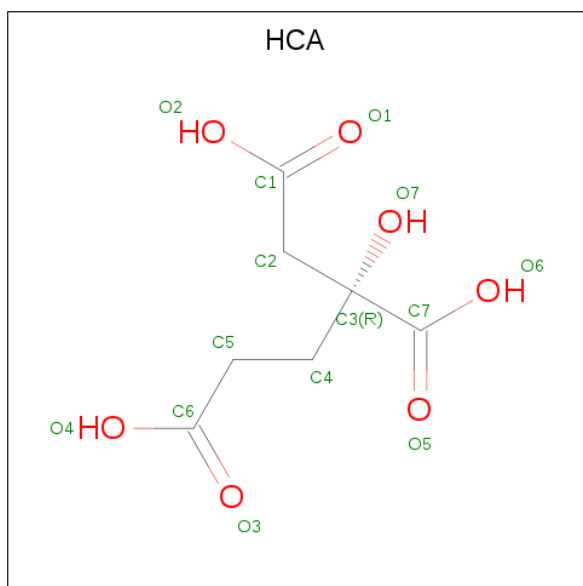
Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	LEU	deletion	UNP P00459
F	?	-	LEU	deletion	UNP P00459
G	?	-	LEU	deletion	UNP P00459

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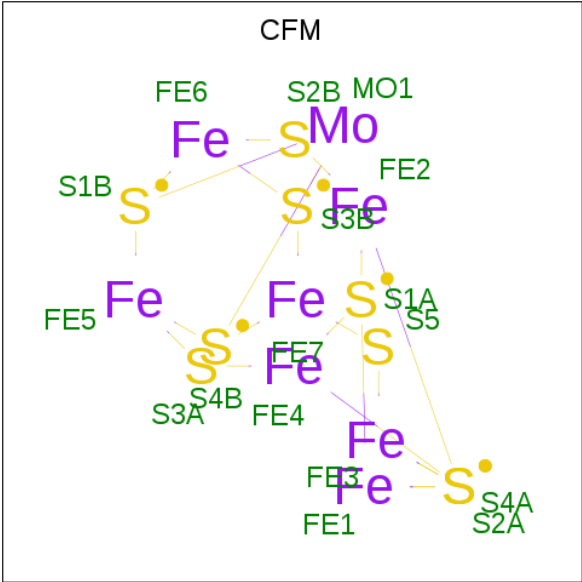
Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	LEU	deletion	UNP P00459

- Molecule 4 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (formula:  $C_7H_{10}O_7$ ).



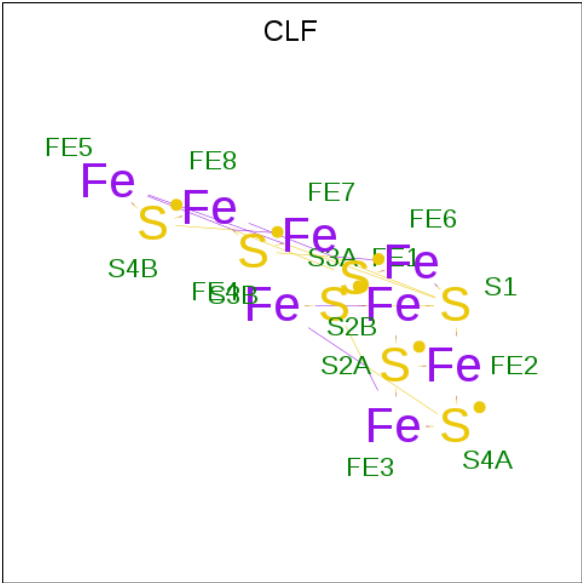
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			14	7	7		
4	C	1	Total	C	O	0	0
			14	7	7		

- Molecule 5 is FE-MO-S CLUSTER (three-letter code: CFM) (formula:  $Fe_7MoS_9$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	Fe	Mo	S	0	0
			17	7	1	9		
5	C	1	Total	Fe	Mo	S	0	0
			17	7	1	9		

- Molecule 6 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula: Fe<sub>8</sub>S<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Fe	S	0	0
			15	8	7		
6	D	1	Total	Fe	S	0	0
			15	8	7		

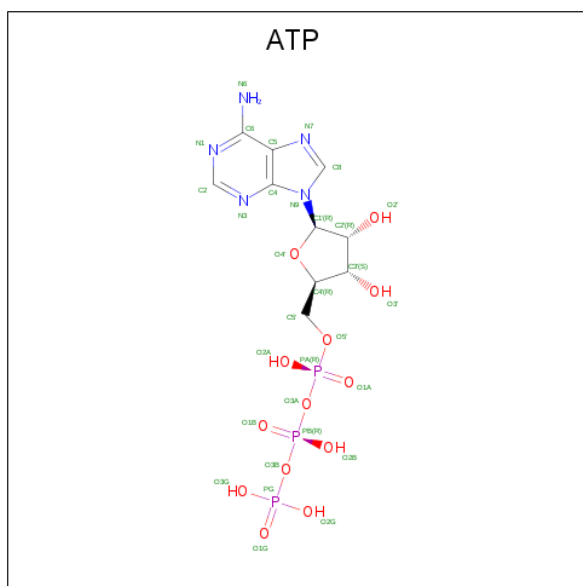
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Ca	0	0
			1	1		
7	D	1	Total	Ca	0	0
			1	1		

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	1	Total	Mg	0	0
			1	1		
8	G	1	Total	Mg	0	0
			1	1		
8	F	1	Total	Mg	0	0
			1	1		
8	E	1	Total	Mg	0	0
			1	1		

- Molecule 9 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



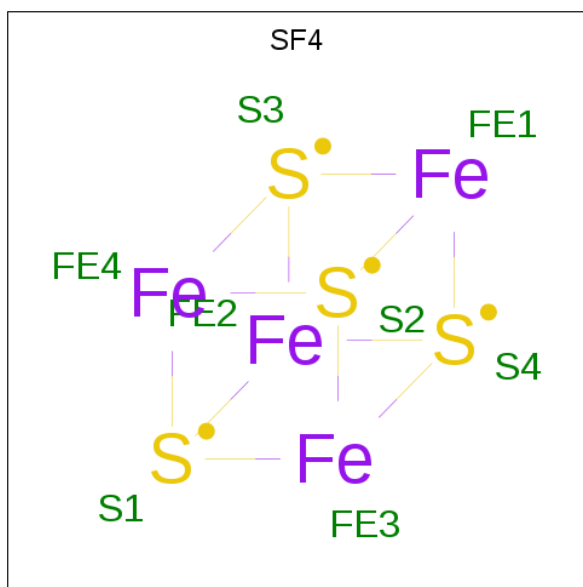
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
9	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
9	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 10 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula:  $\text{Fe}_4\text{S}_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	F	1	Total	Fe	S	0	0
			8	4	4		
10	G	1	Total	Fe	S	0	0
			8	4	4		

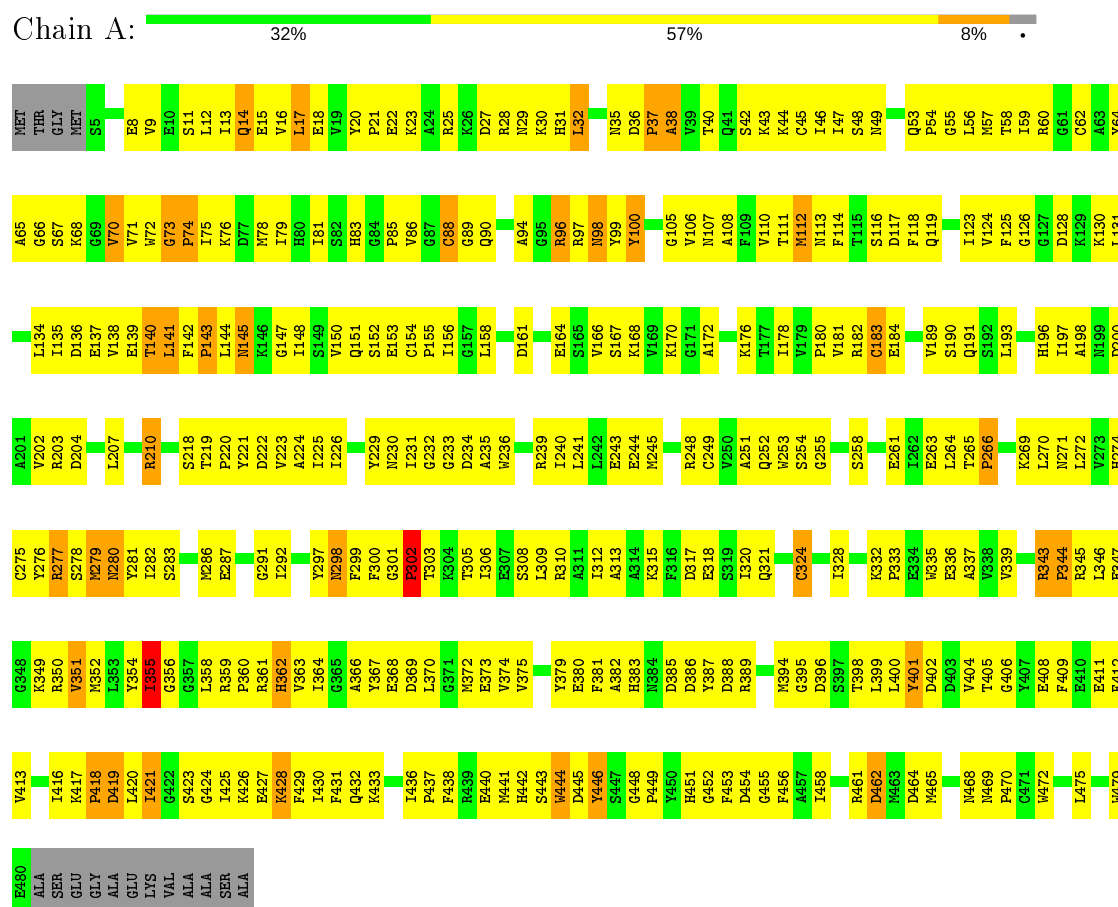


### 3 Residue-property plots

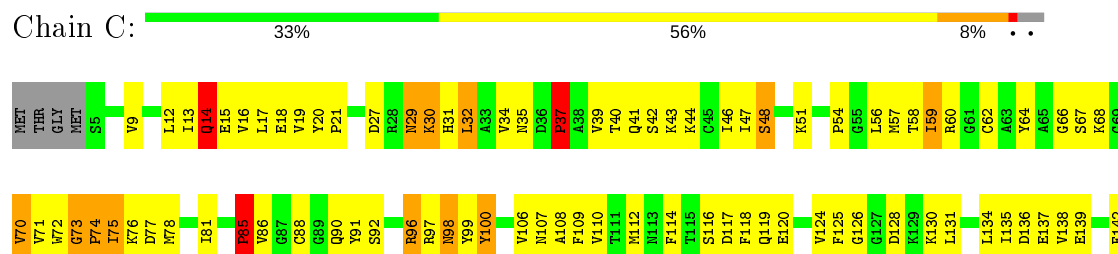
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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.

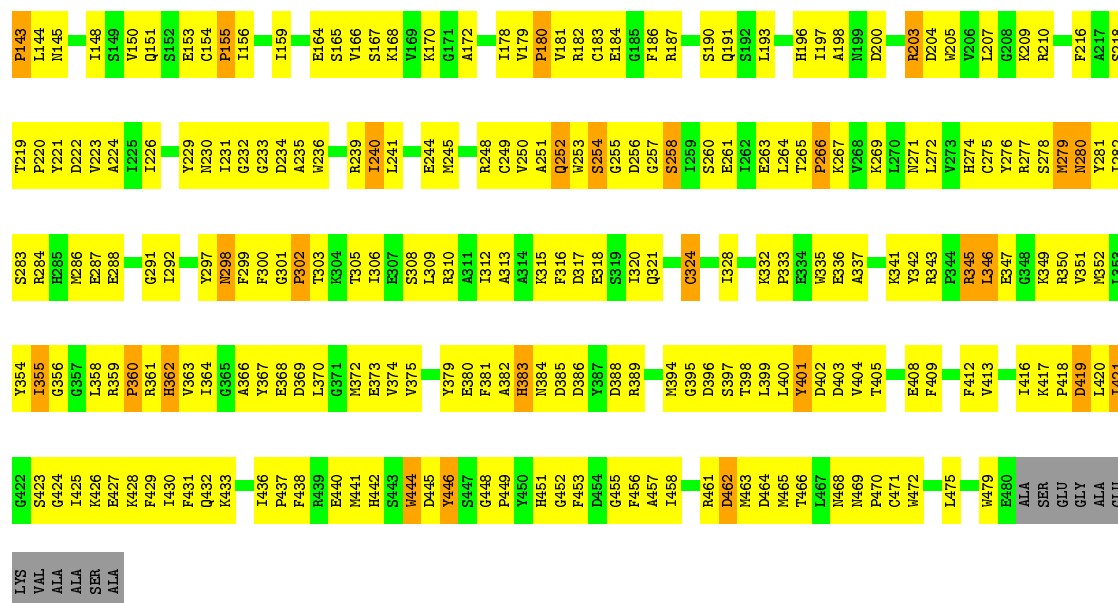
Note EDS was not executed.

#### • Molecule 1: NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN



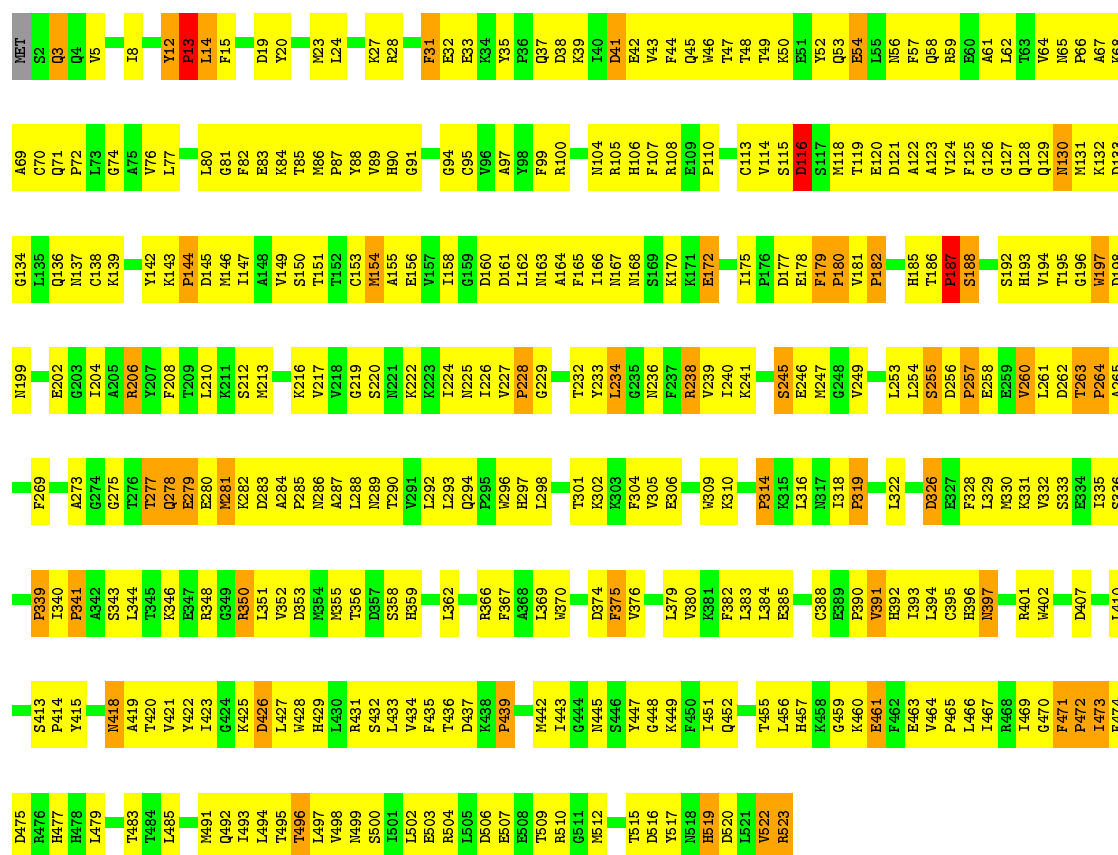
#### • Molecule 1: NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN





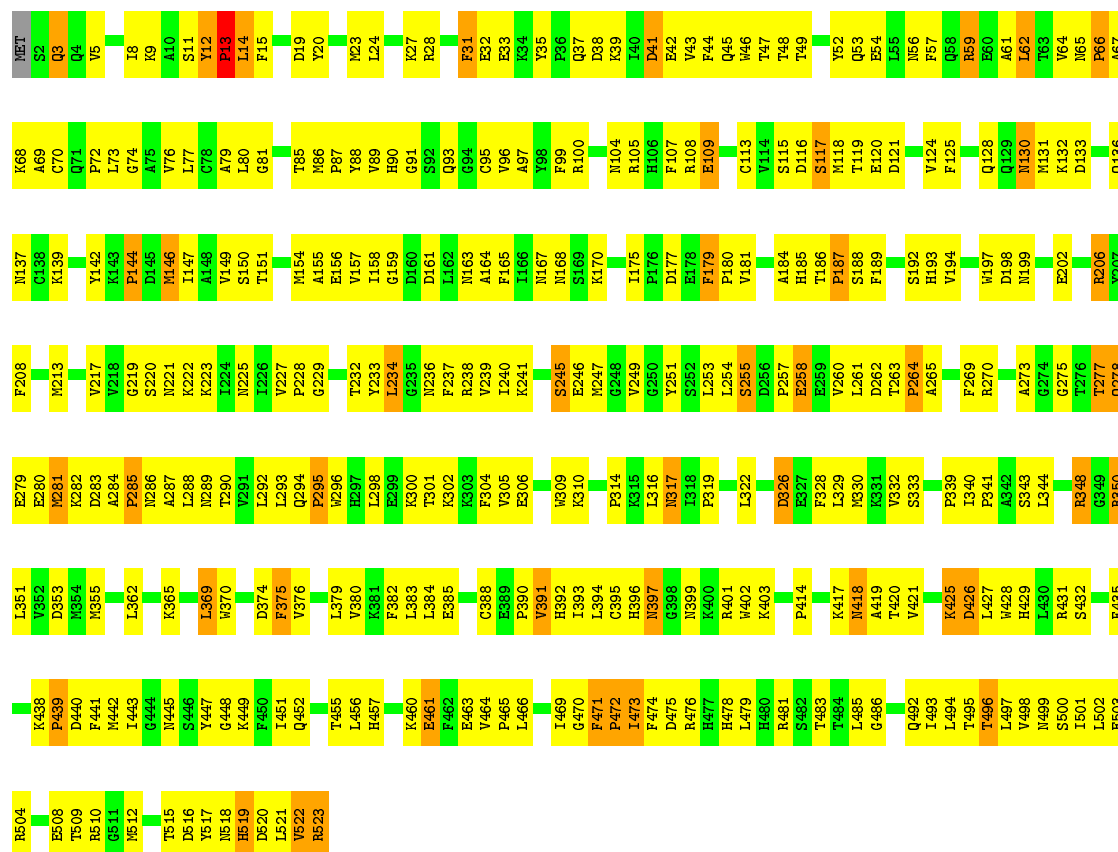
• Molecule 2: NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN

Chain B: 33% 57% 9%



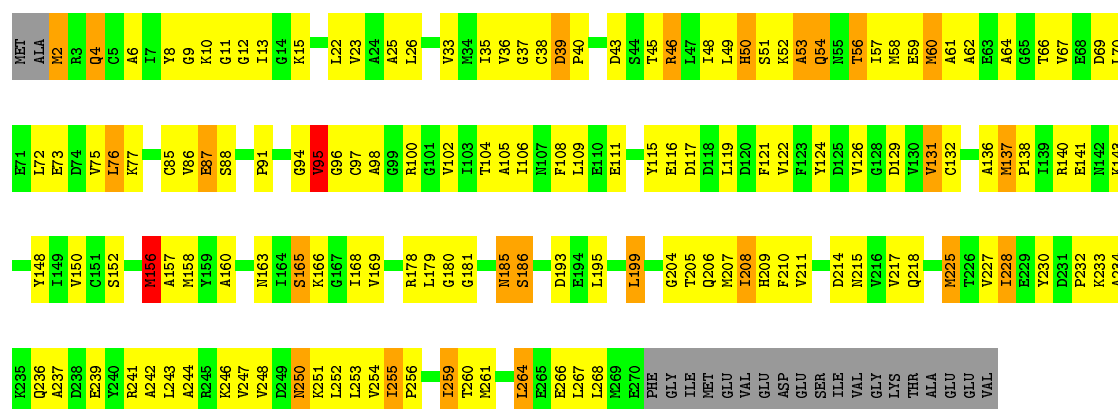
• Molecule 2: NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN

Chain D: 39% 52% 9%



### • Molecule 3: NITROGENASE IRON PROTEIN

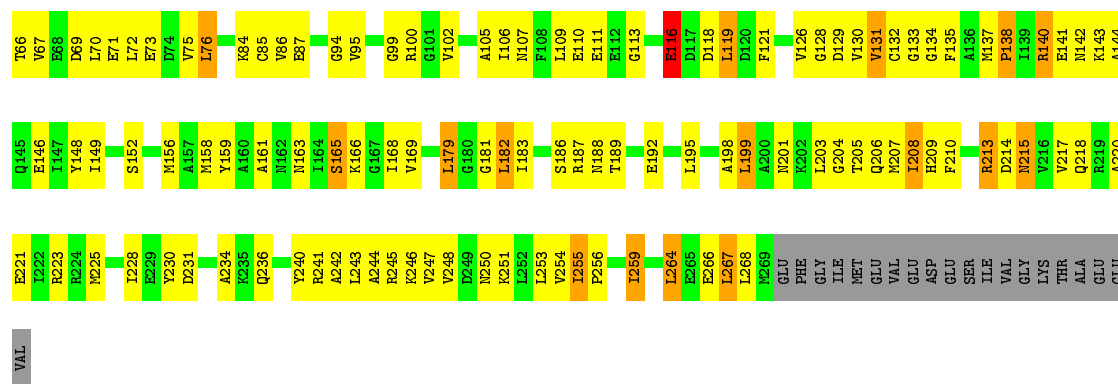
Chain E: 42% 42% 8% 7%



### • Molecule 3: NITROGENASE IRON PROTEIN

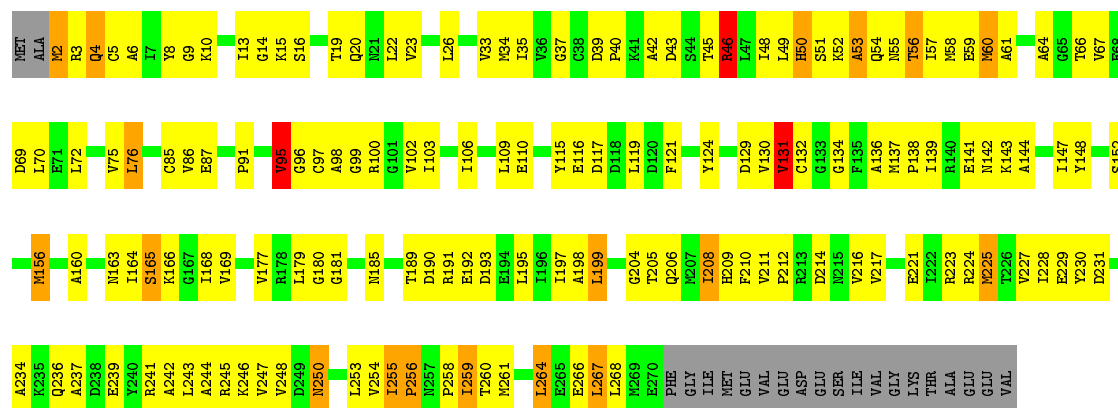
Chain F: 37% 47% 8% 8%





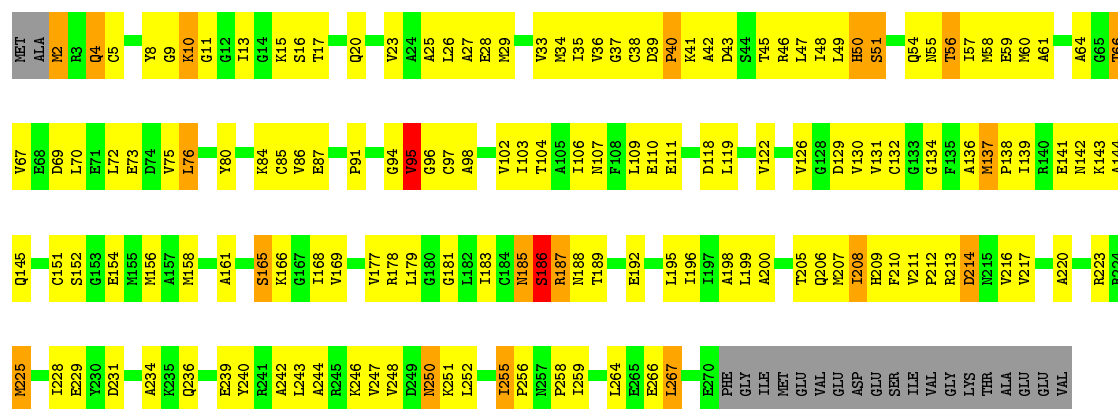
### • Molecule 3: NITROGENASE IRON PROTEIN

Chain G: 40% 46% 6% • 7%



### • Molecule 3: NITROGENASE IRON PROTEIN

Chain H: 39% 46% 7% • 7%



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.50Å 121.50Å 264.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00	Depositor
% Data completeness (in resolution range)	71.6 (20.00-3.00)	Depositor
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.238 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	24237	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CFM, CLF, HCA, ATP, CA, SF4

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	0.50	0/3864	0.73	2/5212 (0.0%)
1	C	0.48	0/3864	0.73	2/5212 (0.0%)
2	B	0.54	0/4276	0.82	7/5782 (0.1%)
2	D	0.50	1/4276 (0.0%)	0.88	15/5782 (0.3%)
3	E	0.51	0/2052	0.80	2/2764 (0.1%)
3	F	0.55	1/2043 (0.0%)	0.84	4/2752 (0.1%)
3	G	0.47	0/2052	0.75	0/2764
3	H	0.54	1/2052 (0.0%)	0.81	1/2764 (0.0%)
All	All	0.51	3/24479 (0.0%)	0.80	33/33032 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	40	PRO	N-CD	5.37	1.55	1.47
3	F	40	PRO	N-CD	5.31	1.55	1.47
2	D	109	GLU	C-N	-5.08	1.24	1.34

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	12	TYR	C-N-CD	-21.77	72.71	120.60
2	B	12	TYR	C-N-CD	-20.40	75.71	120.60
2	B	12	TYR	C-N-CA	13.32	177.95	122.00
2	D	12	TYR	C-N-CA	12.49	174.45	122.00
1	A	88	CYS	CA-CB-SG	-10.83	94.51	114.00
2	D	95	CYS	CA-CB-SG	-10.59	94.93	114.00
2	D	350	ARG	NE-CZ-NH2	9.26	124.93	120.30
2	D	348	ARG	NE-CZ-NH1	-7.22	116.69	120.30
3	F	116	GLU	N-CA-C	7.09	130.14	111.00
2	D	350	ARG	NE-CZ-NH1	-7.08	116.76	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	206	ARG	NE-CZ-NH1	-7.06	116.77	120.30
2	D	348	ARG	NE-CZ-NH2	6.88	123.74	120.30
2	D	13	PRO	CA-N-CD	-6.80	101.98	111.50
2	D	471	PHE	C-N-CD	-6.77	105.71	120.60
2	D	59	ARG	NE-CZ-NH1	-6.75	116.92	120.30
3	F	3	ARG	NE-CZ-NH2	-6.74	116.93	120.30
2	D	431	ARG	NE-CZ-NH1	6.72	123.66	120.30
3	E	156	MET	CG-SD-CE	-6.67	89.53	100.20
2	B	471	PHE	C-N-CD	-6.61	106.06	120.60
3	E	39	ASP	CB-CG-OD2	6.53	124.18	118.30
2	B	13	PRO	CA-N-CD	-6.35	102.61	111.50
3	H	186	SER	N-CA-C	6.29	127.99	111.00
2	B	439	PRO	CA-N-CD	-6.26	102.73	111.50
3	F	3	ARG	NE-CZ-NH1	6.02	123.31	120.30
3	F	119	LEU	N-CA-C	5.99	127.16	111.00
2	D	206	ARG	NE-CZ-NH2	5.84	123.22	120.30
2	D	59	ARG	NE-CZ-NH2	5.80	123.20	120.30
1	A	38	ALA	N-CA-C	5.78	126.61	111.00
2	B	116	ASP	N-CA-C	-5.64	95.78	111.00
1	C	14	GLN	CB-CA-C	5.62	121.64	110.40
2	B	257	PRO	CA-N-CD	-5.61	103.65	111.50
2	D	431	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	C	143	PRO	CA-N-CD	-5.01	104.48	111.50

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	A	3776	0	3709	452	0
1	C	3776	0	3709	490	0
2	B	4170	0	4076	441	0
2	D	4170	0	4076	461	0
3	E	2029	0	2040	150	0
3	F	2020	0	2034	166	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	2029	0	2041	158	0
3	H	2029	0	2041	153	0
4	A	14	0	6	1	0
4	C	14	0	6	2	0
5	A	17	0	0	4	0
5	C	17	0	0	7	0
6	A	15	0	0	1	0
6	D	15	0	0	3	0
7	B	1	0	0	0	0
7	D	1	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
8	G	1	0	0	0	0
8	H	1	0	0	0	0
9	E	31	0	12	4	0
9	F	31	0	12	6	0
9	G	31	0	12	11	0
9	H	31	0	12	6	0
10	F	8	0	0	0	0
10	G	8	0	0	0	0
All	All	24237	0	23786	2236	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 48.

All (2236) 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)
3:F:39:ASP:OD1	3:F:40:PRO:HD2	1.28	1.29
2:D:91:GLY:HA2	2:D:118:MET:CE	1.62	1.28
1:C:124:VAL:HG21	3:H:58:MET:CE	1.70	1.21
1:A:355:ILE:HG23	1:A:356:GLY:H	0.99	1.15
3:F:39:ASP:OD1	3:F:40:PRO:CD	1.95	1.13
2:B:471:PHE:CD2	2:B:472:PRO:HD3	1.83	1.12
1:C:433:LYS:NZ	2:D:263:THR:HG23	1.66	1.10
3:F:106:ILE:CD1	3:F:138:PRO:HD3	1.82	1.09
1:C:355:ILE:CG2	1:C:356:GLY:H	1.63	1.08
2:B:128:GLN:HG3	2:B:132:LYS:HE3	1.09	1.06
1:A:355:ILE:CG2	1:A:360:PRO:CD	2.33	1.06
1:C:124:VAL:HG21	3:H:58:MET:HE2	1.13	1.06
1:A:86:VAL:HG11	2:B:68:LYS:HE3	1.36	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:86:MET:HE2	2:D:87:PRO:HD2	1.37	1.04
1:C:355:ILE:HG22	1:C:356:GLY:N	1.62	1.04
1:C:167:SER:CB	1:C:180:PRO:HG3	1.86	1.04
1:C:167:SER:HB2	1:C:180:PRO:HG3	1.40	1.04
3:G:56:THR:HG23	3:G:59:GLU:HB2	1.40	1.03
2:B:128:GLN:CG	2:B:132:LYS:HE3	1.88	1.03
3:E:156:MET:SD	9:F:6292:ATP:H4'	1.99	1.02
1:A:355:ILE:HG22	1:A:360:PRO:CD	1.89	1.01
1:C:58:THR:HG22	1:C:60:ARG:H	1.25	1.01
2:D:91:GLY:HA2	2:D:118:MET:HE3	1.02	1.01
3:H:56:THR:HG23	3:H:59:GLU:HB2	1.41	1.01
1:C:346:LEU:HD12	1:C:372:MET:SD	2.00	1.01
2:B:212:SER:O	2:B:216:LYS:HE3	1.61	1.00
3:H:23:VAL:HG21	3:H:35:ILE:HD11	1.43	1.00
2:D:86:MET:CE	2:D:87:PRO:HD2	1.92	1.00
2:B:289:ASN:HD21	2:B:314:PRO:HD3	1.27	0.99
3:H:225:MET:HE3	3:H:229:GLU:OE2	1.63	0.99
3:F:242:ALA:O	3:F:246:LYS:HG2	1.62	0.98
1:A:355:ILE:HG23	1:A:356:GLY:N	1.74	0.98
1:A:97:ARG:NH2	1:A:99:TYR:OH	1.95	0.98
9:G:7292:ATP:H5'2	3:H:156:MET:SD	2.02	0.98
1:C:253:TRP:CZ3	1:C:282:ILE:HD13	1.99	0.97
1:C:253:TRP:HZ3	1:C:282:ILE:HD13	1.25	0.97
1:A:355:ILE:CG2	1:A:360:PRO:HD3	1.93	0.97
2:B:220:SER:HB2	2:B:286:ASN:HB3	1.41	0.97
3:E:4:GLN:NE2	3:E:143:LYS:O	1.98	0.97
2:B:260:VAL:HG22	2:B:273:ALA:O	1.64	0.96
1:A:167:SER:HB2	1:A:180:PRO:HG3	1.46	0.96
1:C:426:LYS:HZ1	2:D:97:ALA:HB1	1.26	0.96
2:D:146:MET:HG3	2:D:180:PRO:HB2	1.48	0.96
3:E:56:THR:HG23	3:E:59:GLU:HB3	1.46	0.96
1:C:389:ARG:HG3	1:C:389:ARG:HH11	1.30	0.95
1:A:229:TYR:HA	1:A:254:SER:O	1.68	0.94
1:C:355:ILE:HG22	1:C:356:GLY:H	0.79	0.94
1:A:27:ASP:O	1:A:30:LYS:HG2	1.67	0.94
1:A:346:LEU:HD12	1:A:370:LEU:HD12	1.47	0.94
1:C:59:ILE:HG23	1:C:426:LYS:HD2	1.48	0.94
3:G:217:VAL:HG21	9:G:7292:ATP:H2	1.32	0.94
2:B:206:ARG:HG3	2:B:304:PHE:CZ	2.02	0.93
3:F:56:THR:O	3:F:60:MET:HB2	1.67	0.93
1:C:433:LYS:NZ	2:D:263:THR:CG2	2.31	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:ILE:CG2	1:A:356:GLY:N	2.31	0.93
3:E:35:ILE:CD1	3:E:48:ILE:HD12	1.98	0.93
1:C:209:LYS:HE2	1:C:263:GLU:OE1	1.69	0.93
3:G:189:THR:HG22	3:G:190:ASP:H	1.33	0.92
1:A:355:ILE:CG2	1:A:356:GLY:H	1.78	0.92
3:F:13:ILE:O	3:F:187:ARG:NH2	2.03	0.92
3:F:186:SER:HB3	3:F:210:PHE:CZ	2.04	0.91
1:C:426:LYS:NZ	2:D:97:ALA:HB1	1.84	0.91
1:C:342:TYR:O	1:C:345:ARG:HG3	1.70	0.91
2:D:220:SER:HB2	2:D:286:ASN:HB3	1.49	0.91
2:B:85:THR:HG22	2:B:146:MET:HB3	1.53	0.91
1:A:218:SER:OG	1:A:269:LYS:HE2	1.72	0.90
2:B:238:ARG:HE	2:B:258:GLU:CG	1.85	0.90
2:B:142:TYR:O	2:B:144:PRO:HD3	1.70	0.90
3:F:42:ALA:HA	3:F:87:GLU:OE1	1.72	0.90
2:D:471:PHE:CD2	2:D:472:PRO:HD3	2.07	0.89
1:C:355:ILE:HD12	1:C:359:ARG:HB2	1.52	0.89
2:D:3:GLN:HA	2:D:3:GLN:HE21	1.38	0.89
2:B:3:GLN:HE21	2:B:3:GLN:HA	1.39	0.88
1:C:20:TYR:OH	1:C:408:GLU:HG2	1.72	0.88
1:C:433:LYS:HZ1	2:D:263:THR:HG23	1.37	0.88
1:A:405:THR:OG1	1:A:408:GLU:HG3	1.74	0.88
1:C:138:VAL:HG13	2:D:62:LEU:HD13	1.53	0.88
2:B:457:HIS:HD2	2:D:512:MET:HB3	1.39	0.87
1:A:182:ARG:O	1:A:197:ILE:HG21	1.74	0.87
2:B:77:LEU:HA	2:B:80:LEU:HD12	1.56	0.87
2:D:91:GLY:CA	2:D:118:MET:HE3	1.98	0.87
1:A:167:SER:CB	1:A:180:PRO:HG3	2.04	0.87
1:C:154:CYS:HB2	1:C:155:PRO:HD3	1.56	0.87
1:A:355:ILE:HG21	1:A:360:PRO:HD3	1.55	0.87
1:C:355:ILE:HB	1:C:360:PRO:HD3	1.57	0.87
2:D:91:GLY:CA	2:D:118:MET:CE	2.52	0.87
2:B:512:MET:HB3	2:D:457:HIS:HD2	1.38	0.86
1:A:20:TYR:OH	1:A:408:GLU:HG2	1.74	0.86
2:B:517:TYR:O	1:C:99:TYR:CE1	2.28	0.86
2:B:90:HIS:N	2:B:150:SER:O	2.07	0.86
2:B:90:HIS:HA	2:B:116:ASP:OD1	1.74	0.86
2:D:85:THR:HG22	2:D:146:MET:HB3	1.55	0.86
2:D:64:VAL:O	2:D:426:ASP:OD1	1.94	0.86
3:F:241:ARG:O	3:F:245:ARG:HG3	1.76	0.86
2:B:130:ASN:ND2	2:B:130:ASN:H	1.70	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:VAL:HG11	1:C:198:ALA:HB1	1.58	0.85
3:G:243:LEU:O	3:G:247:VAL:HG23	1.77	0.85
2:B:350:ARG:HG2	2:D:264:PRO:HG3	1.59	0.85
3:F:13:ILE:HA	3:F:187:ARG:HH21	1.42	0.85
2:D:496:THR:O	2:D:500:SER:OG	1.95	0.84
1:A:277:ARG:CZ	1:A:383:HIS:CD2	2.60	0.84
2:D:260:VAL:HG23	2:D:273:ALA:O	1.77	0.84
1:A:58:THR:HG22	1:A:60:ARG:H	1.42	0.84
1:A:388:ASP:OD1	1:A:389:ARG:HG3	1.78	0.84
2:B:206:ARG:HG3	2:B:304:PHE:CE1	2.13	0.84
2:B:161:ASP:O	2:B:165:PHE:CD1	2.31	0.84
2:B:397:ASN:H	2:B:397:ASN:HD22	1.24	0.84
1:A:219:THR:HG22	1:A:221:TYR:H	1.42	0.84
1:C:27:ASP:O	1:C:30:LYS:HG3	1.77	0.84
2:D:238:ARG:HE	2:D:258:GLU:CG	1.90	0.84
2:D:362:LEU:HD11	2:D:498:VAL:HG22	1.59	0.84
3:H:54:GLN:HG3	3:H:55:ASN:H	1.43	0.83
3:G:217:VAL:HG22	3:G:227:VAL:HG21	1.61	0.83
2:D:397:ASN:H	2:D:397:ASN:HD22	1.26	0.83
3:G:42:ALA:HA	3:G:87:GLU:OE1	1.78	0.83
3:E:37:GLY:HA3	3:E:87:GLU:OE2	1.78	0.83
2:B:289:ASN:ND2	2:B:314:PRO:HD3	1.93	0.83
2:B:331:LYS:O	2:B:335:ILE:HG12	1.79	0.83
1:C:182:ARG:O	1:C:197:ILE:HG21	1.78	0.83
1:C:449:PRO:HG2	2:D:15:PHE:HZ	1.43	0.83
2:B:220:SER:N	2:B:286:ASN:O	2.11	0.83
1:C:234:ASP:HB3	1:C:451:HIS:CG	2.14	0.83
3:G:241:ARG:O	3:G:245:ARG:HG3	1.79	0.83
1:A:385:ASP:O	1:A:388:ASP:OD1	1.96	0.82
2:D:452:GLN:NE2	2:D:465:PRO:HA	1.94	0.82
1:A:343:ARG:O	1:A:347:GLU:HG3	1.80	0.82
3:F:106:ILE:HD11	3:F:138:PRO:HD3	1.61	0.82
1:C:219:THR:HG22	1:C:221:TYR:H	1.42	0.82
1:C:167:SER:HB2	1:C:180:PRO:CG	2.08	0.82
3:E:12:GLY:HA2	3:F:156:MET:CE	2.09	0.82
1:C:405:THR:OG1	1:C:408:GLU:HG3	1.79	0.82
2:B:452:GLN:NE2	2:B:465:PRO:HA	1.95	0.82
1:C:298:ASN:HB2	1:C:362:HIS:HE2	1.43	0.82
2:B:397:ASN:H	2:B:397:ASN:ND2	1.79	0.81
1:C:124:VAL:CG2	3:H:58:MET:HE2	2.06	0.81
1:C:57:MET:HE1	2:D:100:ARG:CZ	2.10	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57:MET:CE	2:D:100:ARG:NH2	2.44	0.81
2:D:397:ASN:ND2	2:D:397:ASN:H	1.79	0.81
2:D:326:ASP:OD2	2:D:348:ARG:HD2	1.81	0.81
3:G:37:GLY:HA3	3:G:87:GLU:OE2	1.80	0.81
2:D:161:ASP:O	2:D:165:PHE:CD1	2.34	0.81
2:D:128:GLN:HE22	2:D:165:PHE:HA	1.43	0.81
2:D:130:ASN:H	2:D:130:ASN:ND2	1.79	0.81
2:B:197:TRP:CE3	2:B:229:GLY:HA2	2.15	0.80
3:H:56:THR:O	3:H:60:MET:HB2	1.81	0.80
2:B:59:ARG:NH2	2:B:429:HIS:CE1	2.50	0.80
1:C:210:ARG:HH11	1:C:264:LEU:HD21	1.46	0.80
1:A:355:ILE:HG22	1:A:360:PRO:CG	2.11	0.80
2:B:59:ARG:HH22	2:B:429:HIS:CE1	2.00	0.80
3:H:137:MET:HB3	3:H:138:PRO:HD3	1.63	0.80
1:A:234:ASP:HB3	1:A:451:HIS:CG	2.17	0.80
2:D:238:ARG:HD3	2:D:258:GLU:HG3	1.64	0.80
1:C:186:PHE:HE1	3:G:100:ARG:HH21	1.29	0.80
2:D:151:THR:CG2	2:D:186:THR:H	1.94	0.80
3:H:231:ASP:OD2	3:H:234:ALA:HB2	1.81	0.80
3:H:244:ALA:O	3:H:248:VAL:HG23	1.82	0.80
1:A:355:ILE:HG21	1:A:360:PRO:CD	2.09	0.79
2:B:158:ILE:O	3:F:133:GLY:HA3	1.81	0.79
3:H:106:ILE:CD1	3:H:138:PRO:HD3	2.12	0.79
1:C:97:ARG:NH1	1:C:446:TYR:HA	1.96	0.79
3:G:49:LEU:O	3:G:50:HIS:HB2	1.80	0.79
1:C:59:ILE:HD13	1:C:427:GLU:OE2	1.82	0.79
1:A:31:HIS:O	1:A:46:ILE:HD11	1.83	0.79
1:C:170:LYS:O	1:C:178:ILE:HD12	1.82	0.79
3:F:43:ASP:HB2	3:F:46:ARG:HD3	1.62	0.79
2:D:305:VAL:HG13	2:D:309:TRP:CE3	2.17	0.79
3:F:204:GLY:O	3:F:254:VAL:HG21	1.83	0.79
1:A:97:ARG:HH21	2:D:520:ASP:CG	1.86	0.78
2:B:151:THR:OG1	2:B:155:ALA:HB3	1.82	0.78
2:D:369:LEU:HD21	2:D:393:ILE:HG12	1.65	0.78
2:D:238:ARG:CD	2:D:258:GLU:HG3	2.13	0.78
3:E:35:ILE:HD11	3:E:48:ILE:HD12	1.65	0.78
2:D:238:ARG:NE	2:D:258:GLU:HG3	1.98	0.78
3:E:61:ALA:HB2	3:E:70:LEU:HD12	1.64	0.78
1:A:75:ILE:HG21	1:A:78:MET:CE	2.14	0.78
2:B:65:ASN:O	2:B:427:LEU:HB2	1.82	0.78
2:B:496:THR:O	2:B:500:SER:OG	2.00	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:THR:HG21	2:B:146:MET:HE1	1.66	0.78
2:D:77:LEU:HA	2:D:80:LEU:HD12	1.66	0.78
1:C:167:SER:CB	1:C:180:PRO:CG	2.61	0.78
1:C:389:ARG:CG	1:C:389:ARG:HH11	1.97	0.78
1:C:298:ASN:HD22	1:C:299:PHE:N	1.81	0.78
1:C:58:THR:HG22	1:C:60:ARG:N	1.97	0.78
1:C:433:LYS:HZ3	2:D:263:THR:CG2	1.95	0.78
3:H:49:LEU:O	3:H:50:HIS:HB2	1.84	0.78
2:B:279:GLU:OE1	2:B:282:LYS:HD2	1.83	0.78
2:D:128:GLN:HE22	2:D:168:ASN:HD22	1.31	0.78
2:D:233:TYR:HB2	2:D:236:ASN:HD22	1.50	0.77
2:B:142:TYR:C	2:B:144:PRO:HD3	2.05	0.77
1:C:253:TRP:HE1	1:C:265:THR:HG1	1.31	0.77
2:D:91:GLY:HA2	2:D:118:MET:HE2	1.63	0.77
1:A:433:LYS:NZ	2:B:263:THR:O	2.17	0.77
1:C:57:MET:HE1	2:D:100:ARG:NH2	2.00	0.77
1:A:59:ILE:HG23	1:A:426:LYS:HD2	1.65	0.77
1:A:355:ILE:CG2	1:A:360:PRO:HD2	2.14	0.77
1:C:355:ILE:HD11	1:C:441:MET:HB3	1.67	0.77
3:E:94:GLY:O	3:E:95:VAL:HG23	1.85	0.77
1:A:429:PHE:CB	2:B:110:PRO:HD3	2.15	0.77
1:A:465:MET:O	1:A:469:ASN:HB2	1.85	0.77
1:C:355:ILE:HB	1:C:360:PRO:CD	2.14	0.77
1:C:355:ILE:HB	1:C:360:PRO:HG3	1.65	0.77
1:C:75:ILE:HG21	1:C:78:MET:CE	2.15	0.77
2:B:329:LEU:HD13	2:B:344:LEU:HD13	1.65	0.76
1:C:40:THR:O	1:C:40:THR:HG22	1.86	0.76
2:D:217:VAL:HB	2:D:220:SER:OG	1.84	0.76
1:C:193:LEU:O	1:C:197:ILE:HG13	1.84	0.76
1:C:385:ASP:HA	1:C:388:ASP:OD2	1.85	0.76
1:A:251:ALA:HA	1:A:261:GLU:HG2	1.65	0.76
1:C:131:LEU:O	1:C:135:ILE:HG13	1.86	0.76
1:C:433:LYS:HZ1	2:D:263:THR:CG2	1.95	0.76
1:A:71:VAL:HG11	1:A:198:ALA:HB1	1.68	0.76
2:D:262:ASP:O	2:D:264:PRO:HD3	1.85	0.76
2:B:369:LEU:HD12	2:B:379:LEU:HD23	1.67	0.76
2:D:86:MET:HE2	2:D:87:PRO:CD	2.14	0.76
2:D:116:ASP:HB2	2:D:130:ASN:HB2	1.68	0.75
2:D:329:LEU:HD13	2:D:344:LEU:HD13	1.68	0.75
1:A:355:ILE:HG22	1:A:360:PRO:HD2	1.67	0.75
3:H:186:SER:HB3	3:H:210:PHE:CZ	2.22	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:30:LYS:NZ	1:C:47:ILE:HD13	2.02	0.75
3:H:166:LYS:O	3:H:169:VAL:HG12	1.86	0.75
2:B:197:TRP:CZ3	2:B:229:GLY:HA2	2.22	0.75
2:D:46:TRP:O	2:D:49:THR:HG22	1.86	0.75
2:B:170:LYS:HD2	2:B:177:ASP:HA	1.69	0.75
2:D:49:THR:HG23	2:D:52:TYR:H	1.52	0.75
3:G:56:THR:O	3:G:60:MET:HB2	1.87	0.75
1:A:429:PHE:HB3	2:B:110:PRO:HD3	1.69	0.74
1:A:388:ASP:OD1	1:A:389:ARG:N	2.20	0.74
1:C:355:ILE:HB	1:C:360:PRO:CG	2.17	0.74
1:A:359:ARG:HH11	1:A:359:ARG:HG3	1.50	0.74
3:H:141:GLU:O	3:H:142:ASN:HB2	1.86	0.74
3:G:56:THR:HG23	3:G:59:GLU:CB	2.17	0.74
3:G:181:GLY:HA2	3:G:205:THR:OG1	1.88	0.74
2:B:129:GLN:NE2	2:B:132:LYS:HD2	2.03	0.74
1:C:57:MET:CE	2:D:100:ARG:CZ	2.65	0.74
2:D:68:LYS:HG2	2:D:396:HIS:HD2	1.52	0.74
2:B:217:VAL:HB	2:B:220:SER:OG	1.87	0.74
1:C:251:ALA:HA	1:C:261:GLU:HG2	1.70	0.74
3:F:206:GLN:NE2	3:F:250:ASN:OD1	2.21	0.74
3:H:55:ASN:HB3	3:H:60:MET:SD	2.27	0.74
2:B:233:TYR:HB2	2:B:236:ASN:HD22	1.52	0.74
2:D:170:LYS:HD2	2:D:177:ASP:HA	1.70	0.74
3:F:56:THR:HG23	3:F:59:GLU:HB2	1.70	0.74
1:C:31:HIS:O	1:C:46:ILE:HD11	1.88	0.73
1:A:276:TYR:HB3	1:A:361:ARG:HH22	1.53	0.73
2:B:128:GLN:O	2:B:132:LYS:HG3	1.88	0.73
2:D:28:ARG:HA	2:D:32:GLU:HG3	1.69	0.73
2:D:65:ASN:O	2:D:427:LEU:HB2	1.89	0.73
3:H:106:ILE:HD13	3:H:138:PRO:HD3	1.71	0.73
1:A:131:LEU:O	1:A:135:ILE:HG13	1.88	0.73
3:H:60:MET:HB3	3:H:70:LEU:HD11	1.69	0.73
1:A:360:PRO:HB2	1:A:379:TYR:CE2	2.24	0.73
2:B:151:THR:CG2	2:B:186:THR:H	2.01	0.73
1:C:56:LEU:O	1:C:57:MET:HB2	1.87	0.73
1:A:210:ARG:HH11	1:A:264:LEU:HD21	1.52	0.73
1:A:280:ASN:N	1:A:280:ASN:HD22	1.86	0.73
3:F:183:ILE:HD13	3:F:243:LEU:HD11	1.70	0.73
2:B:178:GLU:O	2:B:180:PRO:HD3	1.89	0.73
1:C:116:SER:O	1:C:130:LYS:HE2	1.86	0.73
1:C:355:ILE:HD12	1:C:359:ARG:CB	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:238:ARG:HE	2:B:258:GLU:HG2	1.53	0.73
3:F:110:GLU:OE2	3:F:143:LYS:NZ	2.22	0.73
3:G:23:VAL:HG21	3:G:35:ILE:HD11	1.70	0.73
1:C:124:VAL:HG21	3:H:58:MET:HE3	1.71	0.73
1:C:86:VAL:HG21	2:D:68:LYS:HE3	1.71	0.73
3:E:57:ILE:HG12	3:E:75:VAL:HG21	1.71	0.73
1:C:98:ASN:H	1:C:98:ASN:ND2	1.87	0.72
3:F:207:MET:CE	3:F:210:PHE:HB2	2.20	0.72
3:F:49:LEU:O	3:F:50:HIS:HB2	1.89	0.72
3:G:106:ILE:HD12	3:G:137:MET:HB3	1.71	0.72
2:B:305:VAL:HG13	2:B:309:TRP:CE3	2.23	0.72
2:D:238:ARG:HE	2:D:258:GLU:HG3	1.50	0.72
3:F:23:VAL:HG21	3:F:35:ILE:HD11	1.71	0.72
1:A:298:ASN:HB2	1:A:362:HIS:HE2	1.54	0.72
3:F:54:GLN:HG3	3:F:55:ASN:H	1.54	0.72
3:H:39:ASP:OD1	3:H:40:PRO:HD2	1.88	0.72
3:E:57:ILE:HG13	3:E:75:VAL:HG11	1.71	0.72
3:G:22:LEU:HD11	3:G:247:VAL:HG21	1.72	0.72
2:B:422:TYR:HD2	2:B:425:LYS:HZ2	1.36	0.72
1:C:280:ASN:HD22	1:C:280:ASN:N	1.87	0.72
1:C:433:LYS:HZ3	2:D:263:THR:HG23	1.53	0.72
2:D:260:VAL:CG2	2:D:273:ALA:O	2.36	0.72
2:B:512:MET:CB	2:D:457:HIS:HD2	2.02	0.72
2:B:362:LEU:HD11	2:B:498:VAL:HG22	1.72	0.72
2:D:124:VAL:HG11	3:G:58:MET:HG3	1.71	0.72
2:D:146:MET:CG	2:D:180:PRO:HB2	2.19	0.72
2:B:139:LYS:HG3	2:B:179:PHE:CE1	2.25	0.72
2:B:14:LEU:HD12	2:B:14:LEU:O	1.90	0.72
1:A:193:LEU:O	1:A:197:ILE:HG13	1.89	0.72
2:D:12:TYR:CD2	2:D:13:PRO:HD3	2.25	0.72
3:F:13:ILE:CA	3:F:187:ARG:HH21	2.03	0.72
1:A:151:GLN:NE2	1:A:181:VAL:HG11	2.04	0.71
2:B:238:ARG:NE	2:B:258:GLU:HG3	2.05	0.71
2:B:49:THR:HG23	2:B:52:TYR:H	1.53	0.71
1:C:15:GLU:O	1:C:18:GLU:HB2	1.90	0.71
2:D:301:THR:O	2:D:305:VAL:HG23	1.89	0.71
2:B:85:THR:HG21	2:B:146:MET:CE	2.20	0.71
1:C:280:ASN:ND2	1:C:281:TYR:H	1.88	0.71
1:A:277:ARG:NE	1:A:383:HIS:CD2	2.58	0.71
2:B:301:THR:O	2:B:305:VAL:HG23	1.89	0.71
2:D:283:ASP:OD1	2:D:283:ASP:O	2.08	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:56:THR:O	3:E:60:MET:HB2	1.91	0.71
1:A:138:VAL:HG21	1:A:148:ILE:CD1	2.20	0.71
1:A:128:ASP:HB3	1:A:166:VAL:HG21	1.70	0.71
1:A:258:SER:HB2	1:A:261:GLU:HB2	1.72	0.71
1:A:479:TRP:HZ3	2:D:326:ASP:HB3	1.53	0.71
3:E:204:GLY:O	3:E:254:VAL:HG21	1.89	0.71
2:B:302:LYS:HE2	2:B:306:GLU:OE2	1.91	0.71
1:A:58:THR:HG22	1:A:60:ARG:N	2.03	0.71
1:A:98:ASN:H	1:A:98:ASN:ND2	1.89	0.71
3:G:141:GLU:O	3:G:142:ASN:HB2	1.90	0.71
1:A:154:CYS:HB2	1:A:155:PRO:HD3	1.72	0.71
2:B:346:LYS:HG3	2:D:264:PRO:HG2	1.73	0.71
3:G:217:VAL:CG2	9:G:7292:ATP:H2	2.03	0.71
2:B:262:ASP:OD2	2:D:350:ARG:NE	2.24	0.71
3:F:60:MET:HB3	3:F:70:LEU:HD11	1.72	0.71
3:G:56:THR:CG2	3:G:59:GLU:HB2	2.19	0.71
1:A:75:ILE:HG21	1:A:78:MET:HE3	1.73	0.70
2:D:130:ASN:ND2	2:D:130:ASN:N	2.39	0.70
2:B:512:MET:HE2	2:D:457:HIS:CB	2.21	0.70
3:F:55:ASN:HB3	3:F:60:MET:SD	2.31	0.70
1:C:360:PRO:HB2	1:C:379:TYR:CE2	2.26	0.70
2:D:146:MET:CE	2:D:208:PHE:CZ	2.73	0.70
1:C:430:ILE:HG12	2:D:269:PHE:CE1	2.26	0.70
3:F:195:LEU:HD21	3:F:268:LEU:HD23	1.73	0.70
1:C:138:VAL:HG21	1:C:148:ILE:CD1	2.21	0.70
1:A:105:GLY:HA2	1:A:112:MET:HE1	1.71	0.70
2:B:45:GLN:O	2:B:48:THR:HG22	1.91	0.70
2:D:292:LEU:O	2:D:295:PRO:HD3	1.90	0.70
3:G:259:ILE:HD12	3:G:264:LEU:HD23	1.72	0.70
1:C:159:ILE:HD12	3:H:97:CYS:HB2	1.72	0.70
1:A:352:MET:HB3	1:A:421:ILE:HG23	1.74	0.70
1:A:298:ASN:HB2	1:A:362:HIS:NE2	2.07	0.70
1:C:346:LEU:CD1	1:C:372:MET:SD	2.79	0.70
3:F:244:ALA:O	3:F:248:VAL:HG23	1.92	0.70
2:B:46:TRP:O	2:B:49:THR:HG22	1.92	0.70
1:C:355:ILE:CG2	5:C:3496:CFM:S3A	2.80	0.70
1:C:425:ILE:HG22	4:C:3494:HCA:C6	2.21	0.70
1:C:465:MET:O	1:C:469:ASN:HB2	1.92	0.70
2:B:238:ARG:CD	2:B:258:GLU:HG3	2.22	0.70
2:D:96:VAL:HG13	2:D:113:CYS:SG	2.32	0.70
3:E:23:VAL:HG12	3:E:33:VAL:HG11	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:142:TYR:O	2:D:144:PRO:HD3	1.90	0.70
3:E:35:ILE:HD12	3:E:48:ILE:HD12	1.73	0.70
3:G:224:ARG:O	3:G:225:MET:HG2	1.92	0.70
3:E:12:GLY:HA2	3:F:156:MET:HE3	1.73	0.69
1:A:350:ARG:HH11	1:A:375:VAL:HG11	1.56	0.69
1:A:35:ASN:HB2	1:A:400:LEU:HD11	1.74	0.69
1:C:30:LYS:HZ2	1:C:47:ILE:HD13	1.55	0.69
3:H:223:ARG:HG2	3:H:223:ARG:O	1.91	0.69
2:B:238:ARG:NE	2:B:258:GLU:CG	2.55	0.69
1:C:355:ILE:HG22	5:C:3496:CFM:S3A	2.31	0.69
2:D:128:GLN:HE22	2:D:168:ASN:ND2	1.89	0.69
1:C:298:ASN:HB2	1:C:362:HIS:NE2	2.06	0.69
2:D:403:LYS:NZ	2:D:421:VAL:HB	2.07	0.69
2:D:45:GLN:O	2:D:48:THR:HG22	1.92	0.69
3:E:11:GLY:HA2	9:E:5292:ATP:O1G	1.93	0.69
1:A:86:VAL:CG1	2:B:68:LYS:HE3	2.19	0.69
2:D:394:LEU:HD23	2:D:395:CYS:N	2.07	0.69
1:C:134:LEU:HD12	2:D:61:ALA:O	1.92	0.69
3:G:156:MET:SD	9:H:8292:ATP:H4'	2.32	0.69
1:A:437:PRO:HA	1:A:472:TRP:CZ2	2.27	0.69
1:A:116:SER:O	1:A:130:LYS:HE2	1.93	0.69
2:B:124:VAL:HG11	3:E:58:MET:HG3	1.74	0.69
3:H:56:THR:HG23	3:H:59:GLU:CB	2.22	0.69
2:D:146:MET:HG3	2:D:180:PRO:CB	2.21	0.69
1:A:421:ILE:HD11	1:A:436:ILE:HG21	1.75	0.69
1:A:64:TYR:CE2	1:A:88:CYS:HB3	2.28	0.69
2:D:213:MET:HE1	2:D:309:TRP:HA	1.74	0.69
1:A:446:TYR:CE2	2:D:522:VAL:HG23	2.28	0.68
2:B:59:ARG:NH2	2:B:426:ASP:OD2	2.26	0.68
1:C:274:HIS:O	1:C:358:LEU:HD11	1.93	0.68
1:A:99:TYR:CE1	2:D:517:TYR:O	2.47	0.68
2:B:130:ASN:HD22	2:B:130:ASN:H	1.41	0.68
3:H:50:HIS:O	3:H:51:SER:HB3	1.94	0.68
1:C:154:CYS:HB2	1:C:155:PRO:CD	2.23	0.68
1:C:62:CYS:O	1:C:191:GLN:HA	1.94	0.68
1:C:449:PRO:HG2	2:D:15:PHE:CZ	2.28	0.68
2:D:322:LEU:O	2:D:326:ASP:OD1	2.12	0.68
3:E:181:GLY:HA2	3:E:205:THR:OG1	1.93	0.68
3:G:192:GLU:HB3	3:G:210:PHE:HE2	1.58	0.68
3:F:26:LEU:HD12	3:F:29:MET:CE	2.23	0.68
3:H:57:ILE:HG12	3:H:75:VAL:HG21	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:VAL:HG23	1:A:190:SER:N	2.08	0.68
1:C:48:SER:HB3	1:C:402:ASP:OD2	1.94	0.68
2:B:238:ARG:HE	2:B:258:GLU:HG3	1.59	0.68
1:C:287:GLU:O	1:C:291:GLY:HA2	1.93	0.68
3:E:23:VAL:HG21	3:E:35:ILE:HD11	1.76	0.68
1:C:359:ARG:HH11	1:C:359:ARG:HG3	1.58	0.68
1:A:105:GLY:HA2	1:A:112:MET:CE	2.23	0.68
1:C:209:LYS:HE2	1:C:263:GLU:CD	2.12	0.68
1:C:343:ARG:O	1:C:347:GLU:HG3	1.94	0.68
1:C:68:LYS:O	1:C:68:LYS:HD3	1.94	0.68
1:C:74:PRO:HG3	1:C:98:ASN:OD1	1.94	0.68
2:B:517:TYR:O	1:C:99:TYR:CD1	2.47	0.68
1:A:280:ASN:ND2	1:A:281:TYR:H	1.92	0.67
1:A:74:PRO:HG3	1:A:98:ASN:OD1	1.94	0.67
1:C:355:ILE:CB	1:C:360:PRO:HD3	2.24	0.67
1:A:449:PRO:HG2	2:B:15:PHE:HZ	1.58	0.67
2:D:222:LYS:HA	2:D:288:LEU:HD21	1.77	0.67
1:C:404:VAL:HG23	1:C:408:GLU:HB2	1.77	0.67
1:C:137:GLU:OE1	2:D:59:ARG:HG3	1.94	0.67
1:A:346:LEU:HD12	1:A:370:LEU:CD1	2.21	0.67
1:A:441:MET:SD	1:A:444:TRP:HZ3	2.17	0.67
2:B:254:LEU:HB3	2:B:281:MET:HE2	1.77	0.67
2:B:91:GLY:HA2	2:B:118:MET:SD	2.34	0.67
1:C:253:TRP:CZ3	1:C:282:ILE:CD1	2.76	0.67
2:B:326:ASP:HB3	1:C:479:TRP:HZ3	1.58	0.67
2:D:375:PHE:HE2	2:D:470:GLY:HA2	1.59	0.67
1:C:437:PRO:HA	1:C:472:TRP:CZ2	2.29	0.67
3:E:10:LYS:H	3:E:13:ILE:CD1	2.08	0.67
3:E:195:LEU:HD21	3:E:268:LEU:HD23	1.77	0.67
2:B:314:PRO:HB3	2:B:316:LEU:HD13	1.75	0.67
1:C:332:LYS:O	1:C:336:GLU:HG3	1.94	0.67
1:C:352:MET:HB3	1:C:421:ILE:HG23	1.77	0.67
1:C:275:CYS:HA	1:C:358:LEU:HD13	1.75	0.67
2:D:225:ASN:HB2	2:D:290:THR:HA	1.77	0.67
3:E:185:ASN:HA	3:E:211:VAL:HB	1.76	0.67
2:B:130:ASN:ND2	2:B:130:ASN:N	2.40	0.67
1:A:168:LYS:O	1:A:172:ALA:HB2	1.94	0.67
1:C:229:TYR:HA	1:C:254:SER:O	1.93	0.67
1:A:178:ILE:O	1:A:180:PRO:HD3	1.95	0.67
3:E:13:ILE:O	3:E:185:ASN:ND2	2.28	0.67
2:D:294:GLN:HB3	2:D:374:ASP:OD2	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:37:GLY:HA3	3:F:87:GLU:OE2	1.95	0.66
1:A:97:ARG:NH2	2:D:520:ASP:OD2	2.28	0.66
1:C:144:LEU:CG	2:D:43:VAL:HG21	2.25	0.66
1:C:265:THR:HB	1:C:266:PRO:HD3	1.78	0.66
3:E:35:ILE:HD11	3:E:48:ILE:CD1	2.24	0.66
1:A:14:GLN:O	1:A:18:GLU:HG3	1.95	0.66
1:A:359:ARG:NH1	1:A:359:ARG:HG3	2.08	0.66
1:A:444:TRP:HA	1:A:444:TRP:CE3	2.28	0.66
2:D:88:TYR:HB2	2:D:147:ILE:HG22	1.77	0.66
3:G:115:TYR:C	3:G:117:ASP:H	1.97	0.66
1:A:239:ARG:HG3	1:A:249:CYS:SG	2.36	0.66
1:A:97:ARG:NH1	1:A:446:TYR:HA	2.10	0.66
1:C:75:ILE:HG21	1:C:78:MET:HE3	1.77	0.66
2:D:81:GLY:HA2	2:D:257:PRO:HD3	1.78	0.66
2:B:37:GLN:HG3	2:B:41:ASP:OD1	1.95	0.66
1:C:433:LYS:NZ	2:D:263:THR:O	2.28	0.66
2:D:220:SER:N	2:D:286:ASN:O	2.28	0.66
2:D:37:GLN:HG3	2:D:41:ASP:OD1	1.95	0.66
2:D:107:PHE:CE2	2:D:261:LEU:HD23	2.31	0.66
1:C:230:ASN:HB2	1:C:235:ALA:CB	2.25	0.66
1:C:235:ALA:HB1	1:C:252:GLN:HE21	1.61	0.66
2:D:146:MET:CE	2:D:208:PHE:CE1	2.79	0.66
3:H:45:THR:HG21	3:H:85:CYS:HB3	1.77	0.66
1:A:303:THR:HG22	1:A:369:ASP:OD1	1.95	0.66
1:C:210:ARG:NH1	1:C:264:LEU:HD21	2.10	0.66
1:C:99:TYR:CE2	1:C:232:GLY:HA2	2.31	0.66
1:C:303:THR:HG22	1:C:369:ASP:OD1	1.95	0.66
1:C:302:PRO:HD3	1:C:456:PHE:CG	2.30	0.66
3:G:179:LEU:HD12	3:G:256:PRO:HG3	1.78	0.66
1:A:425:ILE:HD11	2:B:105:ARG:HG2	1.78	0.66
2:B:107:PHE:CE2	2:B:261:LEU:HD23	2.31	0.66
1:C:85:PRO:HG3	2:D:189:PHE:HB3	1.77	0.66
3:G:231:ASP:OD2	3:G:234:ALA:HB2	1.95	0.66
3:H:86:VAL:HG21	3:H:109:LEU:HD11	1.78	0.66
1:C:138:VAL:HG21	1:C:148:ILE:HD11	1.78	0.65
2:D:146:MET:HE2	2:D:208:PHE:CZ	2.31	0.65
3:E:2:MET:HB2	3:E:119:LEU:O	1.95	0.65
3:G:224:ARG:C	3:G:225:MET:HG2	2.16	0.65
3:G:57:ILE:CG1	3:G:75:VAL:HG11	2.26	0.65
1:A:138:VAL:HG21	1:A:148:ILE:HD11	1.78	0.65
1:A:401:TYR:HB2	1:A:404:VAL:HB	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:106:ILE:HD12	3:F:138:PRO:HD3	1.78	0.65
3:H:137:MET:HB3	3:H:138:PRO:CD	2.25	0.65
2:B:89:VAL:HG22	2:B:150:SER:HB2	1.77	0.65
2:B:164:ALA:O	2:B:168:ASN:ND2	2.28	0.65
1:C:68:LYS:C	1:C:68:LYS:HD3	2.17	0.65
3:G:61:ALA:HB2	3:G:70:LEU:HD12	1.78	0.65
2:D:302:LYS:HE2	2:D:306:GLU:OE2	1.97	0.65
3:F:189:THR:OG1	3:F:192:GLU:HB2	1.95	0.65
1:A:76:LYS:O	1:A:108:ALA:HA	1.95	0.65
1:A:417:LYS:N	1:A:418:PRO:HD3	2.12	0.65
2:B:47:THR:HA	2:B:52:TYR:CG	2.32	0.65
1:A:58:THR:HG21	1:A:60:ARG:HB2	1.77	0.65
3:F:57:ILE:HG12	3:F:75:VAL:HG21	1.78	0.65
3:G:87:GLU:OE2	3:G:87:GLU:HA	1.97	0.65
1:C:35:ASN:HB2	1:C:400:LEU:HD11	1.79	0.65
2:D:146:MET:HA	2:D:179:PHE:HE2	1.61	0.65
2:D:260:VAL:HG22	2:D:273:ALA:H	1.60	0.65
2:D:284:ALA:HB3	2:D:285:PRO:HD3	1.79	0.65
2:B:130:ASN:HD22	2:B:130:ASN:N	1.94	0.65
1:C:350:ARG:HH11	1:C:375:VAL:HG11	1.61	0.65
2:D:56:ASN:O	2:D:59:ARG:HB2	1.97	0.65
3:F:2:MET:HB2	3:F:119:LEU:O	1.97	0.65
1:C:404:VAL:CG2	1:C:408:GLU:HB2	2.27	0.64
3:E:207:MET:CE	3:E:210:PHE:HB2	2.25	0.64
3:E:54:GLN:HG2	3:E:77:LYS:HZ2	1.62	0.64
3:G:189:THR:HG22	3:G:190:ASP:N	2.10	0.64
2:D:81:GLY:CA	2:D:257:PRO:HD3	2.28	0.64
3:E:54:GLN:HG2	3:E:77:LYS:NZ	2.13	0.64
3:H:15:LYS:N	9:H:8292:ATP:O1B	2.29	0.64
1:C:332:LYS:HG2	1:C:336:GLU:OE2	1.98	0.64
2:D:142:TYR:C	2:D:144:PRO:HD3	2.18	0.64
2:B:90:HIS:ND1	2:B:116:ASP:OD2	2.30	0.64
1:C:17:LEU:HD11	1:C:29:ASN:HA	1.78	0.64
1:C:37:PRO:HD3	1:C:396:ASP:HA	1.79	0.64
1:C:355:ILE:O	1:C:380:GLU:HG2	1.97	0.64
2:D:57:PHE:CD2	2:D:425:LYS:NZ	2.66	0.64
1:A:444:TRP:HA	1:A:444:TRP:HE3	1.61	0.64
2:B:397:ASN:ND2	2:B:397:ASN:N	2.45	0.64
2:D:239:VAL:HG11	2:D:483:THR:HG21	1.79	0.64
2:D:362:LEU:HD11	2:D:498:VAL:CG2	2.26	0.64
3:E:52:LYS:O	3:E:53:ALA:HB2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:CYS:SG	1:A:278:SER:HB2	2.38	0.64
2:D:124:VAL:HG21	3:G:58:MET:HE1	1.80	0.64
3:G:206:GLN:NE2	3:G:250:ASN:OD1	2.30	0.64
3:H:187:ARG:NH2	3:H:195:LEU:CD2	2.61	0.64
1:A:99:TYR:CE2	1:A:232:GLY:HA2	2.33	0.64
2:B:146:MET:HA	2:B:179:PHE:HE2	1.61	0.64
2:D:206:ARG:HG2	2:D:304:PHE:CE1	2.33	0.64
2:D:86:MET:CE	2:D:87:PRO:CD	2.71	0.64
3:F:220:ALA:HB1	3:F:225:MET:O	1.97	0.64
3:H:250:ASN:HD22	3:H:250:ASN:C	2.00	0.64
1:A:332:LYS:O	1:A:336:GLU:HG3	1.98	0.64
1:A:405:THR:OG1	1:A:408:GLU:CG	2.46	0.64
2:B:119:THR:HG22	2:B:120:GLU:H	1.63	0.64
1:C:76:LYS:O	1:C:108:ALA:HA	1.98	0.64
3:G:34:MET:HB2	3:G:119:LEU:CD1	2.27	0.64
3:H:37:GLY:HA3	3:H:87:GLU:OE2	1.97	0.64
1:A:35:ASN:CB	1:A:400:LEU:HD11	2.28	0.64
1:C:138:VAL:HG13	2:D:62:LEU:CD1	2.28	0.63
1:C:209:LYS:CE	1:C:263:GLU:OE1	2.45	0.63
1:C:458:ILE:HG23	1:C:461:ARG:NH2	2.14	0.63
2:D:47:THR:HA	2:D:52:TYR:CG	2.32	0.63
1:A:207:LEU:HD11	1:A:266:PRO:CG	2.28	0.63
1:C:144:LEU:HD11	2:D:43:VAL:HG21	1.80	0.63
1:A:302:PRO:HD3	1:A:456:PHE:CG	2.34	0.63
2:B:64:VAL:O	2:B:426:ASP:OD1	2.16	0.63
1:C:276:TYR:O	1:C:280:ASN:HB3	1.99	0.63
1:C:359:ARG:NH1	1:C:359:ARG:HG3	2.12	0.63
1:C:423:SER:HB3	1:C:427:GLU:HG3	1.80	0.63
1:A:230:ASN:HB2	1:A:235:ALA:CB	2.28	0.63
1:C:58:THR:CG2	1:C:60:ARG:H	2.08	0.63
1:C:9:VAL:O	1:C:13:ILE:HG13	1.98	0.63
2:D:128:GLN:NE2	2:D:168:ASN:ND2	2.46	0.63
1:A:276:TYR:O	1:A:280:ASN:HB3	1.99	0.63
1:A:35:ASN:HB2	1:A:400:LEU:CD1	2.29	0.63
2:B:3:GLN:HE21	2:B:3:GLN:CA	2.09	0.63
1:C:12:LEU:O	1:C:16:VAL:HG23	1.98	0.63
1:C:178:ILE:O	1:C:180:PRO:HD2	1.99	0.63
1:C:433:LYS:CE	2:D:263:THR:HG23	2.28	0.63
2:B:238:ARG:HD3	2:B:258:GLU:HG3	1.79	0.63
2:D:3:GLN:HE21	2:D:3:GLN:CA	2.09	0.63
3:E:98:ALA:O	3:E:102:VAL:HG23	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:460:LYS:HE3	2:B:507:GLU:OE2	1.99	0.63
2:D:502:LEU:HD22	2:D:523:ARG:HD3	1.80	0.63
3:E:129:ASP:HB3	3:E:131:VAL:HG12	1.80	0.63
3:G:45:THR:HG21	3:G:85:CYS:HB3	1.81	0.63
1:A:23:LYS:NZ	2:B:133:ASP:OD2	2.15	0.63
3:E:45:THR:HG21	3:E:85:CYS:HB3	1.81	0.63
3:G:13:ILE:O	3:G:185:ASN:ND2	2.32	0.63
2:B:47:THR:OG1	2:B:431:ARG:NH1	2.31	0.63
1:C:167:SER:OG	1:C:180:PRO:HG3	1.98	0.63
1:C:423:SER:CB	1:C:427:GLU:HG3	2.29	0.63
1:A:419:ASP:O	1:A:437:PRO:HD2	1.99	0.62
2:B:225:ASN:HB2	2:B:290:THR:HA	1.81	0.62
1:C:253:TRP:HZ3	1:C:282:ILE:CD1	2.06	0.62
1:C:400:LEU:HD12	1:C:400:LEU:N	2.13	0.62
1:C:309:LEU:HD11	1:C:453:PHE:HE1	1.64	0.62
2:D:90:HIS:ND1	2:D:116:ASP:OD2	2.32	0.62
1:A:58:THR:CG2	1:A:60:ARG:HB2	2.28	0.62
2:B:239:VAL:HG11	2:B:483:THR:HG21	1.80	0.62
3:G:23:VAL:HA	3:G:26:LEU:HB2	1.81	0.62
3:H:134:GLY:O	3:H:137:MET:HB2	1.99	0.62
2:D:222:LYS:HG2	2:D:222:LYS:O	1.97	0.62
3:F:13:ILE:HA	3:F:187:ARG:NH2	2.12	0.62
3:F:7:ILE:HD12	3:F:19:THR:OG1	2.00	0.62
1:A:302:PRO:HD3	1:A:456:PHE:CD1	2.34	0.62
2:D:279:GLU:OE2	2:D:282:LYS:HD2	1.99	0.62
1:C:144:LEU:HD11	2:D:43:VAL:CG2	2.29	0.62
3:E:166:LYS:O	3:E:169:VAL:HG12	2.00	0.62
3:E:91:PRO:HD2	3:E:98:ALA:HB2	1.81	0.62
3:G:57:ILE:HG12	3:G:75:VAL:HG21	1.82	0.62
3:H:42:ALA:HA	3:H:87:GLU:OE1	1.99	0.62
1:A:170:LYS:O	1:A:178:ILE:HD12	1.99	0.62
2:D:284:ALA:HB3	2:D:285:PRO:CD	2.30	0.62
3:E:87:GLU:OE2	3:E:87:GLU:HA	1.99	0.62
2:B:499:ASN:O	2:B:503:GLU:HG3	2.00	0.62
3:H:16:SER:O	3:H:20:GLN:HG3	2.00	0.62
1:A:189:VAL:HG23	1:A:190:SER:H	1.65	0.62
1:A:280:ASN:H	1:A:280:ASN:HD22	1.45	0.62
2:B:392:HIS:ND1	2:B:433:LEU:HD12	2.15	0.62
2:B:509:THR:HA	2:B:515:THR:HB	1.82	0.62
1:C:298:ASN:CG	1:C:362:HIS:CD2	2.74	0.62
2:B:520:ASP:O	2:D:449:LYS:NZ	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:215:ASN:HA	3:E:218:GLN:OE1	2.00	0.62
3:G:212:PRO:HB2	3:G:236:GLN:HE21	1.65	0.62
1:A:75:ILE:HG21	1:A:78:MET:HE2	1.80	0.61
2:B:322:LEU:O	2:B:326:ASP:OD1	2.18	0.61
3:F:57:ILE:HD12	3:F:105:ALA:HB1	1.81	0.61
2:D:369:LEU:HD23	2:D:393:ILE:HA	1.82	0.61
3:F:86:VAL:HG21	3:F:109:LEU:HD11	1.82	0.61
3:F:195:LEU:O	3:F:198:ALA:HB3	2.00	0.61
3:G:129:ASP:HB3	3:G:131:VAL:HG12	1.82	0.61
2:B:375:PHE:HE2	2:B:470:GLY:HA2	1.65	0.61
2:B:471:PHE:CD2	2:B:472:PRO:CD	2.74	0.61
1:C:218:SER:OG	1:C:269:LYS:HE2	2.00	0.61
2:D:238:ARG:HE	2:D:258:GLU:HG2	1.63	0.61
3:G:45:THR:CG2	3:G:85:CYS:HB3	2.31	0.61
1:C:300:PHE:HB3	1:C:366:ALA:HB2	1.82	0.61
1:C:444:TRP:CE3	1:C:444:TRP:HA	2.36	0.61
3:G:204:GLY:O	3:G:254:VAL:HG21	2.00	0.61
3:H:87:GLU:OE2	3:H:87:GLU:HA	2.01	0.61
3:E:131:VAL:HG22	3:E:132:CYS:N	2.15	0.61
1:A:219:THR:HG23	1:A:220:PRO:HD2	1.83	0.61
1:A:225:ILE:HD11	1:A:249:CYS:SG	2.39	0.61
1:C:274:HIS:O	1:C:358:LEU:CD1	2.48	0.61
2:D:70:CYS:O	2:D:193:HIS:HA	2.01	0.61
3:E:217:VAL:HB	9:E:5292:ATP:C2	2.36	0.61
3:E:23:VAL:CG1	3:E:33:VAL:HG11	2.31	0.61
2:B:124:VAL:HG21	3:E:58:MET:HE1	1.82	0.61
3:G:9:GLY:O	3:G:15:LYS:HE2	2.00	0.61
1:A:332:LYS:HG2	1:A:336:GLU:OE2	2.00	0.61
2:B:328:PHE:O	2:B:332:VAL:HG23	2.01	0.61
2:B:56:ASN:O	2:B:59:ARG:HB2	2.01	0.61
1:A:141:LEU:HD23	2:B:59:ARG:HD2	1.81	0.61
1:C:96:ARG:HG2	1:C:96:ARG:HH11	1.66	0.61
2:D:146:MET:CE	2:D:208:PHE:HZ	2.13	0.61
2:D:222:LYS:HA	2:D:288:LEU:CD2	2.31	0.61
2:B:302:LYS:O	2:B:306:GLU:HG3	2.01	0.61
2:D:317:ASN:ND2	2:D:317:ASN:H	1.98	0.61
3:G:223:ARG:O	3:G:224:ARG:HB2	2.01	0.61
3:G:106:ILE:CD1	3:G:137:MET:HB3	2.31	0.61
3:H:64:ALA:HB1	3:H:69:ASP:HB3	1.82	0.61
1:C:57:MET:HE3	2:D:100:ARG:NH1	2.15	0.60
3:F:242:ALA:O	3:F:246:LYS:CG	2.43	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:38:CYS:HB3	3:H:102:VAL:HG13	1.83	0.60
1:A:277:ARG:CZ	1:A:383:HIS:HD2	2.12	0.60
2:B:105:ARG:HB2	2:B:474:PHE:CE2	2.36	0.60
2:D:72:PRO:HB2	2:D:99:PHE:CZ	2.35	0.60
1:C:389:ARG:NH1	1:C:389:ARG:CG	2.61	0.60
3:E:237:ALA:O	3:E:241:ARG:HG3	2.01	0.60
2:D:370:TRP:HH2	2:D:448:GLY:HA3	1.66	0.60
1:A:309:LEU:HD11	1:A:453:PHE:HE1	1.66	0.60
1:A:355:ILE:O	1:A:380:GLU:HG2	2.01	0.60
2:B:422:TYR:HD2	2:B:425:LYS:HD2	1.64	0.60
1:C:178:ILE:HG22	1:C:180:PRO:HD3	1.83	0.60
1:C:222:ASP:OD1	1:C:248:ARG:NH1	2.34	0.60
2:B:131:MET:HG2	2:B:165:PHE:HB3	1.83	0.60
1:A:222:ASP:OD1	1:A:248:ARG:NH1	2.35	0.60
1:A:404:VAL:HG23	1:A:408:GLU:HB2	1.83	0.60
1:C:341:LYS:HD2	2:D:5:VAL:CG1	2.31	0.60
3:G:212:PRO:HB2	3:G:236:GLN:NE2	2.16	0.60
2:B:247:MET:HE3	2:B:340:ILE:HA	1.84	0.60
1:C:421:ILE:HD11	1:C:436:ILE:HG21	1.83	0.60
2:D:499:ASN:O	2:D:503:GLU:HG3	2.01	0.60
3:E:179:LEU:HD12	3:E:256:PRO:HG3	1.82	0.60
3:G:22:LEU:HD23	3:G:22:LEU:O	2.02	0.60
2:B:129:GLN:NE2	2:B:129:GLN:HA	2.17	0.60
2:B:236:ASN:HA	2:B:239:VAL:HG12	1.84	0.60
1:C:35:ASN:CB	1:C:400:LEU:HD11	2.32	0.60
2:D:328:PHE:O	2:D:332:VAL:HG23	2.02	0.60
3:E:243:LEU:O	3:E:247:VAL:HG23	2.02	0.60
2:B:142:TYR:C	2:B:144:PRO:CD	2.69	0.60
1:C:186:PHE:HB3	2:D:154:MET:CE	2.31	0.60
1:C:433:LYS:HE3	2:D:263:THR:O	2.01	0.60
3:H:26:LEU:HD12	3:H:29:MET:CE	2.32	0.60
1:A:9:VAL:O	1:A:13:ILE:HG13	2.01	0.59
2:B:503:GLU:HG2	2:D:476:ARG:HH11	1.66	0.59
1:C:32:LEU:N	1:C:32:LEU:HD23	2.18	0.59
1:C:417:LYS:N	1:C:418:PRO:HD3	2.17	0.59
2:D:119:THR:HG22	2:D:120:GLU:H	1.67	0.59
3:H:243:LEU:O	3:H:247:VAL:HG23	2.01	0.59
3:F:146:GLU:HG2	3:F:253:LEU:HD22	1.83	0.59
3:G:40:PRO:HG3	3:G:98:ALA:HB1	1.84	0.59
2:D:131:MET:HG2	2:D:165:PHE:HB3	1.83	0.59
3:E:10:LYS:O	3:E:13:ILE:HG12	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:LEU:HD11	1:A:266:PRO:HG3	1.84	0.59
1:A:355:ILE:HG21	1:A:359:ARG:HB2	1.83	0.59
2:B:81:GLY:CA	2:B:257:PRO:HD3	2.32	0.59
1:C:230:ASN:HB2	1:C:235:ALA:HB3	1.82	0.59
2:D:394:LEU:HD23	2:D:394:LEU:C	2.23	0.59
2:D:59:ARG:NH1	2:D:429:HIS:CE1	2.71	0.59
3:F:20:GLN:NE2	3:F:47:LEU:HD12	2.18	0.59
3:G:217:VAL:HG22	3:G:227:VAL:CG2	2.31	0.59
1:C:280:ASN:H	1:C:280:ASN:HD22	1.49	0.59
1:C:42:SER:HB3	1:C:46:ILE:HG22	1.83	0.59
1:A:128:ASP:OD1	1:A:161:ASP:HB3	2.02	0.59
1:A:287:GLU:O	1:A:291:GLY:HA2	2.01	0.59
2:B:212:SER:O	2:B:216:LYS:CE	2.45	0.59
2:D:236:ASN:HA	2:D:239:VAL:HG12	1.85	0.59
2:D:448:GLY:C	2:D:466:LEU:HD22	2.22	0.59
1:A:423:SER:OG	1:A:427:GLU:HG3	2.03	0.59
1:A:479:TRP:CZ3	2:D:326:ASP:HB3	2.36	0.59
1:C:96:ARG:HG2	1:C:96:ARG:NH1	2.18	0.59
3:F:45:THR:HG21	3:F:85:CYS:HB3	1.84	0.59
1:C:405:THR:OG1	1:C:408:GLU:CG	2.50	0.59
1:C:424:GLY:CA	1:C:442:HIS:HD2	2.16	0.59
2:D:118:MET:HE1	2:D:155:ALA:HB2	1.85	0.59
2:D:362:LEU:CD1	2:D:498:VAL:HG22	2.30	0.59
2:D:494:LEU:O	2:D:498:VAL:HG23	2.02	0.59
3:F:106:ILE:HD12	3:F:137:MET:CG	2.32	0.59
1:A:425:ILE:CD1	2:B:105:ARG:HG2	2.33	0.59
1:C:355:ILE:CG2	1:C:356:GLY:N	2.36	0.59
3:E:88:SER:HA	3:E:105:ALA:CB	2.33	0.59
3:F:198:ALA:HB1	3:F:267:LEU:HD21	1.84	0.59
2:B:213:MET:HE1	2:B:309:TRP:HA	1.84	0.59
2:B:494:LEU:O	2:B:498:VAL:HG23	2.03	0.59
1:C:230:ASN:OD1	1:C:233:GLY:CA	2.51	0.59
1:C:433:LYS:CE	2:D:263:THR:O	2.50	0.59
3:G:191:ARG:O	3:G:195:LEU:HB2	2.03	0.59
1:A:350:ARG:HD2	1:A:375:VAL:HG11	1.85	0.58
2:B:397:ASN:N	2:B:397:ASN:HD22	1.88	0.58
1:C:128:ASP:HB3	1:C:166:VAL:HG21	1.85	0.58
1:C:230:ASN:OD1	1:C:233:GLY:HA2	2.03	0.58
3:E:255:ILE:HG22	3:E:255:ILE:O	2.02	0.58
3:H:55:ASN:HD22	3:H:55:ASN:N	1.99	0.58
3:H:55:ASN:ND2	3:H:55:ASN:N	2.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:298:ASN:ND2	1:C:298:ASN:C	2.57	0.58
1:A:280:ASN:HD22	1:A:281:TYR:H	1.50	0.58
1:A:32:LEU:HD23	1:A:32:LEU:N	2.18	0.58
2:B:91:GLY:O	2:B:116:ASP:O	2.20	0.58
2:B:162:LEU:HD12	2:B:185:HIS:HD2	1.68	0.58
2:B:375:PHE:C	2:B:375:PHE:HD1	2.06	0.58
2:B:394:LEU:HD23	2:B:395:CYS:N	2.18	0.58
2:B:72:PRO:HB2	2:B:99:PHE:CZ	2.38	0.58
1:A:479:TRP:CD2	2:D:340:ILE:HD12	2.38	0.58
1:A:404:VAL:CG2	1:A:408:GLU:HB2	2.33	0.58
1:C:75:ILE:HG21	1:C:78:MET:HE2	1.86	0.58
2:D:124:VAL:HG21	3:G:58:MET:CE	2.33	0.58
3:F:207:MET:HE3	3:F:210:PHE:HB2	1.86	0.58
3:F:72:LEU:HD11	3:F:76:LEU:HD12	1.86	0.58
2:B:449:LYS:NZ	2:D:520:ASP:O	2.35	0.58
2:B:56:ASN:OD1	2:B:59:ARG:NH1	2.36	0.58
3:H:49:LEU:HD11	3:H:85:CYS:HB2	1.85	0.58
1:A:245:MET:HE1	1:A:309:LEU:HD22	1.84	0.58
1:C:299:PHE:HB3	1:C:452:GLY:H	1.69	0.58
3:E:91:PRO:HB2	3:E:95:VAL:O	2.03	0.58
3:F:148:TYR:CE2	3:F:208:ILE:HD12	2.39	0.58
2:B:283:ASP:O	2:B:283:ASP:OD1	2.22	0.58
2:B:246:GLU:OE2	2:B:343:SER:HB2	2.03	0.58
2:D:128:GLN:O	2:D:132:LYS:HG3	2.03	0.58
2:D:130:ASN:N	2:D:130:ASN:HD22	2.00	0.58
3:F:215:ASN:HA	3:F:218:GLN:OE1	2.04	0.58
3:F:57:ILE:HG13	3:F:75:VAL:HG11	1.86	0.58
1:A:426:LYS:HE3	2:B:97:ALA:O	2.04	0.58
1:C:277:ARG:NH2	1:C:280:ASN:OD1	2.35	0.58
2:D:151:THR:OG1	2:D:155:ALA:HB3	2.03	0.58
1:A:300:PHE:HB3	1:A:366:ALA:HB2	1.85	0.58
1:A:382:ALA:HB1	1:A:386:ASP:HB2	1.84	0.58
2:B:124:VAL:HG21	3:E:58:MET:CE	2.34	0.58
2:B:129:GLN:HE21	2:B:129:GLN:HA	1.69	0.58
1:C:298:ASN:C	1:C:298:ASN:HD22	2.03	0.58
1:C:419:ASP:O	1:C:437:PRO:HD2	2.04	0.58
1:C:440:GLU:HB2	1:C:445:ASP:HB2	1.85	0.58
2:B:523:ARG:HG3	2:D:475:ASP:HA	1.85	0.58
3:E:136:ALA:HB2	3:F:94:GLY:CA	2.34	0.58
1:A:150:VAL:O	1:A:181:VAL:HG12	2.04	0.58
1:A:224:ALA:CB	1:A:251:ALA:HB3	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:314:PRO:CB	2:B:316:LEU:HD13	2.34	0.58
2:B:3:GLN:NE2	2:B:3:GLN:HA	2.17	0.58
2:B:457:HIS:HD2	2:D:512:MET:CB	2.15	0.58
2:B:70:CYS:HB2	2:B:188:SER:HB3	1.85	0.58
3:E:115:TYR:O	3:E:117:ASP:N	2.30	0.58
3:F:13:ILE:C	3:F:187:ARG:NH2	2.57	0.58
1:A:116:SER:O	1:A:130:LYS:CE	2.52	0.57
2:B:370:TRP:HH2	2:B:448:GLY:HA3	1.68	0.57
1:C:444:TRP:HE3	1:C:444:TRP:HA	1.68	0.57
2:D:158:ILE:HG22	3:G:97:CYS:HB2	1.85	0.57
3:F:8:TYR:CE1	3:F:126:VAL:HG21	2.38	0.57
1:A:210:ARG:NH1	1:A:264:LEU:HD21	2.19	0.57
2:B:57:PHE:HE2	2:B:425:LYS:NZ	2.01	0.57
1:C:35:ASN:HB2	1:C:400:LEU:CD1	2.34	0.57
1:C:360:PRO:HB2	1:C:379:TYR:CZ	2.39	0.57
1:C:401:TYR:HB2	1:C:404:VAL:HB	1.85	0.57
1:C:66:GLY:O	1:C:70:VAL:HG22	2.04	0.57
2:D:375:PHE:C	2:D:375:PHE:HD1	2.06	0.57
3:G:131:VAL:HG22	3:G:132:CYS:N	2.19	0.57
1:C:124:VAL:CG2	3:H:58:MET:CE	2.64	0.57
1:A:231:ILE:O	1:A:234:ASP:OD2	2.23	0.57
1:A:400:LEU:N	1:A:400:LEU:HD12	2.19	0.57
2:B:467:ILE:HD13	2:B:497:LEU:HD23	1.87	0.57
1:C:151:GLN:NE2	1:C:181:VAL:HG11	2.19	0.57
2:D:197:TRP:CE3	2:D:229:GLY:HA2	2.39	0.57
2:D:317:ASN:H	2:D:317:ASN:HD22	1.51	0.57
3:F:49:LEU:O	3:F:50:HIS:CB	2.52	0.57
3:G:166:LYS:O	3:G:169:VAL:HG12	2.04	0.57
2:B:471:PHE:HD2	2:B:472:PRO:HD3	1.62	0.57
2:D:375:PHE:C	2:D:375:PHE:CD1	2.77	0.57
2:D:390:PRO:O	2:D:419:ALA:HB1	2.04	0.57
3:F:141:GLU:O	3:F:142:ASN:HB2	2.02	0.57
1:A:167:SER:HB2	1:A:180:PRO:CG	2.28	0.57
1:A:36:ASP:OD1	1:A:38:ALA:HB3	2.04	0.57
1:C:58:THR:HG22	1:C:59:ILE:N	2.19	0.57
2:D:96:VAL:HG21	2:D:115:SER:HB2	1.86	0.57
2:D:91:GLY:CA	2:D:118:MET:HE2	2.28	0.57
3:F:199:LEU:O	3:F:203:LEU:HB2	2.04	0.57
3:G:91:PRO:HB2	3:G:95:VAL:O	2.03	0.57
3:H:45:THR:OG1	3:H:49:LEU:HD12	2.04	0.57
3:H:4:GLN:HB3	3:H:122:VAL:HB	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:375:PHE:C	2:B:375:PHE:CD1	2.77	0.57
2:B:375:PHE:CZ	2:B:469:ILE:HG22	2.39	0.57
2:B:502:LEU:HD22	2:B:523:ARG:HD3	1.84	0.57
1:C:17:LEU:CD1	1:C:29:ASN:HA	2.35	0.57
1:C:299:PHE:CD2	1:C:305:THR:HG23	2.40	0.57
1:C:355:ILE:HD11	1:C:441:MET:CB	2.33	0.57
2:D:397:ASN:N	2:D:397:ASN:HD22	1.89	0.57
1:A:124:VAL:HG21	3:F:58:MET:CE	2.35	0.57
2:B:473:ILE:HG21	2:B:479:LEU:HD22	1.87	0.57
1:C:352:MET:HE1	1:C:413:VAL:HA	1.86	0.57
2:D:154:MET:O	2:D:158:ILE:HG12	2.04	0.57
2:D:128:GLN:NE2	2:D:165:PHE:HA	2.15	0.57
3:F:23:VAL:HA	3:F:26:LEU:HB2	1.86	0.57
3:H:250:ASN:C	3:H:250:ASN:ND2	2.58	0.57
1:C:280:ASN:HD22	1:C:281:TYR:H	1.53	0.57
1:C:298:ASN:ND2	1:C:299:PHE:N	2.53	0.57
1:C:34:VAL:CG1	1:C:397:SER:HA	2.35	0.57
1:C:429:PHE:O	1:C:433:LYS:HG2	2.05	0.57
2:D:238:ARG:NE	2:D:258:GLU:CG	2.60	0.57
2:D:3:GLN:HA	2:D:3:GLN:NE2	2.17	0.57
3:H:35:ILE:CD1	3:H:48:ILE:HD12	2.35	0.57
1:A:287:GLU:HA	1:A:292:ILE:H	1.69	0.57
1:A:446:TYR:HE2	2:D:522:VAL:CG2	2.18	0.57
1:C:234:ASP:HB3	1:C:451:HIS:ND1	2.19	0.57
1:C:280:ASN:ND2	1:C:281:TYR:N	2.52	0.57
1:A:446:TYR:CE2	2:D:522:VAL:CG2	2.87	0.57
3:E:208:ILE:O	3:E:246:LYS:HE3	2.05	0.57
3:E:56:THR:HG23	3:E:59:GLU:CB	2.30	0.57
3:G:57:ILE:HG13	3:G:75:VAL:HG11	1.87	0.57
3:H:26:LEU:HD12	3:H:29:MET:HE3	1.86	0.57
3:H:94:GLY:O	3:H:95:VAL:HG23	2.04	0.57
1:A:230:ASN:OD1	1:A:233:GLY:HA2	2.04	0.57
1:A:251:ALA:HA	1:A:261:GLU:CG	2.34	0.57
2:B:206:ARG:CG	2:B:304:PHE:CE1	2.88	0.57
2:B:459:GLY:HA3	2:B:461:GLU:OE1	2.04	0.57
1:C:207:LEU:HD11	1:C:266:PRO:HD3	1.86	0.57
1:C:425:ILE:HG22	4:C:3494:HCA:O3	2.05	0.57
2:D:62:LEU:HD21	2:D:64:VAL:CG2	2.34	0.57
3:E:100:ARG:O	3:E:100:ARG:HD2	2.04	0.57
3:F:106:ILE:HD11	3:F:138:PRO:CD	2.35	0.57
3:G:16:SER:O	3:G:20:GLN:HG3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ILE:HD11	1:A:436:ILE:CG2	2.34	0.56
1:C:396:ASP:O	1:C:397:SER:HB2	2.05	0.56
1:C:423:SER:OG	1:C:427:GLU:HG3	2.05	0.56
2:D:456:LEU:HD13	2:D:463:GLU:OE2	2.05	0.56
3:F:107:ASN:O	3:F:111:GLU:HB2	2.05	0.56
1:A:68:LYS:HD3	1:A:68:LYS:O	2.06	0.56
3:F:56:THR:HG23	3:F:59:GLU:CB	2.35	0.56
1:A:380:GLU:HG3	1:A:381:PHE:CD2	2.41	0.56
1:A:429:PHE:HB2	2:B:110:PRO:HD3	1.86	0.56
1:A:90:GLN:NE2	2:B:447:TYR:CZ	2.73	0.56
2:B:238:ARG:HD3	2:B:258:GLU:CD	2.26	0.56
2:D:403:LYS:HZ1	2:D:421:VAL:HB	1.68	0.56
3:E:115:TYR:C	3:E:117:ASP:H	2.08	0.56
3:F:45:THR:CG2	3:F:85:CYS:HB3	2.35	0.56
3:G:141:GLU:O	3:G:142:ASN:CB	2.52	0.56
3:H:45:THR:CG2	3:H:85:CYS:HB3	2.34	0.56
1:C:144:LEU:CD1	2:D:43:VAL:HG21	2.35	0.56
1:C:351:VAL:HG11	1:C:367:TYR:CE2	2.40	0.56
2:D:246:GLU:OE2	2:D:343:SER:HB2	2.05	0.56
2:D:442:MET:HG3	2:D:464:VAL:HG12	1.86	0.56
2:D:67:ALA:HB3	2:D:396:HIS:HB2	1.87	0.56
3:G:72:LEU:HD11	3:G:76:LEU:HD12	1.87	0.56
3:G:57:ILE:HG12	3:G:75:VAL:HG11	1.88	0.56
3:G:86:VAL:HG21	3:G:109:LEU:HD11	1.87	0.56
3:H:141:GLU:O	3:H:142:ASN:CB	2.51	0.56
1:A:277:ARG:HE	1:A:383:HIS:HE2	1.52	0.56
2:B:309:TRP:O	2:B:310:LYS:HB2	2.04	0.56
2:B:375:PHE:HZ	2:B:469:ILE:HG22	1.69	0.56
1:C:97:ARG:CZ	1:C:446:TYR:HA	2.34	0.56
2:D:314:PRO:CB	2:D:316:LEU:HD13	2.35	0.56
2:B:503:GLU:HG2	2:D:476:ARG:NH1	2.21	0.56
1:A:97:ARG:NH2	2:D:520:ASP:CG	2.58	0.56
2:B:456:LEU:HD13	2:B:463:GLU:OE2	2.05	0.56
1:A:97:ARG:NH2	2:D:520:ASP:OD1	2.36	0.56
3:G:217:VAL:HG21	9:G:7292:ATP:C2	2.28	0.56
1:A:449:PRO:HG2	2:B:15:PHE:CZ	2.40	0.56
1:A:96:ARG:NH1	1:A:96:ARG:HG2	2.21	0.56
2:B:118:MET:HB3	2:B:154:MET:HE1	1.88	0.56
1:C:239:ARG:NH1	1:C:252:GLN:OE1	2.38	0.56
1:C:351:VAL:HG23	1:C:420:LEU:HB3	1.88	0.56
1:A:458:ILE:HG23	1:A:461:ARG:NH2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:390:PRO:O	2:D:419:ALA:CB	2.54	0.56
2:D:442:MET:HG3	2:D:464:VAL:CG1	2.35	0.56
3:H:57:ILE:HG13	3:H:75:VAL:HG11	1.88	0.56
1:A:265:THR:HG22	1:A:286:MET:HE2	1.87	0.56
1:C:118:PHE:CZ	1:C:156:ILE:HD11	2.41	0.56
1:A:423:SER:CB	1:A:427:GLU:HG3	2.36	0.56
2:B:239:VAL:HG11	2:B:483:THR:CG2	2.36	0.56
1:C:287:GLU:HA	1:C:292:ILE:H	1.69	0.56
1:C:245:MET:HE1	1:C:309:LEU:HD22	1.88	0.56
1:C:426:LYS:NZ	2:D:97:ALA:CB	2.66	0.55
2:D:239:VAL:HG11	2:D:483:THR:CG2	2.36	0.55
2:D:289:ASN:ND2	2:D:314:PRO:HD3	2.21	0.55
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.70	0.55
2:B:50:LYS:HG3	2:B:436:THR:HG22	1.87	0.55
2:D:67:ALA:HB3	2:D:396:HIS:CB	2.37	0.55
3:F:137:MET:HB3	3:F:138:PRO:CD	2.36	0.55
3:F:243:LEU:O	3:F:247:VAL:HG23	2.06	0.55
1:A:280:ASN:ND2	1:A:281:TYR:N	2.54	0.55
2:B:517:TYR:O	1:C:99:TYR:HE1	1.85	0.55
1:C:210:ARG:HH11	1:C:264:LEU:CD2	2.17	0.55
1:C:265:THR:HG22	1:C:286:MET:HE2	1.88	0.55
2:D:59:ARG:HH12	2:D:429:HIS:CE1	2.25	0.55
1:A:17:LEU:HD21	1:A:28:ARG:HB2	1.88	0.55
1:A:70:VAL:CG2	1:A:71:VAL:N	2.69	0.55
1:C:235:ALA:HB1	1:C:252:GLN:NE2	2.20	0.55
1:C:358:LEU:O	1:C:362:HIS:HB2	2.06	0.55
2:D:88:TYR:HB2	2:D:147:ILE:CG2	2.37	0.55
2:B:125:PHE:CZ	3:E:58:MET:O	2.58	0.55
3:F:43:ASP:CB	3:F:46:ARG:HD3	2.34	0.55
1:A:37:PRO:HD3	1:A:396:ASP:HA	1.87	0.55
1:C:119:GLN:HA	1:C:119:GLN:OE1	2.05	0.55
1:C:358:LEU:HD22	5:C:3496:CFM:S4A	2.47	0.55
3:E:15:LYS:N	9:E:5292:ATP:O1B	2.40	0.55
3:E:8:TYR:CE1	3:E:126:VAL:HG21	2.42	0.55
1:A:136:ASP:O	1:A:140:THR:HG22	2.07	0.55
1:A:351:VAL:HG11	1:A:367:TYR:CE2	2.41	0.55
2:B:238:ARG:HD3	2:B:258:GLU:CG	2.36	0.55
2:B:228:PRO:O	2:B:294:GLN:HG3	2.07	0.55
2:B:422:TYR:CD2	2:B:425:LYS:HD2	2.42	0.55
1:A:144:LEU:CG	2:B:43:VAL:HG21	2.37	0.55
1:C:346:LEU:HG	1:C:370:LEU:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:351:VAL:CG1	1:C:374:VAL:HG22	2.36	0.55
2:D:260:VAL:HG22	2:D:273:ALA:N	2.21	0.55
3:G:61:ALA:HB2	3:G:70:LEU:CD1	2.36	0.55
1:A:277:ARG:NE	1:A:383:HIS:NE2	2.53	0.55
1:A:355:ILE:CB	1:A:360:PRO:HD3	2.37	0.55
1:C:433:LYS:NZ	2:D:263:THR:HG22	2.22	0.55
2:D:90:HIS:O	2:D:151:THR:HA	2.05	0.55
3:F:13:ILE:C	3:F:187:ARG:HH21	2.09	0.55
3:G:14:GLY:HA3	3:G:185:ASN:HD22	1.70	0.55
3:H:20:GLN:OE1	3:H:47:LEU:HB2	2.06	0.55
1:C:98:ASN:N	1:C:98:ASN:ND2	2.52	0.55
3:E:178:ARG:HB2	3:E:253:LEU:HB3	1.89	0.55
3:F:26:LEU:HD12	3:F:29:MET:HE3	1.87	0.55
1:A:138:VAL:HG23	1:A:139:GLU:H	1.72	0.55
1:A:151:GLN:HA	1:A:181:VAL:HG13	1.89	0.55
1:A:332:LYS:N	1:A:333:PRO:HD2	2.21	0.55
3:E:208:ILE:HG22	3:E:209:HIS:N	2.22	0.55
1:A:138:VAL:HG13	2:B:62:LEU:HD22	1.88	0.55
2:D:128:GLN:NE2	2:D:168:ASN:HD22	2.01	0.55
3:E:23:VAL:HA	3:E:26:LEU:HB2	1.88	0.55
3:G:239:GLU:O	3:G:242:ALA:HB3	2.07	0.55
3:H:138:PRO:O	3:H:143:LYS:CB	2.55	0.55
1:A:275:CYS:HA	1:A:358:LEU:HD13	1.87	0.54
1:C:380:GLU:HG3	1:C:381:PHE:CD2	2.42	0.54
3:F:181:GLY:HA2	3:F:205:THR:OG1	2.07	0.54
1:A:99:TYR:CD1	2:D:517:TYR:O	2.61	0.54
2:B:70:CYS:O	2:B:193:HIS:HA	2.06	0.54
2:B:434:VAL:HG12	2:B:439:PRO:HG2	1.88	0.54
2:B:512:MET:HB3	2:D:457:HIS:CD2	2.30	0.54
1:C:224:ALA:CB	1:C:251:ALA:HB3	2.38	0.54
1:C:346:LEU:HD11	1:C:463:MET:HB2	1.88	0.54
2:D:219:GLY:N	2:D:287:ALA:O	2.40	0.54
1:A:225:ILE:CD1	1:A:249:CYS:SG	2.95	0.54
1:A:239:ARG:NH1	1:A:252:GLN:OE1	2.40	0.54
1:C:332:LYS:N	1:C:333:PRO:HD2	2.22	0.54
1:C:355:ILE:CG2	1:C:360:PRO:HD3	2.37	0.54
3:E:61:ALA:HB1	3:E:67:VAL:HA	1.89	0.54
3:H:2:MET:HB2	3:H:119:LEU:O	2.07	0.54
3:H:144:ALA:O	3:H:177:VAL:HG23	2.08	0.54
3:H:39:ASP:OD1	3:H:40:PRO:CD	2.56	0.54
1:A:134:LEU:HD12	2:B:61:ALA:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:324:CYS:SG	1:C:328:ILE:HD11	2.48	0.54
1:C:41:GLN:HE21	1:C:43:LYS:HG3	1.73	0.54
2:B:457:HIS:CD2	2:D:512:MET:HB3	2.31	0.54
3:F:213:ARG:HG2	9:F:6292:ATP:H2	1.72	0.54
1:A:131:LEU:HD12	1:A:166:VAL:HG11	1.89	0.54
2:B:227:VAL:HG12	2:B:298:LEU:HD13	1.90	0.54
3:E:12:GLY:HA2	3:F:156:MET:HE1	1.86	0.54
2:B:217:VAL:O	2:B:286:ASN:HA	2.07	0.54
2:B:413:SER:OG	2:B:415:TYR:HD1	1.90	0.54
1:C:358:LEU:CD2	5:C:3496:CFM:S4A	2.96	0.54
2:D:401:ARG:HB2	2:D:401:ARG:HH11	1.73	0.54
3:G:244:ALA:O	3:G:248:VAL:HG23	2.07	0.54
3:H:198:ALA:HB1	3:H:267:LEU:HD21	1.89	0.54
1:A:298:ASN:ND2	1:A:300:PHE:H	2.06	0.54
1:A:35:ASN:HD21	1:A:394:MET:HB2	1.73	0.54
1:A:81:ILE:HD13	1:A:134:LEU:CD2	2.37	0.54
2:B:118:MET:CE	2:B:127:GLY:HA3	2.37	0.54
2:B:146:MET:HA	2:B:179:PHE:CE2	2.41	0.54
2:D:375:PHE:HZ	2:D:469:ILE:HG22	1.72	0.54
3:E:195:LEU:HD21	3:E:268:LEU:CD2	2.38	0.54
3:E:165:SER:HB2	3:E:256:PRO:HB3	1.89	0.54
3:E:43:ASP:HB2	3:E:46:ARG:HH11	1.73	0.54
3:F:25:ALA:HB2	3:F:228:ILE:CD1	2.38	0.54
1:A:265:THR:HB	1:A:266:PRO:HD3	1.88	0.54
1:A:356:GLY:O	1:A:379:TYR:HD2	1.91	0.54
2:B:81:GLY:O	2:B:275:GLY:HA2	2.07	0.54
2:B:356:THR:HG22	1:C:471:CYS:SG	2.48	0.54
1:C:81:ILE:HD13	1:C:134:LEU:CD2	2.37	0.54
1:C:239:ARG:HG3	1:C:249:CYS:SG	2.48	0.54
2:D:91:GLY:N	2:D:116:ASP:OD1	2.34	0.54
2:D:188:SER:HB3	6:D:3498:CLF:S3B	2.48	0.54
2:D:314:PRO:HB2	2:D:316:LEU:HD13	1.88	0.54
2:D:473:ILE:HG21	2:D:479:LEU:HD22	1.90	0.54
3:H:187:ARG:NH2	3:H:195:LEU:HD22	2.23	0.54
1:A:230:ASN:HB2	1:A:235:ALA:HB3	1.87	0.54
2:B:81:GLY:HA2	2:B:257:PRO:HD3	1.90	0.54
1:C:430:ILE:HG23	2:D:269:PHE:CD1	2.43	0.54
2:D:124:VAL:HG11	3:G:58:MET:HE2	1.88	0.54
3:F:179:LEU:HB2	3:F:256:PRO:HG3	1.90	0.54
3:G:193:ASP:O	3:G:197:ILE:HG13	2.07	0.54
3:H:242:ALA:O	3:H:246:LYS:HG2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:SER:HB3	1:A:427:GLU:HG3	1.90	0.54
2:B:39:LYS:O	2:B:43:VAL:HG23	2.08	0.54
1:A:106:VAL:HG21	2:B:44:PHE:HB2	1.90	0.54
2:B:442:MET:HG3	2:B:464:VAL:HG12	1.90	0.54
1:C:240:ILE:HG23	1:C:241:LEU:N	2.23	0.54
2:D:161:ASP:O	2:D:165:PHE:HD1	1.86	0.54
2:D:236:ASN:HB3	2:D:485:LEU:HD22	1.89	0.54
3:F:166:LYS:O	3:F:169:VAL:HG12	2.07	0.54
3:H:23:VAL:HA	3:H:26:LEU:HB2	1.88	0.54
2:D:238:ARG:HD3	2:D:258:GLU:CG	2.36	0.53
2:D:39:LYS:HA	2:D:42:GLU:HB2	1.90	0.53
3:E:186:SER:N	3:E:211:VAL:O	2.26	0.53
3:F:25:ALA:O	3:F:28:GLU:HB3	2.08	0.53
3:F:15:LYS:N	9:F:6292:ATP:O1B	2.41	0.53
3:G:189:THR:HB	3:G:192:GLU:HG2	1.90	0.53
9:G:7292:ATP:C5'	3:H:156:MET:SD	2.89	0.53
1:A:298:ASN:C	1:A:298:ASN:HD22	2.11	0.53
2:B:418:ASN:ND2	2:B:418:ASN:O	2.41	0.53
1:C:458:ILE:HG22	1:C:462:ASP:OD2	2.08	0.53
1:C:70:VAL:CG2	1:C:71:VAL:N	2.71	0.53
3:E:57:ILE:CG1	3:E:75:VAL:HG11	2.38	0.53
3:F:207:MET:HE1	3:F:210:PHE:HB2	1.91	0.53
3:F:3:ARG:HG3	3:F:3:ARG:HH11	1.73	0.53
1:A:99:TYR:HE2	1:A:232:GLY:HA2	1.73	0.53
1:C:230:ASN:O	1:C:230:ASN:OD1	2.26	0.53
1:C:350:ARG:HD2	1:C:375:VAL:HG11	1.91	0.53
1:C:37:PRO:HD2	1:C:396:ASP:CG	2.29	0.53
1:C:57:MET:HB2	2:D:142:TYR:OH	2.09	0.53
3:F:186:SER:HB2	3:F:192:GLU:OE1	2.07	0.53
1:A:224:ALA:HB1	1:A:251:ALA:HB3	1.90	0.53
1:C:417:LYS:N	1:C:418:PRO:CD	2.72	0.53
1:C:60:ARG:HD3	1:C:190:SER:HB3	1.89	0.53
2:D:91:GLY:O	2:D:116:ASP:O	2.27	0.53
3:G:95:VAL:HG12	3:G:95:VAL:O	2.09	0.53
1:A:299:PHE:CD2	1:A:305:THR:HG23	2.43	0.53
1:A:35:ASN:ND2	1:A:394:MET:HB2	2.23	0.53
2:B:394:LEU:HD23	2:B:394:LEU:C	2.28	0.53
1:C:186:PHE:HE1	3:G:100:ARG:NH2	2.02	0.53
1:C:30:LYS:NZ	1:C:47:ILE:CD1	2.71	0.53
1:C:62:CYS:SG	1:C:64:TYR:HB3	2.49	0.53
2:D:369:LEU:CD2	2:D:393:ILE:HA	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:131:VAL:CG2	3:G:132:CYS:N	2.71	0.53
1:A:15:GLU:O	1:A:18:GLU:HB2	2.09	0.53
1:A:59:ILE:HD13	1:A:427:GLU:OE2	2.09	0.53
2:B:241:LYS:O	2:B:245:SER:HB2	2.08	0.53
1:C:14:GLN:O	1:C:18:GLU:HG3	2.08	0.53
1:C:306:ILE:HD11	1:C:335:TRP:NE1	2.23	0.53
2:D:156:GLU:HG3	2:D:187:PRO:HA	1.91	0.53
2:D:375:PHE:CZ	2:D:469:ILE:HG22	2.42	0.53
3:G:255:ILE:HG22	3:G:255:ILE:O	2.07	0.53
3:H:138:PRO:O	3:H:143:LYS:HB2	2.08	0.53
1:C:271:ASN:OD1	1:C:286:MET:HE2	2.09	0.53
1:C:90:GLN:HG3	1:C:90:GLN:O	2.09	0.53
3:E:35:ILE:CD1	3:E:48:ILE:CD1	2.79	0.53
3:F:259:ILE:HD12	3:F:264:LEU:HD23	1.89	0.53
3:F:39:ASP:OD1	3:F:40:PRO:N	2.42	0.53
1:A:124:VAL:HG21	3:F:58:MET:HE1	1.91	0.53
2:B:129:GLN:CA	2:B:129:GLN:HE21	2.22	0.53
1:C:99:TYR:HE2	1:C:232:GLY:HA2	1.74	0.53
1:C:277:ARG:NE	1:C:277:ARG:HA	2.23	0.53
1:C:302:PRO:HD3	1:C:456:PHE:CD1	2.44	0.53
2:D:139:LYS:HG3	2:D:179:PHE:CE1	2.43	0.53
2:D:322:LEU:HD11	2:D:348:ARG:HH21	1.73	0.53
3:E:61:ALA:N	3:E:70:LEU:HD11	2.24	0.53
1:C:57:MET:HE3	2:D:100:ARG:CZ	2.38	0.53
2:D:451:ILE:O	2:D:455:THR:HG23	2.09	0.53
2:D:76:VAL:HG13	2:D:87:PRO:HB3	1.90	0.53
3:G:237:ALA:O	3:G:241:ARG:HG3	2.09	0.53
3:H:61:ALA:HB1	3:H:67:VAL:HA	1.91	0.53
1:A:354:TYR:CZ	1:A:404:VAL:HG12	2.44	0.53
2:B:351:LEU:O	2:B:355:MET:HG3	2.09	0.53
2:B:38:ASP:O	2:B:42:GLU:HG3	2.08	0.53
1:C:200:ASP:O	1:C:203:ARG:HG3	2.09	0.53
1:C:298:ASN:ND2	1:C:300:PHE:H	2.07	0.53
1:C:382:ALA:HB1	1:C:386:ASP:HB2	1.90	0.53
1:C:428:LYS:HD2	1:C:440:GLU:HG3	1.91	0.53
2:D:289:ASN:HD21	2:D:314:PRO:HD3	1.74	0.53
3:H:217:VAL:HG11	9:H:8292:ATP:C8	2.44	0.53
1:A:355:ILE:HD13	1:A:359:ARG:HB2	1.91	0.52
1:A:424:GLY:HA2	1:A:442:HIS:HD2	1.73	0.52
3:G:33:VAL:HG22	3:G:121:PHE:HB2	1.91	0.52
3:H:137:MET:CB	3:H:138:PRO:CD	2.87	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:428:LYS:HD2	1:C:440:GLU:CG	2.39	0.52
2:D:81:GLY:O	2:D:275:GLY:HA2	2.08	0.52
2:D:43:VAL:O	2:D:47:THR:HG23	2.10	0.52
2:D:516:ASP:O	2:D:519:HIS:HB2	2.09	0.52
3:E:4:GLN:CD	3:E:143:LYS:O	2.48	0.52
3:G:4:GLN:NE2	3:G:124:TYR:OH	2.41	0.52
3:H:217:VAL:HG11	9:H:8292:ATP:N7	2.24	0.52
1:A:413:VAL:HG21	1:A:431:PHE:CE2	2.44	0.52
2:B:219:GLY:N	2:B:287:ALA:O	2.42	0.52
1:C:13:ILE:O	1:C:17:LEU:HG	2.08	0.52
1:C:224:ALA:HB1	1:C:251:ALA:HB3	1.91	0.52
2:D:184:ALA:O	2:D:186:THR:HG23	2.10	0.52
1:C:144:LEU:HG	2:D:43:VAL:HG21	1.90	0.52
1:C:138:VAL:CG1	2:D:62:LEU:HD13	2.34	0.52
3:F:64:ALA:HB1	3:F:69:ASP:HB3	1.90	0.52
3:G:64:ALA:HB1	3:G:69:ASP:HB3	1.90	0.52
1:A:387:TYR:OH	1:A:402:ASP:HB2	2.10	0.52
1:A:67:SER:OG	1:A:183:CYS:HB3	2.10	0.52
2:B:510:ARG:HG2	2:B:510:ARG:O	2.08	0.52
1:C:207:LEU:HD11	1:C:266:PRO:CD	2.40	0.52
1:C:440:GLU:HB2	1:C:445:ASP:CB	2.39	0.52
2:B:116:ASP:OD1	2:B:116:ASP:N	2.29	0.52
2:B:57:PHE:CE2	2:B:425:LYS:NZ	2.77	0.52
1:C:216:PHE:CE1	1:C:264:LEU:HD13	2.45	0.52
1:C:58:THR:HG21	1:C:60:ARG:HB2	1.90	0.52
2:D:68:LYS:HG2	2:D:396:HIS:CD2	2.39	0.52
3:E:10:LYS:HZ3	3:E:156:MET:HG3	1.75	0.52
3:F:87:GLU:HA	3:F:87:GLU:OE2	2.10	0.52
3:H:154:GLU:O	3:H:158:MET:HG3	2.10	0.52
1:A:355:ILE:HG21	1:A:360:PRO:HD2	1.87	0.52
2:B:448:GLY:C	2:B:466:LEU:HD22	2.30	0.52
2:B:340:ILE:HD12	1:C:479:TRP:CD2	2.44	0.52
2:D:510:ARG:HB2	2:D:519:HIS:NE2	2.24	0.52
3:E:10:LYS:H	3:E:13:ILE:HD11	1.74	0.52
3:E:33:VAL:HG22	3:E:121:PHE:HB2	1.91	0.52
3:F:195:LEU:HD12	3:F:267:LEU:HD22	1.91	0.52
1:A:382:ALA:HB1	1:A:386:ASP:CB	2.40	0.52
2:B:59:ARG:NH2	2:B:429:HIS:HE1	2.07	0.52
3:E:131:VAL:CG2	3:E:132:CYS:N	2.71	0.52
3:F:106:ILE:HD13	3:F:138:PRO:HD3	1.86	0.52
3:F:186:SER:HA	3:F:192:GLU:CD	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:151:THR:HG23	2:B:186:THR:H	1.74	0.52
2:B:452:GLN:CD	2:D:510:ARG:NH1	2.63	0.52
2:B:451:ILE:O	2:B:455:THR:HG23	2.09	0.52
3:E:61:ALA:HB2	3:E:70:LEU:CD1	2.35	0.52
3:H:212:PRO:HG2	3:H:239:GLU:OE2	2.09	0.52
2:B:442:MET:HG3	2:B:464:VAL:CG1	2.39	0.52
2:D:391:VAL:HG12	2:D:392:HIS:CE1	2.45	0.52
2:D:397:ASN:ND2	2:D:397:ASN:N	2.45	0.52
2:D:88:TYR:CB	2:D:147:ILE:HG22	2.40	0.52
1:A:72:TRP:CZ2	1:A:202:VAL:HG22	2.45	0.52
1:C:159:ILE:CD1	3:H:97:CYS:HB2	2.39	0.52
1:C:424:GLY:HA2	1:C:442:HIS:HD2	1.75	0.52
2:D:241:LYS:O	2:D:245:SER:HB2	2.10	0.52
2:D:302:LYS:O	2:D:306:GLU:HG3	2.10	0.52
1:A:136:ASP:OD1	1:A:170:LYS:NZ	2.28	0.51
1:C:421:ILE:HD11	1:C:436:ILE:CG2	2.38	0.51
3:F:106:ILE:HD12	3:F:137:MET:HG2	1.93	0.51
3:F:57:ILE:CG1	3:F:75:VAL:HG11	2.40	0.51
3:G:185:ASN:HA	3:G:211:VAL:HB	1.92	0.51
1:A:131:LEU:HD11	1:A:135:ILE:HD11	1.93	0.51
1:A:355:ILE:CD1	1:A:359:ARG:HB2	2.40	0.51
2:B:391:VAL:HG12	2:B:392:HIS:CE1	2.45	0.51
1:C:40:THR:O	1:C:40:THR:CG2	2.57	0.51
2:D:197:TRP:HZ2	2:D:255:SER:HG	1.55	0.51
3:G:223:ARG:HG2	3:G:223:ARG:O	2.11	0.51
1:A:299:PHE:HB3	1:A:452:GLY:H	1.75	0.51
1:A:55:GLY:HA2	2:B:114:VAL:HB	1.92	0.51
1:C:385:ASP:OD2	1:C:385:ASP:C	2.48	0.51
2:D:317:ASN:ND2	2:D:317:ASN:N	2.57	0.51
1:C:250:VAL:HG13	2:D:31:PHE:CD2	2.45	0.51
2:D:247:MET:HE3	2:D:340:ILE:HA	1.91	0.51
2:D:456:LEU:HD11	2:D:460:LYS:HD2	1.92	0.51
3:E:45:THR:CG2	3:E:85:CYS:HB3	2.40	0.51
1:A:116:SER:HA	1:A:134:LEU:CD1	2.40	0.51
2:B:156:GLU:HG3	2:B:187:PRO:HA	1.93	0.51
2:B:82:PHE:CZ	2:B:255:SER:HB2	2.46	0.51
1:C:385:ASP:OD2	1:C:386:ASP:OD1	2.29	0.51
2:D:309:TRP:O	2:D:310:LYS:HB2	2.10	0.51
2:D:293:LEU:HD22	2:D:319:PRO:HG2	1.91	0.51
2:B:512:MET:HE1	2:D:44:PHE:HE1	1.76	0.51
2:B:512:MET:HE2	2:D:457:HIS:CG	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:148:TYR:CE2	3:G:208:ILE:HD12	2.45	0.51
2:B:118:MET:HE3	2:B:160:ASP:OD2	2.11	0.51
2:B:289:ASN:ND2	2:B:314:PRO:CD	2.71	0.51
2:B:434:VAL:HA	2:B:439:PRO:HD2	1.92	0.51
1:C:35:ASN:ND2	1:C:395:GLY:O	2.44	0.51
1:C:72:TRP:O	1:C:73:GLY:C	2.49	0.51
2:D:351:LEU:O	2:D:355:MET:HG3	2.09	0.51
2:B:76:VAL:HG13	2:B:87:PRO:HB3	1.92	0.51
1:C:116:SER:HA	1:C:134:LEU:CD1	2.41	0.51
1:C:221:TYR:O	1:C:223:VAL:HG13	2.10	0.51
1:C:42:SER:O	1:C:46:ILE:O	2.28	0.51
1:C:449:PRO:CG	2:D:15:PHE:HZ	2.18	0.51
2:D:509:THR:HG21	2:D:518:ASN:HD22	1.76	0.51
3:G:160:ALA:HA	3:G:163:ASN:HB3	1.93	0.51
1:A:337:ALA:HB1	2:B:5:VAL:HG21	1.93	0.51
1:C:275:CYS:SG	1:C:278:SER:HB2	2.51	0.51
1:C:364:ILE:O	1:C:367:TYR:HB2	2.11	0.51
2:D:206:ARG:HG2	2:D:304:PHE:CZ	2.45	0.51
2:D:263:THR:OG1	2:D:270:ARG:HD2	2.11	0.51
3:F:186:SER:HB3	3:F:210:PHE:HZ	1.65	0.51
3:G:208:ILE:O	3:G:246:LYS:HD3	2.11	0.51
2:B:445:ASN:OD1	2:B:447:TYR:HB2	2.11	0.51
3:E:217:VAL:HG22	3:E:227:VAL:HG21	1.93	0.51
3:E:206:GLN:NE2	3:E:250:ASN:OD1	2.44	0.51
3:E:73:GLU:OE1	3:E:73:GLU:N	2.44	0.51
3:H:40:PRO:HG3	3:H:98:ALA:HB1	1.93	0.51
1:A:53:GLN:HB2	1:A:56:LEU:HD12	1.91	0.51
2:B:181:VAL:N	2:B:182:PRO:HD3	2.26	0.51
2:B:422:TYR:HB3	2:B:425:LYS:HD2	1.91	0.51
1:C:277:ARG:HE	1:C:277:ARG:HA	1.76	0.51
3:F:10:LYS:O	3:F:13:ILE:HG12	2.11	0.51
3:G:98:ALA:O	3:G:102:VAL:HG23	2.10	0.51
1:A:16:VAL:HG11	1:A:408:GLU:HA	1.92	0.51
1:A:280:ASN:N	1:A:280:ASN:ND2	2.58	0.51
1:A:355:ILE:HG22	1:A:360:PRO:HG2	1.92	0.51
1:A:277:ARG:NE	1:A:383:HIS:HE2	2.08	0.51
1:C:134:LEU:HG	2:D:62:LEU:HB2	1.92	0.51
1:C:200:ASP:HA	1:C:203:ARG:HG2	1.92	0.51
1:C:258:SER:HB2	1:C:261:GLU:HB2	1.93	0.51
2:D:125:PHE:HA	3:G:91:PRO:HB3	1.93	0.51
2:B:523:ARG:CG	2:D:475:ASP:HA	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:10:LYS:H	3:E:13:ILE:HD13	1.75	0.51
3:F:236:GLN:HG2	3:F:240:TYR:CE2	2.45	0.51
3:F:16:SER:OG	9:F:6292:ATP:O2A	2.29	0.51
3:H:72:LEU:HD11	3:H:76:LEU:CD1	2.41	0.51
1:A:355:ILE:HG23	5:A:1496:CFM:S3A	2.51	0.50
1:A:234:ASP:HB3	1:A:451:HIS:ND1	2.26	0.50
2:B:118:MET:HE2	2:B:127:GLY:HA3	1.93	0.50
2:B:88:TYR:HB2	2:B:147:ILE:HG23	1.92	0.50
1:C:351:VAL:HG12	1:C:374:VAL:HG22	1.94	0.50
3:E:52:LYS:O	3:E:53:ALA:CB	2.60	0.50
3:H:131:VAL:HG22	3:H:132:CYS:SG	2.51	0.50
3:H:49:LEU:O	3:H:50:HIS:CB	2.57	0.50
1:A:141:LEU:CD2	2:B:59:ARG:HD2	2.41	0.50
1:A:361:ARG:HB3	1:A:379:TYR:OH	2.12	0.50
2:B:222:LYS:HD3	2:B:288:LEU:HD21	1.93	0.50
2:B:390:PRO:O	2:B:419:ALA:HB1	2.11	0.50
1:C:230:ASN:HB2	1:C:235:ALA:HB2	1.92	0.50
1:C:241:LEU:HD21	1:C:453:PHE:HD1	1.75	0.50
1:C:266:PRO:O	1:C:292:ILE:HD11	2.11	0.50
1:C:34:VAL:HG13	1:C:397:SER:HA	1.94	0.50
1:C:471:CYS:SG	1:C:472:TRP:N	2.83	0.50
1:C:239:ARG:HB3	2:D:23:MET:HE1	1.94	0.50
3:F:52:LYS:O	3:F:53:ALA:HB2	2.11	0.50
3:H:107:ASN:O	3:H:111:GLU:HB2	2.10	0.50
3:H:207:MET:CE	3:H:210:PHE:HB2	2.41	0.50
1:A:151:GLN:CD	1:A:181:VAL:HG11	2.32	0.50
1:A:332:LYS:HA	1:A:335:TRP:NE1	2.26	0.50
2:B:118:MET:HB3	2:B:154:MET:CE	2.41	0.50
2:B:369:LEU:HD21	2:B:393:ILE:HG12	1.93	0.50
2:B:70:CYS:CB	2:B:188:SER:HB3	2.41	0.50
1:C:405:THR:H	1:C:408:GLU:HG3	1.76	0.50
2:D:146:MET:HA	2:D:179:PHE:CE2	2.45	0.50
2:D:146:MET:HE3	2:D:208:PHE:CZ	2.46	0.50
3:G:115:TYR:C	3:G:117:ASP:N	2.64	0.50
3:G:96:GLY:O	3:H:132:CYS:HB2	2.12	0.50
3:H:179:LEU:HB2	3:H:256:PRO:HG3	1.94	0.50
1:A:46:ILE:HG12	1:A:47:ILE:N	2.25	0.50
2:B:284:ALA:HB3	2:B:285:PRO:CD	2.41	0.50
2:B:206:ARG:CG	2:B:304:PHE:CZ	2.88	0.50
1:A:144:LEU:HD22	2:B:35:TYR:CD1	2.46	0.50
2:B:95:CYS:HB3	2:B:99:PHE:CZ	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:ILE:HG23	1:C:279:MET:HG2	1.93	0.50
1:C:343:ARG:HG3	1:C:370:LEU:O	2.11	0.50
1:C:429:PHE:CZ	2:D:108:ARG:HA	2.46	0.50
1:C:186:PHE:HB3	2:D:154:MET:HE2	1.93	0.50
2:D:146:MET:HE3	2:D:208:PHE:HZ	1.76	0.50
3:H:73:GLU:N	3:H:73:GLU:OE1	2.44	0.50
2:B:422:TYR:HD2	2:B:425:LYS:CD	2.23	0.50
1:C:106:VAL:HG21	2:D:44:PHE:HB2	1.93	0.50
1:C:277:ARG:NH1	1:C:383:HIS:CG	2.79	0.50
2:D:91:GLY:N	2:D:118:MET:HE2	2.25	0.50
2:D:234:LEU:O	2:D:238:ARG:HG2	2.12	0.50
2:D:254:LEU:HD13	2:D:281:MET:HE1	1.93	0.50
2:D:254:LEU:HB3	2:D:281:MET:HE2	1.94	0.50
3:F:165:SER:HA	3:F:168:ILE:HD12	1.91	0.50
3:G:264:LEU:O	3:G:267:LEU:HB2	2.11	0.50
3:G:52:LYS:O	3:G:53:ALA:HB2	2.12	0.50
2:B:522:VAL:HG23	1:C:446:TYR:CE2	2.46	0.50
1:C:164:GLU:HA	1:C:180:PRO:HB3	1.93	0.50
2:D:39:LYS:O	2:D:43:VAL:HG23	2.12	0.50
3:E:148:TYR:CD2	3:E:208:ILE:HD12	2.46	0.50
3:G:225:MET:CE	3:G:230:TYR:HA	2.41	0.50
3:H:54:GLN:HG3	3:H:55:ASN:N	2.21	0.50
1:A:430:ILE:HG12	2:B:269:PHE:CE1	2.47	0.50
1:A:57:MET:HE3	2:B:100:ARG:CZ	2.42	0.50
1:A:57:MET:CG	2:B:142:TYR:CZ	2.94	0.50
1:C:151:GLN:HA	1:C:181:VAL:HG13	1.93	0.50
3:E:4:GLN:HB3	3:E:122:VAL:HB	1.94	0.50
3:G:100:ARG:HD2	3:G:100:ARG:O	2.10	0.50
3:G:137:MET:CB	3:G:138:PRO:HD3	2.42	0.50
1:A:230:ASN:HB2	1:A:235:ALA:HB2	1.92	0.50
1:A:359:ARG:HB2	1:A:360:PRO:HD3	1.93	0.50
1:C:342:TYR:O	1:C:343:ARG:C	2.50	0.50
3:F:201:ASN:C	3:F:203:LEU:H	2.15	0.50
1:A:354:TYR:CE1	1:A:404:VAL:HG12	2.46	0.50
1:C:231:ILE:O	1:C:234:ASP:OD2	2.30	0.50
2:D:180:PRO:HG2	2:D:278:GLN:OE1	2.12	0.50
2:D:382:PHE:HD1	2:D:385:GLU:OE2	1.95	0.50
2:D:445:ASN:OD1	2:D:447:TYR:HB2	2.12	0.50
3:F:131:VAL:HG22	3:F:132:CYS:SG	2.51	0.50
3:F:231:ASP:OD2	3:F:234:ALA:HB2	2.11	0.50
3:H:103:ILE:HG12	3:H:137:MET:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:141:GLU:HA	3:H:141:GLU:OE1	2.12	0.50
1:A:385:ASP:O	1:A:388:ASP:CG	2.51	0.49
2:B:326:ASP:HB3	1:C:479:TRP:CZ3	2.43	0.49
2:B:326:ASP:OD2	2:B:348:ARG:NE	2.43	0.49
1:C:349:LYS:O	1:C:372:MET:HA	2.12	0.49
2:D:510:ARG:O	2:D:510:ARG:CG	2.60	0.49
1:A:151:GLN:HA	1:A:181:VAL:CG1	2.42	0.49
1:A:62:CYS:O	1:A:191:GLN:HA	2.12	0.49
1:A:351:VAL:CG1	1:A:374:VAL:HG22	2.42	0.49
1:A:40:THR:O	1:A:40:THR:HG22	2.13	0.49
1:C:107:ASN:O	1:C:107:ASN:ND2	2.45	0.49
1:C:138:VAL:HG23	1:C:139:GLU:H	1.77	0.49
3:G:55:ASN:HB3	3:G:60:MET:SD	2.52	0.49
3:H:161:ALA:O	3:H:165:SER:OG	2.30	0.49
1:A:106:VAL:HG12	1:A:144:LEU:HD12	1.94	0.49
1:A:221:TYR:CE2	1:A:320:ILE:HD11	2.47	0.49
2:B:236:ASN:HB3	2:B:485:LEU:HD22	1.93	0.49
2:B:53:GLN:OE1	2:B:432:SER:HB3	2.12	0.49
1:C:37:PRO:HG2	1:C:396:ASP:HB2	1.93	0.49
3:G:43:ASP:HB2	3:G:46:ARG:HD3	1.93	0.49
1:A:298:ASN:C	1:A:298:ASN:ND2	2.65	0.49
2:B:156:GLU:CD	2:B:187:PRO:HG3	2.33	0.49
2:B:224:ILE:HD12	2:B:249:VAL:CG1	2.42	0.49
2:B:247:MET:HB3	2:B:249:VAL:HG23	1.93	0.49
2:D:251:TYR:CD1	2:D:251:TYR:C	2.85	0.49
2:D:495:THR:HG22	2:D:499:ASN:ND2	2.27	0.49
3:E:141:GLU:OE1	3:E:141:GLU:HA	2.13	0.49
3:G:34:MET:HB2	3:G:119:LEU:HD11	1.92	0.49
1:A:35:ASN:ND2	1:A:395:GLY:O	2.46	0.49
2:B:59:ARG:CZ	2:B:429:HIS:CE1	2.96	0.49
2:B:43:VAL:O	2:B:47:THR:HG23	2.12	0.49
1:C:125:PHE:O	1:C:126:GLY:O	2.30	0.49
2:D:93:GLN:HB3	2:D:117:SER:OG	2.13	0.49
1:C:236:TRP:HA	2:D:23:MET:HE1	1.95	0.49
2:D:403:LYS:HZ2	2:D:421:VAL:HB	1.77	0.49
3:F:72:LEU:HD11	3:F:76:LEU:CD1	2.42	0.49
3:G:102:VAL:O	3:G:106:ILE:HG13	2.13	0.49
1:A:83:HIS:O	1:A:153:GLU:HG3	2.12	0.49
1:A:203:ARG:HA	1:A:207:LEU:HB3	1.93	0.49
1:A:196:HIS:HA	1:A:281:TYR:CD1	2.47	0.49
1:A:359:ARG:HG2	5:A:1496:CFM:S3A	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:THR:H	1:A:408:GLU:HG3	1.77	0.49
2:B:222:LYS:HA	2:B:288:LEU:HD21	1.95	0.49
1:C:280:ASN:N	1:C:280:ASN:ND2	2.59	0.49
3:F:195:LEU:HD21	3:F:268:LEU:CD2	2.40	0.49
3:G:192:GLU:HB3	3:G:210:PHE:CE2	2.44	0.49
1:C:272:LEU:HD13	1:C:312:ILE:HD13	1.93	0.49
2:D:19:ASP:OD2	2:D:20:TYR:N	2.45	0.49
3:E:10:LYS:O	3:E:11:GLY:C	2.49	0.49
3:E:180:GLY:HA2	3:E:253:LEU:HD23	1.93	0.49
3:G:110:GLU:OE2	3:G:143:LYS:NZ	2.45	0.49
2:B:249:VAL:HG13	2:B:336:SER:HB2	1.94	0.49
1:C:399:LEU:HD21	1:C:412:PHE:CD2	2.47	0.49
3:G:50:HIS:NE2	3:G:229:GLU:OE2	2.40	0.49
1:A:203:ARG:HG3	1:A:204:ASP:OD2	2.12	0.49
1:A:210:ARG:HG3	1:A:263:GLU:HB3	1.95	0.49
2:B:206:ARG:HH11	2:B:210:LEU:HD22	1.78	0.49
2:B:296:TRP:CZ3	2:B:402:TRP:HA	2.47	0.49
1:C:144:LEU:HD21	2:D:43:VAL:HG21	1.94	0.49
1:C:196:HIS:HA	1:C:281:TYR:CD1	2.47	0.49
1:C:280:ASN:O	1:C:284:ARG:HG3	2.13	0.49
2:B:125:PHE:HE2	3:E:62:ALA:HB2	1.78	0.49
1:A:399:LEU:HD21	1:A:412:PHE:CD2	2.47	0.49
2:B:39:LYS:HA	2:B:42:GLU:HB2	1.95	0.49
1:C:76:LYS:HD3	1:C:256:ASP:OD2	2.13	0.49
1:C:342:TYR:OH	2:D:8:ILE:HD11	2.12	0.49
1:C:41:GLN:HG3	1:C:43:LYS:H	1.76	0.49
2:D:197:TRP:CZ3	2:D:229:GLY:HA2	2.48	0.49
2:D:64:VAL:HB	2:D:428:TRP:CB	2.43	0.49
2:D:44:PHE:CD2	2:D:44:PHE:C	2.86	0.49
1:A:138:VAL:HG23	1:A:139:GLU:N	2.27	0.48
2:B:107:PHE:CZ	2:B:232:THR:HB	2.48	0.48
2:B:133:ASP:O	2:B:136:GLN:N	2.46	0.48
2:B:227:VAL:CG1	2:B:298:LEU:HD13	2.43	0.48
1:C:342:TYR:HA	1:C:345:ARG:HD2	1.94	0.48
2:D:254:LEU:O	2:D:255:SER:CB	2.61	0.48
3:E:264:LEU:O	3:E:267:LEU:HB2	2.13	0.48
3:E:43:ASP:HB2	3:E:46:ARG:HD3	1.93	0.48
3:F:186:SER:C	3:F:188:ASN:H	2.17	0.48
3:F:61:ALA:HB1	3:F:67:VAL:HA	1.95	0.48
3:G:39:ASP:OD1	3:G:40:PRO:HD2	2.13	0.48
3:H:231:ASP:OD2	3:H:234:ALA:CB	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:ASN:HD22	1:A:299:PHE:N	2.10	0.48
1:A:349:LYS:O	1:A:372:MET:HA	2.13	0.48
1:A:449:PRO:CG	2:B:15:PHE:HZ	2.25	0.48
2:B:161:ASP:O	2:B:165:PHE:HD1	1.89	0.48
2:B:241:LYS:NZ	2:B:256:ASP:OD2	2.45	0.48
1:C:167:SER:HB3	1:C:180:PRO:HD3	1.95	0.48
1:C:98:ASN:HD22	1:C:98:ASN:N	2.09	0.48
2:D:146:MET:CE	2:D:208:PHE:HE1	2.26	0.48
2:D:495:THR:HG22	2:D:499:ASN:HD22	1.78	0.48
3:E:38:CYS:HB3	3:E:102:VAL:HG13	1.95	0.48
3:F:255:ILE:HG22	3:F:255:ILE:O	2.12	0.48
3:G:2:MET:HB2	3:G:119:LEU:O	2.13	0.48
1:A:110:VAL:C	1:A:112:MET:H	2.15	0.48
2:B:422:TYR:OH	2:B:433:LEU:HD11	2.13	0.48
2:D:12:TYR:O	2:D:12:TYR:CD2	2.66	0.48
2:D:199:ASN:HD22	2:D:199:ASN:N	2.10	0.48
1:A:58:THR:HG22	1:A:59:ILE:N	2.28	0.48
2:B:278:GLN:HG2	2:B:278:GLN:H	1.50	0.48
1:C:66:GLY:HA2	1:C:70:VAL:HG13	1.95	0.48
3:G:115:TYR:O	3:G:117:ASP:N	2.38	0.48
3:H:23:VAL:HG21	3:H:35:ILE:CD1	2.28	0.48
1:A:167:SER:HB3	1:A:178:ILE:HG22	1.94	0.48
1:A:416:ILE:C	1:A:418:PRO:HD3	2.34	0.48
2:B:186:THR:N	2:B:187:PRO:HD3	2.29	0.48
1:C:251:ALA:HA	1:C:261:GLU:CG	2.41	0.48
1:C:430:ILE:HG12	2:D:269:PHE:HE1	1.75	0.48
3:H:165:SER:HA	3:H:168:ILE:HD12	1.96	0.48
1:C:245:MET:CE	1:C:309:LEU:HD22	2.43	0.48
3:G:224:ARG:C	3:G:225:MET:CG	2.82	0.48
1:A:68:LYS:C	1:A:68:LYS:HD3	2.34	0.48
1:A:72:TRP:O	1:A:73:GLY:C	2.51	0.48
2:B:471:PHE:CE2	2:B:472:PRO:HD3	2.41	0.48
2:D:238:ARG:NH1	2:D:262:ASP:OD2	2.46	0.48
3:E:156:MET:HG2	3:E:157:ALA:N	2.29	0.48
2:B:388:CYS:O	2:B:390:PRO:HD3	2.14	0.48
2:B:44:PHE:CD2	2:B:44:PHE:C	2.86	0.48
1:C:389:ARG:NH1	1:C:389:ARG:HG3	2.11	0.48
2:D:479:LEU:N	2:D:479:LEU:HD12	2.28	0.48
3:G:14:GLY:HA3	3:G:185:ASN:ND2	2.29	0.48
1:A:219:THR:C	1:A:221:TYR:H	2.17	0.48
1:A:324:CYS:SG	1:A:328:ILE:HD11	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:VAL:HG23	1:A:420:LEU:HB3	1.95	0.48
1:A:373:GLU:HG3	1:A:373:GLU:O	2.12	0.48
1:A:81:ILE:HD12	1:A:148:ILE:HG21	1.95	0.48
2:B:192:SER:OG	2:B:194:VAL:HG22	2.14	0.48
2:B:247:MET:HA	2:B:341:PRO:HG3	1.96	0.48
2:B:362:LEU:HD11	2:B:498:VAL:CG2	2.42	0.48
2:B:81:GLY:HA3	2:B:257:PRO:HD3	1.96	0.48
1:C:125:PHE:C	1:C:126:GLY:O	2.49	0.48
2:D:20:TYR:O	2:D:24:LEU:HG	2.13	0.48
3:E:160:ALA:HA	3:E:163:ASN:HB3	1.96	0.48
3:E:72:LEU:HD11	3:E:76:LEU:CD1	2.44	0.48
1:A:119:GLN:HA	1:A:119:GLN:OE1	2.12	0.48
2:B:247:MET:CE	2:B:340:ILE:HA	2.44	0.48
2:B:475:ASP:HA	2:D:523:ARG:HG3	1.95	0.48
1:C:355:ILE:HG21	1:C:359:ARG:HB2	1.96	0.48
2:D:146:MET:HG2	2:D:180:PRO:O	2.13	0.48
3:G:72:LEU:HD11	3:G:76:LEU:CD1	2.43	0.48
3:H:151:CYS:SG	3:H:196:ILE:HD12	2.54	0.48
2:B:181:VAL:O	2:B:181:VAL:HG12	2.12	0.47
2:B:108:ARG:NH2	2:B:477:HIS:CD2	2.82	0.47
1:C:428:LYS:O	1:C:432:GLN:HG3	2.14	0.47
1:C:457:ALA:CB	2:D:3:GLN:HG2	2.44	0.47
3:F:16:SER:O	3:F:20:GLN:HG3	2.13	0.47
3:G:132:CYS:HB2	3:H:96:GLY:O	2.14	0.47
1:A:240:ILE:HG23	1:A:241:LEU:N	2.29	0.47
1:A:280:ASN:H	1:A:280:ASN:ND2	2.10	0.47
2:B:86:MET:HG2	2:B:138:CYS:SG	2.55	0.47
1:C:138:VAL:O	1:C:142:PHE:N	2.42	0.47
1:C:337:ALA:HB1	2:D:5:VAL:HG21	1.96	0.47
2:D:238:ARG:HG3	2:D:238:ARG:HH21	1.78	0.47
2:D:89:VAL:HG22	2:D:150:SER:HB2	1.96	0.47
3:E:22:LEU:O	3:E:22:LEU:HD23	2.14	0.47
3:F:201:ASN:C	3:F:203:LEU:N	2.66	0.47
3:F:213:ARG:HG2	9:F:6292:ATP:C2	2.49	0.47
3:H:56:THR:CG2	3:H:59:GLU:HB2	2.28	0.47
1:A:301:GLY:HA2	1:A:456:PHE:CD1	2.48	0.47
2:B:254:LEU:O	2:B:255:SER:HB3	2.14	0.47
2:B:180:PRO:HG2	2:B:278:GLN:OE1	2.14	0.47
2:B:475:ASP:HA	2:D:523:ARG:CG	2.44	0.47
1:C:142:PHE:O	1:C:145:ASN:ND2	2.47	0.47
1:C:277:ARG:HD2	1:C:386:ASP:OD2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:192:SER:OG	2:D:194:VAL:HG22	2.14	0.47
2:D:379:LEU:HD21	2:D:443:ILE:HG21	1.95	0.47
3:E:106:ILE:HD12	3:E:137:MET:HB3	1.95	0.47
3:E:207:MET:HE3	3:E:210:PHE:HB2	1.94	0.47
3:H:179:LEU:HD23	3:H:181:GLY:H	1.79	0.47
1:A:355:ILE:CG2	5:A:1496:CFM:S3A	3.02	0.47
1:A:16:VAL:HG21	1:A:412:PHE:CE1	2.48	0.47
1:A:449:PRO:O	1:A:455:GLY:HA2	2.13	0.47
2:B:139:LYS:CG	2:B:179:PHE:CE1	2.97	0.47
2:B:85:THR:CG2	2:B:146:MET:CE	2.91	0.47
2:B:71:GLN:HG2	2:B:192:SER:O	2.15	0.47
2:B:318:ILE:O	2:B:318:ILE:HG23	2.15	0.47
1:C:219:THR:HG23	1:C:220:PRO:HD2	1.96	0.47
1:C:302:PRO:O	1:C:306:ILE:HG13	2.15	0.47
2:D:217:VAL:O	2:D:286:ASN:HA	2.14	0.47
2:D:247:MET:HB3	2:D:249:VAL:HG23	1.95	0.47
2:D:509:THR:HA	2:D:515:THR:HB	1.96	0.47
3:G:216:VAL:O	3:G:216:VAL:HG12	2.15	0.47
3:H:208:ILE:HG22	3:H:209:HIS:N	2.30	0.47
2:B:247:MET:HE2	2:B:339:PRO:O	2.13	0.47
1:C:361:ARG:HB3	1:C:379:TYR:OH	2.13	0.47
1:C:20:TYR:HH	1:C:408:GLU:HG2	1.73	0.47
3:E:10:LYS:NZ	3:E:156:MET:HG3	2.29	0.47
3:E:236:GLN:O	3:E:236:GLN:CG	2.62	0.47
3:H:179:LEU:HD12	3:H:256:PRO:HG3	1.96	0.47
1:A:118:PHE:CZ	1:A:156:ILE:HD11	2.49	0.47
1:A:298:ASN:CG	1:A:362:HIS:CD2	2.88	0.47
1:A:399:LEU:HD23	1:A:416:ILE:HD11	1.97	0.47
1:A:427:GLU:HB2	1:A:431:PHE:HE1	1.78	0.47
1:A:424:GLY:CA	1:A:442:HIS:HD2	2.27	0.47
2:B:382:PHE:HD1	2:B:385:GLU:OE2	1.98	0.47
2:B:392:HIS:CG	2:B:433:LEU:HD12	2.49	0.47
1:C:203:ARG:HG3	1:C:204:ASP:OD2	2.15	0.47
2:D:369:LEU:HD23	2:D:369:LEU:O	2.14	0.47
2:B:522:VAL:HB	2:D:474:PHE:HB3	1.96	0.47
2:D:494:LEU:HD23	2:D:494:LEU:C	2.35	0.47
2:D:509:THR:O	2:D:516:ASP:HA	2.15	0.47
3:F:3:ARG:NH2	3:F:146:GLU:OE1	2.43	0.47
3:G:34:MET:HB2	3:G:119:LEU:HD13	1.96	0.47
1:A:144:LEU:HG	2:B:43:VAL:HG21	1.96	0.47
1:A:210:ARG:HH11	1:A:264:LEU:CD2	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:MET:CE	1:A:418:PRO:HG2	2.45	0.47
1:A:42:SER:C	1:A:44:LYS:N	2.65	0.47
1:A:57:MET:SD	2:B:113:CYS:O	2.73	0.47
1:A:58:THR:CG2	1:A:60:ARG:H	2.20	0.47
2:B:512:MET:CB	2:D:457:HIS:CD2	2.92	0.47
2:B:512:MET:HE2	2:D:457:HIS:HB2	1.94	0.47
1:C:354:TYR:CZ	1:C:404:VAL:HG12	2.50	0.47
2:D:254:LEU:O	2:D:255:SER:HB3	2.14	0.47
3:F:26:LEU:CD1	3:F:244:ALA:HB1	2.43	0.47
3:G:137:MET:O	3:G:143:LYS:HG3	2.15	0.47
3:G:147:ILE:HD11	3:G:177:VAL:HG21	1.97	0.47
1:A:100:TYR:CD2	1:A:100:TYR:N	2.83	0.47
1:A:168:LYS:O	1:A:172:ALA:CB	2.61	0.47
2:B:367:PHE:CD2	2:B:443:ILE:HD11	2.49	0.47
2:B:71:GLN:O	2:B:196:GLY:HA3	2.15	0.47
1:C:138:VAL:HG23	1:C:139:GLU:N	2.30	0.47
1:C:168:LYS:O	1:C:172:ALA:HB2	2.15	0.47
1:C:346:LEU:HB3	1:C:372:MET:CG	2.45	0.47
1:C:60:ARG:HG2	1:C:380:GLU:O	2.14	0.47
3:E:57:ILE:HD12	3:E:105:ALA:HB1	1.96	0.47
3:F:223:ARG:O	3:F:223:ARG:HG2	2.14	0.47
3:G:180:GLY:HA2	3:G:253:LEU:HD23	1.96	0.47
3:G:50:HIS:O	3:G:51:SER:HB3	2.14	0.47
1:A:359:ARG:O	1:A:363:VAL:HG13	2.15	0.47
2:B:379:LEU:HD21	2:B:443:ILE:HG21	1.96	0.47
2:B:495:THR:HG22	2:B:499:ASN:ND2	2.30	0.47
1:C:442:HIS:HA	5:C:3496:CFM:S4B	2.55	0.47
1:C:373:GLU:O	1:C:373:GLU:HG3	2.15	0.47
2:D:96:VAL:CG1	2:D:113:CYS:SG	3.03	0.47
3:E:39:ASP:OD1	3:E:40:PRO:N	2.47	0.47
3:F:13:ILE:CA	3:F:187:ARG:NH2	2.73	0.47
3:F:146:GLU:HG2	3:F:253:LEU:CD2	2.45	0.47
3:G:199:LEU:CD1	3:G:259:ILE:HD11	2.45	0.47
1:A:145:ASN:ND2	1:A:147:GLY:H	2.13	0.47
1:A:158:LEU:HD21	2:B:123:ALA:HB1	1.96	0.47
1:A:253:TRP:CZ3	1:A:282:ILE:HG12	2.49	0.47
1:A:426:LYS:HA	2:B:104:ASN:HD21	1.79	0.47
1:C:20:TYR:OH	1:C:408:GLU:CG	2.56	0.47
1:C:413:VAL:HG21	1:C:431:PHE:CE2	2.49	0.47
1:C:464:ASP:OD1	1:C:468:ASN:ND2	2.48	0.47
1:C:97:ARG:NH1	1:C:446:TYR:CA	2.74	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:90:HIS:HA	2:D:116:ASP:OD1	2.15	0.47
2:D:284:ALA:CB	2:D:285:PRO:CD	2.92	0.47
3:E:156:MET:HE3	3:F:12:GLY:HA2	1.97	0.47
3:F:43:ASP:N	3:F:43:ASP:OD1	2.47	0.47
3:G:195:LEU:HD21	3:G:268:LEU:CD2	2.45	0.47
3:G:223:ARG:HD2	3:G:230:TYR:CE1	2.50	0.47
1:A:428:LYS:HG2	1:A:438:PHE:CD2	2.50	0.47
2:B:106:HIS:CE1	2:B:471:PHE:HD1	2.32	0.47
2:B:163:ASN:OD1	2:B:167:ASN:ND2	2.48	0.47
1:C:207:LEU:HD11	1:C:266:PRO:CG	2.45	0.47
1:C:399:LEU:C	1:C:400:LEU:HD12	2.35	0.47
2:D:456:LEU:CD1	2:D:460:LYS:HD2	2.44	0.47
3:H:57:ILE:CG1	3:H:75:VAL:HG11	2.45	0.47
3:F:46:ARG:NH2	3:F:221:GLU:HG3	2.30	0.46
1:A:62:CYS:SG	1:A:64:TYR:HB3	2.55	0.46
2:B:380:VAL:O	2:B:383:LEU:HB2	2.15	0.46
2:B:506:ASP:O	2:B:510:ARG:HB2	2.15	0.46
2:D:370:TRP:HA	2:D:394:LEU:O	2.15	0.46
2:D:105:ARG:HB2	2:D:474:PHE:CE2	2.50	0.46
3:E:250:ASN:ND2	3:E:252:LEU:H	2.14	0.46
3:G:148:TYR:CE2	3:G:208:ILE:CD1	2.99	0.46
3:G:22:LEU:HD23	3:G:22:LEU:C	2.34	0.46
1:A:245:MET:HG3	1:A:324:CYS:HA	1.97	0.46
2:B:238:ARG:CD	2:B:258:GLU:CG	2.90	0.46
2:B:376:VAL:O	2:B:380:VAL:HG23	2.14	0.46
1:A:86:VAL:HG21	2:B:68:LYS:HE2	1.97	0.46
1:C:428:LYS:HG3	1:C:438:PHE:CD2	2.51	0.46
2:D:163:ASN:OD1	2:D:167:ASN:ND2	2.49	0.46
2:D:493:ILE:O	2:D:497:LEU:HG	2.14	0.46
1:C:91:TYR:OH	2:D:73:LEU:HB2	2.15	0.46
3:G:19:THR:O	3:G:23:VAL:HG22	2.16	0.46
1:C:150:VAL:O	1:C:181:VAL:HG12	2.15	0.46
1:C:203:ARG:NE	1:C:204:ASP:OD2	2.48	0.46
1:C:64:TYR:HB2	6:D:3498:CLF:S3A	2.56	0.46
2:D:62:LEU:CD2	2:D:64:VAL:HG23	2.46	0.46
3:E:22:LEU:C	3:E:22:LEU:HD23	2.36	0.46
1:A:48:SER:HB3	1:A:387:TYR:CE1	2.51	0.46
2:B:226:ILE:O	2:B:228:PRO:HD3	2.15	0.46
2:B:401:ARG:HH11	2:B:401:ARG:HB2	1.81	0.46
3:H:187:ARG:O	3:H:188:ASN:HB3	2.16	0.46
3:H:41:LYS:O	3:H:42:ALA:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:PHE:N	1:A:143:PRO:HD3	2.31	0.46
1:A:358:LEU:HD12	1:A:361:ARG:HH21	1.80	0.46
1:A:385:ASP:OD1	1:A:386:ASP:OD1	2.33	0.46
1:A:89:GLY:C	1:A:113:ASN:ND2	2.69	0.46
2:B:326:ASP:O	2:B:330:MET:HG3	2.15	0.46
1:C:229:TYR:N	1:C:229:TYR:CD1	2.83	0.46
1:C:276:TYR:O	1:C:276:TYR:CG	2.68	0.46
2:D:369:LEU:HD12	2:D:379:LEU:HD23	1.97	0.46
3:E:148:TYR:CE2	3:E:208:ILE:CD1	2.99	0.46
3:F:73:GLU:N	3:F:73:GLU:OE1	2.45	0.46
3:H:61:ALA:HB2	3:H:70:LEU:HD12	1.96	0.46
3:H:66:THR:O	3:H:69:ASP:HB2	2.15	0.46
1:A:98:ASN:H	1:A:98:ASN:HD22	1.61	0.46
2:B:474:PHE:HB3	2:D:522:VAL:HB	1.96	0.46
3:G:39:ASP:OD1	3:G:40:PRO:N	2.49	0.46
3:H:187:ARG:HH21	3:H:195:LEU:HD22	1.80	0.46
3:H:39:ASP:OD2	3:H:41:LYS:HB2	2.16	0.46
3:H:76:LEU:HD21	3:H:84:LYS:HD3	1.97	0.46
1:A:128:ASP:HB3	1:A:166:VAL:CG2	2.41	0.46
1:A:425:ILE:HG22	4:A:1494:HCA:C6	2.46	0.46
1:A:131:LEU:CD1	1:A:166:VAL:HG11	2.45	0.46
1:A:90:GLN:NE2	2:B:447:TYR:CE1	2.84	0.46
1:C:51:LYS:HE3	2:D:119:THR:OG1	2.15	0.46
2:D:448:GLY:O	2:D:466:LEU:HD22	2.15	0.46
2:D:90:HIS:HB3	2:D:150:SER:O	2.15	0.46
3:F:57:ILE:HG13	3:F:87:GLU:O	2.16	0.46
3:G:212:PRO:O	9:G:7292:ATP:N6	2.44	0.46
3:H:183:ILE:HD13	3:H:243:LEU:HD11	1.98	0.46
1:A:458:ILE:HG22	1:A:462:ASP:OD2	2.16	0.46
2:B:227:VAL:HG12	2:B:298:LEU:CD1	2.45	0.46
2:B:257:PRO:HB3	2:B:261:LEU:HD22	1.98	0.46
2:B:222:LYS:HA	2:B:288:LEU:CD2	2.46	0.46
1:C:58:THR:CG2	1:C:60:ARG:HB2	2.45	0.46
3:G:179:LEU:CD1	3:G:256:PRO:HG3	2.46	0.46
3:H:129:ASP:HB3	3:H:131:VAL:HG12	1.98	0.46
3:H:181:GLY:HA2	3:H:205:THR:OG1	2.16	0.46
1:A:22:GLU:HA	1:A:25:ARG:HB3	1.98	0.46
2:B:318:ILE:HD12	2:B:374:ASP:HB3	1.98	0.46
1:C:144:LEU:CD2	2:D:43:VAL:HG21	2.46	0.46
1:C:168:LYS:O	1:C:172:ALA:CB	2.64	0.46
1:C:302:PRO:HG3	1:C:335:TRP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:449:PRO:O	1:C:455:GLY:HA2	2.16	0.46
2:D:157:VAL:C	2:D:159:GLY:H	2.19	0.46
2:D:418:ASN:ND2	2:D:418:ASN:O	2.49	0.46
3:E:58:MET:SD	3:E:104:THR:HG21	2.56	0.46
1:C:186:PHE:CE1	3:G:100:ARG:NH2	2.81	0.46
2:B:147:ILE:O	2:B:181:VAL:HA	2.15	0.45
2:B:390:PRO:O	2:B:419:ALA:CB	2.64	0.45
1:C:416:ILE:C	1:C:418:PRO:HD3	2.37	0.45
2:D:38:ASP:O	2:D:42:GLU:HG3	2.16	0.45
3:E:50:HIS:O	3:E:51:SER:HB3	2.15	0.45
3:E:72:LEU:HD11	3:E:76:LEU:HD12	1.98	0.45
3:H:72:LEU:HD11	3:H:76:LEU:HD12	1.98	0.45
1:A:297:TYR:HB2	1:A:308:SER:OG	2.16	0.45
2:B:227:VAL:HB	2:B:292:LEU:HD23	1.97	0.45
1:C:165:SER:O	1:C:168:LYS:HB2	2.16	0.45
1:C:380:GLU:HG3	1:C:381:PHE:HD2	1.81	0.45
2:D:380:VAL:O	2:D:383:LEU:HB2	2.17	0.45
1:A:272:LEU:HD13	1:A:312:ILE:HD13	1.98	0.45
2:B:329:LEU:CD1	2:B:344:LEU:HD13	2.41	0.45
1:C:107:ASN:C	1:C:107:ASN:ND2	2.67	0.45
1:C:110:VAL:C	1:C:112:MET:H	2.20	0.45
1:C:239:ARG:HD3	2:D:23:MET:SD	2.55	0.45
2:D:257:PRO:HB3	2:D:261:LEU:HD22	1.98	0.45
1:C:144:LEU:HD22	2:D:35:TYR:CD1	2.51	0.45
3:H:192:GLU:HA	3:H:195:LEU:HB3	1.98	0.45
1:A:219:THR:HG22	1:A:221:TYR:N	2.21	0.45
1:A:245:MET:CE	1:A:309:LEU:HD22	2.47	0.45
1:A:56:LEU:O	1:A:405:THR:HB	2.16	0.45
2:B:67:ALA:HB3	2:B:396:HIS:HB2	1.98	0.45
1:C:230:ASN:O	1:C:230:ASN:CG	2.54	0.45
1:C:359:ARG:O	1:C:363:VAL:HG13	2.16	0.45
1:C:46:ILE:HG12	1:C:47:ILE:N	2.31	0.45
2:D:185:HIS:C	2:D:187:PRO:HD3	2.36	0.45
3:G:8:TYR:HD2	3:G:130:VAL:HG22	1.82	0.45
3:H:43:ASP:OD1	3:H:43:ASP:N	2.49	0.45
1:A:125:PHE:C	1:A:126:GLY:O	2.54	0.45
1:A:239:ARG:HD3	2:B:23:MET:SD	2.57	0.45
1:C:298:ASN:CB	1:C:362:HIS:NE2	2.79	0.45
2:D:56:ASN:O	2:D:59:ARG:CB	2.64	0.45
3:E:158:MET:HE1	3:E:195:LEU:HG	1.99	0.45
3:F:23:VAL:HG12	3:F:33:VAL:HG11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:136:ALA:HB2	3:F:94:GLY:HA2	1.98	0.45
3:H:8:TYR:CE1	3:H:126:VAL:HG21	2.52	0.45
1:A:141:LEU:HA	1:A:141:LEU:HD12	1.84	0.45
1:A:189:VAL:CG2	1:A:190:SER:N	2.76	0.45
1:A:57:MET:HE3	2:B:100:ARG:NH1	2.32	0.45
2:B:119:THR:HG22	2:B:120:GLU:N	2.31	0.45
2:B:122:ALA:HB3	2:B:154:MET:HE1	1.99	0.45
2:B:472:PRO:HB3	2:B:474:PHE:CE2	2.51	0.45
2:B:90:HIS:O	2:B:151:THR:HA	2.16	0.45
1:C:239:ARG:HD3	2:D:23:MET:CG	2.47	0.45
1:C:253:TRP:NE1	1:C:265:THR:OG1	2.34	0.45
1:C:58:THR:CG2	1:C:59:ILE:N	2.79	0.45
2:D:330:MET:O	2:D:333:SER:HB3	2.16	0.45
3:E:207:MET:HE1	3:E:210:PHE:HB2	1.96	0.45
3:F:113:GLY:HA2	3:F:116:GLU:OE1	2.17	0.45
3:F:38:CYS:HB3	3:F:102:VAL:HG13	1.98	0.45
3:G:4:GLN:HE21	3:G:124:TYR:HE2	1.65	0.45
3:H:103:ILE:HA	3:H:137:MET:HG3	1.99	0.45
1:A:276:TYR:O	1:A:280:ASN:CB	2.64	0.45
1:A:360:PRO:HB2	1:A:379:TYR:CZ	2.52	0.45
1:A:448:GLY:HA3	1:A:458:ILE:HD13	1.98	0.45
2:B:85:THR:HA	2:B:146:MET:O	2.17	0.45
2:B:234:LEU:O	2:B:238:ARG:HG2	2.17	0.45
2:B:56:ASN:O	2:B:59:ARG:HD3	2.17	0.45
1:C:81:ILE:HD12	1:C:148:ILE:HG21	1.98	0.45
2:D:233:TYR:CB	2:D:236:ASN:HD22	2.25	0.45
1:C:210:ARG:HH22	2:D:33:GLU:CD	2.20	0.45
3:E:255:ILE:O	3:E:255:ILE:CG2	2.63	0.45
3:E:25:ALA:HB2	3:E:228:ILE:CD1	2.47	0.45
3:F:3:ARG:NH1	3:F:3:ARG:HG3	2.31	0.45
1:A:343:ARG:N	1:A:344:PRO:CD	2.80	0.45
1:A:36:ASP:O	1:A:38:ALA:N	2.50	0.45
1:A:381:PHE:CZ	5:A:1496:CFM:S2B	3.10	0.45
1:A:35:ASN:ND2	1:A:394:MET:CB	2.80	0.45
1:A:350:ARG:O	1:A:419:ASP:OD1	2.35	0.45
1:A:98:ASN:ND2	1:A:98:ASN:N	2.57	0.45
2:B:122:ALA:O	2:B:126:GLY:N	2.48	0.45
2:B:494:LEU:HD23	2:B:494:LEU:C	2.37	0.45
1:C:457:ALA:HB3	2:D:3:GLN:HG2	1.99	0.45
3:E:49:LEU:O	3:E:50:HIS:HB2	2.17	0.45
3:F:3:ARG:NH1	3:F:121:PHE:CZ	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:217:VAL:HG11	9:F:6292:ATP:N7	2.32	0.45
1:A:90:GLN:N	1:A:113:ASN:HD21	2.15	0.45
1:A:190:SER:HB2	1:A:381:PHE:HB3	1.99	0.45
1:C:167:SER:HB3	1:C:178:ILE:HG22	1.98	0.45
1:C:337:ALA:CB	2:D:5:VAL:HG21	2.46	0.45
1:C:448:GLY:HA3	1:C:458:ILE:HD13	1.99	0.45
2:D:137:ASN:HD22	2:D:137:ASN:N	2.14	0.45
2:D:284:ALA:CB	2:D:285:PRO:HD3	2.45	0.45
2:D:232:THR:HG21	2:D:471:PHE:CD1	2.50	0.45
3:E:244:ALA:O	3:E:248:VAL:HG23	2.17	0.45
2:B:212:SER:C	2:B:216:LYS:HE3	2.36	0.45
2:B:70:CYS:HB2	2:B:72:PRO:HD2	1.99	0.45
1:C:221:TYR:CE2	1:C:320:ILE:HD11	2.52	0.45
1:C:297:TYR:HB2	1:C:308:SER:OG	2.17	0.45
1:C:37:PRO:HD2	1:C:396:ASP:OD1	2.17	0.45
2:D:90:HIS:CE1	2:D:116:ASP:OD2	2.70	0.45
2:D:277:THR:O	2:D:280:GLU:HB3	2.16	0.45
2:D:497:LEU:O	2:D:500:SER:N	2.50	0.45
3:H:231:ASP:OD2	3:H:234:ALA:N	2.50	0.45
2:D:147:ILE:O	2:D:181:VAL:HA	2.16	0.44
1:C:260:SER:HB2	2:D:33:GLU:OE1	2.17	0.44
3:E:158:MET:CE	3:E:195:LEU:HG	2.47	0.44
3:F:149:ILE:O	3:F:182:LEU:HA	2.16	0.44
3:G:160:ALA:O	3:G:164:ILE:HG13	2.17	0.44
1:A:9:VAL:O	1:A:12:LEU:HB3	2.16	0.44
1:A:253:TRP:CH2	1:A:282:ILE:HG12	2.52	0.44
1:A:271:ASN:OD1	1:A:286:MET:HE2	2.17	0.44
1:A:310:ARG:O	1:A:313:ALA:HB3	2.17	0.44
1:A:35:ASN:HB3	1:A:398:THR:OG1	2.16	0.44
1:C:124:VAL:O	3:H:97:CYS:N	2.42	0.44
1:C:232:GLY:O	1:C:449:PRO:HG3	2.17	0.44
2:D:426:ASP:OD1	2:D:428:TRP:N	2.49	0.44
2:B:512:MET:HG2	2:D:457:HIS:CD2	2.52	0.44
3:E:136:ALA:HB2	3:F:94:GLY:HA3	1.99	0.44
3:E:225:MET:CE	3:E:230:TYR:HA	2.47	0.44
3:H:220:ALA:HB1	3:H:225:MET:O	2.17	0.44
1:A:306:ILE:HD11	1:A:335:TRP:NE1	2.33	0.44
2:B:284:ALA:HB3	2:B:285:PRO:HD3	2.00	0.44
1:C:186:PHE:CB	2:D:154:MET:CE	2.95	0.44
2:D:81:GLY:HA3	2:D:257:PRO:HD3	2.00	0.44
3:E:129:ASP:CB	3:E:131:VAL:HG12	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:43:ASP:N	3:G:43:ASP:OD1	2.50	0.44
9:G:7292:ATP:H4'	3:H:156:MET:SD	2.57	0.44
3:H:236:GLN:HE22	9:H:8292:ATP:N6	2.15	0.44
1:A:144:LEU:HD21	2:B:43:VAL:HG21	1.99	0.44
2:B:353:ASP:OD2	2:D:109:GLU:OE2	2.35	0.44
2:B:67:ALA:HB3	2:B:396:HIS:CB	2.46	0.44
1:C:219:THR:C	1:C:221:TYR:H	2.19	0.44
2:D:133:ASP:O	2:D:136:GLN:N	2.50	0.44
2:D:14:LEU:HD12	2:D:14:LEU:O	2.17	0.44
2:D:369:LEU:CD2	2:D:369:LEU:N	2.80	0.44
2:D:426:ASP:H	2:D:429:HIS:CE1	2.36	0.44
3:E:148:TYR:CE2	3:E:208:ILE:HD12	2.52	0.44
1:A:277:ARG:NH2	1:A:383:HIS:CD2	2.84	0.44
1:A:417:LYS:N	1:A:418:PRO:CD	2.78	0.44
2:B:168:ASN:O	2:B:172:GLU:HB2	2.17	0.44
2:B:314:PRO:HB3	2:B:316:LEU:CD1	2.46	0.44
1:C:280:ASN:H	1:C:280:ASN:ND2	2.14	0.44
2:D:285:PRO:HG3	2:D:309:TRP:CD1	2.53	0.44
2:B:12:TYR:OH	2:D:508:GLU:HB3	2.17	0.44
3:H:138:PRO:O	3:H:143:LYS:HB3	2.17	0.44
3:H:255:ILE:HG22	3:H:255:ILE:O	2.16	0.44
3:H:213:ARG:HG3	9:H:8292:ATP:H2	1.83	0.44
1:A:100:TYR:OH	1:A:111:THR:HG23	2.16	0.44
1:A:57:MET:HG2	2:B:142:TYR:CE1	2.53	0.44
2:B:88:TYR:O	2:B:150:SER:N	2.50	0.44
1:C:35:ASN:HD21	1:C:394:MET:HB2	1.83	0.44
1:C:59:ILE:CD1	1:C:427:GLU:OE2	2.58	0.44
3:E:165:SER:HA	3:E:168:ILE:HD12	2.00	0.44
3:E:64:ALA:HB1	3:E:69:ASP:HB3	1.99	0.44
3:F:102:VAL:HG21	3:F:135:PHE:CE1	2.53	0.44
3:H:110:GLU:OE2	3:H:143:LYS:NZ	2.51	0.44
1:A:475:LEU:HD13	2:B:265:ALA:O	2.17	0.44
2:B:143:LYS:N	2:B:144:PRO:CD	2.80	0.44
1:C:193:LEU:HG	1:C:197:ILE:HD11	1.98	0.44
1:C:265:THR:HG22	1:C:286:MET:CE	2.48	0.44
2:D:146:MET:HE1	2:D:208:PHE:HE1	1.83	0.44
2:D:365:LYS:HG3	2:D:501:ILE:CD1	2.47	0.44
3:E:6:ALA:HA	3:E:124:TYR:HB2	1.99	0.44
3:F:195:LEU:CD1	3:F:267:LEU:HD22	2.48	0.44
3:G:189:THR:CG2	3:G:190:ASP:H	2.15	0.44
1:A:274:HIS:HB2	1:A:297:TYR:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:ASN:CG	1:A:470:PRO:HD2	2.37	0.44
1:A:57:MET:HG3	2:B:142:TYR:CZ	2.53	0.44
2:B:158:ILE:HG22	3:E:97:CYS:HB2	2.00	0.44
1:C:70:VAL:CG2	1:C:71:VAL:HG23	2.47	0.44
2:D:124:VAL:HG22	3:G:100:ARG:HG3	2.00	0.44
3:E:86:VAL:HG21	3:E:109:LEU:HD11	2.00	0.44
3:F:159:TYR:HA	3:F:264:LEU:HD11	2.00	0.44
3:F:4:GLN:HB2	3:F:144:ALA:HA	2.00	0.44
3:G:198:ALA:HB1	3:G:267:LEU:HD21	2.00	0.44
3:G:33:VAL:HG12	3:G:34:MET:N	2.33	0.44
3:H:50:HIS:HE1	3:H:225:MET:HB3	1.81	0.44
3:H:25:ALA:O	3:H:28:GLU:HB3	2.17	0.44
2:B:41:ASP:O	2:B:45:GLN:HG2	2.18	0.44
2:D:278:GLN:HG2	2:D:278:GLN:H	1.51	0.44
2:D:479:LEU:N	2:D:479:LEU:CD1	2.81	0.44
3:E:9:GLY:C	3:E:15:LYS:HE3	2.39	0.44
3:F:76:LEU:HD21	3:F:84:LYS:HB3	1.99	0.44
3:G:39:ASP:OD1	3:G:40:PRO:CD	2.66	0.44
3:H:23:VAL:O	3:H:27:ALA:N	2.47	0.44
1:A:181:VAL:HG13	1:A:181:VAL:O	2.18	0.43
1:A:229:TYR:CD1	1:A:229:TYR:N	2.86	0.43
1:A:283:SER:HA	1:A:286:MET:HB2	2.00	0.43
1:A:64:TYR:C	1:A:66:GLY:N	2.71	0.43
1:C:168:LYS:HE3	1:C:205:TRP:HH2	1.82	0.43
1:C:332:LYS:HA	1:C:335:TRP:NE1	2.32	0.43
1:C:469:ASN:CG	1:C:470:PRO:HD2	2.38	0.43
3:F:46:ARG:HH21	3:F:221:GLU:HG3	1.83	0.43
3:G:165:SER:HA	3:G:168:ILE:HD12	2.00	0.43
3:G:86:VAL:HG21	3:G:109:LEU:CD1	2.49	0.43
3:G:91:PRO:HD2	3:G:98:ALA:HB2	1.99	0.43
1:A:364:ILE:O	1:A:367:TYR:HB2	2.18	0.43
2:B:208:PHE:HB3	2:B:282:LYS:HA	1.98	0.43
2:B:198:ASP:CG	2:B:298:LEU:HA	2.38	0.43
2:B:426:ASP:OD1	2:B:428:TRP:N	2.50	0.43
2:B:437:ASP:O	2:B:439:PRO:HD3	2.18	0.43
1:C:427:GLU:HB2	1:C:431:PHE:HE1	1.83	0.43
1:C:359:ARG:CZ	1:C:444:TRP:CZ2	3.01	0.43
2:D:375:PHE:CE2	2:D:470:GLY:HA2	2.46	0.43
3:F:152:SER:HB2	3:F:187:ARG:HG2	2.00	0.43
3:F:61:ALA:HB2	3:F:70:LEU:HD12	2.00	0.43
3:G:61:ALA:HB1	3:G:67:VAL:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:15:LYS:N	9:G:7292:ATP:O1B	2.51	0.43
1:A:305:THR:O	1:A:309:LEU:HG	2.17	0.43
2:B:293:LEU:HD22	2:B:319:PRO:HG2	2.00	0.43
2:B:512:MET:CE	2:D:457:HIS:CG	3.01	0.43
2:B:512:MET:HE3	2:D:457:HIS:CD2	2.53	0.43
1:C:179:VAL:O	1:C:181:VAL:N	2.49	0.43
1:C:283:SER:HA	1:C:286:MET:HB2	2.01	0.43
2:D:49:THR:CG2	2:D:52:TYR:H	2.28	0.43
9:E:5292:ATP:H4'	3:F:156:MET:SD	2.58	0.43
3:H:206:GLN:NE2	3:H:250:ASN:OD1	2.50	0.43
1:A:125:PHE:O	1:A:126:GLY:O	2.35	0.43
2:B:175:ILE:HG13	2:B:175:ILE:O	2.18	0.43
2:B:228:PRO:HG3	2:B:253:LEU:HD11	2.00	0.43
1:C:35:ASN:ND2	1:C:394:MET:HB2	2.33	0.43
2:B:352:VAL:HG11	1:C:475:LEU:HD22	2.01	0.43
2:D:104:ASN:O	2:D:108:ARG:N	2.44	0.43
1:A:433:LYS:HE2	2:D:353:ASP:OD2	2.19	0.43
2:D:53:GLN:OE1	2:D:432:SER:HB3	2.18	0.43
2:D:472:PRO:HB3	2:D:474:PHE:CE2	2.54	0.43
1:C:138:VAL:CG1	2:D:62:LEU:CD1	2.94	0.43
3:F:42:ALA:CA	3:F:87:GLU:OE1	2.55	0.43
3:H:48:ILE:HG23	3:H:80:TYR:HB3	2.00	0.43
1:A:431:PHE:N	1:A:431:PHE:CD1	2.87	0.43
1:A:70:VAL:CG2	1:A:71:VAL:HG23	2.48	0.43
1:A:57:MET:HG2	2:B:142:TYR:CZ	2.53	0.43
2:B:71:GLN:OE1	2:B:195:THR:HG22	2.19	0.43
1:C:100:TYR:N	1:C:100:TYR:CD2	2.87	0.43
1:C:219:THR:HG22	1:C:221:TYR:N	2.22	0.43
1:C:312:ILE:O	1:C:316:PHE:CD1	2.71	0.43
1:C:97:ARG:NH2	1:C:99:TYR:OH	2.44	0.43
2:D:69:ALA:HB3	2:D:193:HIS:HB3	2.00	0.43
2:D:41:ASP:O	2:D:45:GLN:HG2	2.19	0.43
3:G:260:THR:O	3:G:261:MET:C	2.56	0.43
1:A:20:TYR:OH	1:A:408:GLU:CG	2.58	0.43
1:A:240:ILE:O	1:A:244:GLU:HG3	2.18	0.43
1:A:361:ARG:HG2	1:A:362:HIS:N	2.34	0.43
2:B:475:ASP:O	2:D:502:LEU:HD13	2.18	0.43
1:C:136:ASP:CG	1:C:170:LYS:HZ1	2.22	0.43
2:D:208:PHE:HB3	2:D:282:LYS:HA	2.01	0.43
2:D:227:VAL:HG12	2:D:298:LEU:HD13	2.00	0.43
3:G:208:ILE:HG22	3:G:209:HIS:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LYS:HA	1:A:110:VAL:HG23	2.01	0.43
1:A:148:ILE:O	1:A:178:ILE:HA	2.18	0.43
1:A:276:TYR:CD1	1:A:280:ASN:HB3	2.53	0.43
1:A:8:GLU:O	1:A:12:LEU:N	2.49	0.43
2:B:346:LYS:HG3	2:D:264:PRO:CG	2.47	0.43
2:B:369:LEU:N	2:B:369:LEU:HD23	2.33	0.43
1:A:337:ALA:CB	2:B:5:VAL:HG21	2.49	0.43
1:C:142:PHE:N	1:C:143:PRO:CD	2.81	0.43
1:C:298:ASN:HD21	1:C:300:PHE:HD1	1.64	0.43
1:C:315:LYS:HA	1:C:315:LYS:HD3	1.72	0.43
1:C:413:VAL:HG11	1:C:431:PHE:HD2	1.84	0.43
2:D:14:LEU:C	2:D:14:LEU:HD12	2.38	0.43
3:G:195:LEU:HD11	3:G:268:LEU:HD23	2.01	0.43
3:H:236:GLN:HG2	3:H:240:TYR:CE2	2.53	0.43
1:A:158:LEU:CD2	2:B:123:ALA:HB1	2.48	0.43
1:A:65:ALA:O	1:A:70:VAL:HG13	2.19	0.43
1:C:57:MET:CG	2:D:142:TYR:CZ	3.01	0.43
1:C:98:ASN:HB3	1:C:229:TYR:O	2.19	0.43
2:D:329:LEU:CD1	2:D:344:LEU:HD13	2.44	0.43
3:E:199:LEU:CD1	3:E:259:ILE:HD11	2.47	0.43
3:F:141:GLU:O	3:F:142:ASN:CB	2.67	0.43
3:F:225:MET:HE2	3:F:230:TYR:HA	2.01	0.43
1:A:54:PRO:HB2	2:B:134:GLY:CA	2.48	0.43
2:B:137:ASN:HD22	2:B:137:ASN:N	2.17	0.43
2:B:199:ASN:N	2:B:199:ASN:HD22	2.16	0.43
2:D:238:ARG:HG3	2:D:238:ARG:NH2	2.34	0.43
3:F:19:THR:O	3:F:23:VAL:HG22	2.17	0.43
3:G:6:ALA:HA	3:G:124:TYR:HB2	2.01	0.43
1:A:134:LEU:HG	2:B:62:LEU:HD13	2.00	0.43
1:A:399:LEU:C	1:A:400:LEU:HD12	2.40	0.43
2:B:179:PHE:C	2:B:179:PHE:CD2	2.93	0.43
1:C:88:CYS:HB2	1:C:153:GLU:OE1	2.19	0.43
2:D:124:VAL:HG11	3:G:58:MET:CG	2.46	0.43
2:D:228:PRO:HD2	2:D:254:LEU:O	2.18	0.43
2:D:498:VAL:O	2:D:502:LEU:HG	2.19	0.43
3:F:11:GLY:HA2	3:F:15:LYS:HE3	2.01	0.43
3:G:217:VAL:CG2	9:G:7292:ATP:C2	2.96	0.43
1:A:89:GLY:C	1:A:113:ASN:HD21	2.22	0.42
1:A:223:VAL:HG12	1:A:270:LEU:HB3	2.00	0.42
1:A:440:GLU:HB2	1:A:445:ASP:HB2	2.00	0.42
2:B:256:ASP:C	2:B:256:ASP:OD1	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:322:LEU:HD11	2:B:348:ARG:NE	2.34	0.42
2:B:362:LEU:CD1	2:B:498:VAL:HG22	2.47	0.42
2:B:71:GLN:N	2:B:72:PRO:CD	2.81	0.42
2:B:94:GLY:O	2:B:97:ALA:HB3	2.19	0.42
1:C:71:VAL:CG1	1:C:198:ALA:HB1	2.40	0.42
1:C:310:ARG:O	1:C:313:ALA:HB3	2.19	0.42
1:C:359:ARG:CG	1:C:359:ARG:HH11	2.27	0.42
1:C:431:PHE:N	1:C:431:PHE:CD1	2.86	0.42
2:D:198:ASP:CG	2:D:298:LEU:HA	2.40	0.42
2:D:86:MET:HE3	2:D:87:PRO:CD	2.48	0.42
2:D:8:ILE:H	2:D:8:ILE:HG13	1.66	0.42
3:E:115:TYR:C	3:E:117:ASP:N	2.72	0.42
3:G:139:ILE:HG21	3:G:147:ILE:HD11	2.02	0.42
3:G:217:VAL:O	3:G:221:GLU:HB3	2.19	0.42
3:G:212:PRO:C	3:G:236:GLN:HE22	2.22	0.42
3:H:67:VAL:HG21	3:H:104:THR:HG21	2.00	0.42
3:H:33:VAL:HG12	3:H:34:MET:N	2.34	0.42
1:A:282:ILE:HD12	1:A:282:ILE:O	2.19	0.42
1:A:363:VAL:O	1:A:367:TYR:HD1	2.02	0.42
2:B:197:TRP:CE3	2:B:298:LEU:HD21	2.53	0.42
2:B:498:VAL:O	2:B:502:LEU:HG	2.19	0.42
1:C:356:GLY:CA	1:C:381:PHE:CE2	3.02	0.42
1:C:383:HIS:N	1:C:383:HIS:ND1	2.67	0.42
1:C:90:GLN:HE22	2:D:66:PRO:C	2.21	0.42
1:C:210:ARG:NH2	2:D:33:GLU:OE1	2.47	0.42
2:B:502:LEU:HD13	2:D:475:ASP:O	2.18	0.42
2:D:64:VAL:HG12	2:D:428:TRP:HB2	2.01	0.42
1:A:176:LYS:HB2	1:A:176:LYS:HE3	1.84	0.42
1:A:226:ILE:HG23	1:A:279:MET:HG2	2.01	0.42
1:A:464:ASP:OD1	1:A:468:ASN:ND2	2.51	0.42
1:A:49:ASN:ND2	1:A:189:VAL:HG21	2.34	0.42
2:B:233:TYR:CB	2:B:236:ASN:HD22	2.28	0.42
2:B:443:ILE:HA	2:B:467:ILE:O	2.19	0.42
1:A:302:PRO:HG3	1:A:335:TRP:HB2	2.01	0.42
1:A:303:THR:HG22	1:A:369:ASP:CG	2.39	0.42
2:B:181:VAL:N	2:B:182:PRO:CD	2.83	0.42
2:B:19:ASP:OD2	2:B:20:TYR:N	2.51	0.42
2:B:492:GLN:O	2:B:493:ILE:C	2.58	0.42
1:C:77:ASP:N	1:C:77:ASP:OD2	2.52	0.42
3:E:108:PHE:O	3:E:111:GLU:N	2.52	0.42
3:F:9:GLY:O	3:F:15:LYS:HE2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:138:PRO:O	3:G:144:ALA:HB3	2.18	0.42
3:H:10:LYS:H	3:H:13:ILE:HD13	1.84	0.42
3:H:145:GLN:HA	3:H:177:VAL:HA	2.01	0.42
3:H:217:VAL:CG2	3:H:236:GLN:HE21	2.32	0.42
1:A:114:PHE:HE2	1:A:142:PHE:CE1	2.37	0.42
1:A:193:LEU:HG	1:A:197:ILE:HD11	2.01	0.42
1:A:222:ASP:OD1	1:A:248:ARG:HG2	2.20	0.42
1:A:54:PRO:HB3	2:B:116:ASP:HA	2.01	0.42
2:B:149:VAL:HG21	2:B:166:ILE:HD11	2.01	0.42
2:B:407:ASP:O	2:B:410:LEU:HB2	2.19	0.42
1:C:274:HIS:HE2	1:C:300:PHE:HE1	1.65	0.42
1:C:363:VAL:O	1:C:367:TYR:HD1	2.01	0.42
1:C:442:HIS:CE1	5:C:3496:CFM:S1B	3.12	0.42
2:D:199:ASN:ND2	2:D:199:ASN:N	2.67	0.42
2:D:3:GLN:OE1	2:D:9:LYS:O	2.37	0.42
3:F:137:MET:HB3	3:F:138:PRO:HD3	2.02	0.42
3:G:99:GLY:O	3:G:134:GLY:HA3	2.19	0.42
1:A:440:GLU:HB2	1:A:445:ASP:CB	2.49	0.42
1:A:86:VAL:HG21	2:B:68:LYS:CE	2.49	0.42
1:A:57:MET:SD	2:B:114:VAL:HG12	2.59	0.42
2:B:339:PRO:O	2:B:341:PRO:HD3	2.19	0.42
1:C:109:PHE:CD1	1:C:109:PHE:N	2.87	0.42
1:C:167:SER:HB3	1:C:180:PRO:CD	2.50	0.42
1:C:382:ALA:HB1	1:C:386:ASP:CB	2.49	0.42
3:F:179:LEU:CB	3:F:256:PRO:HG3	2.49	0.42
1:A:219:THR:HG23	1:A:220:PRO:CD	2.49	0.42
1:A:274:HIS:HE1	1:A:299:PHE:H	1.68	0.42
1:A:389:ARG:HG3	1:A:389:ARG:HH11	1.84	0.42
1:A:239:ARG:NH2	2:B:27:LYS:HG3	2.35	0.42
2:B:522:VAL:CG2	1:C:446:TYR:CE2	3.03	0.42
1:C:356:GLY:HA2	1:C:381:PHE:CE2	2.55	0.42
1:C:405:THR:CB	1:C:408:GLU:HG3	2.49	0.42
2:D:240:ILE:HA	2:D:240:ILE:HD13	1.94	0.42
2:D:426:ASP:OD1	2:D:426:ASP:C	2.57	0.42
3:E:137:MET:CB	3:E:138:PRO:HD3	2.49	0.42
3:E:40:PRO:HG3	3:E:98:ALA:HB1	2.02	0.42
3:E:45:THR:OG1	3:E:49:LEU:HD12	2.18	0.42
3:E:36:VAL:HA	3:E:86:VAL:HG23	2.01	0.42
3:F:179:LEU:HB2	3:F:256:PRO:CG	2.50	0.42
3:F:20:GLN:O	3:F:48:ILE:HD11	2.18	0.42
3:G:14:GLY:CA	9:G:7292:ATP:O1B	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:250:ASN:ND2	3:H:251:LYS:N	2.67	0.42
1:A:12:LEU:O	1:A:16:VAL:HG23	2.19	0.42
1:A:189:VAL:CG2	1:A:190:SER:H	2.30	0.42
1:A:193:LEU:HA	1:A:193:LEU:HD12	1.85	0.42
2:B:28:ARG:HA	2:B:32:GLU:HG3	2.02	0.42
1:A:138:VAL:CG1	2:B:62:LEU:HD22	2.48	0.42
2:D:74:GLY:HA3	2:D:193:HIS:O	2.19	0.42
3:H:185:ASN:HD21	3:H:211:VAL:CG1	2.33	0.42
1:A:298:ASN:HD21	1:A:300:PHE:HB2	1.85	0.42
1:A:48:SER:CB	1:A:402:ASP:OD2	2.68	0.42
2:B:236:ASN:OD1	2:B:485:LEU:N	2.53	0.42
1:A:239:ARG:NH1	2:B:27:LYS:HD2	2.35	0.42
1:A:144:LEU:HD11	2:B:43:VAL:HG21	2.02	0.42
2:B:469:ILE:HD13	2:B:493:ILE:CD1	2.50	0.42
1:C:114:PHE:N	1:C:114:PHE:CD1	2.88	0.42
1:C:57:MET:CE	2:D:100:ARG:NH1	2.82	0.42
2:D:165:PHE:H	2:D:165:PHE:HD1	1.67	0.42
2:D:322:LEU:HD11	2:D:348:ARG:NH2	2.34	0.42
2:D:339:PRO:O	2:D:341:PRO:HD3	2.19	0.42
2:D:438:LYS:HA	2:D:439:PRO:HD2	1.95	0.42
1:C:86:VAL:CG2	2:D:68:LYS:HE3	2.47	0.42
3:F:158:MET:HE1	3:F:195:LEU:HG	2.01	0.42
3:G:23:VAL:HG12	3:G:33:VAL:HG11	2.02	0.42
2:B:57:PHE:C	2:B:59:ARG:H	2.22	0.42
1:C:128:ASP:HB3	1:C:166:VAL:CG2	2.49	0.42
1:C:355:ILE:HG21	5:C:3496:CFM:S3A	2.59	0.42
3:G:136:ALA:HB2	3:H:94:GLY:HA2	2.01	0.42
1:A:141:LEU:HD21	2:B:56:ASN:HA	2.02	0.41
1:A:318:GLU:HA	1:A:321:GLN:OE1	2.20	0.41
1:A:352:MET:HE1	1:A:418:PRO:HG2	2.00	0.41
1:A:425:ILE:HG23	1:A:426:LYS:N	2.35	0.41
1:A:98:ASN:HD22	1:A:98:ASN:N	2.16	0.41
2:B:204:ILE:HG23	2:B:208:PHE:HE1	1.85	0.41
1:C:112:MET:HE1	2:D:428:TRP:CZ3	2.54	0.41
1:C:239:ARG:NH1	2:D:27:LYS:HD2	2.35	0.41
1:C:318:GLU:HA	1:C:321:GLN:OE1	2.20	0.41
1:C:39:VAL:HG23	1:C:39:VAL:O	2.19	0.41
1:C:302:PRO:CD	1:C:456:PHE:CD1	3.03	0.41
2:D:146:MET:HE2	2:D:208:PHE:CE1	2.49	0.41
2:D:206:ARG:CG	2:D:304:PHE:CZ	3.03	0.41
2:D:365:LYS:O	2:D:388:CYS:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:375:PHE:HE2	2:D:470:GLY:CA	2.31	0.41
3:E:260:THR:O	3:E:261:MET:C	2.58	0.41
3:F:186:SER:HA	3:F:192:GLU:OE2	2.20	0.41
3:F:4:GLN:HB2	3:F:143:LYS:O	2.20	0.41
3:H:136:ALA:O	3:H:139:ILE:HG12	2.20	0.41
3:H:185:ASN:HD21	3:H:211:VAL:HG12	1.85	0.41
1:A:134:LEU:HG	2:B:62:LEU:CD1	2.50	0.41
1:A:277:ARG:HD3	1:A:386:ASP:OD2	2.21	0.41
1:A:355:ILE:HB	1:A:360:PRO:HD3	2.02	0.41
1:A:96:ARG:NH1	1:A:98:ASN:OD1	2.53	0.41
2:B:118:MET:HE3	2:B:127:GLY:HA3	2.02	0.41
2:B:330:MET:O	2:B:333:SER:HB3	2.19	0.41
1:C:76:LYS:HG2	1:C:257:GLY:O	2.20	0.41
1:C:427:GLU:O	1:C:431:PHE:CD1	2.73	0.41
2:D:221:ASN:O	2:D:223:LYS:HG3	2.20	0.41
3:E:96:GLY:O	3:F:132:CYS:HB2	2.19	0.41
3:G:103:ILE:HG12	3:G:137:MET:HG2	2.02	0.41
3:H:166:LYS:HA	3:H:258:PRO:HG3	2.02	0.41
3:H:185:ASN:HD22	3:H:185:ASN:HA	1.40	0.41
3:H:98:ALA:O	3:H:102:VAL:HG23	2.20	0.41
1:A:239:ARG:O	1:A:243:GLU:HG3	2.20	0.41
1:A:70:VAL:HG23	1:A:71:VAL:N	2.35	0.41
2:B:393:ILE:HD12	2:B:410:LEU:HD11	2.03	0.41
2:B:395:CYS:O	2:B:423:ILE:HA	2.21	0.41
1:C:226:ILE:O	1:C:226:ILE:HG22	2.20	0.41
1:C:210:ARG:HG3	1:C:263:GLU:HB3	2.01	0.41
2:D:388:CYS:O	2:D:390:PRO:HD3	2.21	0.41
3:E:100:ARG:C	3:E:100:ARG:HD2	2.40	0.41
3:F:36:VAL:HA	3:F:86:VAL:HG23	2.02	0.41
3:H:165:SER:HB3	3:H:179:LEU:HD12	2.02	0.41
6:A:1498:CLF:S3B	2:B:72:PRO:HG2	2.60	0.41
1:A:221:TYR:O	1:A:223:VAL:HG13	2.20	0.41
1:A:454:ASP:HB3	2:B:14:LEU:HD21	2.01	0.41
2:B:277:THR:O	2:B:280:GLU:HB3	2.20	0.41
2:B:294:GLN:HB2	2:B:297:HIS:CE1	2.55	0.41
1:C:358:LEU:HD11	1:C:362:HIS:ND1	2.36	0.41
1:C:364:ILE:O	1:C:368:GLU:HG2	2.21	0.41
2:D:237:PHE:O	2:D:241:LYS:HG3	2.21	0.41
2:D:369:LEU:HD11	2:D:380:VAL:CG2	2.50	0.41
2:D:375:PHE:O	2:D:375:PHE:HD1	2.03	0.41
2:D:414:PRO:HA	2:D:417:LYS:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:492:GLN:O	2:D:493:ILE:C	2.56	0.41
3:F:163:ASN:O	3:F:166:LYS:HB3	2.21	0.41
3:F:198:ALA:CB	3:F:267:LEU:HD21	2.50	0.41
3:G:185:ASN:OD1	9:G:7292:ATP:N6	2.54	0.41
3:H:214:ASP:OD2	3:H:216:VAL:HG23	2.20	0.41
1:A:131:LEU:HD13	1:A:131:LEU:C	2.40	0.41
1:A:230:ASN:OD1	1:A:233:GLY:CA	2.68	0.41
1:A:339:VAL:HG13	1:A:343:ARG:HB2	2.01	0.41
1:A:411:GLU:HA	1:A:411:GLU:OE1	2.19	0.41
1:A:352:MET:HE1	1:A:413:VAL:HA	2.02	0.41
1:A:349:LYS:HD3	1:A:419:ASP:OD2	2.20	0.41
1:A:236:TRP:HA	2:B:23:MET:HE1	2.02	0.41
1:A:144:LEU:HD22	2:B:35:TYR:CE1	2.56	0.41
2:B:366:ARG:HB3	2:B:391:VAL:HG21	2.01	0.41
2:B:39:LYS:HD2	2:B:42:GLU:OE1	2.21	0.41
1:C:346:LEU:HB3	1:C:372:MET:HG3	2.02	0.41
1:C:37:PRO:HD2	1:C:396:ASP:CB	2.51	0.41
1:C:349:LYS:HD3	1:C:419:ASP:OD2	2.20	0.41
2:D:170:LYS:HD3	2:D:175:ILE:HG13	2.02	0.41
2:D:146:MET:HE2	2:D:208:PHE:HZ	1.79	0.41
2:D:427:LEU:HD23	2:D:427:LEU:HA	1.91	0.41
3:H:200:ALA:O	3:H:205:THR:O	2.39	0.41
3:H:36:VAL:HA	3:H:86:VAL:HG23	2.02	0.41
1:A:141:LEU:HD12	2:B:52:TYR:CE1	2.56	0.41
1:A:67:SER:HB3	1:A:151:GLN:NE2	2.35	0.41
1:A:405:THR:O	1:A:406:GLY:C	2.57	0.41
2:B:262:ASP:O	2:B:264:PRO:HD3	2.21	0.41
2:B:74:GLY:HA3	2:B:193:HIS:O	2.19	0.41
1:C:30:LYS:HZ1	1:C:47:ILE:CD1	2.33	0.41
1:C:404:VAL:HG22	1:C:408:GLU:HB2	2.02	0.41
1:C:16:VAL:HG21	1:C:412:PHE:CE1	2.55	0.41
3:E:106:ILE:CD1	3:E:137:MET:HB3	2.50	0.41
2:B:125:PHE:CE2	3:E:62:ALA:HB2	2.55	0.41
3:F:100:ARG:O	3:F:100:ARG:HD2	2.20	0.41
1:A:164:GLU:HA	1:A:180:PRO:HB3	2.03	0.41
1:A:364:ILE:O	1:A:368:GLU:HG2	2.20	0.41
2:B:84:LYS:HD3	2:B:145:ASP:CG	2.41	0.41
2:D:227:VAL:HB	2:D:292:LEU:HD23	2.02	0.41
2:D:362:LEU:HD21	2:D:497:LEU:HB2	2.03	0.41
2:D:440:ASP:HB3	2:D:441:PHE:CE1	2.56	0.41
2:D:481:ARG:HB3	2:D:481:ARG:CZ	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:242:ALA:O	3:E:246:LYS:HG2	2.21	0.41
3:F:102:VAL:HG21	3:F:135:PHE:CD1	2.56	0.41
3:F:23:VAL:CG1	3:F:33:VAL:HG11	2.51	0.41
3:H:195:LEU:O	3:H:198:ALA:HB3	2.21	0.41
3:H:91:PRO:HB2	3:H:95:VAL:O	2.20	0.41
2:B:309:TRP:CD1	2:B:309:TRP:N	2.85	0.41
2:B:31:PHE:CD1	2:B:31:PHE:N	2.89	0.41
2:B:358:SER:OG	2:D:478:HIS:NE2	2.53	0.41
2:B:76:VAL:O	2:B:80:LEU:HG	2.20	0.41
1:C:106:VAL:HG12	1:C:144:LEU:HD12	2.02	0.41
1:C:277:ARG:HE	1:C:277:ARG:CA	2.33	0.41
1:C:359:ARG:N	1:C:360:PRO:CD	2.83	0.41
1:C:402:ASP:O	1:C:403:ASP:HB3	2.21	0.41
1:C:475:LEU:HD13	2:D:265:ALA:O	2.21	0.41
1:C:67:SER:HB3	1:C:183:CYS:HB3	2.02	0.41
2:D:142:TYR:C	2:D:144:PRO:CD	2.88	0.41
2:D:179:PHE:CD2	2:D:179:PHE:C	2.94	0.41
2:D:186:THR:N	2:D:187:PRO:HD3	2.36	0.41
2:D:445:ASN:HB2	2:D:472:PRO:O	2.20	0.41
2:D:510:ARG:O	2:D:510:ARG:HG2	2.21	0.41
2:B:125:PHE:HZ	3:E:58:MET:O	2.03	0.41
3:F:99:GLY:O	3:F:134:GLY:HA3	2.20	0.41
3:F:208:ILE:HG22	3:F:209:HIS:N	2.35	0.41
3:G:26:LEU:CD1	3:G:244:ALA:HB1	2.51	0.41
1:A:207:LEU:HD11	1:A:266:PRO:HD3	2.03	0.41
1:A:428:LYS:O	1:A:432:GLN:HG3	2.20	0.41
2:B:421:VAL:HG12	2:B:422:TYR:N	2.35	0.41
2:B:495:THR:HG22	2:B:499:ASN:HD22	1.86	0.41
1:C:346:LEU:HB3	1:C:372:MET:SD	2.61	0.41
1:C:86:VAL:HB	1:C:117:ASP:OD2	2.19	0.41
2:D:188:SER:HB2	6:D:3498:CLF:S2B	2.61	0.41
2:D:365:LYS:HG3	2:D:501:ILE:HD11	2.02	0.41
2:D:296:TRP:CZ3	2:D:402:TRP:HA	2.55	0.41
2:D:461:GLU:HG3	2:D:461:GLU:O	2.21	0.41
3:G:95:VAL:CG1	3:G:95:VAL:O	2.62	0.41
3:H:9:GLY:C	3:H:15:LYS:HE3	2.41	0.41
3:H:214:ASP:O	3:H:217:VAL:HG23	2.21	0.41
3:H:23:VAL:HG12	3:H:33:VAL:HG11	2.03	0.41
3:H:70:LEU:HD23	3:H:70:LEU:HA	1.76	0.41
1:A:224:ALA:HB2	1:A:251:ALA:HB3	2.01	0.41
1:A:443:SER:C	1:A:445:ASP:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:ARG:HG3	2:B:8:ILE:HD12	2.03	0.41
2:B:170:LYS:HD3	2:B:175:ILE:HG13	2.03	0.41
2:B:20:TYR:O	2:B:24:LEU:HG	2.21	0.41
2:B:512:MET:CE	2:D:457:HIS:CD2	3.04	0.41
2:D:399:ASN:C	2:D:399:ASN:OD1	2.60	0.41
2:D:70:CYS:O	2:D:193:HIS:CA	2.69	0.41
3:E:4:GLN:NE2	3:E:124:TYR:OH	2.54	0.41
3:F:161:ALA:O	3:F:165:SER:OG	2.39	0.41
1:A:79:ILE:HG13	1:A:145:ASN:HB2	2.02	0.41
1:A:241:LEU:HD11	1:A:453:PHE:CD1	2.56	0.41
1:A:57:MET:CE	2:B:100:ARG:CZ	2.99	0.41
1:C:222:ASP:OD1	1:C:248:ARG:HG2	2.20	0.41
1:C:301:GLY:HA2	1:C:456:PHE:CD1	2.56	0.41
2:D:221:ASN:CG	2:D:223:LYS:HD3	2.41	0.41
2:D:456:LEU:HD11	2:D:460:LYS:CD	2.51	0.41
2:B:125:PHE:HZ	3:E:59:GLU:HA	1.86	0.41
3:F:129:ASP:HB3	3:F:131:VAL:HG12	2.03	0.41
3:F:179:LEU:HD12	3:F:256:PRO:HG3	2.02	0.41
3:F:41:LYS:HB3	3:F:43:ASP:OD1	2.21	0.41
3:G:100:ARG:NH1	3:G:103:ILE:CG2	2.84	0.41
3:G:199:LEU:HD11	3:G:259:ILE:HD11	2.03	0.41
1:A:107:ASN:O	1:A:107:ASN:ND2	2.53	0.40
1:A:90:GLN:N	1:A:113:ASN:ND2	2.68	0.40
1:A:413:VAL:HG11	1:A:431:PHE:HD2	1.85	0.40
1:A:48:SER:HB2	1:A:402:ASP:OD2	2.21	0.40
2:B:69:ALA:HB3	2:B:193:HIS:HB3	2.03	0.40
2:B:510:ARG:CG	2:B:510:ARG:O	2.70	0.40
2:B:54:GLU:O	2:B:58:GLN:HG3	2.22	0.40
1:C:148:ILE:O	1:C:178:ILE:HA	2.21	0.40
1:C:240:ILE:O	1:C:244:GLU:HG3	2.21	0.40
1:C:96:ARG:HH11	1:C:96:ARG:CG	2.33	0.40
2:D:233:TYR:HB2	2:D:236:ASN:ND2	2.27	0.40
3:E:225:MET:HE2	3:E:230:TYR:HB2	2.03	0.40
3:E:61:ALA:HA	3:E:70:LEU:HG	2.03	0.40
1:A:207:LEU:HD11	1:A:266:PRO:CD	2.52	0.40
1:A:218:SER:OG	1:A:269:LYS:CE	2.57	0.40
1:A:258:SER:HB2	1:A:261:GLU:H	1.86	0.40
1:A:42:SER:O	1:A:43:LYS:C	2.60	0.40
1:A:94:ALA:HB3	2:D:521:LEU:HD22	2.03	0.40
1:C:204:ASP:HB2	1:C:205:TRP:CD1	2.57	0.40
2:D:247:MET:CE	2:D:340:ILE:HA	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:62:LEU:HD23	2:D:64:VAL:HG23	2.02	0.40
3:E:13:ILE:HD12	3:E:150:VAL:O	2.20	0.40
2:B:185:HIS:CE1	3:F:140:ARG:HH12	2.39	0.40
3:F:158:MET:CE	3:F:195:LEU:HG	2.51	0.40
3:G:223:ARG:O	3:G:224:ARG:CB	2.63	0.40
3:H:186:SER:CB	3:H:210:PHE:CZ	3.00	0.40
3:H:50:HIS:O	3:H:51:SER:CB	2.61	0.40
1:A:200:ASP:HA	1:A:203:ARG:HG2	2.03	0.40
1:A:367:TYR:O	1:A:368:GLU:C	2.59	0.40
1:A:427:GLU:HB2	1:A:431:PHE:CE1	2.56	0.40
2:B:224:ILE:HD12	2:B:249:VAL:HG11	2.03	0.40
2:B:32:GLU:O	2:B:33:GLU:C	2.59	0.40
1:C:16:VAL:O	1:C:19:VAL:HG22	2.21	0.40
1:C:43:LYS:HE2	1:C:384:ASN:ND2	2.36	0.40
2:D:79:ALA:O	2:D:80:LEU:C	2.58	0.40
3:E:131:VAL:HG22	3:E:132:CYS:SG	2.61	0.40
3:E:179:LEU:HB2	3:E:256:PRO:HG3	2.02	0.40
1:A:118:PHE:HD1	1:A:123:ILE:HD13	1.86	0.40
1:A:67:SER:HB2	1:A:183:CYS:CB	2.52	0.40
1:A:265:THR:HG22	1:A:286:MET:CE	2.49	0.40
1:A:315:LYS:HD3	1:A:315:LYS:HA	1.79	0.40
1:A:8:GLU:O	1:A:11:SER:N	2.55	0.40
2:B:293:LEU:O	2:B:318:ILE:HA	2.20	0.40
2:B:415:TYR:CD1	2:B:415:TYR:N	2.90	0.40
1:C:250:VAL:HA	2:D:31:PHE:CE2	2.55	0.40
1:C:245:MET:HG3	1:C:324:CYS:HA	2.04	0.40
1:C:9:VAL:HB	1:C:34:VAL:HG22	2.04	0.40
2:D:247:MET:CB	2:D:249:VAL:HG23	2.50	0.40
3:E:233:LYS:O	3:E:234:ALA:C	2.59	0.40
3:E:239:GLU:OE1	3:E:239:GLU:HA	2.22	0.40
3:E:94:GLY:O	3:E:95:VAL:CG2	2.64	0.40
3:G:106:ILE:HD12	3:G:137:MET:CB	2.46	0.40
3:H:185:ASN:ND2	3:H:211:VAL:CG1	2.84	0.40
1:A:137:GLU:O	1:A:141:LEU:HB2	2.21	0.40
1:A:229:TYR:O	1:A:230:ASN:HB3	2.21	0.40
2:B:161:ASP:OD2	2:B:164:ALA:HB2	2.21	0.40
2:B:227:VAL:HA	2:B:228:PRO:HD2	1.95	0.40
2:B:240:ILE:HA	2:B:240:ILE:HD13	1.96	0.40
2:B:359:HIS:NE2	1:C:466:THR:HG23	2.36	0.40
2:B:43:VAL:O	2:B:46:TRP:HB3	2.21	0.40
2:B:516:ASP:O	2:B:519:HIS:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:106:VAL:HG21	2:D:44:PHE:HD1	1.87	0.40
1:C:437:PRO:HA	1:C:472:TRP:CH2	2.55	0.40
2:D:131:MET:CE	2:D:149:VAL:HG11	2.51	0.40
2:D:161:ASP:OD2	2:D:164:ALA:HB2	2.21	0.40
2:D:376:VAL:O	2:D:380:VAL:HG23	2.21	0.40
3:F:187:ARG:HD3	3:F:187:ARG:HA	1.90	0.40
3:F:26:LEU:HD12	3:F:244:ALA:HB1	2.03	0.40
3:F:26:LEU:HD12	3:F:29:MET:HE2	2.02	0.40
3:H:250:ASN:ND2	3:H:252:LEU:N	2.70	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	474/492 (96%)	420 (89%)	47 (10%)	7 (2%)	10	42
1	C	474/492 (96%)	415 (88%)	52 (11%)	7 (2%)	10	42
2	B	520/523 (99%)	470 (90%)	43 (8%)	7 (1%)	12	45
2	D	520/523 (99%)	450 (86%)	60 (12%)	10 (2%)	8	36
3	E	266/289 (92%)	232 (87%)	29 (11%)	5 (2%)	8	36
3	F	265/289 (92%)	232 (88%)	25 (9%)	8 (3%)	4	24
3	G	266/289 (92%)	225 (85%)	33 (12%)	8 (3%)	4	24
3	H	266/289 (92%)	234 (88%)	24 (9%)	8 (3%)	4	24
All	All	3051/3186 (96%)	2678 (88%)	313 (10%)	60 (2%)	7	34

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	13	PRO

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Mol	Chain	Res	Type
2	B	391	VAL
2	D	13	PRO
2	D	439	PRO
3	E	53	ALA
3	F	50	HIS
3	G	95	VAL
3	H	50	HIS
3	H	186	SER
2	D	391	VAL
3	E	95	VAL
3	E	116	GLU
3	F	53	ALA
3	F	116	GLU
3	G	50	HIS
3	G	53	ALA
3	H	118	ASP
1	C	37	PRO
2	D	117	SER
2	D	255	SER
3	F	128	GLY
3	G	258	PRO
1	A	302	PRO
1	C	85	PRO
3	F	215	ASN
3	G	116	GLU
3	G	131	VAL
3	H	51	SER
1	A	355	ILE
2	B	255	SER
2	D	187	PRO
3	E	140	ARG
3	H	189	THR
1	A	73	GLY
1	A	117	ASP
1	A	255	GLY
2	B	187	PRO
2	B	473	ILE
1	C	73	GLY
1	C	254	SER
2	D	258	GLU
3	E	50	HIS
3	G	46	ARG

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Mol	Chain	Res	Type
1	C	255	GLY
3	F	14	GLY
3	F	130	VAL
1	A	37	PRO
1	C	180	PRO
2	D	473	ILE
3	H	130	VAL
2	B	228	PRO
1	C	355	ILE
2	D	66	PRO
2	D	486	GLY
3	H	11	GLY
3	H	95	VAL
1	A	85	PRO
2	B	319	PRO
3	F	138	PRO
3	G	256	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	405/415 (98%)	362 (89%)	43 (11%)	6	26
1	C	405/415 (98%)	357 (88%)	48 (12%)	5	22
2	B	453/455 (100%)	398 (88%)	55 (12%)	5	21
2	D	453/455 (100%)	411 (91%)	42 (9%)	9	33
3	E	216/233 (93%)	186 (86%)	30 (14%)	3	16
3	F	215/233 (92%)	190 (88%)	25 (12%)	5	23
3	G	216/233 (93%)	188 (87%)	28 (13%)	4	19
3	H	216/233 (93%)	189 (88%)	27 (12%)	4	20
All	All	2579/2672 (96%)	2281 (88%)	298 (12%)	5	23

All (298) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	17	LEU
1	A	21	PRO
1	A	29	ASN
1	A	32	LEU
1	A	45	CYS
1	A	70	VAL
1	A	74	PRO
1	A	96	ARG
1	A	98	ASN
1	A	100	TYR
1	A	112	MET
1	A	140	THR
1	A	141	LEU
1	A	143	PRO
1	A	145	ASN
1	A	152	SER
1	A	183	CYS
1	A	184	GLU
1	A	210	ARG
1	A	266	PRO
1	A	277	ARG
1	A	279	MET
1	A	280	ASN
1	A	298	ASN
1	A	302	PRO
1	A	317	ASP
1	A	324	CYS
1	A	343	ARG
1	A	344	PRO
1	A	345	ARG
1	A	351	VAL
1	A	355	ILE
1	A	362	HIS
1	A	401	TYR
1	A	409	PHE
1	A	418	PRO
1	A	419	ASP
1	A	421	ILE
1	A	428	LYS
1	A	444	TRP
1	A	446	TYR
1	A	462	ASP

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Mol	Chain	Res	Type
2	B	3	GLN
2	B	13	PRO
2	B	14	LEU
2	B	31	PHE
2	B	41	ASP
2	B	54	GLU
2	B	66	PRO
2	B	83	GLU
2	B	115	SER
2	B	116	ASP
2	B	121	ASP
2	B	130	ASN
2	B	144	PRO
2	B	153	CYS
2	B	154	MET
2	B	172	GLU
2	B	179	PHE
2	B	180	PRO
2	B	182	PRO
2	B	187	PRO
2	B	188	SER
2	B	197	TRP
2	B	202	GLU
2	B	206	ARG
2	B	234	LEU
2	B	238	ARG
2	B	245	SER
2	B	260	VAL
2	B	263	THR
2	B	264	PRO
2	B	277	THR
2	B	278	GLN
2	B	279	GLU
2	B	281	MET
2	B	314	PRO
2	B	326	ASP
2	B	339	PRO
2	B	341	PRO
2	B	350	ARG
2	B	375	PHE
2	B	384	LEU
2	B	397	ASN

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Mol	Chain	Res	Type
2	B	414	PRO
2	B	418	ASN
2	B	420	THR
2	B	426	ASP
2	B	435	PHE
2	B	461	GLU
2	B	472	PRO
2	B	491	MET
2	B	496	THR
2	B	504	ARG
2	B	519	HIS
2	B	522	VAL
2	B	523	ARG
1	C	14	GLN
1	C	21	PRO
1	C	29	ASN
1	C	30	LYS
1	C	32	LEU
1	C	37	PRO
1	C	44	LYS
1	C	48	SER
1	C	54	PRO
1	C	59	ILE
1	C	70	VAL
1	C	74	PRO
1	C	75	ILE
1	C	85	PRO
1	C	92	SER
1	C	96	ARG
1	C	98	ASN
1	C	100	TYR
1	C	120	GLU
1	C	155	PRO
1	C	184	GLU
1	C	187	ARG
1	C	203	ARG
1	C	240	ILE
1	C	252	GLN
1	C	258	SER
1	C	266	PRO
1	C	267	LYS
1	C	279	MET

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Mol	Chain	Res	Type
1	C	280	ASN
1	C	288	GLU
1	C	298	ASN
1	C	302	PRO
1	C	317	ASP
1	C	324	CYS
1	C	345	ARG
1	C	346	LEU
1	C	360	PRO
1	C	362	HIS
1	C	383	HIS
1	C	398	THR
1	C	401	TYR
1	C	409	PHE
1	C	419	ASP
1	C	421	ILE
1	C	444	TRP
1	C	446	TYR
1	C	462	ASP
2	D	3	GLN
2	D	11	SER
2	D	13	PRO
2	D	14	LEU
2	D	31	PHE
2	D	41	ASP
2	D	54	GLU
2	D	62	LEU
2	D	121	ASP
2	D	130	ASN
2	D	144	PRO
2	D	146	MET
2	D	179	PHE
2	D	202	GLU
2	D	234	LEU
2	D	245	SER
2	D	253	LEU
2	D	264	PRO
2	D	277	THR
2	D	278	GLN
2	D	281	MET
2	D	285	PRO
2	D	295	PRO

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Mol	Chain	Res	Type
2	D	300	LYS
2	D	317	ASN
2	D	326	ASP
2	D	369	LEU
2	D	375	PHE
2	D	384	LEU
2	D	397	ASN
2	D	418	ASN
2	D	420	THR
2	D	425	LYS
2	D	426	ASP
2	D	435	PHE
2	D	461	GLU
2	D	472	PRO
2	D	496	THR
2	D	504	ARG
2	D	519	HIS
2	D	522	VAL
2	D	523	ARG
3	E	2	MET
3	E	4	GLN
3	E	46	ARG
3	E	54	GLN
3	E	56	THR
3	E	60	MET
3	E	66	THR
3	E	76	LEU
3	E	87	GLU
3	E	95	VAL
3	E	131	VAL
3	E	137	MET
3	E	152	SER
3	E	156	MET
3	E	165	SER
3	E	185	ASN
3	E	186	SER
3	E	193	ASP
3	E	199	LEU
3	E	208	ILE
3	E	214	ASP
3	E	225	MET
3	E	228	ILE

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Mol	Chain	Res	Type
3	E	232	PRO
3	E	250	ASN
3	E	251	LYS
3	E	255	ILE
3	E	259	ILE
3	E	264	LEU
3	E	266	GLU
3	F	2	MET
3	F	3	ARG
3	F	48	ILE
3	F	56	THR
3	F	60	MET
3	F	66	THR
3	F	71	GLU
3	F	76	LEU
3	F	95	VAL
3	F	118	ASP
3	F	131	VAL
3	F	140	ARG
3	F	165	SER
3	F	179	LEU
3	F	182	LEU
3	F	199	LEU
3	F	208	ILE
3	F	213	ARG
3	F	214	ASP
3	F	251	LYS
3	F	255	ILE
3	F	259	ILE
3	F	264	LEU
3	F	266	GLU
3	F	267	LEU
3	G	2	MET
3	G	3	ARG
3	G	4	GLN
3	G	5	CYS
3	G	10	LYS
3	G	46	ARG
3	G	48	ILE
3	G	54	GLN
3	G	56	THR
3	G	60	MET

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Mol	Chain	Res	Type
3	G	66	THR
3	G	76	LEU
3	G	95	VAL
3	G	131	VAL
3	G	152	SER
3	G	156	MET
3	G	165	SER
3	G	199	LEU
3	G	208	ILE
3	G	214	ASP
3	G	225	MET
3	G	228	ILE
3	G	250	ASN
3	G	255	ILE
3	G	259	ILE
3	G	264	LEU
3	G	266	GLU
3	G	267	LEU
3	H	2	MET
3	H	4	GLN
3	H	5	CYS
3	H	10	LYS
3	H	17	THR
3	H	46	ARG
3	H	56	THR
3	H	66	THR
3	H	76	LEU
3	H	95	VAL
3	H	137	MET
3	H	152	SER
3	H	165	SER
3	H	178	ARG
3	H	185	ASN
3	H	187	ARG
3	H	199	LEU
3	H	208	ILE
3	H	214	ASP
3	H	225	MET
3	H	228	ILE
3	H	250	ASN
3	H	255	ILE
3	H	259	ILE

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Mol	Chain	Res	Type
3	H	264	LEU
3	H	266	GLU
3	H	267	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (81) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	49	ASN
1	A	53	GLN
1	A	113	ASN
1	A	145	ASN
1	A	191	GLN
1	A	199	ASN
1	A	274	HIS
1	A	280	ASN
1	A	298	ASN
1	A	362	HIS
1	A	432	GLN
1	A	442	HIS
2	B	3	GLN
2	B	18	GLN
2	B	71	GLN
2	B	128	GLN
2	B	129	GLN
2	B	130	ASN
2	B	137	ASN
2	B	167	ASN
2	B	168	ASN
2	B	185	HIS
2	B	225	ASN
2	B	289	ASN
2	B	397	ASN
2	B	418	ASN
2	B	429	HIS
2	B	452	GLN
2	B	457	HIS
2	B	480	HIS
2	B	518	ASN
1	C	35	ASN
1	C	151	GLN
1	C	280	ASN

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Mol	Chain	Res	Type
1	C	298	ASN
1	C	362	HIS
1	C	384	ASN
1	C	432	GLN
1	C	476	GLN
2	D	3	GLN
2	D	18	GLN
2	D	58	GLN
2	D	104	ASN
2	D	129	GLN
2	D	130	ASN
2	D	137	ASN
2	D	167	ASN
2	D	168	ASN
2	D	199	ASN
2	D	225	ASN
2	D	268	GLN
2	D	294	GLN
2	D	317	ASN
2	D	396	HIS
2	D	397	ASN
2	D	452	GLN
2	D	457	HIS
2	D	518	ASN
3	E	4	GLN
3	E	107	ASN
3	E	206	GLN
3	E	236	GLN
3	E	250	ASN
3	F	4	GLN
3	F	107	ASN
3	F	206	GLN
3	F	250	ASN
3	G	4	GLN
3	G	54	GLN
3	G	206	GLN
3	G	236	GLN
3	G	250	ASN
3	H	4	GLN
3	H	54	GLN
3	H	55	ASN
3	H	107	ASN

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Mol	Chain	Res	Type
3	H	185	ASN
3	H	206	GLN
3	H	236	GLN
3	H	250	ASN

### 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 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	$\# Z  > 2$
5	CFM	C	3496	1	0,24,24	0.00	-	-		
9	ATP	F	6292	8	26,33,33	1.08	0	31,52,52	1.56	5 (16%)
4	HCA	A	1494	-	4,13,13	0.58	0	4,18,18	2.64	2 (50%)
5	CFM	A	1496	1	0,24,24	0.00	-	-		
10	SF4	G	7290	3	0,12,12	0.00	-	-		
9	ATP	G	7292	8	26,33,33	1.84	7 (26%)	31,52,52	1.40	4 (12%)
10	SF4	F	5290	3	0,12,12	0.00	-	-		
6	CLF	D	3498	1,2	0,24,24	0.00	-	-		
9	ATP	H	8292	8	26,33,33	1.19	3 (11%)	31,52,52	1.50	5 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	ATP	E	5292	8	26,33,33	1.20	2 (7%)	31,52,52	1.42	4 (12%)
4	HCA	C	3494	-	4,13,13	0.54	0	4,18,18	1.18	0
6	CLF	A	1498	1,2	0,24,24	0.00	-	-		

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
9	ATP	H	8292	8	-	3/18/38/38	0/3/3/3
6	CLF	A	1498	1,2	-	-	0/12/10/10
4	HCA	A	1494	-	-	6/7/17/17	-
10	SF4	G	7290	3	-	-	0/6/5/5
9	ATP	G	7292	8	-	6/18/38/38	0/3/3/3
10	SF4	F	5290	3	-	-	0/6/5/5
6	CLF	D	3498	1,2	-	-	0/12/10/10
9	ATP	E	5292	8	-	5/18/38/38	0/3/3/3
4	HCA	C	3494	-	-	4/7/17/17	-
9	ATP	F	6292	8	-	8/18/38/38	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	G	7292	ATP	C4-N3	5.32	1.43	1.35
9	G	7292	ATP	O4'-C1'	4.21	1.47	1.41
9	G	7292	ATP	C2-N3	3.09	1.37	1.32
9	E	5292	ATP	C4-N3	3.01	1.39	1.35
9	H	8292	ATP	C8-N7	-2.64	1.30	1.34
9	G	7292	ATP	C2'-C1'	2.42	1.57	1.53
9	E	5292	ATP	C8-N7	-2.25	1.30	1.34
9	H	8292	ATP	PB-O2B	-2.15	1.45	1.55
9	H	8292	ATP	C4-N3	2.14	1.38	1.35
9	G	7292	ATP	PG-O2G	-2.06	1.46	1.54
9	G	7292	ATP	C8-N7	-2.03	1.31	1.34
9	G	7292	ATP	PB-O2B	-2.01	1.45	1.55

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1494	HCA	C4-C3-C7	-4.82	103.03	111.52
9	E	5292	ATP	O4'-C1'-C2'	-4.74	99.99	106.93
9	H	8292	ATP	O4'-C1'-C2'	-4.55	100.27	106.93
9	G	7292	ATP	O4'-C1'-C2'	-4.42	100.47	106.93
9	F	6292	ATP	O4'-C1'-C2'	-4.32	100.62	106.93
9	F	6292	ATP	C3'-C2'-C1'	3.95	106.93	100.98
9	G	7292	ATP	O3'-C3'-C4'	-3.32	101.46	111.05
9	F	6292	ATP	C4-C5-N7	3.27	112.80	109.40
9	H	8292	ATP	C4-C5-N7	3.18	112.71	109.40
9	H	8292	ATP	C3'-C2'-C1'	3.16	105.73	100.98
9	F	6292	ATP	O3'-C3'-C4'	-2.75	103.11	111.05
9	E	5292	ATP	O3G-PG-O2G	2.63	117.68	107.64
9	H	8292	ATP	O3G-PG-O2G	2.56	117.41	107.64
9	G	7292	ATP	C3'-C2'-C1'	2.51	104.75	100.98
9	E	5292	ATP	C4-C5-N7	2.47	111.97	109.40
9	H	8292	ATP	O3'-C3'-C4'	-2.23	104.60	111.05
9	E	5292	ATP	C3'-C2'-C1'	2.20	104.28	100.98
9	F	6292	ATP	O3G-PG-O2G	2.11	115.68	107.64
4	A	1494	HCA	C3-C2-C1	2.01	118.20	114.98
9	G	7292	ATP	O3G-PG-O2G	2.01	115.30	107.64

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	F	6292	ATP	PB-O3B-PG-O2G
9	F	6292	ATP	C5'-O5'-PA-O3A
9	E	5292	ATP	PB-O3B-PG-O2G
9	E	5292	ATP	C5'-O5'-PA-O3A
4	A	1494	HCA	C2-C3-C4-C5
4	A	1494	HCA	C7-C3-C4-C5
4	A	1494	HCA	O7-C3-C4-C5
9	G	7292	ATP	C5'-O5'-PA-O1A
9	G	7292	ATP	C5'-O5'-PA-O2A
9	G	7292	ATP	C5'-O5'-PA-O3A
9	H	8292	ATP	C5'-O5'-PA-O3A
4	C	3494	HCA	C2-C3-C4-C5
4	C	3494	HCA	C7-C3-C4-C5
4	C	3494	HCA	O7-C3-C4-C5
9	G	7292	ATP	C3'-C4'-C5'-O5'
4	A	1494	HCA	C1-C2-C3-C4
9	G	7292	ATP	O4'-C4'-C5'-O5'
4	C	3494	HCA	C3-C4-C5-C6

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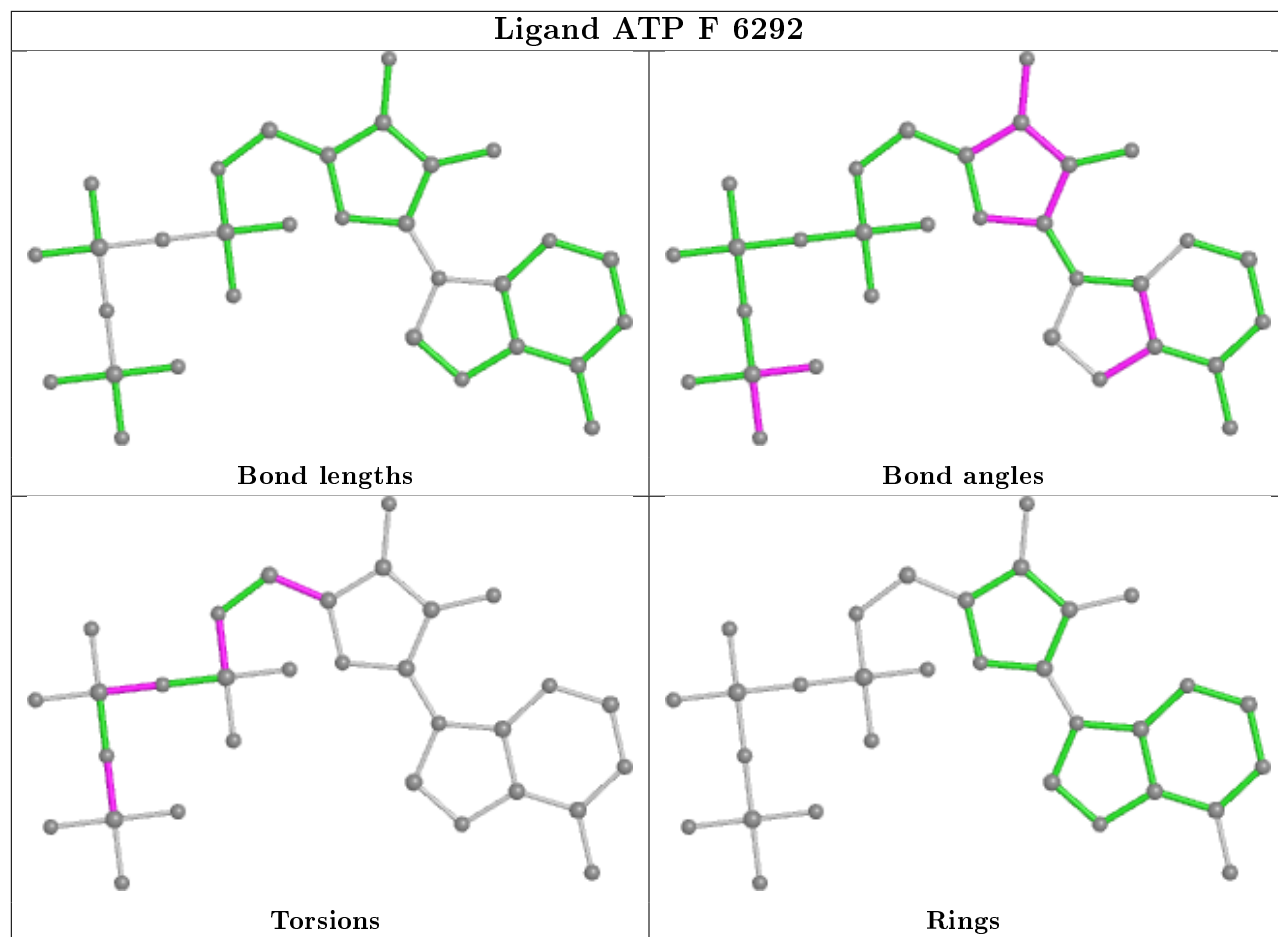
Mol	Chain	Res	Type	Atoms
9	F	6292	ATP	PA-O3A-PB-O1B
9	E	5292	ATP	PA-O3A-PB-O1B
9	F	6292	ATP	C5'-O5'-PA-O1A
9	F	6292	ATP	C5'-O5'-PA-O2A
4	A	1494	HCA	C1-C2-C3-C7
9	F	6292	ATP	O4'-C4'-C5'-O5'
9	G	7292	ATP	PB-O3B-PG-O2G
9	F	6292	ATP	C3'-C4'-C5'-O5'
9	F	6292	ATP	PA-O3A-PB-O2B
9	E	5292	ATP	PA-O3A-PB-O2B
9	H	8292	ATP	PA-O3A-PB-O1B
4	A	1494	HCA	C1-C2-C3-O7
9	E	5292	ATP	C5'-O5'-PA-O1A
9	H	8292	ATP	C5'-O5'-PA-O1A

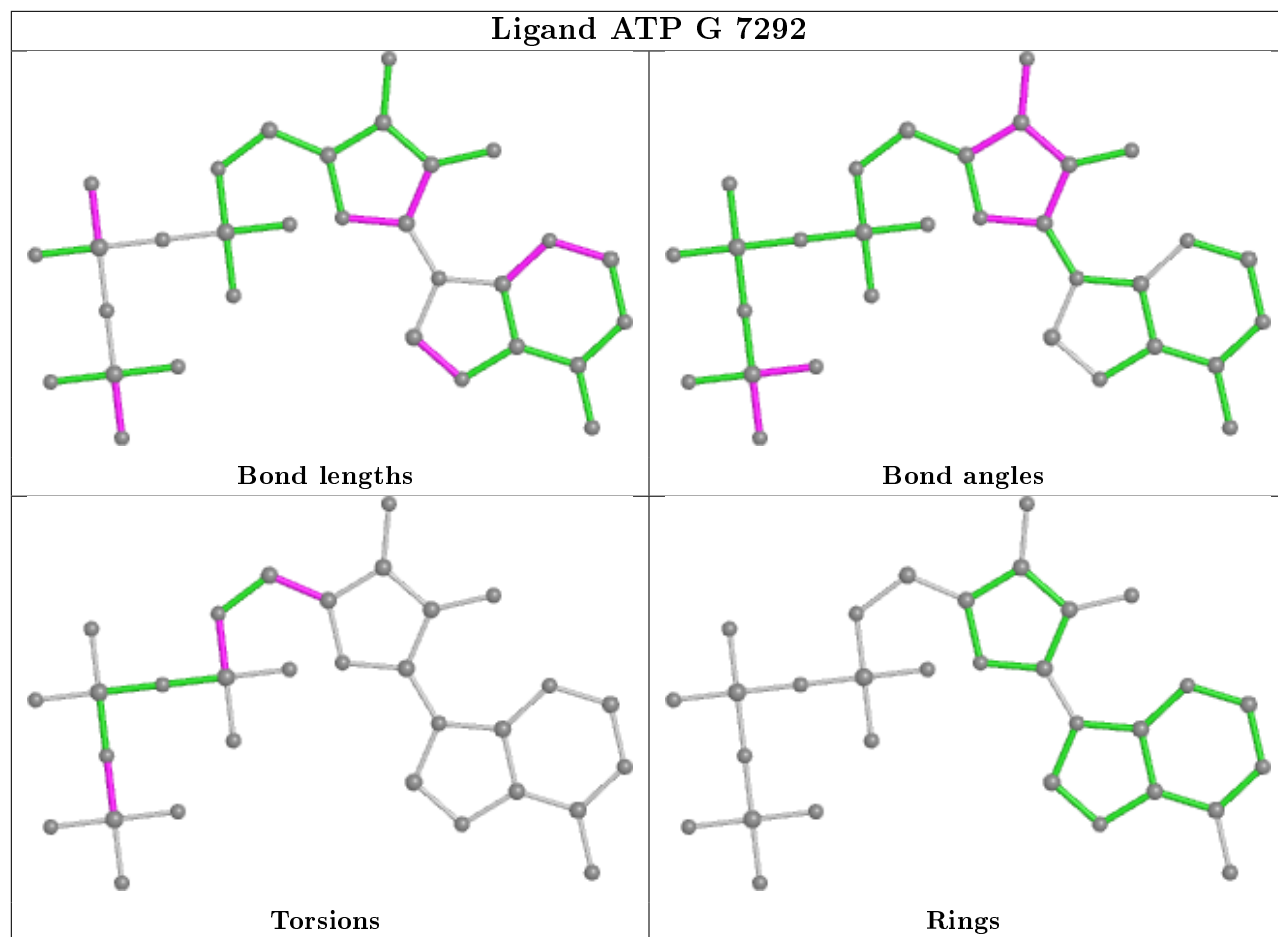
There are no ring outliers.

10 monomers are involved in 45 short contacts:

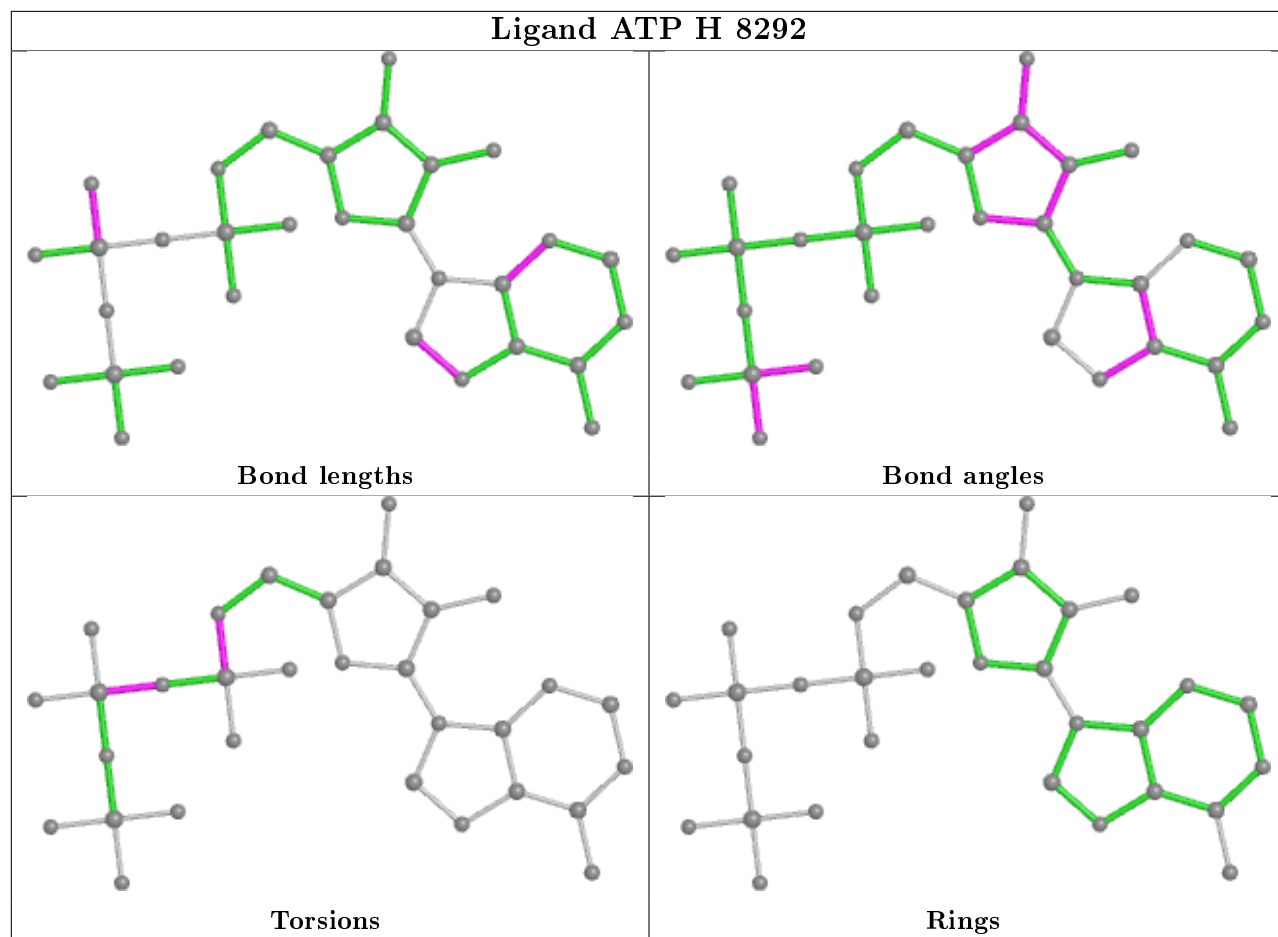
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	3496	CFM	7	0
9	F	6292	ATP	6	0
4	A	1494	HCA	1	0
5	A	1496	CFM	4	0
9	G	7292	ATP	11	0
6	D	3498	CLF	3	0
9	H	8292	ATP	6	0
9	E	5292	ATP	4	0
4	C	3494	HCA	2	0
6	A	1498	CLF	1	0

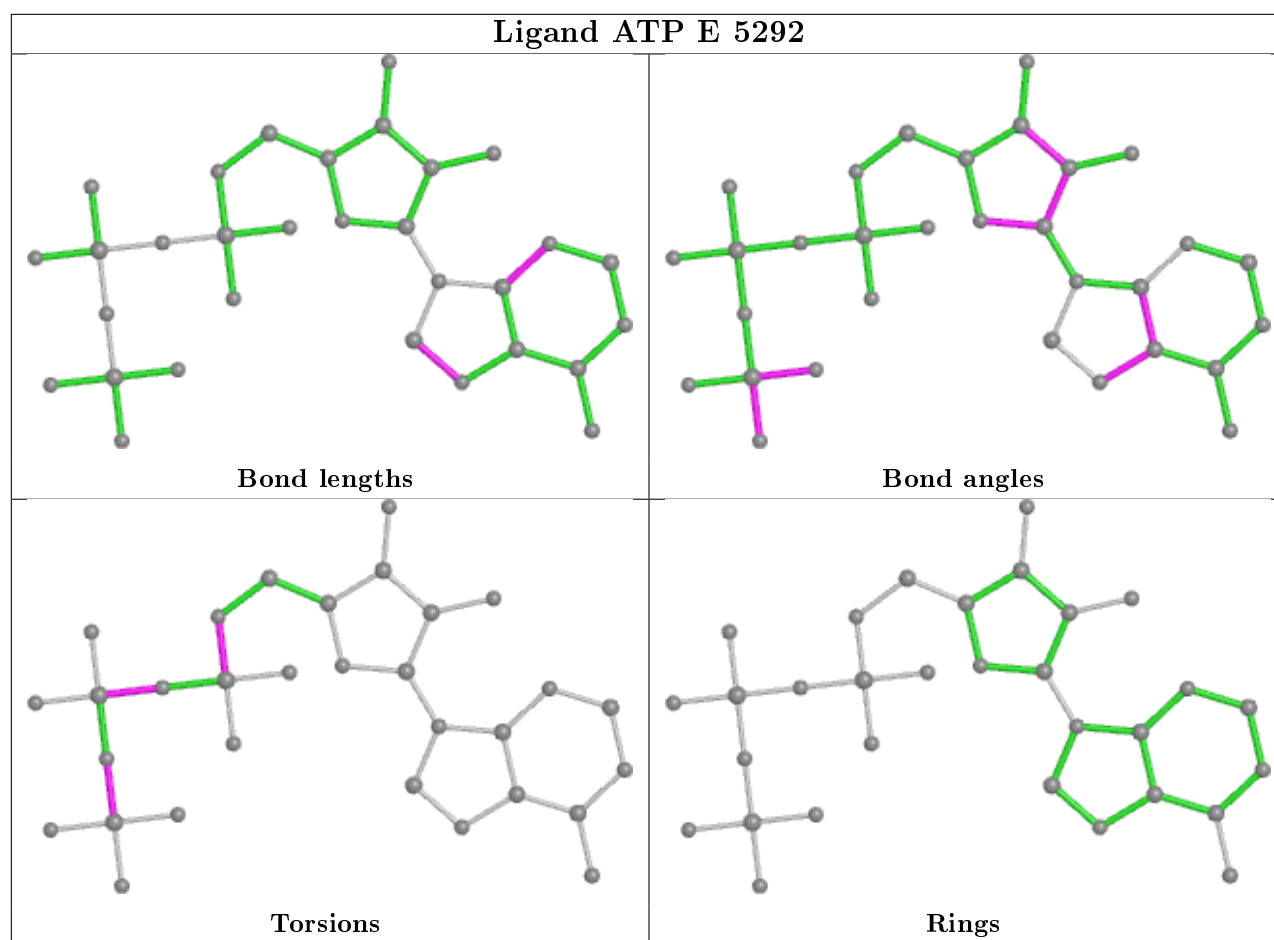
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.