



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2022 – 08:06 PM JST

PDB ID : 7W0J  
Title : Acyl-CoA dehydrogenase, Tfu\_1647  
Authors : Liu, L.X.; Zhou, S.H.; Deng, Y.  
Deposited on : 2021-11-18  
Resolution : 3.13 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

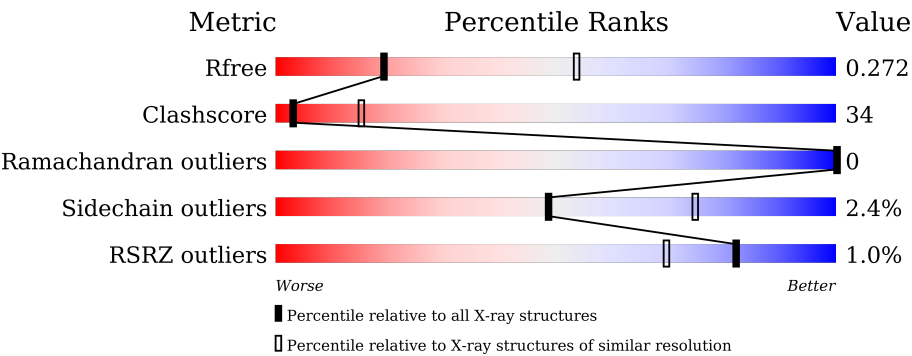
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.13 Å.

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





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1626 (3.18-3.10)
Clashscore	141614	1735 (3.18-3.10)
Ramachandran outliers	138981	1677 (3.18-3.10)
Sidechain outliers	138945	1677 (3.18-3.10)
RSRZ outliers	127900	1588 (3.18-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	385	<div><div>%</div><div><div></div><div>40%</div><div>54%</div><div></div></div><div>..</div></div>
1	B	385	<div><div>%</div><div><div></div><div>45%</div><div>54%</div><div></div></div><div>..</div></div>
1	C	385	<div><div></div><div><div></div><div>47%</div><div>51%</div><div></div></div><div>..</div></div>
1	D	385	<div><div>2%</div><div><div></div><div>46%</div><div>51%</div><div></div></div><div>..</div></div>
1	E	385	<div><div>%</div><div><div></div><div>48%</div><div>49%</div><div></div></div><div>..</div></div>
1	F	385	<div><div>2%</div><div><div></div><div>45%</div><div>51%</div><div></div></div><div>..</div></div>

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Mol	Chain	Length	Quality of chain
1	G	385	
1	H	385	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	875	E	401	-	-	-	X
2	875	E	402	-	-	-	X
2	875	H	401	-	-	-	X

## 2 Entry composition

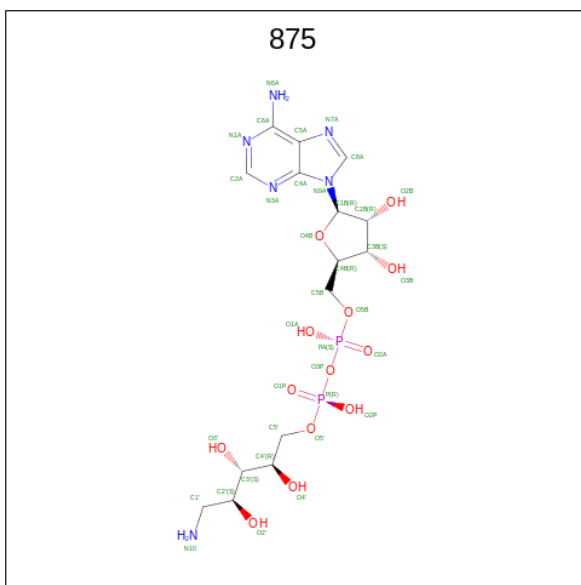
There are 2 unique types of molecules in this entry. The entry contains 23345 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Acyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	0	0
			2844	1777	502	550	15			
1	D	376	Total	C	N	O	S	0	0	0
			2894	1813	505	561	15			
1	G	379	Total	C	N	O	S	0	0	0
			2912	1821	514	562	15			
1	F	379	Total	C	N	O	S	0	0	0
			2906	1818	511	562	15			
1	B	380	Total	C	N	O	S	0	0	0
			2920	1825	515	565	15			
1	C	380	Total	C	N	O	S	0	0	0
			2914	1822	512	565	15			
1	E	382	Total	C	N	O	S	0	0	0
			2933	1835	514	569	15			
1	H	380	Total	C	N	O	S	0	0	0
			2914	1822	512	565	15			

- Molecule 2 is [[(2R,3S,4R,5R)-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] [(2R,3S,4S)-5-azanyl-2,3,4-tris(oxidanyl)pentyl] hydrogen phosphate (three-letter code: 875) (formula: C<sub>15</sub>H<sub>26</sub>N<sub>6</sub>O<sub>13</sub>P<sub>2</sub>).

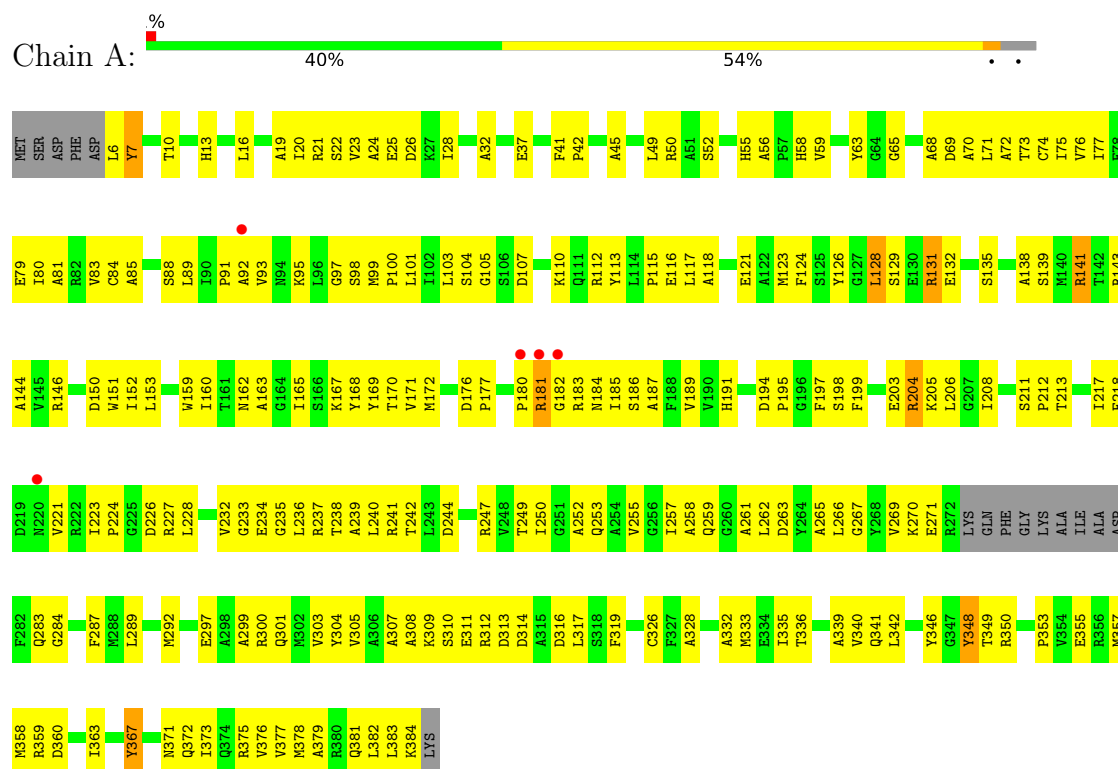


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	E	1	Total 36	C 15	N 6	O 13	P 2	0	0
2	E	1	Total 36	C 15	N 6	O 13	P 2	0	0
2	H	1	Total 36	C 15	N 6	O 13	P 2	0	0

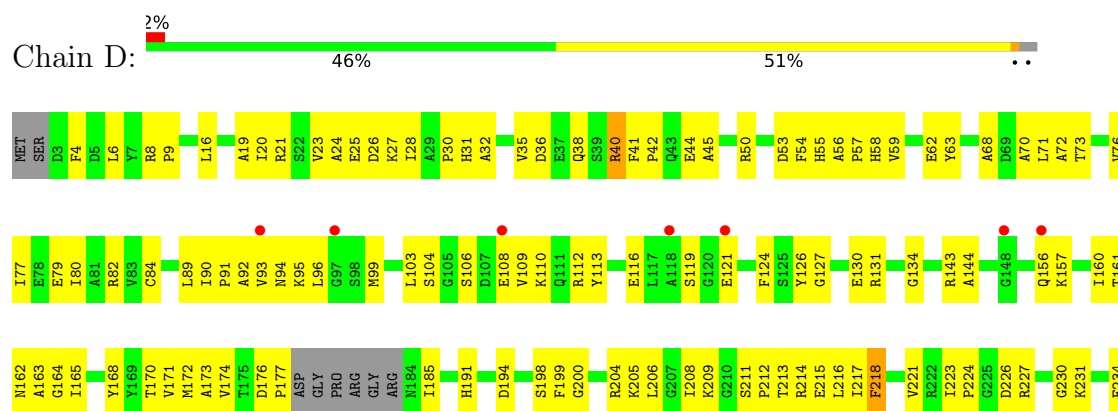
### 3 Residue-property plots

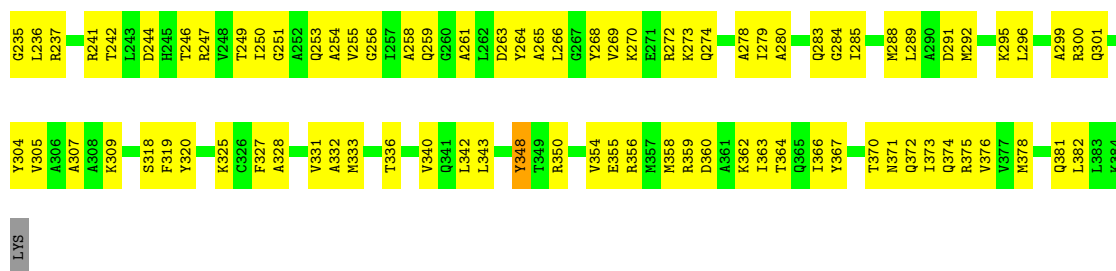
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

#### • Molecule 1: Acyl-CoA dehydrogenase

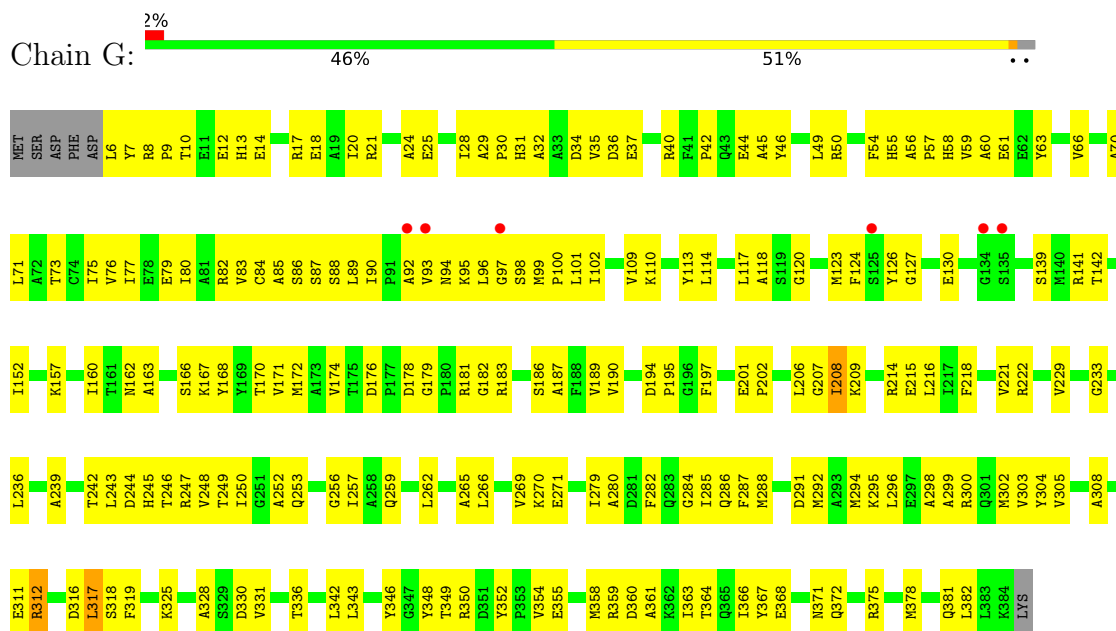


#### • Molecule 1: Acyl-CoA dehydrogenase

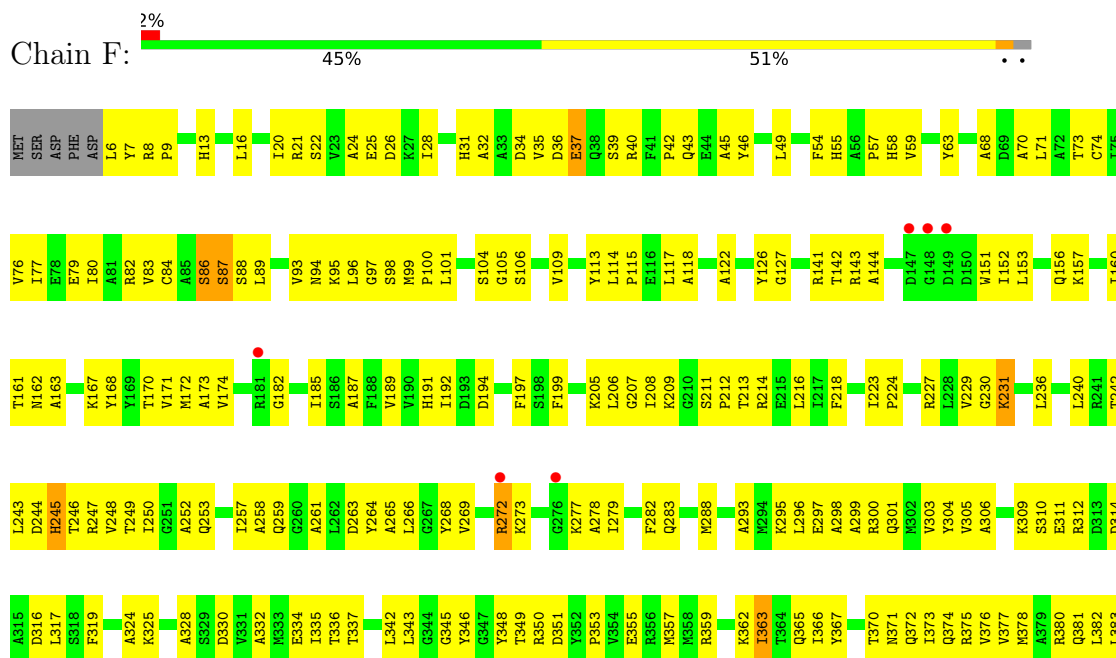




• Molecule 1: Acyl-CoA dehydrogenase




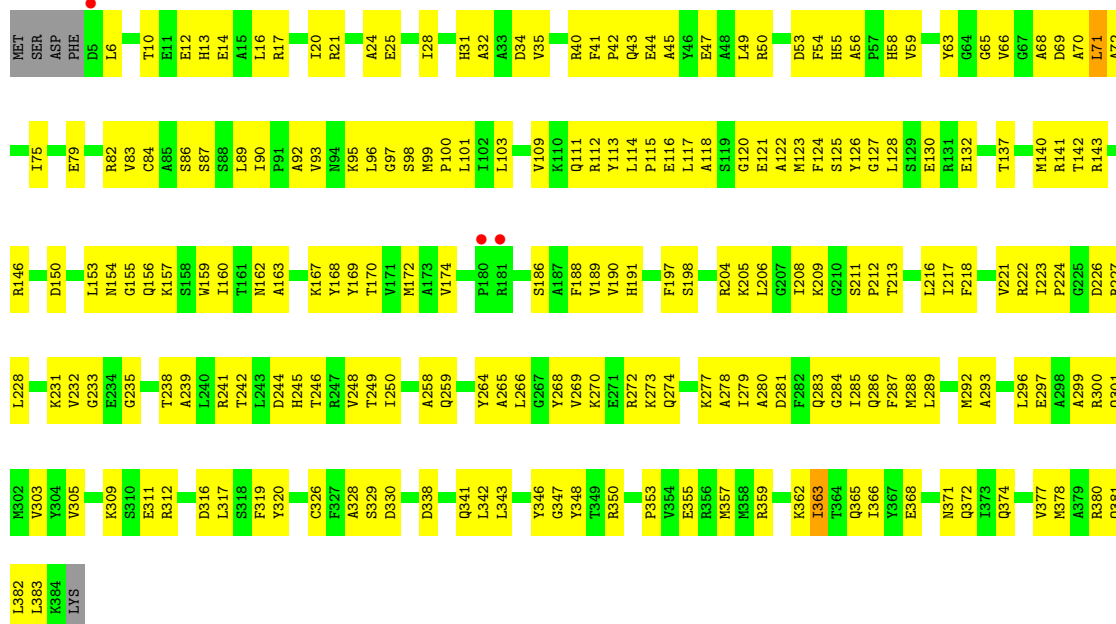
• Molecule 1: Acyl-CoA dehydrogenase



K384  
LYS

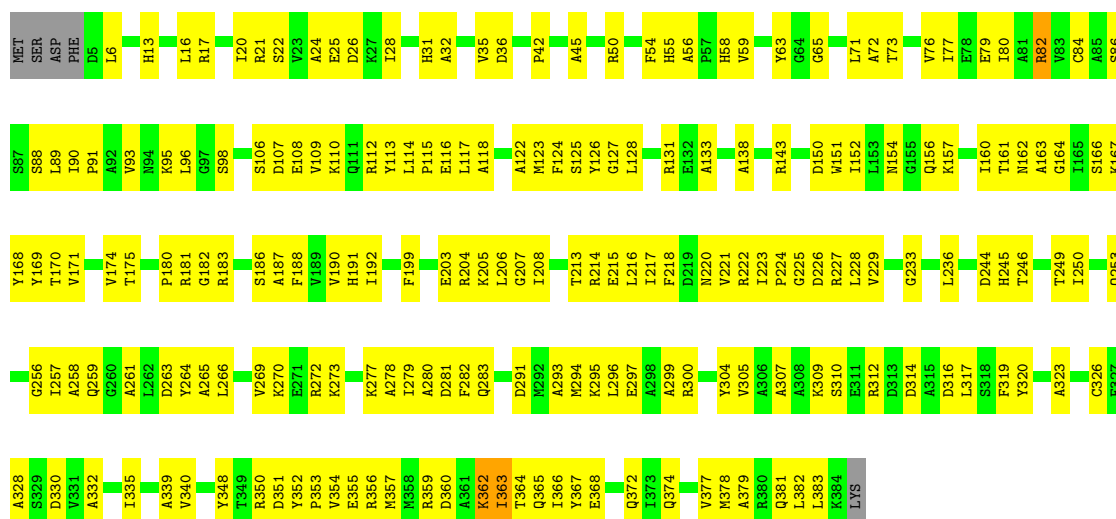
- Molecule 1: Acyl-CoA dehydrogenase

Chain B: 



- Molecule 1: Acyl-CoA dehydrogenase

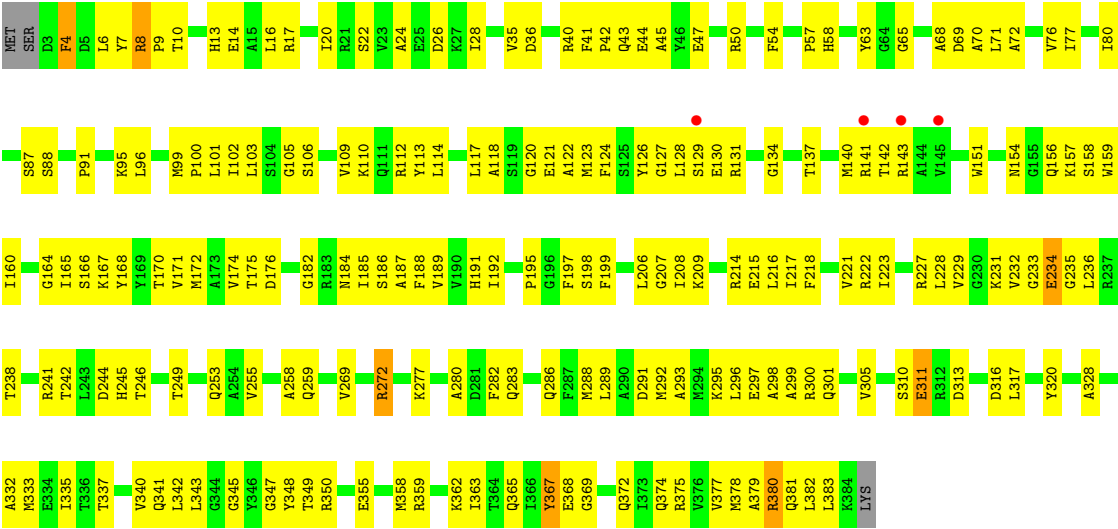
Chain C: 



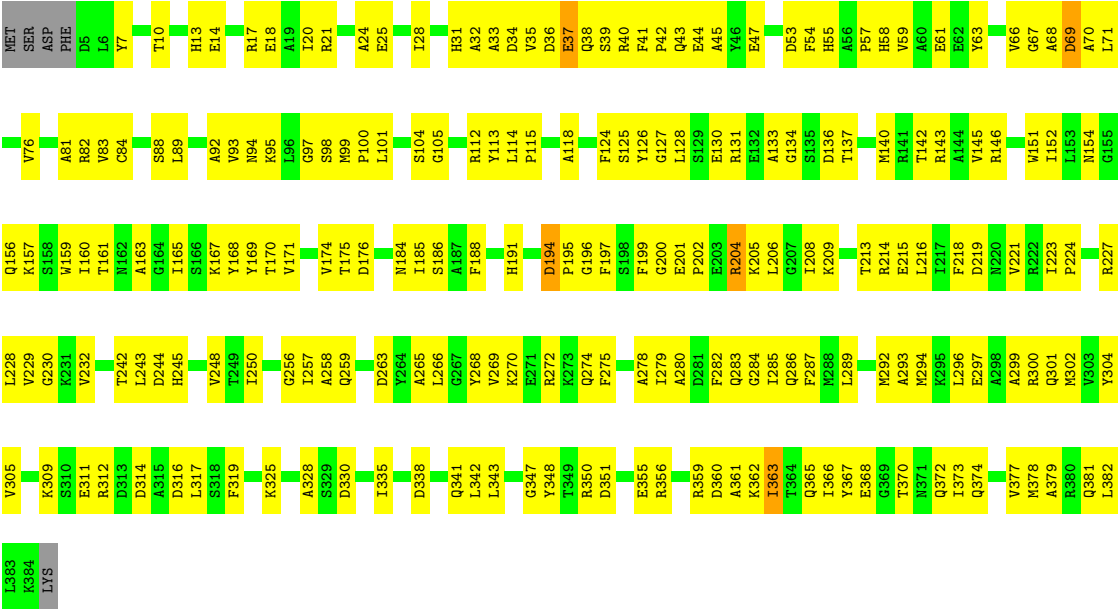
- Molecule 1: Acyl-CoA dehydrogenase

Chain E: 





● Molecule 1: Acyl-CoA dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.12Å 88.91Å 97.18Å 90.19° 91.93° 112.09°	Depositor
Resolution (Å)	27.46 – 3.13 27.46 – 3.13	Depositor EDS
% Data completeness (in resolution range)	92.5 (27.46-3.13) 92.6 (27.46-3.13)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.32 (at 3.11Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, $R_{free}$	0.215 , 0.270 0.216 , 0.272	Depositor DCC
$R_{free}$ test set	2009 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.1	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 20.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	23345	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:  
875

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	0.58	0/2892	0.81	2/3907 (0.1%)
1	B	0.57	0/2970	0.84	0/4012
1	C	0.58	0/2964	0.83	0/4005
1	D	0.54	0/2943	0.81	1/3975 (0.0%)
1	E	0.59	0/2984	0.82	0/4032
1	F	0.57	0/2956	0.83	0/3994
1	G	0.55	0/2962	0.79	0/4001
1	H	0.56	0/2964	0.82	0/4005
All	All	0.57	0/23635	0.82	3/31931 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	348	TYR	CB-CG-CD1	-7.98	116.21	121.00
1	A	348	TYR	CB-CG-CD1	5.86	124.51	121.00
1	A	348	TYR	CB-CG-CD2	-5.62	117.63	121.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2844	0	2805	231	0
1	B	2920	0	2881	204	0
1	C	2914	0	2870	231	0
1	D	2894	0	2850	201	0
1	E	2933	0	2883	199	0
1	F	2906	0	2866	215	0
1	G	2912	0	2877	223	0
1	H	2914	0	2870	232	0
2	E	72	0	0	5	0
2	H	36	0	0	3	0
All	All	23345	0	22902	1557	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 34.

All (1557) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:277:LYS:HZ3	1:H:38:GLN:HG2	1.09	1.16
1:G:245:HIS:CD2	1:G:317:LEU:HD11	1.81	1.15
1:C:363:ILE:HD12	1:C:367:TYR:CE2	1.82	1.15
1:C:363:ILE:CD1	1:C:367:TYR:HE2	1.60	1.14
1:F:223:ILE:HB	1:F:227:ARG:HD2	1.36	1.06
1:C:205:LYS:CE	1:C:208:ILE:HG23	1.87	1.04
1:C:363:ILE:HB	1:C:367:TYR:CE2	1.93	1.04
1:F:277:LYS:NZ	1:H:38:GLN:HG2	1.77	0.99
1:H:223:ILE:HB	1:H:227:ARG:HD2	1.44	0.98
1:C:363:ILE:HG23	1:H:348:TYR:CZ	1.99	0.97
1:A:131:ARG:HB3	1:A:131:ARG:NH1	1.81	0.96
1:A:144:ALA:HB2	1:A:153:LEU:CD2	1.96	0.96
1:H:35:VAL:HG11	1:H:42:PRO:HB3	1.45	0.96
1:A:383:LEU:HD21	1:D:280:ALA:HB1	1.48	0.95
1:C:363:ILE:CD1	1:C:367:TYR:CE2	2.47	0.95
1:A:206:LEU:HB2	1:G:355:GLU:HG3	1.48	0.93
1:C:363:ILE:HB	1:C:367:TYR:CD2	2.04	0.93
1:B:206:LEU:HD13	1:E:355:GLU:HG2	1.49	0.93
1:H:31:HIS:O	1:H:35:VAL:HG23	1.68	0.93
1:B:159:TRP:HB3	2:E:401:875:C1'	2.01	0.91
1:C:205:LYS:CE	1:C:208:ILE:CG2	2.48	0.90
1:E:130:GLU:H	1:E:134:GLY:HA2	1.32	0.90
1:G:245:HIS:HD2	1:G:317:LEU:HD11	1.32	0.89
1:C:86:SER:HA	1:C:208:ILE:HD11	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:VAL:HG21	1:A:289:LEU:HD11	1.56	0.88
1:B:59:VAL:HG23	1:B:65:GLY:HA3	1.56	0.88
1:B:84:CYS:HG	1:B:87:SER:HG	1.22	0.86
1:H:39:SER:HB2	1:H:209:LYS:HE2	1.58	0.85
1:A:116:GLU:HG3	1:A:121:GLU:HB2	1.56	0.85
1:D:206:LEU:HD12	1:F:355:GLU:HG2	1.56	0.85
1:C:205:LYS:HE2	1:C:208:ILE:HG23	1.57	0.84
1:A:311:GLU:HG2	1:D:4:PHE:CE1	2.13	0.84
1:C:205:LYS:HE3	1:C:208:ILE:CG2	2.07	0.83
1:C:363:ILE:HG23	1:H:348:TYR:CE1	2.12	0.83
1:C:157:LYS:HB2	1:C:216:LEU:HB2	1.59	0.83
1:C:330:ASP:HA	1:C:365:GLN:HE21	1.42	0.83
1:A:311:GLU:HB3	1:D:4:PHE:HE1	1.43	0.83
1:D:156:GLN:HG2	1:D:217:ILE:HG22	1.59	0.83
1:E:199:PHE:HB3	1:E:214:ARG:HD2	1.61	0.82
1:H:130:GLU:H	1:H:134:GLY:HA2	1.45	0.82
1:F:63:TYR:HB3	1:F:115:PRO:HG3	1.60	0.82
1:D:231:LYS:HB2	1:D:234:GLU:HB3	1.62	0.81
1:A:363:ILE:HB	1:G:348:TYR:CZ	2.16	0.80
1:G:245:HIS:CD2	1:G:317:LEU:CD1	2.63	0.80
1:D:21:ARG:O	1:D:25:GLU:HG2	1.82	0.80
1:C:206:LEU:HD12	1:H:355:GLU:HG2	1.64	0.80
1:B:50:ARG:HD2	1:B:120:GLY:HA3	1.63	0.80
1:H:244:ASP:HB3	1:H:317:LEU:HD23	1.64	0.79
1:F:182:GLY:HA2	1:F:236:LEU:HD13	1.64	0.79
1:D:355:GLU:HG2	1:F:206:LEU:HD13	1.62	0.79
1:C:207:GLY:O	1:C:208:ILE:HG22	1.82	0.79
1:G:42:PRO:HB2	1:G:45:ALA:HB3	1.65	0.79
1:C:363:ILE:HD12	1:C:367:TYR:CZ	2.17	0.79
1:C:127:GLY:HA2	1:C:160:ILE:HD12	1.65	0.79
1:A:144:ALA:HB2	1:A:153:LEU:HD23	1.64	0.78
1:B:286:GLN:HG2	1:C:379:ALA:HB1	1.63	0.78
1:C:59:VAL:HG23	1:C:65:GLY:HA3	1.65	0.78
1:C:205:LYS:HE2	1:C:208:ILE:CG2	2.11	0.78
1:F:363:ILE:HB	1:F:367:TYR:CD1	2.18	0.78
1:F:24:ALA:HA	1:F:28:ILE:HG13	1.64	0.77
1:F:32:ALA:HB2	1:F:84:CYS:HB2	1.67	0.77
1:G:176:ASP:HB3	1:G:179:GLY:H	1.49	0.77
1:F:163:ALA:HB3	1:F:214:ARG:HB2	1.67	0.77
1:D:38:GLN:HB2	1:D:40:ARG:HG2	1.67	0.77
1:D:247:ARG:HH12	1:D:318:SER:HA	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:348:TYR:CZ	1:F:206:LEU:HB3	2.20	0.77
1:C:86:SER:HA	1:C:208:ILE:CD1	2.15	0.77
1:E:151:TRP:O	1:E:222:ARG:HA	1.85	0.77
1:B:205:LYS:HD2	1:B:213:THR:HB	1.67	0.76
1:A:42:PRO:HB2	1:A:45:ALA:HB3	1.67	0.76
1:B:162:ASN:HA	1:B:212:PRO:HD2	1.66	0.76
1:F:244:ASP:HB3	1:F:317:LEU:HD22	1.66	0.76
1:D:305:VAL:O	1:D:309:LYS:HG3	1.86	0.76
1:H:143:ARG:HA	1:H:174:VAL:HG22	1.68	0.76
1:F:345:GLY:HA2	1:F:348:TYR:CE2	2.20	0.75
1:C:180:PRO:HG2	1:C:183:ARG:HB2	1.65	0.75
1:C:363:ILE:CB	1:C:367:TYR:CE2	2.70	0.75
1:A:73:THR:HG21	1:A:95:LYS:HD2	1.68	0.75
1:E:337:THR:HA	1:E:358:MET:HE3	1.68	0.75
1:H:296:LEU:HB2	1:H:335:ILE:HD11	1.68	0.75
1:G:269:VAL:HG12	1:G:280:ALA:HB2	1.69	0.75
1:A:153:LEU:HB2	1:A:221:VAL:CG2	2.16	0.75
1:D:185:ILE:HD11	1:D:236:LEU:HD13	1.67	0.75
1:A:153:LEU:HB2	1:A:221:VAL:HG22	1.68	0.75
1:H:55:HIS:NE2	1:H:118:ALA:O	2.20	0.75
1:H:363:ILE:HD12	1:H:366:ILE:HB	1.68	0.75
1:E:171:VAL:HG21	1:E:218:PHE:HZ	1.51	0.75
1:E:231:LYS:O	1:E:234:GLU:HB3	1.87	0.75
1:A:131:ARG:HB3	1:A:131:ARG:CZ	2.17	0.74
1:G:330:ASP:OD1	1:G:371:ASN:ND2	2.20	0.74
1:H:58:HIS:NE2	1:H:98:SER:OG	2.20	0.74
1:B:21:ARG:O	1:B:25:GLU:HG2	1.87	0.74
1:C:269:VAL:HG23	1:C:280:ALA:HB2	1.68	0.74
1:H:127:GLY:HA2	1:H:160:ILE:HD12	1.69	0.74
1:E:102:ILE:HG12	1:E:114:LEU:HD21	1.68	0.74
1:H:33:ALA:O	1:H:37:GLU:HB2	1.87	0.74
1:F:97:GLY:HA2	1:F:126:TYR:HB2	1.70	0.74
1:B:288:MET:O	1:B:292:MET:HG3	1.87	0.74
1:E:269:VAL:HG21	1:E:289:LEU:HD11	1.69	0.74
1:G:7:TYR:CE2	1:F:304:TYR:HB3	2.22	0.74
1:G:97:GLY:HA2	1:G:126:TYR:HB2	1.70	0.74
1:F:63:TYR:HB3	1:F:115:PRO:CG	2.18	0.74
1:G:7:TYR:HB3	1:F:305:VAL:HG22	1.69	0.73
1:H:258:ALA:HB1	1:H:335:ILE:HD12	1.69	0.73
1:F:185:ILE:HG21	1:F:236:LEU:HB2	1.68	0.73
1:A:126:TYR:OH	1:A:128:LEU:HD22	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ALA:HB2	1:A:153:LEU:HD21	1.71	0.73
1:G:14:GLU:OE1	1:G:17:ARG:HD2	1.87	0.73
1:D:269:VAL:HG21	1:D:289:LEU:HD11	1.70	0.73
1:G:325:LYS:NZ	1:G:371:ASN:OD1	2.22	0.73
1:E:103:LEU:HB3	1:E:241:ARG:HH21	1.54	0.72
1:A:50:ARG:HA	1:A:55:HIS:ND1	2.03	0.72
1:E:7:TYR:HB3	1:H:305:VAL:HG22	1.70	0.72
1:H:269:VAL:HG21	1:H:289:LEU:HD11	1.71	0.72
1:E:157:LYS:HB2	1:E:216:LEU:HB2	1.71	0.72
1:F:84:CYS:HG	1:F:87:SER:HG	0.73	0.72
1:A:132:GLU:OE2	1:A:141:ARG:CB	2.38	0.72
1:E:231:LYS:O	1:E:234:GLU:CB	2.38	0.71
1:D:50:ARG:HA	1:D:55:HIS:ND1	2.05	0.71
1:G:31:HIS:CE1	1:G:44:GLU:HG2	2.25	0.71
1:F:277:LYS:HZ3	1:H:38:GLN:CG	1.96	0.71
1:H:330:ASP:HA	1:H:365:GLN:HE21	1.55	0.71
1:D:288:MET:O	1:D:292:MET:HG3	1.91	0.71
1:G:382:LEU:HD23	1:F:266:LEU:HD21	1.73	0.71
1:G:8:ARG:HH12	1:F:312:ARG:HH21	1.36	0.71
1:D:103:LEU:O	1:D:241:ARG:NH2	2.24	0.70
1:G:288:MET:O	1:G:292:MET:HG3	1.90	0.70
1:C:107:ASP:HA	1:C:110:LYS:HE2	1.73	0.70
1:E:244:ASP:HB3	1:E:317:LEU:HD22	1.72	0.70
1:B:350:ARG:HH12	1:E:209:LYS:HD3	1.56	0.70
1:C:363:ILE:HD12	1:C:367:TYR:OH	1.92	0.70
1:G:269:VAL:HG13	1:G:279:ILE:HG13	1.72	0.70
1:A:311:GLU:CB	1:D:4:PHE:HE1	2.04	0.70
1:G:7:TYR:HD1	1:F:7:TYR:CD1	2.08	0.70
1:F:259:GLN:NE2	1:F:263:ASP:OD1	2.25	0.70
1:A:143:ARG:HH12	1:A:177:PRO:HG3	1.57	0.69
1:D:209:LYS:NZ	1:F:350:ARG:HH21	1.90	0.69
1:G:182:GLY:HA2	1:G:236:LEU:HD13	1.75	0.69
1:H:28:ILE:HG12	1:H:45:ALA:HA	1.73	0.69
1:D:54:PHE:HA	1:D:57:PRO:HG3	1.74	0.69
1:D:131:ARG:NH2	1:D:215:GLU:OE2	2.25	0.69
1:C:163:ALA:HB3	1:C:214:ARG:HB2	1.74	0.69
1:G:17:ARG:NH2	1:G:75:ILE:CD1	2.56	0.69
1:A:383:LEU:CD2	1:D:280:ALA:HB1	2.22	0.69
1:G:7:TYR:CE2	1:F:71:LEU:HD11	2.28	0.69
1:B:143:ARG:N	1:B:154:ASN:O	2.25	0.69
1:B:223:ILE:HB	1:B:227:ARG:HG3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:GLN:O	1:A:305:VAL:HG23	1.93	0.69
1:D:68:ALA:HB1	1:D:72:ALA:HB3	1.75	0.69
1:D:246:THR:O	1:D:249:THR:HG22	1.93	0.69
1:C:191:HIS:CE1	1:C:227:ARG:HH12	2.10	0.69
1:E:310:SER:HA	1:E:317:LEU:HD11	1.75	0.69
1:F:259:GLN:OE1	1:F:300:ARG:NH2	2.25	0.68
1:B:34:ASP:HB3	1:B:40:ARG:HH21	1.56	0.68
1:C:133:ALA:HA	1:H:274:GLN:HE22	1.58	0.68
1:F:277:LYS:NZ	1:H:38:GLN:CG	2.56	0.68
1:A:262:LEU:HD13	1:A:292:MET:HB3	1.74	0.68
1:G:17:ARG:HH21	1:G:75:ILE:CD1	2.06	0.68
1:B:266:LEU:O	1:B:270:LYS:HG3	1.93	0.68
1:H:24:ALA:HB1	1:H:83:VAL:HG21	1.75	0.68
1:D:208:ILE:CG1	1:D:363:ILE:HG21	2.23	0.68
1:F:100:PRO:HG2	1:F:170:THR:HG21	1.74	0.68
1:E:372:GLN:N	1:E:372:GLN:OE1	2.25	0.68
1:A:297:GLU:OE1	1:A:300:ARG:NH1	2.26	0.68
1:B:112:ARG:HG2	1:B:112:ARG:HH11	1.59	0.68
1:A:132:GLU:OE2	1:A:141:ARG:HD3	1.94	0.68
1:A:167:LYS:HB3	1:A:168:TYR:CD1	2.29	0.68
1:E:171:VAL:HG21	1:E:218:PHE:CZ	2.28	0.68
1:C:138:ALA:HB1	1:C:181:ARG:HG3	1.73	0.67
1:H:296:LEU:HB2	1:H:335:ILE:CD1	2.24	0.67
1:B:58:HIS:NE2	1:B:98:SER:OG	2.27	0.67
1:C:191:HIS:ND1	1:C:227:ARG:NH1	2.42	0.67
1:A:103:LEU:HD12	1:A:242:THR:HG22	1.77	0.67
1:C:17:ARG:NH2	1:C:304:TYR:OH	2.26	0.67
1:C:160:ILE:HG13	1:C:216:LEU:HG	1.76	0.67
1:C:204:ARG:NH2	1:H:351:ASP:OD1	2.26	0.67
1:H:268:TYR:CG	1:H:343:LEU:HD22	2.30	0.67
1:F:24:ALA:HA	1:F:28:ILE:CG1	2.24	0.67
1:H:330:ASP:HA	1:H:365:GLN:NE2	2.09	0.67
1:D:90:ILE:O	1:D:94:ASN:ND2	2.27	0.67
1:C:244:ASP:HB3	1:C:317:LEU:HD23	1.76	0.67
1:E:16:LEU:HD23	1:E:72:ALA:HB1	1.77	0.67
1:G:245:HIS:O	1:G:248:VAL:HG22	1.95	0.67
1:A:186:SER:HB3	1:A:233:GLY:H	1.60	0.66
1:G:265:ALA:O	1:G:269:VAL:HG23	1.96	0.66
1:F:250:ILE:HG21	1:F:325:LYS:HE2	1.76	0.66
1:F:349:THR:HG22	1:F:351:ASP:H	1.60	0.66
1:D:103:LEU:HB3	1:D:241:ARG:HH21	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:13:HIS:CD2	1:E:72:ALA:HB2	2.31	0.66
1:H:69:ASP:N	1:H:69:ASP:OD1	2.29	0.66
1:A:144:ALA:CB	1:A:153:LEU:HD23	2.26	0.66
1:A:283:GLN:OE1	1:F:282:PHE:HB3	1.96	0.66
1:F:34:ASP:OD2	1:F:40:ARG:NH2	2.29	0.66
1:A:311:GLU:HG2	1:D:4:PHE:HE1	1.60	0.66
1:E:238:THR:O	1:E:242:THR:HG23	1.96	0.66
1:H:100:PRO:HG2	1:H:170:THR:HG21	1.78	0.66
1:B:100:PRO:HG2	1:B:170:THR:HG21	1.78	0.65
1:C:330:ASP:HA	1:C:365:GLN:NE2	2.10	0.65
1:B:250:ILE:HG13	1:B:368:GLU:HG3	1.76	0.65
1:G:208:ILE:HB	1:G:363:ILE:HD13	1.78	0.65
1:D:99:MET:HB3	1:D:242:THR:HG22	1.78	0.65
1:A:363:ILE:HD13	1:G:348:TYR:CD2	2.32	0.65
1:D:363:ILE:HD12	1:D:366:ILE:HB	1.78	0.65
1:G:20:ILE:HG12	1:G:76:VAL:HG13	1.78	0.65
1:B:56:ALA:O	1:B:59:VAL:HG22	1.97	0.65
1:E:126:TYR:O	1:E:160:ILE:HD12	1.96	0.65
1:A:238:THR:O	1:A:242:THR:HG23	1.97	0.65
1:A:299:ALA:O	1:A:303:VAL:HG23	1.97	0.65
1:C:316:ASP:N	1:C:316:ASP:OD1	2.29	0.65
1:F:127:GLY:HA2	1:F:160:ILE:HD12	1.77	0.65
1:B:24:ALA:HA	1:B:28:ILE:HD12	1.79	0.65
1:C:25:GLU:OE2	1:C:82:ARG:NH2	2.30	0.65
1:H:55:HIS:O	1:H:94:ASN:ND2	2.28	0.64
1:F:76:VAL:O	1:F:80:ILE:HG13	1.97	0.64
1:B:95:LYS:HD3	1:B:249:THR:HG21	1.79	0.64
1:C:250:ILE:HD12	1:C:367:TYR:HE1	1.62	0.64
1:H:128:LEU:HD11	1:H:137:THR:HG23	1.78	0.64
1:H:285:ILE:HG23	1:H:342:LEU:HD22	1.78	0.64
1:A:355:GLU:HG3	1:G:206:LEU:HB2	1.79	0.64
1:G:375:ARG:HA	1:G:378:MET:HE2	1.78	0.64
1:F:86:SER:HB3	1:F:211:SER:H	1.61	0.64
1:C:355:GLU:OE2	1:C:359:ARG:NE	2.29	0.64
1:E:50:ARG:NH2	1:E:121:GLU:OE1	2.30	0.64
1:A:336:THR:HB	1:A:358:MET:HA	1.79	0.64
1:C:363:ILE:O	1:C:366:ILE:N	2.25	0.64
1:A:113:TYR:CE2	1:A:189:VAL:HG11	2.32	0.64
1:A:311:GLU:HB3	1:D:4:PHE:CE1	2.31	0.64
1:D:208:ILE:HG12	1:D:363:ILE:HG21	1.79	0.64
1:A:340:VAL:HG12	1:G:366:ILE:HD11	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:139:SER:HB2	1:G:181:ARG:NH2	2.13	0.64
1:F:372:GLN:O	1:F:376:VAL:HG23	1.97	0.64
1:B:348:TYR:CE2	1:E:363:ILE:HD12	2.32	0.64
1:E:288:MET:O	1:E:292:MET:HG3	1.97	0.64
1:A:312:ARG:HD3	1:D:4:PHE:O	1.98	0.64
1:D:77:ILE:HD13	1:D:249:THR:OG1	1.97	0.64
1:F:330:ASP:HA	1:F:365:GLN:HE21	1.60	0.64
1:G:245:HIS:NE2	1:G:317:LEU:HD11	2.13	0.64
1:G:360:ASP:O	1:G:363:ILE:HG12	1.98	0.64
1:B:268:TYR:CE2	1:B:272:ARG:HD2	2.32	0.64
1:C:151:TRP:CD1	1:C:225:GLY:HA2	2.32	0.64
1:H:221:VAL:HG12	1:H:223:ILE:HG23	1.80	0.64
1:H:305:VAL:O	1:H:309:LYS:HG3	1.98	0.64
1:F:89:LEU:HD13	1:F:161:THR:HG21	1.78	0.63
1:C:123:MET:SD	1:C:162:ASN:ND2	2.70	0.63
1:G:100:PRO:HD3	1:G:242:THR:HG21	1.80	0.63
1:G:266:LEU:HD21	1:F:382:LEU:HB3	1.78	0.63
1:A:63:TYR:HB3	1:A:115:PRO:HG3	1.79	0.63
1:A:16:LEU:CD2	1:A:72:ALA:HB1	2.28	0.63
1:D:268:TYR:CG	1:D:343:LEU:HG	2.33	0.63
1:C:163:ALA:O	1:C:214:ARG:HD2	1.98	0.63
1:B:273:LYS:O	1:B:274:GLN:NE2	2.31	0.63
1:E:4:PHE:HE1	1:E:6:LEU:HD12	1.64	0.63
1:A:311:GLU:CG	1:D:4:PHE:HE1	2.12	0.63
1:D:299:ALA:HB1	1:D:328:ALA:HA	1.80	0.62
1:F:43:GLN:HE22	1:F:46:TYR:HD2	1.47	0.62
1:C:348:TYR:CZ	1:H:363:ILE:HB	2.34	0.62
1:C:245:HIS:HD2	1:C:310:SER:HB2	1.63	0.62
1:C:89:LEU:HD13	1:C:161:THR:HG21	1.80	0.62
1:E:4:PHE:CE1	1:E:6:LEU:HB2	2.33	0.62
1:C:150:ASP:HB2	1:C:224:PRO:HA	1.81	0.62
1:G:17:ARG:NH1	1:G:17:ARG:HG3	2.13	0.62
1:G:157:LYS:HB2	1:G:216:LEU:HB2	1.81	0.62
1:G:259:GLN:OE1	1:G:300:ARG:NH1	2.31	0.62
1:C:63:TYR:HB3	1:C:115:PRO:HD3	1.80	0.62
1:H:171:VAL:HG11	1:H:218:PHE:HZ	1.63	0.62
1:D:103:LEU:HB3	1:D:241:ARG:NH2	2.14	0.62
1:B:265:ALA:O	1:B:269:VAL:HG13	2.00	0.62
1:H:205:LYS:NZ	1:H:208:ILE:O	2.32	0.62
1:D:237:ARG:O	1:D:241:ARG:HG3	1.98	0.62
1:B:150:ASP:HB2	1:B:223:ILE:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:208:ILE:HG13	1:E:363:ILE:HG21	1.82	0.62
1:D:162:ASN:HA	1:D:212:PRO:HD2	1.82	0.62
1:G:244:ASP:OD1	1:G:247:ARG:NH2	2.33	0.62
1:F:371:ASN:HA	1:F:374:GLN:HG2	1.81	0.62
1:B:269:VAL:HG23	1:B:280:ALA:HB2	1.81	0.62
1:A:311:GLU:CG	1:D:4:PHE:CE1	2.83	0.62
1:G:101:LEU:HD21	1:G:113:TYR:HB2	1.82	0.62
1:C:208:ILE:HG23	1:C:208:ILE:O	1.99	0.62
1:E:50:ARG:NE	1:E:120:GLY:O	2.32	0.62
1:F:197:PHE:HE1	1:F:216:LEU:HD13	1.64	0.62
1:C:206:LEU:HB2	1:H:355:GLU:HG3	1.80	0.62
1:C:374:GLN:O	1:C:378:MET:HG3	1.99	0.62
1:H:42:PRO:HB2	1:H:45:ALA:HB3	1.80	0.62
1:A:197:PHE:HB2	1:A:221:VAL:HG11	1.82	0.61
1:D:205:LYS:NZ	1:D:211:SER:O	2.21	0.61
1:G:186:SER:HB3	1:G:233:GLY:H	1.64	0.61
1:C:36:ASP:CG	1:C:359:ARG:HH22	2.03	0.61
1:C:266:LEU:O	1:C:270:LYS:HG3	1.99	0.61
1:E:122:ALA:HA	1:E:167:LYS:HD3	1.81	0.61
1:D:56:ALA:O	1:D:59:VAL:HG23	2.00	0.61
1:B:286:GLN:HG2	1:C:379:ALA:CB	2.30	0.61
1:B:305:VAL:O	1:B:309:LYS:HG3	2.00	0.61
1:A:28:ILE:HD11	1:A:49:LEU:HD21	1.80	0.61
1:G:163:ALA:HB3	1:G:214:ARG:HB2	1.80	0.61
1:G:181:ARG:HB3	1:H:201:GLU:HB2	1.81	0.61
1:F:127:GLY:O	1:F:157:LYS:HE3	2.00	0.61
1:B:132:GLU:OE1	1:B:132:GLU:N	2.33	0.61
1:B:142:THR:HA	1:B:155:GLY:HA3	1.83	0.61
1:C:16:LEU:HD22	1:C:72:ALA:HB1	1.83	0.61
1:H:205:LYS:HD3	1:H:213:THR:HB	1.83	0.61
1:H:297:GLU:OE1	1:H:300:ARG:NH1	2.33	0.61
1:A:183:ARG:HD2	1:A:237:ARG:HH12	1.64	0.61
1:A:379:ALA:HA	1:A:382:LEU:HD12	1.81	0.61
1:H:160:ILE:HG13	1:H:216:LEU:HG	1.81	0.61
1:B:84:CYS:SG	1:B:87:SER:OG	2.46	0.61
1:A:363:ILE:HD13	1:G:348:TYR:CG	2.35	0.61
1:F:126:TYR:HE1	1:F:172:MET:HE2	1.65	0.61
1:A:180:PRO:HB2	1:A:183:ARG:HG3	1.82	0.61
1:A:319:PHE:CE1	1:A:378:MET:HG2	2.35	0.61
1:E:208:ILE:O	1:E:208:ILE:HG22	2.01	0.61
1:D:40:ARG:HH22	1:D:44:GLU:CD	2.04	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:171:VAL:HG21	1:D:218:PHE:CZ	2.35	0.61
1:D:333:MET:HE1	1:D:358:MET:HG3	1.82	0.61
1:G:294:MET:HB2	1:F:378:MET:CE	2.31	0.61
1:H:157:LYS:HB3	1:H:160:ILE:HD11	1.82	0.61
1:H:228:LEU:HD11	1:H:232:VAL:HG22	1.82	0.61
1:G:17:ARG:HG3	1:G:17:ARG:HH11	1.66	0.61
1:F:95:LYS:O	1:F:99:MET:HG2	2.00	0.61
1:A:73:THR:O	1:A:77:ILE:HG13	2.01	0.60
1:A:247:ARG:NH2	1:A:377:VAL:HG21	2.15	0.60
1:G:17:ARG:NH2	1:G:75:ILE:HD13	2.16	0.60
1:D:71:LEU:HD12	1:D:307:ALA:HB3	1.81	0.60
1:D:112:ARG:NH1	1:D:226:ASP:OD1	2.34	0.60
1:F:43:GLN:NE2	1:F:46:TYR:HB3	2.14	0.60
1:H:82:ARG:HA	1:H:256:GLY:O	2.01	0.60
1:A:197:PHE:CZ	1:A:199:PHE:HE1	2.20	0.60
1:E:77:ILE:HG12	1:E:91:PRO:HG2	1.83	0.60
1:H:43:GLN:O	1:H:47:GLU:HG2	2.02	0.60
1:C:205:LYS:HE3	1:C:208:ILE:HG21	1.83	0.60
1:A:247:ARG:HH21	1:A:377:VAL:HG21	1.66	0.60
1:D:174:VAL:HA	1:D:185:ILE:HG22	1.82	0.60
1:H:200:GLY:O	1:H:214:ARG:NH2	2.35	0.60
1:F:101:LEU:HA	1:F:229:VAL:HG21	1.82	0.60
1:D:32:ALA:HB2	1:D:84:CYS:HB2	1.82	0.60
1:D:244:ASP:HA	1:D:247:ARG:NH1	2.17	0.60
1:G:280:ALA:O	1:G:286:GLN:NE2	2.35	0.60
1:C:350:ARG:HH12	1:H:209:LYS:NZ	1.99	0.60
1:B:329:SER:OG	1:B:371:ASN:ND2	2.29	0.60
1:B:355:GLU:HG2	1:E:206:LEU:HD13	1.83	0.60
1:C:82:ARG:NH1	1:C:263:ASP:OD2	2.35	0.60
1:E:367:TYR:HB2	2:E:402:875:C2'	2.31	0.60
1:H:355:GLU:OE2	1:H:359:ARG:NE	2.33	0.59
1:D:82:ARG:HA	1:D:256:GLY:O	2.01	0.59
1:F:162:ASN:HA	1:F:212:PRO:HD2	1.83	0.59
1:G:70:ALA:HB3	1:G:311:GLU:HG2	1.83	0.59
1:D:274:GLN:HB2	1:D:279:ILE:HG22	1.84	0.59
1:G:96:LEU:HA	1:G:246:THR:HG21	1.84	0.59
1:F:345:GLY:HA2	1:F:348:TYR:HE2	1.67	0.59
1:H:269:VAL:HG12	1:H:279:ILE:HD11	1.84	0.59
1:D:209:LYS:HZ2	1:F:350:ARG:HH21	1.48	0.59
1:G:25:GLU:O	1:G:29:ALA:HB3	2.02	0.59
1:C:245:HIS:CD2	1:C:310:SER:HB2	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:176:ASP:HB3	1:G:179:GLY:N	2.18	0.59
1:F:268:TYR:CG	1:F:343:LEU:HD22	2.37	0.59
1:D:360:ASP:O	1:D:363:ILE:HG22	2.03	0.59
1:B:59:VAL:HG12	1:B:114:LEU:HD23	1.84	0.59
1:A:41:PHE:CD1	1:A:42:PRO:HD2	2.38	0.59
1:C:90:ILE:HG23	1:C:123:MET:HE3	1.83	0.59
1:C:272:ARG:O	1:C:279:ILE:HG23	2.03	0.59
1:E:4:PHE:CD1	1:E:6:LEU:HB2	2.38	0.59
1:E:272:ARG:NH2	2:E:401:875:O2A	2.32	0.59
1:A:309:LYS:HA	1:A:314:ASP:OD2	2.03	0.58
1:D:171:VAL:HG21	1:D:218:PHE:HZ	1.68	0.58
1:F:143:ARG:O	1:F:153:LEU:HA	2.03	0.58
1:B:20:ILE:HD13	1:B:54:PHE:CD2	2.38	0.58
1:B:128:LEU:HD11	1:B:137:THR:HG21	1.84	0.58
1:B:372:GLN:HE22	1:E:341:GLN:HG2	1.68	0.58
1:D:247:ARG:NH1	1:D:318:SER:HA	2.18	0.58
1:G:21:ARG:O	1:G:25:GLU:HG2	2.02	0.58
1:F:261:ALA:HB2	1:F:336:THR:HG22	1.85	0.58
1:F:272:ARG:O	1:F:278:ALA:HA	2.02	0.58
1:E:186:SER:HB3	1:E:232:VAL:HA	1.85	0.58
1:H:20:ILE:HG12	1:H:76:VAL:HG13	1.84	0.58
1:A:21:ARG:NH2	1:A:79:GLU:OE2	2.36	0.58
1:D:363:ILE:O	1:D:366:ILE:N	2.26	0.58
1:F:31:HIS:O	1:F:35:VAL:HG23	2.04	0.58
1:F:36:ASP:OD2	1:F:359:ARG:NH2	2.32	0.58
1:H:35:VAL:CG1	1:H:42:PRO:HB3	2.28	0.58
1:A:7:TYR:OH	1:D:9:PRO:HD3	2.03	0.58
1:F:205:LYS:NZ	1:F:211:SER:O	2.36	0.58
1:B:103:LEU:HD13	1:B:241:ARG:HB3	1.86	0.58
1:A:379:ALA:O	1:A:383:LEU:HD12	2.02	0.58
1:H:99:MET:CB	1:H:242:THR:HG23	2.34	0.58
1:G:7:TYR:HD1	1:F:7:TYR:HD1	1.50	0.58
1:G:49:LEU:HD11	1:G:80:ILE:HD13	1.85	0.58
1:B:189:VAL:O	1:B:227:ARG:HD2	2.03	0.58
1:B:383:LEU:HD21	1:C:280:ALA:HB1	1.85	0.58
1:C:112:ARG:HD2	1:C:113:TYR:CE1	2.38	0.58
1:H:167:LYS:HD3	1:H:168:TYR:CZ	2.39	0.58
1:A:297:GLU:O	1:A:301:GLN:HG2	2.03	0.58
1:C:151:TRP:HD1	1:C:225:GLY:HA2	1.68	0.58
1:A:113:TYR:HH	1:A:191:HIS:HE2	1.50	0.58
1:G:7:TYR:HE2	1:F:71:LEU:HD11	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:GLN:HA	1:B:286:GLN:HB2	1.86	0.58
1:E:43:GLN:O	1:E:47:GLU:HG2	2.04	0.58
1:E:142:THR:HA	1:E:154:ASN:O	2.04	0.58
1:H:17:ARG:NH2	1:H:304:TYR:OH	2.30	0.58
1:D:265:ALA:O	1:D:269:VAL:HG13	2.04	0.58
1:G:89:LEU:HA	1:G:92:ALA:HB3	1.86	0.58
1:F:363:ILE:HD13	1:F:367:TYR:CE1	2.39	0.58
1:B:209:LYS:HD2	1:B:359:ARG:HH12	1.69	0.58
1:B:224:PRO:HB2	1:B:226:ASP:OD1	2.03	0.58
1:C:123:MET:HB2	1:C:166:SER:HA	1.86	0.58
1:E:297:GLU:HG3	1:H:319:PHE:HE2	1.68	0.58
1:A:182:GLY:HA2	1:A:236:LEU:CD2	2.34	0.58
1:H:191:HIS:HB2	1:H:194:ASP:OD1	2.03	0.58
1:A:132:GLU:OE2	1:A:141:ARG:CG	2.52	0.57
1:A:144:ALA:HA	1:A:152:ILE:O	2.03	0.57
1:D:31:HIS:O	1:D:35:VAL:HG23	2.03	0.57
1:G:60:ALA:HB3	1:G:63:TYR:HD2	1.68	0.57
1:B:273:LYS:HG2	1:B:278:ALA:HA	1.86	0.57
1:C:250:ILE:HG13	1:C:368:GLU:HB2	1.86	0.57
1:D:291:ASP:HB3	1:D:295:LYS:HE3	1.86	0.57
1:B:16:LEU:O	1:B:20:ILE:HG22	2.04	0.57
1:E:4:PHE:CD2	1:H:311:GLU:HG2	2.39	0.57
1:E:195:PRO:O	1:E:221:VAL:HG22	2.04	0.57
1:G:100:PRO:HG3	1:G:126:TYR:CE1	2.39	0.57
1:B:127:GLY:HA2	1:B:160:ILE:HD12	1.87	0.57
1:C:312:ARG:NH1	1:C:314:ASP:OD2	2.37	0.57
1:E:77:ILE:HD13	1:E:249:THR:HG23	1.85	0.57
1:E:188:PHE:HA	1:E:227:ARG:O	2.04	0.57
1:A:171:VAL:HG11	1:A:218:PHE:HZ	1.70	0.57
1:D:325:LYS:NZ	1:D:364:THR:O	2.37	0.57
1:E:70:ALA:HB3	1:E:311:GLU:HB2	1.85	0.57
1:D:42:PRO:HB2	1:D:45:ALA:HB3	1.85	0.57
1:G:245:HIS:NE2	1:G:317:LEU:CD1	2.67	0.57
1:B:238:THR:O	1:B:242:THR:HG23	2.04	0.57
1:D:204:ARG:NH1	1:F:37:GLU:OE2	2.38	0.57
1:G:318:SER:OG	1:G:381:GLN:NE2	2.38	0.57
1:F:173:ALA:O	1:F:185:ILE:HD12	2.05	0.57
1:H:368:GLU:O	1:H:374:GLN:NE2	2.38	0.57
1:A:131:ARG:HB3	1:A:131:ARG:HH11	1.67	0.57
1:D:200:GLY:HA3	1:D:215:GLU:HB2	1.86	0.57
1:B:343:LEU:HB2	1:B:347:GLY:HA3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:ALA:N	1:A:311:GLU:OE2	2.31	0.57
1:E:24:ALA:HA	1:E:28:ILE:HB	1.87	0.57
1:G:89:LEU:HB3	1:G:93:VAL:HG23	1.87	0.57
1:F:122:ALA:HB1	1:F:167:LYS:HB2	1.86	0.57
1:F:309:LYS:HD3	1:F:314:ASP:HB2	1.86	0.57
1:C:76:VAL:O	1:C:80:ILE:HG13	2.05	0.57
1:E:140:MET:HE1	1:E:185:ILE:HG21	1.85	0.57
1:B:40:ARG:HH12	1:B:44:GLU:CD	2.08	0.57
1:A:7:TYR:CD2	1:D:71:LEU:HD21	2.40	0.56
1:D:70:ALA:HA	1:D:73:THR:HG22	1.86	0.56
1:G:50:ARG:HA	1:G:55:HIS:ND1	2.20	0.56
1:B:116:GLU:HG3	1:B:121:GLU:HB2	1.87	0.56
1:C:354:VAL:HA	1:C:357:MET:CE	2.35	0.56
1:H:55:HIS:HE2	1:H:118:ALA:C	2.08	0.56
1:D:375:ARG:HA	1:D:378:MET:HE3	1.88	0.56
1:H:372:GLN:OE1	1:H:372:GLN:N	2.38	0.56
1:D:247:ARG:HG2	1:D:374:GLN:HE22	1.69	0.56
1:D:370:THR:O	1:D:373:ILE:N	2.39	0.56
1:G:295:LYS:HB3	1:G:331:VAL:HG13	1.86	0.56
1:F:16:LEU:O	1:F:20:ILE:HG22	2.05	0.56
1:F:21:ARG:NH1	1:F:79:GLU:OE1	2.38	0.56
1:B:70:ALA:N	1:B:311:GLU:OE1	2.35	0.56
1:B:96:LEU:HA	1:B:246:THR:HG21	1.87	0.56
1:E:380:ARG:HE	1:E:380:ARG:HA	1.69	0.56
1:F:167:LYS:HA	1:F:192:ILE:HG13	1.87	0.56
1:C:187:ALA:HB3	1:C:229:VAL:HG23	1.87	0.56
1:G:95:LYS:HD3	1:G:249:THR:HG21	1.88	0.56
1:G:382:LEU:HD21	1:F:293:ALA:HB2	1.88	0.56
1:F:173:ALA:C	1:F:185:ILE:HD12	2.26	0.56
1:C:21:ARG:O	1:C:25:GLU:HG3	2.04	0.56
1:C:372:GLN:OE1	1:H:341:GLN:NE2	2.34	0.56
1:G:142:THR:O	1:G:174:VAL:HG22	2.06	0.56
1:E:100:PRO:HG2	1:E:170:THR:HG21	1.87	0.56
1:E:320:TYR:OH	1:H:297:GLU:OE2	2.24	0.56
1:H:21:ARG:O	1:H:25:GLU:HG2	2.05	0.56
1:A:333:MET:HE3	1:A:333:MET:O	2.06	0.56
1:D:40:ARG:NH2	1:D:44:GLU:OE2	2.37	0.56
1:C:88:SER:O	1:C:91:PRO:HD2	2.06	0.56
1:A:266:LEU:O	1:A:270:LYS:HG3	2.05	0.56
1:D:224:PRO:HG2	1:D:227:ARG:HG2	1.87	0.56
1:B:245:HIS:O	1:B:248:VAL:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:348:TYR:CZ	1:E:363:ILE:HB	2.41	0.56
1:C:340:VAL:HB	1:H:362:LYS:HE2	1.88	0.56
1:C:377:VAL:O	1:C:381:GLN:HG2	2.06	0.56
1:E:16:LEU:CD2	1:E:72:ALA:HB1	2.35	0.56
1:H:330:ASP:OD1	1:H:365:GLN:NE2	2.39	0.56
1:H:363:ILE:HG13	1:H:367:TYR:CE2	2.41	0.56
1:G:127:GLY:HA2	1:G:160:ILE:CD1	2.36	0.56
1:C:259:GLN:NE2	1:C:263:ASP:OD1	2.39	0.56
1:E:130:GLU:HG2	1:E:156:GLN:O	2.06	0.56
1:H:363:ILE:HG13	1:H:367:TYR:CD2	2.41	0.56
1:G:152:ILE:HD11	1:G:222:ARG:NH2	2.21	0.56
1:F:74:CYS:HB3	1:F:252:ALA:HB2	1.87	0.56
1:D:41:PHE:CD1	1:D:42:PRO:HD2	2.40	0.55
1:F:63:TYR:HB3	1:F:115:PRO:CD	2.35	0.55
1:B:197:PHE:CE1	1:B:218:PHE:HE1	2.24	0.55
1:H:151:TRP:HB2	1:H:223:ILE:HG13	1.87	0.55
1:G:71:LEU:HD13	1:F:6:LEU:HD21	1.87	0.55
1:C:258:ALA:HB3	1:C:296:LEU:HD13	1.88	0.55
1:F:316:ASP:N	1:F:316:ASP:OD1	2.39	0.55
1:B:191:HIS:CD2	1:B:227:ARG:NH2	2.74	0.55
1:C:166:SER:O	1:C:192:ILE:HD12	2.06	0.55
1:A:126:TYR:OH	1:A:128:LEU:CD2	2.55	0.55
1:A:172:MET:HE1	1:A:235:GLY:C	2.26	0.55
1:H:343:LEU:HB2	1:H:347:GLY:CA	2.36	0.55
1:A:172:MET:HG2	1:A:187:ALA:HB2	1.88	0.55
1:F:39:SER:HB3	1:F:209:LYS:HB3	1.89	0.55
1:F:297:GLU:O	1:F:301:GLN:HG2	2.06	0.55
1:H:125:SER:HB2	1:H:169:TYR:CD2	2.41	0.55
1:H:145:VAL:HG23	1:H:152:ILE:HB	1.87	0.55
1:C:24:ALA:HA	1:C:28:ILE:HB	1.89	0.55
1:C:122:ALA:HB1	1:C:167:LYS:HB2	1.89	0.55
1:C:125:SER:HB2	1:C:161:THR:O	2.07	0.55
1:A:236:LEU:O	1:A:240:LEU:HG	2.06	0.55
1:D:318:SER:HB2	1:D:381:GLN:CD	2.27	0.55
1:G:17:ARG:NH2	1:G:304:TYR:OH	2.40	0.55
1:C:95:LYS:HD2	1:C:249:THR:HG21	1.88	0.55
1:E:131:ARG:NH2	1:E:215:GLU:OE1	2.40	0.55
1:D:68:ALA:HB1	1:D:72:ALA:CB	2.36	0.55
1:F:156:GLN:O	1:F:157:LYS:HD3	2.06	0.55
1:B:259:GLN:OE1	1:B:300:ARG:NH2	2.37	0.55
1:H:35:VAL:HG11	1:H:42:PRO:CB	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ALA:HB1	1:A:83:VAL:CG2	2.37	0.55
1:G:77:ILE:HD13	1:G:249:THR:HB	1.89	0.55
1:F:265:ALA:HB1	1:F:342:LEU:HD12	1.89	0.55
1:B:266:LEU:HD21	1:C:382:LEU:HD23	1.87	0.55
1:C:362:LYS:HD2	1:C:362:LYS:O	2.05	0.55
1:C:363:ILE:CB	1:C:367:TYR:CD2	2.87	0.55
1:H:97:GLY:HA2	1:H:126:TYR:HB2	1.89	0.55
1:A:309:LYS:NZ	1:A:316:ASP:OD1	2.35	0.55
1:A:131:ARG:CZ	1:A:131:ARG:CB	2.85	0.54
1:G:84:CYS:SG	1:G:87:SER:OG	2.57	0.54
1:F:172:MET:SD	1:F:187:ALA:HB2	2.47	0.54
1:F:189:VAL:O	1:F:227:ARG:HD3	2.07	0.54
1:C:355:GLU:HG2	1:H:206:LEU:HD13	1.89	0.54
1:A:292:MET:HG2	1:A:335:ILE:HG12	1.89	0.54
1:D:231:LYS:HD3	1:D:234:GLU:HG2	1.90	0.54
1:D:350:ARG:HH12	1:F:209:LYS:HE3	1.72	0.54
1:G:113:TYR:HD1	1:G:168:TYR:CD2	2.25	0.54
1:A:205:LYS:HZ1	1:A:208:ILE:HG13	1.71	0.54
1:F:96:LEU:HD13	1:F:246:THR:HG21	1.89	0.54
1:E:172:MET:SD	1:E:187:ALA:HB2	2.48	0.54
1:C:363:ILE:HD13	1:C:367:TYR:HE2	1.64	0.54
1:H:89:LEU:HD22	1:H:161:THR:HG21	1.87	0.54
1:H:224:PRO:HG2	1:H:227:ARG:HE	1.73	0.54
1:A:58:HIS:NE2	1:A:98:SER:OG	2.38	0.54
1:A:383:LEU:HA	1:D:270:LYS:HD3	1.88	0.54
1:F:363:ILE:HB	1:F:367:TYR:HD1	1.69	0.54
1:C:224:PRO:HB2	1:C:226:ASP:OD1	2.07	0.54
1:A:228:LEU:HD11	1:A:232:VAL:HG12	1.88	0.54
1:G:123:MET:HB2	1:G:166:SER:HA	1.90	0.54
1:G:294:MET:HB2	1:F:378:MET:HE1	1.89	0.54
1:F:223:ILE:CB	1:F:227:ARG:HD2	2.25	0.54
1:D:23:VAL:O	1:D:27:LYS:HB2	2.08	0.54
1:G:96:LEU:HG	1:G:126:TYR:HB3	1.90	0.54
1:F:49:LEU:HD23	1:F:54:PHE:HB3	1.88	0.54
1:F:104:SER:O	1:F:230:GLY:HA2	2.08	0.54
1:F:113:TYR:HD1	1:F:168:TYR:CD2	2.26	0.54
1:B:71:LEU:HD12	1:C:6:LEU:HD13	1.90	0.54
1:C:112:ARG:HD2	1:C:113:TYR:CZ	2.42	0.54
1:E:255:VAL:HG21	1:E:300:ARG:HA	1.89	0.54
1:H:24:ALA:HB1	1:H:83:VAL:CG2	2.38	0.54
1:D:89:LEU:HD13	1:D:161:THR:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:GLN:HG2	1:C:217:ILE:HG23	1.90	0.54
1:H:194:ASP:OD2	1:H:223:ILE:HG22	2.08	0.54
1:A:310:SER:O	1:A:313:ASP:N	2.39	0.54
1:G:361:ALA:O	1:G:364:THR:OG1	2.20	0.54
1:B:188:PHE:HE1	1:B:228:LEU:HD13	1.73	0.54
1:C:59:VAL:HG21	1:C:118:ALA:HB2	1.90	0.54
1:C:169:TYR:HB2	1:C:190:VAL:HG22	1.90	0.54
1:E:100:PRO:HB3	1:E:238:THR:HG22	1.89	0.54
1:A:101:LEU:HD12	1:A:124:PHE:HE2	1.72	0.53
1:D:163:ALA:HB3	1:D:214:ARG:HB2	1.90	0.53
1:F:172:MET:HG3	1:F:185:ILE:HG13	1.90	0.53
1:B:142:THR:O	1:B:174:VAL:HG12	2.08	0.53
1:F:58:HIS:NE2	1:F:98:SER:OG	2.31	0.53
1:B:258:ALA:HB3	1:B:296:LEU:HD13	1.91	0.53
1:B:270:LYS:HE3	1:C:383:LEU:HA	1.91	0.53
1:C:182:GLY:HA2	1:C:236:LEU:HD22	1.90	0.53
1:E:382:LEU:HB3	1:H:266:LEU:HD11	1.90	0.53
1:D:301:GLN:HA	1:D:301:GLN:OE1	2.09	0.53
1:F:142:THR:O	1:F:174:VAL:HG12	2.09	0.53
1:E:40:ARG:HB2	1:E:40:ARG:NH1	2.23	0.53
1:H:105:GLY:HA3	1:H:229:VAL:HG23	1.88	0.53
1:G:34:ASP:OD2	1:G:40:ARG:NE	2.38	0.53
1:C:350:ARG:HE	1:H:204:ARG:HB3	1.72	0.53
1:C:354:VAL:HA	1:C:357:MET:HE2	1.91	0.53
1:B:10:THR:HG22	1:C:6:LEU:HD21	1.91	0.53
1:B:59:VAL:HG23	1:B:65:GLY:CA	2.34	0.53
1:B:362:LYS:NZ	1:B:365:GLN:OE1	2.31	0.53
1:C:204:ARG:NH1	1:H:37:GLU:OE1	2.41	0.53
1:C:296:LEU:HB2	1:C:335:ILE:CD1	2.39	0.53
1:H:101:LEU:HA	1:H:229:VAL:HG21	1.90	0.53
1:H:133:ALA:HB1	1:H:136:ASP:O	2.08	0.53
1:H:370:THR:O	1:H:373:ILE:N	2.40	0.53
1:A:103:LEU:CD1	1:A:242:THR:HG22	2.37	0.53
1:A:132:GLU:OE2	1:A:141:ARG:CD	2.55	0.53
1:G:266:LEU:O	1:G:270:LYS:HG3	2.09	0.53
1:B:130:GLU:OE1	1:B:140:MET:HB2	2.08	0.53
1:E:367:TYR:HD1	1:E:367:TYR:C	2.11	0.53
1:A:383:LEU:HD21	1:D:280:ALA:CB	2.29	0.53
1:G:61:GLU:CD	1:G:61:GLU:H	2.11	0.53
1:G:139:SER:HB2	1:G:181:ARG:HH22	1.73	0.53
1:G:302:MET:HE2	1:F:298:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:30:PRO:HG2	1:D:31:HIS:HD2	1.74	0.53
1:D:268:TYR:CD1	1:D:343:LEU:HG	2.44	0.53
1:G:7:TYR:OH	1:F:9:PRO:HD3	2.08	0.53
1:G:100:PRO:HB2	1:G:170:THR:HG21	1.90	0.53
1:G:243:LEU:HG	1:G:247:ARG:NH1	2.24	0.53
1:F:246:THR:HA	1:F:249:THR:HG23	1.91	0.53
1:F:258:ALA:HB2	1:F:332:ALA:HA	1.91	0.53
1:F:377:VAL:O	1:F:381:GLN:HG2	2.09	0.53
1:C:269:VAL:HG12	1:C:279:ILE:HD11	1.90	0.53
1:H:20:ILE:HD13	1:H:54:PHE:CD2	2.44	0.53
1:A:265:ALA:O	1:A:269:VAL:HG23	2.09	0.53
1:G:79:GLU:OE1	1:G:82:ARG:NH1	2.41	0.53
1:G:171:VAL:HG21	1:G:218:PHE:CZ	2.44	0.53
1:F:171:VAL:O	1:F:187:ALA:HA	2.09	0.53
1:D:269:VAL:HG23	1:D:280:ALA:HB2	1.90	0.53
1:G:299:ALA:HB1	1:G:328:ALA:HA	1.90	0.53
1:B:382:LEU:HD11	1:C:293:ALA:HB2	1.89	0.53
1:C:55:HIS:NE2	1:C:118:ALA:O	2.42	0.53
1:A:113:TYR:HD1	1:A:168:TYR:CD2	2.27	0.52
1:A:292:MET:HG2	1:A:335:ILE:HG23	1.91	0.52
1:A:372:GLN:O	1:A:376:VAL:HG23	2.10	0.52
1:G:330:ASP:OD2	1:G:375:ARG:NH2	2.37	0.52
1:D:4:PHE:CE2	1:D:6:LEU:HB2	2.45	0.52
1:D:348:TYR:OH	1:F:359:ARG:O	2.26	0.52
1:D:350:ARG:NH1	1:F:209:LYS:HE3	2.22	0.52
1:G:57:PRO:O	1:G:66:VAL:HG12	2.09	0.52
1:G:63:TYR:CZ	1:G:110:LYS:HG2	2.45	0.52
1:F:199:PHE:HB3	1:F:214:ARG:HE	1.73	0.52
1:E:127:GLY:C	1:E:157:LYS:HD2	2.29	0.52
1:E:316:ASP:OD1	1:E:316:ASP:N	2.42	0.52
1:F:277:LYS:HB2	1:H:34:ASP:OD2	2.09	0.52
1:B:198:SER:OG	1:B:217:ILE:HB	2.09	0.52
1:B:209:LYS:HD2	1:B:359:ARG:NH1	2.25	0.52
1:B:287:PHE:CE2	1:H:284:GLY:HA3	2.44	0.52
1:C:283:GLN:OE1	1:E:282:PHE:HB3	2.09	0.52
1:E:113:TYR:CE2	1:E:189:VAL:HG11	2.44	0.52
1:E:379:ALA:HB1	1:H:286:GLN:HG2	1.91	0.52
1:D:44:GLU:CD	1:D:44:GLU:H	2.12	0.52
1:F:89:LEU:O	1:F:93:VAL:HG23	2.09	0.52
1:H:95:LYS:O	1:H:99:MET:HG2	2.10	0.52
1:A:205:LYS:NZ	1:A:213:THR:HG23	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:218:PHE:HB3	1:D:221:VAL:HG23	1.92	0.52
1:B:285:ILE:HD11	1:E:372:GLN:HG2	1.91	0.52
1:E:6:LEU:O	1:H:312:ARG:NH1	2.24	0.52
1:E:22:SER:O	1:E:26:ASP:HB2	2.09	0.52
1:H:59:VAL:HG13	1:H:114:LEU:HD23	1.92	0.52
1:A:265:ALA:HB1	1:A:342:LEU:HD13	1.90	0.52
1:G:25:GLU:OE2	1:G:82:ARG:NH2	2.37	0.52
1:F:74:CYS:HB3	1:F:252:ALA:CB	2.39	0.52
1:E:128:LEU:HD13	1:E:172:MET:HG3	1.92	0.52
1:H:146:ARG:HD2	1:H:151:TRP:CZ2	2.44	0.52
1:A:69:ASP:HB2	1:A:311:GLU:OE2	2.09	0.52
1:A:259:GLN:NE2	1:A:263:ASP:OD1	2.37	0.52
1:F:194:ASP:OD2	1:F:227:ARG:NH1	2.43	0.52
1:B:293:ALA:HB2	1:C:382:LEU:HD21	1.92	0.52
1:F:187:ALA:HB3	1:F:229:VAL:HG13	1.92	0.52
1:B:330:ASP:HA	1:B:365:GLN:HE21	1.75	0.52
1:H:250:ILE:HD12	1:H:367:TYR:HE1	1.74	0.52
1:G:178:ASP:HB3	1:C:352:TYR:OH	2.10	0.52
1:B:42:PRO:HB2	1:B:45:ALA:HB3	1.92	0.52
1:C:264:TYR:CE1	1:C:353:PRO:HG3	2.45	0.52
1:E:362:LYS:NZ	1:E:365:GLN:OE1	2.32	0.52
1:H:258:ALA:HB3	1:H:296:LEU:HD13	1.91	0.52
1:A:16:LEU:HD21	1:A:72:ALA:HB1	1.92	0.51
1:A:355:GLU:CG	1:G:206:LEU:HB2	2.40	0.51
1:A:360:ASP:O	1:A:363:ILE:HG22	2.09	0.51
1:D:89:LEU:HB3	1:D:93:VAL:HG23	1.91	0.51
1:B:374:GLN:O	1:B:378:MET:HE2	2.10	0.51
1:H:272:ARG:NH2	2:H:401:875:O2A	2.39	0.51
1:A:74:CYS:HB3	1:A:252:ALA:HB2	1.92	0.51
1:G:8:ARG:NH1	1:F:312:ARG:HH21	2.07	0.51
1:F:163:ALA:CB	1:F:214:ARG:HB2	2.37	0.51
1:F:269:VAL:HG12	1:F:279:ILE:HD11	1.90	0.51
1:C:363:ILE:HG23	1:H:348:TYR:CE2	2.44	0.51
1:E:4:PHE:HE2	1:H:69:ASP:HB3	1.75	0.51
1:F:310:SER:HA	1:F:317:LEU:HD11	1.91	0.51
1:B:89:LEU:HA	1:B:92:ALA:HB3	1.92	0.51
1:B:208:ILE:HG13	1:B:363:ILE:HG12	1.92	0.51
1:C:63:TYR:OH	1:C:110:LYS:HE3	2.10	0.51
1:G:187:ALA:HB3	1:G:229:VAL:HG22	1.93	0.51
1:C:50:ARG:HA	1:C:55:HIS:ND1	2.26	0.51
1:E:69:ASP:OD2	1:E:71:LEU:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:PRO:HB2	1:A:226:ASP:OD1	2.11	0.51
1:G:363:ILE:HG13	1:G:364:THR:N	2.25	0.51
1:B:266:LEU:HD23	1:B:289:LEU:HD22	1.92	0.51
1:E:141:ARG:O	1:E:143:ARG:HG3	2.11	0.51
1:E:343:LEU:HB2	1:E:347:GLY:HA3	1.93	0.51
1:H:44:GLU:O	1:H:47:GLU:HB2	2.11	0.51
1:A:191:HIS:CD2	1:A:227:ARG:CZ	2.93	0.51
1:D:36:ASP:OD2	1:D:359:ARG:NH2	2.32	0.51
1:D:163:ALA:C	1:D:165:ILE:H	2.12	0.51
1:D:363:ILE:HD13	1:F:348:TYR:CE2	2.45	0.51
1:G:70:ALA:N	1:G:311:GLU:OE2	2.36	0.51
1:G:207:GLY:O	1:G:208:ILE:HG22	2.10	0.51
1:F:296:LEU:HB2	1:F:335:ILE:CD1	2.40	0.51
1:A:128:LEU:CD2	1:A:239:ALA:HB1	2.40	0.51
1:A:204:ARG:HB3	1:G:350:ARG:NE	2.26	0.51
1:A:335:ILE:O	1:A:339:ALA:N	2.34	0.51
1:A:383:LEU:CD2	1:D:280:ALA:CB	2.88	0.51
1:D:73:THR:HG21	1:D:95:LYS:HE3	1.93	0.51
1:D:127:GLY:HA2	1:D:160:ILE:HD12	1.93	0.51
1:G:302:MET:CE	1:F:298:ALA:HB2	2.40	0.51
1:B:366:ILE:HD11	1:E:340:VAL:HG12	1.93	0.51
1:C:90:ILE:HB	1:C:91:PRO:HD3	1.93	0.51
1:E:96:LEU:HD13	1:E:368:GLU:OE2	2.10	0.51
1:A:76:VAL:O	1:A:80:ILE:HG13	2.10	0.51
1:A:132:GLU:OE2	1:A:141:ARG:HB2	2.10	0.51
1:A:138:ALA:O	1:A:181:ARG:HB3	2.11	0.51
1:F:35:VAL:HG21	1:F:42:PRO:HB3	1.93	0.51
1:C:96:LEU:HA	1:C:246:THR:HG21	1.92	0.51
1:E:128:LEU:HD13	1:E:172:MET:CG	2.41	0.51
1:A:16:LEU:O	1:A:20:ILE:HG22	2.11	0.51
1:G:35:VAL:HG13	1:G:40:ARG:O	2.11	0.51
1:G:194:ASP:O	1:G:197:PHE:HB3	2.11	0.51
1:E:175:THR:HG21	1:E:186:SER:OG	2.10	0.51
1:H:283:GLN:HA	1:H:286:GLN:HB2	1.93	0.51
1:D:113:TYR:HB3	1:D:124:PHE:HZ	1.75	0.50
1:G:10:THR:OG1	1:G:12:GLU:HB3	2.11	0.50
1:G:45:ALA:O	1:G:49:LEU:HG	2.11	0.50
1:F:106:SER:O	1:F:109:VAL:HG12	2.11	0.50
1:B:53:ASP:O	1:B:66:VAL:HG21	2.11	0.50
1:B:63:TYR:O	1:B:115:PRO:HA	2.10	0.50
1:A:153:LEU:CB	1:A:221:VAL:HG22	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LYS:HB3	1:A:168:TYR:CE1	2.45	0.50
1:D:325:LYS:HE2	1:D:374:GLN:HE21	1.76	0.50
1:B:103:LEU:HD12	1:B:242:THR:HG22	1.93	0.50
1:B:150:ASP:OD2	1:B:222:ARG:NH1	2.45	0.50
1:H:41:PHE:CE2	1:H:165:ILE:HG21	2.46	0.50
1:H:377:VAL:O	1:H:381:GLN:HG2	2.11	0.50
1:A:143:ARG:NH1	1:A:177:PRO:HG3	2.25	0.50
1:B:41:PHE:HE1	1:B:162:ASN:HD21	1.58	0.50
1:H:28:ILE:HG23	1:H:45:ALA:HB2	1.93	0.50
1:H:81:ALA:HA	1:H:84:CYS:O	2.11	0.50
1:H:268:TYR:CD1	1:H:343:LEU:HD22	2.45	0.50
1:G:127:GLY:HA2	1:G:160:ILE:HD11	1.92	0.50
1:F:268:TYR:HH	1:F:346:TYR:HD2	1.56	0.50
1:C:106:SER:O	1:C:109:VAL:HG12	2.10	0.50
1:E:367:TYR:C	1:E:367:TYR:CD1	2.84	0.50
1:H:99:MET:HB2	1:H:242:THR:HG23	1.92	0.50
1:D:273:LYS:HA	1:D:278:ALA:HA	1.92	0.50
1:G:46:TYR:OH	1:G:120:GLY:O	2.26	0.50
1:F:268:TYR:CD2	1:F:343:LEU:HD22	2.46	0.50
1:C:73:THR:HG21	1:C:95:LYS:HE2	1.94	0.50
1:E:185:ILE:O	1:E:235:GLY:N	2.44	0.50
1:A:19:ALA:O	1:A:23:VAL:HG23	2.11	0.50
1:A:198:SER:OG	1:A:217:ILE:HD11	2.11	0.50
1:A:336:THR:O	1:A:340:VAL:HG23	2.12	0.50
1:D:333:MET:CE	1:D:358:MET:HG3	2.41	0.50
1:D:355:GLU:OE2	1:D:359:ARG:NH2	2.44	0.50
1:B:160:ILE:HG21	1:B:216:LEU:HD11	1.94	0.50
1:C:63:TYR:CD1	1:C:63:TYR:N	2.79	0.50
1:H:156:GLN:HG3	1:H:215:GLU:OE2	2.11	0.50
1:H:338:ASP:O	1:H:342:LEU:N	2.43	0.50
1:A:206:LEU:HB2	1:G:355:GLU:CG	2.32	0.50
1:G:208:ILE:HB	1:G:363:ILE:CD1	2.40	0.50
1:F:6:LEU:HD12	1:F:7:TYR:N	2.26	0.50
1:C:150:ASP:HA	1:C:225:GLY:N	2.27	0.50
1:H:272:ARG:O	1:H:278:ALA:HA	2.12	0.50
1:D:174:VAL:CA	1:D:185:ILE:HG22	2.42	0.50
1:D:191:HIS:HB2	1:D:194:ASP:OD1	2.12	0.50
1:F:21:ARG:O	1:F:25:GLU:HG2	2.12	0.50
1:F:89:LEU:HD21	1:F:367:TYR:OH	2.11	0.50
1:F:236:LEU:HD23	1:F:240:LEU:HG	1.93	0.50
1:H:40:ARG:NH2	1:H:44:GLU:OE2	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:223:ILE:HB	1:D:227:ARG:HG3	1.93	0.50
1:F:370:THR:O	1:F:373:ILE:N	2.44	0.50
1:B:125:SER:O	1:B:169:TYR:HA	2.12	0.50
1:A:85:ALA:O	1:A:88:SER:OG	2.25	0.49
1:G:130:GLU:OE1	1:G:141:ARG:HG2	2.12	0.49
1:C:58:HIS:CE1	1:C:95:LYS:HA	2.47	0.49
1:C:82:ARG:HA	1:C:256:GLY:O	2.12	0.49
1:E:110:LYS:HA	1:E:114:LEU:HD13	1.93	0.49
1:G:73:THR:HG21	1:G:95:LYS:HD2	1.94	0.49
1:B:259:GLN:OE1	1:B:300:ARG:NH1	2.43	0.49
1:E:259:GLN:OE1	1:E:296:LEU:HD21	2.12	0.49
1:H:101:LEU:HD22	1:H:124:PHE:CZ	2.47	0.49
1:D:261:ALA:HB2	1:D:336:THR:HG22	1.94	0.49
1:B:50:ARG:HA	1:B:55:HIS:ND1	2.27	0.49
1:C:89:LEU:HD12	1:C:208:ILE:HD11	1.94	0.49
1:H:265:ALA:O	1:H:269:VAL:HG22	2.12	0.49
1:A:185:ILE:O	1:A:235:GLY:N	2.46	0.49
1:F:208:ILE:HG22	1:F:208:ILE:O	2.13	0.49
1:C:167:LYS:O	1:C:192:ILE:HB	2.12	0.49
1:C:261:ALA:HB1	1:C:339:ALA:HB2	1.94	0.49
1:E:44:GLU:HA	1:E:47:GLU:HG3	1.95	0.49
1:A:10:THR:OG1	1:D:6:LEU:HD11	2.13	0.49
1:A:21:ARG:O	1:A:25:GLU:HG3	2.11	0.49
1:A:135:SER:OG	1:A:373:ILE:HD11	2.12	0.49
1:A:241:ARG:O	1:A:244:ASP:HB2	2.13	0.49
1:D:251:GLY:O	1:D:254:ALA:N	2.45	0.49
1:D:259:GLN:OE1	1:D:296:LEU:HD21	2.12	0.49
1:G:167:LYS:NZ	1:G:168:TYR:OH	2.43	0.49
1:B:284:GLY:H	1:H:283:GLN:HB3	1.77	0.49
1:C:162:ASN:HB3	1:C:166:SER:OG	2.11	0.49
1:E:305:VAL:HG22	1:H:7:TYR:HB3	1.94	0.49
1:A:41:PHE:CG	1:A:165:ILE:HD13	2.48	0.49
1:A:93:VAL:HG12	1:A:124:PHE:O	2.11	0.49
1:A:341:GLN:HG2	1:G:372:GLN:HE22	1.77	0.49
1:D:96:LEU:HA	1:D:246:THR:HG21	1.94	0.49
1:C:63:TYR:HD2	1:C:115:PRO:HD3	1.76	0.49
1:C:89:LEU:HD22	1:C:93:VAL:HG23	1.95	0.49
1:E:382:LEU:HD11	1:H:293:ALA:CB	2.43	0.49
1:A:176:ASP:O	1:A:184:ASN:HB2	2.13	0.49
1:C:59:VAL:HG12	1:C:114:LEU:HD22	1.95	0.49
1:C:203:GLU:HG2	1:C:213:THR:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:372:GLN:CD	1:C:372:GLN:N	2.66	0.49
1:H:128:LEU:HD11	1:H:137:THR:CG2	2.42	0.49
1:A:206:LEU:HD13	1:G:355:GLU:HG2	1.95	0.49
1:F:319:PHE:HE2	1:F:382:LEU:HD11	1.77	0.49
1:B:343:LEU:HB2	1:B:347:GLY:CA	2.41	0.49
1:A:21:ARG:HG2	1:A:25:GLU:OE2	2.12	0.49
1:A:284:GLY:H	1:F:283:GLN:HB3	1.77	0.49
1:D:255:VAL:HG21	1:D:300:ARG:HA	1.95	0.49
1:F:365:GLN:HA	1:F:371:ASN:ND2	2.26	0.49
1:C:207:GLY:O	1:C:208:ILE:CG2	2.56	0.49
1:E:16:LEU:HD12	1:E:16:LEU:O	2.12	0.49
1:E:122:ALA:HB1	1:E:167:LYS:HB2	1.94	0.49
1:H:199:PHE:HB3	1:H:214:ARG:HE	1.77	0.49
1:A:297:GLU:HG3	1:A:301:GLN:HE21	1.78	0.49
1:A:379:ALA:O	1:A:382:LEU:N	2.45	0.49
1:D:131:ARG:HG3	1:D:131:ARG:NH1	2.27	0.49
1:B:59:VAL:HG21	1:B:118:ALA:HB2	1.94	0.49
1:B:319:PHE:HB2	1:B:381:GLN:HG3	1.94	0.49
1:C:264:TYR:CZ	1:C:353:PRO:HG3	2.48	0.49
1:C:326:CYS:HB3	1:C:378:MET:HE1	1.95	0.49
1:H:20:ILE:HD13	1:H:54:PHE:CG	2.48	0.49
1:A:71:LEU:HD11	1:A:304:TYR:HB3	1.95	0.48
1:A:350:ARG:NH2	1:G:209:LYS:NZ	2.61	0.48
1:D:30:PRO:HG2	1:D:31:HIS:CD2	2.48	0.48
1:D:350:ARG:HG3	1:D:355:GLU:CD	2.32	0.48
1:B:160:ILE:O	1:B:163:ALA:HB2	2.13	0.48
1:C:265:ALA:O	1:C:269:VAL:HG22	2.13	0.48
1:C:350:ARG:HG2	1:C:355:GLU:CD	2.33	0.48
1:E:296:LEU:HB2	1:E:335:ILE:CD1	2.42	0.48
1:E:355:GLU:OE2	1:E:359:ARG:NE	2.46	0.48
1:A:16:LEU:HD23	1:A:72:ALA:HB1	1.94	0.48
1:A:261:ALA:HB1	1:A:339:ALA:CB	2.43	0.48
1:D:157:LYS:HB2	1:D:216:LEU:HB2	1.94	0.48
1:B:10:THR:HG23	1:C:6:LEU:HD11	1.95	0.48
1:B:268:TYR:CB	1:B:343:LEU:HD22	2.43	0.48
1:B:283:GLN:OE1	1:H:284:GLY:N	2.38	0.48
1:C:131:ARG:NH2	1:C:215:GLU:OE2	2.46	0.48
1:E:176:ASP:O	1:E:184:ASN:HB2	2.12	0.48
1:H:130:GLU:OE2	1:H:140:MET:HB2	2.12	0.48
1:G:7:TYR:HE2	1:F:304:TYR:HB3	1.74	0.48
1:G:36:ASP:OD2	1:G:359:ARG:NH2	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:37:GLU:OE2	1:G:350:ARG:NH1	2.46	0.48
1:F:63:TYR:CB	1:F:115:PRO:HG3	2.36	0.48
1:B:100:PRO:CG	1:B:170:THR:HG21	2.43	0.48
1:B:190:VAL:HG22	1:B:223:ILE:HG21	1.94	0.48
1:B:316:ASP:OD1	1:B:316:ASP:N	2.36	0.48
1:H:325:LYS:HE3	1:H:368:GLU:HB3	1.95	0.48
1:G:171:VAL:HG21	1:G:218:PHE:CE2	2.49	0.48
1:F:100:PRO:CG	1:F:170:THR:HG21	2.40	0.48
1:F:377:VAL:HA	1:F:380:ARG:HD2	1.95	0.48
1:H:104:SER:O	1:H:230:GLY:HA2	2.13	0.48
1:D:54:PHE:C	1:D:57:PRO:HD3	2.34	0.48
1:G:7:TYR:CD1	1:F:7:TYR:HD1	2.31	0.48
1:B:43:GLN:O	1:B:47:GLU:HG2	2.14	0.48
1:A:159:TRP:HH2	1:G:346:TYR:CE2	2.31	0.48
1:D:104:SER:O	1:D:230:GLY:HA2	2.14	0.48
1:D:274:GLN:CB	1:D:279:ILE:HG22	2.43	0.48
1:G:266:LEU:HD21	1:F:382:LEU:HD23	1.96	0.48
1:B:299:ALA:HB1	1:B:328:ALA:HA	1.95	0.48
1:H:175:THR:HG21	1:H:186:SER:HB2	1.94	0.48
1:G:59:VAL:HG11	1:G:118:ALA:HB2	1.96	0.48
1:C:55:HIS:HD2	1:C:56:ALA:HB3	1.79	0.48
1:C:191:HIS:CE1	1:C:227:ARG:NH1	2.79	0.48
1:C:360:ASP:O	1:C:363:ILE:HG13	2.13	0.48
1:E:185:ILE:O	1:E:235:GLY:HA3	2.14	0.48
1:E:258:ALA:HB2	1:E:332:ALA:HA	1.96	0.48
1:D:285:ILE:HD12	1:D:342:LEU:CD2	2.43	0.48
1:F:205:LYS:HD3	1:F:213:THR:HB	1.95	0.48
1:B:121:GLU:O	1:B:167:LYS:NZ	2.30	0.48
1:C:163:ALA:CB	1:C:214:ARG:HB2	2.44	0.48
1:E:8:ARG:NH1	1:H:312:ARG:HD2	2.29	0.48
1:E:245:HIS:CE1	1:E:317:LEU:HD11	2.48	0.48
1:H:57:PRO:HB2	1:H:68:ALA:HB2	1.96	0.48
1:A:258:ALA:HB2	1:A:332:ALA:HA	1.95	0.48
1:A:292:MET:CE	1:A:342:LEU:HD11	2.44	0.48
1:D:269:VAL:HG12	1:D:279:ILE:HD11	1.96	0.48
1:F:24:ALA:HB1	1:F:83:VAL:HG21	1.95	0.48
1:F:73:THR:HG21	1:F:95:LYS:HD2	1.95	0.48
1:F:144:ALA:HA	1:F:152:ILE:O	2.14	0.48
1:E:127:GLY:O	1:E:157:LYS:HD2	2.13	0.48
1:E:192:ILE:HA	1:E:197:PHE:CE2	2.49	0.48
1:H:14:GLU:O	1:H:18:GLU:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:70:ALA:HB3	1:H:311:GLU:HB2	1.96	0.48
1:H:285:ILE:HG23	1:H:342:LEU:CD2	2.43	0.48
1:A:163:ALA:O	1:A:169:TYR:OH	2.32	0.48
1:A:353:PRO:O	1:A:357:MET:HG3	2.14	0.48
1:D:96:LEU:HG	1:D:126:TYR:CB	2.43	0.48
1:D:283:GLN:HB3	1:G:284:GLY:H	1.78	0.48
1:G:24:ALA:HB1	1:G:83:VAL:CG2	2.44	0.48
1:F:247:ARG:NH2	1:F:377:VAL:HG21	2.28	0.48
1:C:32:ALA:HB2	1:C:84:CYS:HB2	1.95	0.48
1:C:36:ASP:OD1	1:C:356:ARG:HG3	2.13	0.48
1:A:144:ALA:CB	1:A:153:LEU:CD2	2.80	0.47
1:G:20:ILE:HD13	1:G:54:PHE:CG	2.49	0.47
1:G:343:LEU:HD22	1:G:354:VAL:HG21	1.95	0.47
1:C:126:TYR:OH	1:C:128:LEU:HD13	2.14	0.47
1:C:253:GLN:O	1:C:257:ILE:HG13	2.13	0.47
1:E:293:ALA:HB2	1:H:382:LEU:HD11	1.96	0.47
1:E:372:GLN:N	1:E:372:GLN:CD	2.68	0.47
1:A:183:ARG:CD	1:A:237:ARG:HH12	2.27	0.47
1:A:194:ASP:OD1	1:A:195:PRO:HD2	2.14	0.47
1:A:205:LYS:HE3	1:A:205:LYS:HB2	1.68	0.47
1:G:152:ILE:HD11	1:G:222:ARG:HH21	1.80	0.47
1:B:34:ASP:HB3	1:B:40:ARG:NH2	2.28	0.47
1:C:250:ILE:HD12	1:C:367:TYR:CE1	2.47	0.47
1:C:363:ILE:CB	1:C:367:TYR:HE2	2.21	0.47
1:C:379:ALA:O	1:C:383:LEU:HG	2.14	0.47
1:E:16:LEU:HD11	1:E:76:VAL:HG22	1.95	0.47
1:E:40:ARG:HB2	1:E:40:ARG:CZ	2.43	0.47
1:H:99:MET:HB3	1:H:242:THR:HG23	1.95	0.47
1:H:131:ARG:HD3	1:H:215:GLU:OE2	2.14	0.47
1:A:113:TYR:OH	1:A:191:HIS:NE2	2.40	0.47
1:D:24:ALA:HA	1:D:28:ILE:HD12	1.95	0.47
1:F:37:GLU:OE2	1:F:350:ARG:NH1	2.47	0.47
1:B:112:ARG:HG2	1:B:112:ARG:NH1	2.29	0.47
1:B:186:SER:OG	1:B:233:GLY:N	2.35	0.47
1:E:10:THR:OG1	1:E:13:HIS:ND1	2.44	0.47
1:E:191:HIS:CD2	1:E:227:ARG:CZ	2.98	0.47
1:A:183:ARG:CD	1:A:237:ARG:NH1	2.77	0.47
1:A:355:GLU:HG2	1:G:206:LEU:HD13	1.96	0.47
1:D:250:ILE:O	1:D:253:GLN:HB3	2.14	0.47
1:C:13:HIS:CE1	1:C:71:LEU:HD23	2.49	0.47
1:H:142:THR:O	1:H:174:VAL:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:GLY:O	1:A:110:LYS:HE2	2.14	0.47
1:D:371:ASN:HA	1:D:374:GLN:HB2	1.96	0.47
1:B:93:VAL:HG12	1:B:124:PHE:O	2.14	0.47
1:B:157:LYS:HB2	1:B:216:LEU:HB2	1.96	0.47
1:C:363:ILE:CG1	1:C:367:TYR:HE2	2.21	0.47
1:E:109:VAL:O	1:E:113:TYR:HD2	1.98	0.47
1:E:297:GLU:OE2	1:E:300:ARG:NH1	2.48	0.47
1:H:202:PRO:HD3	1:H:214:ARG:NH1	2.29	0.47
1:B:268:TYR:HB3	1:B:343:LEU:HD22	1.97	0.47
1:H:101:LEU:HD12	1:H:229:VAL:HG21	1.95	0.47
1:H:130:GLU:CD	1:H:140:MET:HB2	2.35	0.47
1:H:143:ARG:HA	1:H:174:VAL:CG2	2.41	0.47
1:H:266:LEU:HD23	1:H:289:LEU:HD22	1.95	0.47
1:A:37:GLU:OE2	1:A:350:ARG:NH1	2.48	0.47
1:A:113:TYR:CD1	1:A:168:TYR:CD2	3.03	0.47
1:A:299:ALA:HB1	1:A:328:ALA:HA	1.97	0.47
1:G:99:MET:CB	1:G:242:THR:HG23	2.45	0.47
1:G:294:MET:HB2	1:F:378:MET:HE3	1.96	0.47
1:G:363:ILE:HD12	1:G:367:TYR:CE2	2.49	0.47
1:F:273:LYS:HG2	1:F:278:ALA:N	2.30	0.47
1:B:24:ALA:HB1	1:B:83:VAL:HG21	1.97	0.47
1:C:250:ILE:HG13	1:C:368:GLU:CB	2.43	0.47
1:E:310:SER:HA	1:E:317:LEU:CD1	2.43	0.47
1:H:40:ARG:HH12	1:H:44:GLU:CD	2.18	0.47
1:H:105:GLY:HA2	1:H:230:GLY:H	1.80	0.47
1:H:208:ILE:O	1:H:208:ILE:HG22	2.15	0.47
1:H:299:ALA:HB1	1:H:328:ALA:HA	1.95	0.47
1:H:343:LEU:HB2	1:H:347:GLY:HA3	1.97	0.47
1:G:73:THR:O	1:G:77:ILE:HD12	2.14	0.47
1:B:172:MET:SD	1:B:239:ALA:HB2	2.55	0.47
1:H:10:THR:HG1	1:H:13:HIS:CG	2.27	0.47
1:H:245:HIS:O	1:H:248:VAL:HG22	2.15	0.47
1:H:312:ARG:HB3	1:H:314:ASP:OD1	2.15	0.47
1:A:107:ASP:HA	1:A:110:LYS:HE3	1.96	0.47
1:D:366:ILE:HG23	1:D:370:THR:HG22	1.96	0.47
1:E:101:LEU:O	1:E:105:GLY:HA3	2.15	0.47
1:E:228:LEU:HD22	1:E:232:VAL:HG23	1.96	0.47
1:H:157:LYS:HB3	1:H:160:ILE:CD1	2.43	0.47
1:A:13:HIS:O	1:A:16:LEU:HB3	2.15	0.47
1:A:71:LEU:HD12	1:A:307:ALA:HB3	1.95	0.47
1:A:100:PRO:HG2	1:A:170:THR:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:ALA:HB3	1:D:307:ALA:O	2.14	0.47
1:G:90:ILE:O	1:G:94:ASN:HB2	2.15	0.47
1:B:204:ARG:HB3	1:E:350:ARG:NH1	2.30	0.47
1:B:346:TYR:CE2	1:E:159:TRP:HZ2	2.32	0.47
1:A:32:ALA:HB2	1:A:84:CYS:HB2	1.97	0.46
1:C:167:LYS:HD2	1:C:192:ILE:HG21	1.97	0.46
1:H:105:GLY:HA2	1:H:230:GLY:N	2.30	0.46
1:A:171:VAL:HG11	1:A:218:PHE:CZ	2.51	0.46
1:A:236:LEU:HD12	1:A:239:ALA:HB3	1.97	0.46
1:D:99:MET:CB	1:D:242:THR:HG22	2.43	0.46
1:G:24:ALA:HB1	1:G:83:VAL:HG21	1.97	0.46
1:G:29:ALA:HB2	1:G:83:VAL:HB	1.97	0.46
1:G:172:MET:CE	1:G:239:ALA:HB2	2.45	0.46
1:B:368:GLU:O	1:B:374:GLN:NE2	2.48	0.46
1:C:350:ARG:HH21	1:H:204:ARG:HB3	1.79	0.46
1:E:57:PRO:HB2	1:E:68:ALA:HB3	1.97	0.46
1:E:106:SER:N	1:E:109:VAL:HG12	2.30	0.46
1:E:313:ASP:HA	1:E:317:LEU:HD12	1.98	0.46
1:E:377:VAL:O	1:E:381:GLN:HG2	2.16	0.46
1:D:258:ALA:HB2	1:D:332:ALA:HA	1.97	0.46
1:G:17:ARG:HH11	1:G:17:ARG:CG	2.26	0.46
1:E:156:GLN:HB2	1:E:215:GLU:OE2	2.15	0.46
1:H:191:HIS:CD2	1:H:227:ARG:NH1	2.83	0.46
1:D:72:ALA:O	1:D:76:VAL:HG23	2.15	0.46
1:D:191:HIS:CD2	1:D:227:ARG:NH1	2.84	0.46
1:D:261:ALA:CB	1:D:336:THR:HG22	2.45	0.46
1:G:167:LYS:HG2	1:G:168:TYR:CE1	2.50	0.46
1:G:245:HIS:HE2	1:G:317:LEU:CD1	2.28	0.46
1:F:353:PRO:HB2	1:F:357:MET:HE2	1.96	0.46
1:B:68:ALA:HB1	1:B:72:ALA:HB3	1.96	0.46
1:B:380:ARG:HH11	1:B:380:ARG:HB3	1.81	0.46
1:C:171:VAL:HG21	1:C:218:PHE:CZ	2.51	0.46
1:H:223:ILE:HB	1:H:227:ARG:CD	2.31	0.46
1:H:259:GLN:HA	1:H:296:LEU:HD21	1.97	0.46
1:A:71:LEU:O	1:A:75:ILE:HG13	2.15	0.46
1:A:150:ASP:HB3	1:A:223:ILE:O	2.15	0.46
1:A:237:ARG:H	1:A:237:ARG:HG3	1.40	0.46
1:D:164:GLY:C	1:D:165:ILE:HD12	2.36	0.46
1:G:182:GLY:O	1:G:236:LEU:HB3	2.15	0.46
1:F:99:MET:HB2	1:F:242:THR:HG23	1.97	0.46
1:C:266:LEU:HD23	1:C:266:LEU:HA	1.70	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:333:MET:SD	1:E:362:LYS:HA	2.55	0.46
1:H:10:THR:O	1:H:13:HIS:N	2.49	0.46
1:H:36:ASP:OD2	1:H:209:LYS:HG3	2.16	0.46
1:F:59:VAL:HG11	1:F:118:ALA:HB2	1.96	0.46
1:F:105:GLY:HA2	1:F:229:VAL:HG23	1.97	0.46
1:B:97:GLY:HA3	1:B:124:PHE:HB3	1.98	0.46
1:B:250:ILE:CG1	1:B:368:GLU:HG3	2.45	0.46
1:C:258:ALA:HB2	1:C:332:ALA:HA	1.97	0.46
1:C:309:LYS:HG2	1:C:314:ASP:OD2	2.16	0.46
1:E:20:ILE:HD13	1:E:54:PHE:CD2	2.51	0.46
1:E:36:ASP:CG	1:E:359:ARG:HH22	2.18	0.46
1:A:255:VAL:HG21	1:A:300:ARG:HA	1.98	0.46
1:D:4:PHE:HD2	1:D:6:LEU:HD23	1.80	0.46
1:F:94:ASN:ND2	1:F:117:LEU:HD11	2.30	0.46
1:B:264:TYR:CE2	1:B:353:PRO:HG3	2.51	0.46
1:B:269:VAL:HG12	1:B:279:ILE:HD11	1.97	0.46
1:C:123:MET:O	1:C:166:SER:HB3	2.16	0.46
1:C:164:GLY:HA2	1:C:199:PHE:CE2	2.51	0.46
1:E:117:LEU:HD13	1:E:124:PHE:CD1	2.51	0.46
1:E:301:GLN:CD	1:H:305:VAL:HG21	2.36	0.46
1:H:209:LYS:HE2	1:H:209:LYS:HB3	1.61	0.46
1:A:375:ARG:NE	1:D:291:ASP:OD1	2.37	0.46
1:D:172:MET:HE3	1:D:235:GLY:HA3	1.98	0.46
1:G:77:ILE:HG23	1:G:88:SER:HB2	1.98	0.46
1:F:126:TYR:HE1	1:F:172:MET:CE	2.28	0.46
1:B:383:LEU:HA	1:C:270:LYS:HD3	1.98	0.46
1:E:4:PHE:HD2	1:H:311:GLU:HG2	1.80	0.46
1:H:176:ASP:O	1:H:184:ASN:HB2	2.15	0.46
1:A:23:VAL:HG21	1:A:52:SER:OG	2.16	0.46
1:G:9:PRO:HG2	1:G:14:GLU:OE2	2.16	0.46
1:F:167:LYS:HA	1:F:192:ILE:CG1	2.45	0.46
1:B:99:MET:N	1:B:100:PRO:HD2	2.30	0.46
1:B:122:ALA:HB1	1:B:167:LYS:HB2	1.98	0.46
1:B:283:GLN:OE1	1:H:282:PHE:HB3	2.16	0.46
1:C:205:LYS:HB3	1:H:348:TYR:CE2	2.51	0.46
1:C:299:ALA:HB1	1:C:328:ALA:HA	1.98	0.46
1:D:77:ILE:HG13	1:D:91:PRO:HG2	1.98	0.46
1:F:70:ALA:N	1:F:311:GLU:OE1	2.49	0.46
1:F:295:LYS:NZ	1:F:334:GLU:OE2	2.36	0.46
1:B:377:VAL:HG22	1:B:380:ARG:NH2	2.31	0.46
1:C:258:ALA:CB	1:C:296:LEU:HD13	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:100:PRO:HD3	1:E:242:THR:HG21	1.98	0.46
1:E:164:GLY:HA3	1:E:214:ARG:HH21	1.81	0.46
1:A:191:HIS:CD2	1:A:191:HIS:N	2.85	0.45
1:G:9:PRO:HD3	1:F:7:TYR:OH	2.16	0.45
1:G:298:ALA:HB1	1:F:298:ALA:HB1	1.98	0.45
1:F:243:LEU:HD23	1:F:247:ARG:NH2	2.31	0.45
1:C:253:GLN:OE1	1:C:367:TYR:OH	2.33	0.45
1:G:32:ALA:HB2	1:G:84:CYS:HB2	1.98	0.45
1:G:89:LEU:HA	1:G:89:LEU:HD23	1.84	0.45
1:B:141:ARG:HH22	1:B:143:ARG:HH12	1.64	0.45
1:E:7:TYR:HD1	1:H:7:TYR:CD2	2.34	0.45
1:E:16:LEU:O	1:E:20:ILE:HG22	2.15	0.45
1:A:24:ALA:HB1	1:A:83:VAL:HG21	1.98	0.45
1:G:292:MET:HB3	1:G:292:MET:HE2	1.58	0.45
1:F:231:LYS:HD2	1:F:231:LYS:HA	1.37	0.45
1:B:188:PHE:HD1	1:B:228:LEU:HA	1.80	0.45
1:C:175:THR:HG21	1:C:186:SER:OG	2.16	0.45
1:H:100:PRO:HG3	1:H:126:TYR:HE1	1.80	0.45
1:H:174:VAL:HG12	1:H:185:ILE:HD13	1.98	0.45
1:A:182:GLY:HA2	1:A:236:LEU:HD22	1.98	0.45
1:D:119:SER:OG	1:D:121:GLU:HG3	2.16	0.45
1:G:124:PHE:CE1	1:G:168:TYR:HB2	2.51	0.45
1:G:250:ILE:HG13	1:G:368:GLU:HG2	1.97	0.45
1:C:188:PHE:HA	1:C:227:ARG:O	2.16	0.45
1:E:4:PHE:CE1	1:E:6:LEU:HD12	2.49	0.45
1:E:95:LYS:HG3	1:E:99:MET:CE	2.46	0.45
1:E:258:ALA:HB3	1:E:296:LEU:HD13	1.98	0.45
1:A:305:VAL:HG21	1:D:301:GLN:HG3	1.97	0.45
1:D:16:LEU:O	1:D:19:ALA:HB3	2.16	0.45
1:D:198:SER:OG	1:D:217:ILE:HG13	2.17	0.45
1:G:190:VAL:HG11	1:G:197:PHE:CD1	2.51	0.45
1:F:160:ILE:HG21	1:F:216:LEU:HD21	1.98	0.45
1:B:124:PHE:CE1	1:B:168:TYR:HD2	2.33	0.45
1:C:273:LYS:HA	1:C:278:ALA:HA	1.99	0.45
1:E:198:SER:HB3	1:E:217:ILE:HB	1.99	0.45
1:A:6:LEU:HD23	1:A:7:TYR:HB2	1.99	0.45
1:G:71:LEU:HD11	1:F:7:TYR:CD2	2.51	0.45
1:G:113:TYR:CE1	1:G:189:VAL:HG11	2.52	0.45
1:F:365:GLN:HA	1:F:371:ASN:HD21	1.81	0.45
1:F:371:ASN:O	1:F:375:ARG:HG3	2.17	0.45
1:C:24:ALA:HA	1:C:28:ILE:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:HIS:CE1	1:E:95:LYS:HA	2.51	0.45
1:H:338:ASP:HA	1:H:341:GLN:HB3	1.99	0.45
1:G:46:TYR:HD1	1:G:90:ILE:HG21	1.82	0.45
1:G:317:LEU:O	1:G:317:LEU:HD23	2.16	0.45
1:F:95:LYS:HG3	1:F:99:MET:HE3	1.98	0.45
1:B:90:ILE:HG23	1:B:123:MET:CE	2.47	0.45
1:B:153:LEU:HB2	1:B:221:VAL:HB	1.99	0.45
1:C:36:ASP:OD2	1:C:359:ARG:NH2	2.38	0.45
1:C:199:PHE:HB3	1:C:214:ARG:HD3	1.99	0.45
1:H:112:ARG:NH2	1:H:168:TYR:OH	2.49	0.45
1:A:128:LEU:HD12	1:A:128:LEU:O	2.16	0.45
1:G:262:LEU:HD23	1:G:296:LEU:HD23	1.98	0.45
1:F:317:LEU:HD23	1:F:317:LEU:O	2.17	0.45
1:B:269:VAL:HG21	1:B:289:LEU:HD11	1.97	0.45
1:B:283:GLN:HE22	2:H:401:875:C2A	2.29	0.45
1:B:309:LYS:HG2	1:B:312:ARG:NH2	2.32	0.45
1:E:6:LEU:HD23	1:E:6:LEU:HA	1.73	0.45
1:E:221:VAL:HG12	1:E:223:ILE:HG23	1.99	0.45
1:E:375:ARG:HA	1:E:378:MET:HE3	1.99	0.45
1:A:172:MET:SD	1:A:239:ALA:HB2	2.57	0.45
1:A:205:LYS:NZ	1:A:211:SER:O	2.47	0.45
1:D:21:ARG:NH2	1:D:79:GLU:OE2	2.47	0.45
1:G:300:ARG:HG3	1:G:304:TYR:CZ	2.52	0.45
1:F:244:ASP:O	1:F:317:LEU:HD21	2.16	0.45
1:F:299:ALA:HB1	1:F:328:ALA:HA	1.99	0.45
1:C:297:GLU:OE2	1:C:300:ARG:NH1	2.49	0.45
1:E:189:VAL:O	1:E:227:ARG:HD2	2.16	0.45
1:H:105:GLY:CA	1:H:229:VAL:HG23	2.46	0.45
1:H:292:MET:HB3	1:H:292:MET:HE2	1.77	0.45
1:H:374:GLN:O	1:H:378:MET:HE2	2.16	0.45
1:A:223:ILE:O	1:A:223:ILE:HG13	2.17	0.45
1:A:311:GLU:CB	1:D:4:PHE:CE1	2.93	0.45
1:D:348:TYR:HE1	1:F:362:LYS:HB3	1.80	0.45
1:G:336:THR:OG1	1:G:358:MET:HA	2.17	0.45
1:F:299:ALA:O	1:F:303:VAL:HG13	2.17	0.45
1:E:186:SER:HA	1:E:235:GLY:HA3	1.99	0.45
1:G:202:PRO:HD3	1:G:214:ARG:NH1	2.31	0.44
1:F:191:HIS:CE1	1:F:227:ARG:NH2	2.85	0.44
1:B:326:CYS:SG	1:C:294:MET:HE1	2.57	0.44
1:C:169:TYR:HB2	1:C:190:VAL:CG2	2.47	0.44
1:E:7:TYR:CE2	1:H:304:TYR:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:123:MET:HE2	1:E:165:ILE:HG22	1.98	0.44
1:A:205:LYS:NZ	1:A:208:ILE:HG13	2.31	0.44
1:D:56:ALA:HB1	1:D:58:HIS:CE1	2.52	0.44
1:F:21:ARG:NH1	1:F:82:ARG:HD3	2.32	0.44
1:B:14:GLU:HA	1:B:14:GLU:OE1	2.16	0.44
1:B:79:GLU:O	1:B:82:ARG:HB3	2.16	0.44
1:E:182:GLY:HA2	1:E:236:LEU:HD22	1.99	0.44
1:H:140:MET:HE3	1:H:140:MET:HB3	1.75	0.44
1:D:164:GLY:HA2	1:D:199:PHE:CE2	2.51	0.44
1:C:186:SER:OG	1:C:233:GLY:N	2.43	0.44
1:H:82:ARG:NE	1:H:263:ASP:OD2	2.51	0.44
1:A:80:ILE:HD12	1:A:91:PRO:HG3	1.98	0.44
1:A:250:ILE:HD12	1:A:367:TYR:HE1	1.82	0.44
1:D:144:ALA:HB2	1:D:173:ALA:HB3	2.00	0.44
1:G:85:ALA:HB3	1:G:360:ASP:OD2	2.16	0.44
1:G:285:ILE:HG23	1:G:342:LEU:HD22	1.98	0.44
1:F:57:PRO:HB2	1:F:68:ALA:HB2	1.99	0.44
1:F:245:HIS:O	1:F:248:VAL:HG22	2.18	0.44
1:F:268:TYR:CB	1:F:343:LEU:HD22	2.47	0.44
1:F:309:LYS:HD3	1:F:314:ASP:CB	2.47	0.44
1:F:363:ILE:H	1:F:363:ILE:HG13	1.62	0.44
1:B:6:LEU:O	1:C:312:ARG:NH2	2.48	0.44
1:B:17:ARG:HH21	1:B:75:ILE:HD13	1.81	0.44
1:C:188:PHE:CD1	1:C:228:LEU:HA	2.53	0.44
1:E:35:VAL:HA	1:E:40:ARG:NH1	2.33	0.44
1:E:106:SER:O	1:E:109:VAL:HG12	2.18	0.44
1:H:208:ILE:HD13	1:H:208:ILE:HA	1.76	0.44
1:A:153:LEU:HB2	1:A:221:VAL:HG23	1.99	0.44
1:A:244:ASP:HB3	1:A:317:LEU:HD23	2.00	0.44
1:D:89:LEU:HA	1:D:92:ALA:HB3	1.98	0.44
1:D:106:SER:O	1:D:109:VAL:HG12	2.17	0.44
1:F:101:LEU:HA	1:F:229:VAL:CG2	2.47	0.44
1:F:223:ILE:HB	1:F:227:ARG:CD	2.27	0.44
1:F:259:GLN:HE21	1:F:263:ASP:CG	2.20	0.44
1:B:224:PRO:HD2	1:B:227:ARG:CZ	2.47	0.44
1:C:154:ASN:OD1	1:C:220:ASN:N	2.44	0.44
1:E:126:TYR:OH	1:E:128:LEU:HD22	2.17	0.44
1:E:129:SER:HB2	1:E:158:SER:O	2.17	0.44
1:A:383:LEU:HD12	1:A:383:LEU:N	2.32	0.44
1:D:362:LYS:HD3	1:F:337:THR:HG23	2.00	0.44
1:G:9:PRO:HD3	1:F:7:TYR:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:172:MET:SD	1:G:187:ALA:HB2	2.57	0.44
1:G:317:LEU:CD2	1:G:317:LEU:C	2.85	0.44
1:F:45:ALA:HB1	1:F:87:SER:HB3	1.99	0.44
1:F:101:LEU:HD22	1:F:114:LEU:HG	2.00	0.44
1:F:310:SER:HA	1:F:317:LEU:CD1	2.48	0.44
1:B:41:PHE:O	1:B:43:GLN:N	2.49	0.44
1:B:117:LEU:HD12	1:B:122:ALA:O	2.17	0.44
1:C:21:ARG:HG3	1:C:79:GLU:OE1	2.17	0.44
1:C:124:PHE:CE1	1:C:168:TYR:HB2	2.53	0.44
1:E:63:TYR:CZ	1:E:110:LYS:HB3	2.53	0.44
1:E:65:GLY:HA2	1:E:118:ALA:HB1	1.99	0.44
1:E:88:SER:OG	1:E:253:GLN:HG3	2.17	0.44
1:H:101:LEU:HD21	1:H:113:TYR:HB2	1.99	0.44
1:H:355:GLU:CD	1:H:359:ARG:HE	2.19	0.44
1:A:180:PRO:HB2	1:A:183:ARG:CG	2.48	0.44
1:D:130:GLU:H	1:D:134:GLY:HA2	1.83	0.44
1:F:113:TYR:HD1	1:F:168:TYR:CE2	2.36	0.44
1:F:143:ARG:HA	1:F:174:VAL:HG12	2.00	0.44
1:F:224:PRO:O	1:F:227:ARG:HG2	2.17	0.44
1:C:221:VAL:HG12	1:C:223:ILE:HG23	2.00	0.44
1:C:223:ILE:HD12	1:C:227:ARG:CB	2.48	0.44
1:H:59:VAL:HG11	1:H:118:ALA:HB2	2.00	0.44
1:A:6:LEU:HD23	1:A:7:TYR:N	2.31	0.44
1:A:266:LEU:HD21	1:D:382:LEU:HD23	1.98	0.44
1:D:156:GLN:HA	1:D:216:LEU:O	2.18	0.44
1:D:372:GLN:HE21	1:F:288:MET:HE1	1.83	0.44
1:B:292:MET:HB3	1:B:292:MET:HE2	1.57	0.44
1:B:301:GLN:O	1:B:305:VAL:HG23	2.18	0.44
1:C:250:ILE:HG13	1:C:368:GLU:HG3	2.00	0.44
1:E:186:SER:HB3	1:E:233:GLY:H	1.82	0.44
1:E:296:LEU:HB2	1:E:335:ILE:HD13	1.99	0.44
1:E:299:ALA:HB1	1:E:328:ALA:HA	2.00	0.44
1:H:81:ALA:HB2	1:H:88:SER:OG	2.17	0.44
1:A:172:MET:HG2	1:A:187:ALA:CB	2.47	0.44
1:A:267:GLY:O	1:A:271:GLU:HG3	2.18	0.44
1:G:28:ILE:HG12	1:G:45:ALA:HA	1.99	0.44
1:G:89:LEU:HD23	1:G:92:ALA:HB3	1.99	0.44
1:G:308:ALA:HB1	1:G:312:ARG:NH2	2.33	0.44
1:F:303:VAL:HA	1:F:324:ALA:HB1	1.98	0.44
1:E:24:ALA:HA	1:E:28:ILE:HD12	1.99	0.44
1:E:100:PRO:HA	1:E:238:THR:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:GLN:O	1:A:257:ILE:HG13	2.17	0.43
1:A:312:ARG:HE	1:D:8:ARG:HH21	1.65	0.43
1:D:21:ARG:NE	1:D:79:GLU:OE1	2.51	0.43
1:D:266:LEU:HD23	1:D:289:LEU:HD13	2.00	0.43
1:F:144:ALA:HB1	1:F:151:TRP:CE3	2.53	0.43
1:F:261:ALA:CB	1:F:336:THR:HG22	2.47	0.43
1:H:39:SER:O	1:H:39:SER:OG	2.35	0.43
1:D:25:GLU:HB2	1:D:26:ASP:OD1	2.18	0.43
1:G:6:LEU:CD1	1:F:71:LEU:HD13	2.48	0.43
1:G:10:THR:HG23	1:G:13:HIS:CE1	2.53	0.43
1:G:109:VAL:HG11	1:G:229:VAL:HG12	2.00	0.43
1:B:96:LEU:HD21	1:B:126:TYR:HD2	1.83	0.43
1:C:355:GLU:OE1	1:C:356:ARG:N	2.51	0.43
1:E:187:ALA:HB3	1:E:229:VAL:CG2	2.48	0.43
1:H:269:VAL:HG23	1:H:280:ALA:HB2	1.99	0.43
1:A:77:ILE:CD1	1:A:249:THR:HB	2.48	0.43
1:A:183:ARG:HD3	1:A:237:ARG:NH1	2.33	0.43
1:D:272:ARG:NH1	1:D:272:ARG:HG3	2.33	0.43
1:F:8:ARG:HG2	1:F:8:ARG:HH11	1.83	0.43
1:F:21:ARG:HH11	1:F:82:ARG:HD3	1.83	0.43
1:F:22:SER:O	1:F:26:ASP:HB2	2.17	0.43
1:F:55:HIS:NE2	1:F:117:LEU:O	2.48	0.43
1:F:243:LEU:HD12	1:F:243:LEU:HA	1.91	0.43
1:F:253:GLN:O	1:F:257:ILE:HG13	2.18	0.43
1:B:31:HIS:NE2	1:B:44:GLU:HG2	2.34	0.43
1:B:160:ILE:HG13	1:B:216:LEU:HG	2.00	0.43
1:C:20:ILE:HD13	1:C:54:PHE:CD2	2.53	0.43
1:C:22:SER:O	1:C:26:ASP:CB	2.67	0.43
1:C:363:ILE:HG12	1:H:348:TYR:OH	2.19	0.43
1:E:50:ARG:NH2	1:E:121:GLU:HA	2.33	0.43
1:E:137:THR:O	1:E:140:MET:HG3	2.17	0.43
1:E:298:ALA:HB2	1:H:302:MET:CE	2.48	0.43
1:A:359:ARG:HD3	1:G:359:ARG:HD3	2.01	0.43
1:D:185:ILE:HD13	1:D:185:ILE:HG21	1.80	0.43
1:G:291:ASP:HB3	1:G:295:LYS:HE3	2.01	0.43
1:B:16:LEU:CD2	1:B:72:ALA:HB1	2.49	0.43
1:B:40:ARG:NH1	1:B:44:GLU:OE1	2.47	0.43
1:B:124:PHE:HA	1:B:168:TYR:O	2.18	0.43
1:C:22:SER:O	1:C:26:ASP:HB2	2.19	0.43
1:C:42:PRO:HB2	1:C:45:ALA:HB3	2.01	0.43
1:E:292:MET:HB3	1:E:292:MET:HE2	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:367:TYR:HD1	1:E:367:TYR:O	2.01	0.43
1:A:7:TYR:CE2	1:D:9:PRO:HD3	2.54	0.43
1:D:70:ALA:HA	1:D:73:THR:CG2	2.48	0.43
1:D:89:LEU:HD11	1:D:208:ILE:HG21	2.01	0.43
1:B:197:PHE:HE1	1:B:218:PHE:HE1	1.66	0.43
1:B:204:ARG:HD2	1:E:350:ARG:NH1	2.33	0.43
1:B:342:LEU:HD23	1:B:342:LEU:HA	1.93	0.43
1:C:208:ILE:HB	1:C:363:ILE:CD1	2.48	0.43
1:H:63:TYR:HD2	1:H:115:PRO:HD3	1.83	0.43
1:H:89:LEU:HA	1:H:92:ALA:HB3	2.00	0.43
1:A:63:TYR:HB3	1:A:115:PRO:CG	2.47	0.43
1:A:165:ILE:HD12	1:A:212:PRO:CG	2.48	0.43
1:G:113:TYR:CZ	1:G:189:VAL:HG11	2.53	0.43
1:G:127:GLY:O	1:G:157:LYS:HE3	2.18	0.43
1:B:186:SER:OG	1:B:232:VAL:HA	2.18	0.43
1:E:231:LYS:O	1:E:234:GLU:HB2	2.16	0.43
1:H:243:LEU:O	1:H:244:ASP:C	2.57	0.43
1:A:373:ILE:O	1:A:377:VAL:HG22	2.19	0.43
1:D:199:PHE:HD1	1:D:216:LEU:HD23	1.84	0.43
1:G:58:HIS:NE2	1:G:98:SER:OG	2.39	0.43
1:G:82:ARG:HA	1:G:256:GLY:O	2.18	0.43
1:F:208:ILE:HG22	1:F:211:SER:HB3	2.00	0.43
1:E:130:GLU:N	1:E:134:GLY:HA2	2.15	0.43
1:E:223:ILE:HB	1:E:227:ARG:HG3	2.01	0.43
1:H:159:TRP:HA	1:H:213:THR:CG2	2.49	0.43
1:A:159:TRP:HH2	1:G:346:TYR:CD2	2.37	0.43
1:D:58:HIS:CG	1:D:95:LYS:HG3	2.54	0.43
1:D:96:LEU:HG	1:D:126:TYR:HB3	2.01	0.43
1:G:157:LYS:HG3	1:G:171:VAL:HG23	1.99	0.43
1:G:252:ALA:HA	1:G:303:VAL:HG11	1.99	0.43
1:G:319:PHE:CD1	1:G:319:PHE:C	2.91	0.43
1:F:157:LYS:HB3	1:F:160:ILE:HD11	2.00	0.43
1:B:101:LEU:HD21	1:B:113:TYR:HB2	2.00	0.43
1:C:143:ARG:NH2	1:C:154:ASN:HB2	2.34	0.43
1:C:236:LEU:HD12	1:C:236:LEU:HA	1.76	0.43
1:E:80:ILE:HD12	1:E:91:PRO:HG3	2.00	0.43
1:A:172:MET:HE1	1:A:235:GLY:O	2.19	0.43
1:D:62:GLU:HB3	1:D:63:TYR:CD1	2.53	0.43
1:D:63:TYR:CE2	1:D:110:LYS:HB3	2.54	0.43
1:D:205:LYS:HD3	1:D:213:THR:HB	1.99	0.43
1:G:79:GLU:OE1	1:G:79:GLU:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:160:ILE:HD13	1:G:160:ILE:HA	1.79	0.43
1:G:250:ILE:HD13	1:G:250:ILE:HA	1.71	0.43
1:G:346:TYR:HB3	1:G:352:TYR:CE1	2.53	0.43
1:C:6:LEU:HD23	1:C:6:LEU:HA	1.82	0.43
1:C:188:PHE:HD1	1:C:228:LEU:HA	1.84	0.43
1:H:257:ILE:HG21	1:H:361:ALA:HB2	2.00	0.43
1:D:116:GLU:OE1	1:D:168:TYR:OH	2.26	0.43
1:G:123:MET:HE1	1:G:162:ASN:OD1	2.19	0.43
1:F:362:LYS:HE3	1:F:366:ILE:HD11	2.01	0.43
1:B:223:ILE:HD12	1:B:227:ARG:HB2	2.00	0.43
1:B:284:GLY:N	1:H:283:GLN:HB3	2.34	0.43
1:H:259:GLN:NE2	1:H:263:ASP:OD1	2.50	0.43
1:G:36:ASP:O	1:G:209:LYS:HD3	2.19	0.42
1:G:94:ASN:CG	1:G:117:LEU:HD11	2.39	0.42
1:B:32:ALA:HB2	1:B:84:CYS:HB2	2.01	0.42
1:B:233:GLY:C	1:B:235:GLY:H	2.22	0.42
1:B:274:GLN:HG3	2:E:402:875:O1A	2.19	0.42
1:C:143:ARG:HB2	1:C:143:ARG:CZ	2.48	0.42
1:C:208:ILE:O	1:C:208:ILE:HG13	2.19	0.42
1:C:363:ILE:O	1:C:364:THR:C	2.55	0.42
1:E:369:GLY:O	1:E:374:GLN:NE2	2.46	0.42
2:E:402:875:N1A	1:H:283:GLN:NE2	2.67	0.42
1:H:224:PRO:HG2	1:H:227:ARG:NE	2.34	0.42
1:A:22:SER:O	1:A:26:ASP:HB3	2.18	0.42
1:D:31:HIS:CE1	1:D:44:GLU:HG2	2.53	0.42
1:G:253:GLN:NE2	1:G:367:TYR:OH	2.50	0.42
1:F:268:TYR:OH	1:F:346:TYR:HD2	2.02	0.42
1:B:13:HIS:CE1	1:B:69:ASP:OD2	2.71	0.42
1:B:204:ARG:HD2	1:E:350:ARG:HH12	1.84	0.42
1:C:170:THR:O	1:C:170:THR:OG1	2.33	0.42
1:C:350:ARG:NE	1:H:204:ARG:HB3	2.34	0.42
1:E:207:GLY:O	1:E:208:ILE:HB	2.20	0.42
1:A:381:GLN:OE1	1:A:384:LYS:HE3	2.18	0.42
1:D:319:PHE:HD2	1:D:320:TYR:CD1	2.38	0.42
1:C:89:LEU:HD12	1:C:208:ILE:CD1	2.50	0.42
1:C:261:ALA:HB1	1:C:339:ALA:CB	2.48	0.42
1:E:362:LYS:HA	1:E:362:LYS:HD2	1.50	0.42
1:D:340:VAL:HG12	1:F:366:ILE:HD11	2.02	0.42
1:D:363:ILE:HD13	1:F:348:TYR:CD2	2.55	0.42
1:B:35:VAL:HG22	1:B:42:PRO:HA	2.01	0.42
1:B:141:ARG:NH2	1:B:143:ARG:HH12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:GLY:HA3	1:H:287:PHE:CE2	2.55	0.42
1:B:285:ILE:HD12	1:B:342:LEU:CD2	2.50	0.42
1:C:116:GLU:OE2	1:C:168:TYR:OH	2.38	0.42
1:C:205:LYS:NZ	1:C:208:ILE:HG23	2.32	0.42
1:H:174:VAL:HG12	1:H:185:ILE:CD1	2.49	0.42
1:A:56:ALA:O	1:A:59:VAL:HG23	2.20	0.42
1:D:268:TYR:CE2	1:D:343:LEU:HA	2.54	0.42
1:D:343:LEU:HD13	1:D:354:VAL:HG11	2.01	0.42
1:D:348:TYR:OH	1:F:207:GLY:N	2.52	0.42
1:B:112:ARG:HD3	1:B:113:TYR:CZ	2.55	0.42
1:C:291:ASP:HB3	1:C:295:LYS:HE3	2.00	0.42
1:E:96:LEU:HA	1:E:246:THR:HG21	2.02	0.42
1:H:61:GLU:H	1:H:61:GLU:HG2	1.54	0.42
1:H:188:PHE:CE2	1:H:228:LEU:HD12	2.54	0.42
1:H:309:LYS:C	1:H:317:LEU:HD13	2.40	0.42
1:D:71:LEU:HD11	1:D:304:TYR:O	2.19	0.42
1:D:327:PHE:CE2	1:D:331:VAL:HG21	2.55	0.42
1:G:29:ALA:N	1:G:30:PRO:HD2	2.35	0.42
1:G:215:GLU:O	1:G:216:LEU:HD23	2.20	0.42
1:G:363:ILE:O	1:G:367:TYR:N	2.45	0.42
1:B:140:MET:HE3	1:B:172:MET:O	2.20	0.42
1:B:231:LYS:HD2	1:B:231:LYS:HA	1.67	0.42
1:E:10:THR:HG1	1:E:13:HIS:CG	2.37	0.42
1:E:13:HIS:HD2	1:E:72:ALA:HB2	1.82	0.42
1:E:291:ASP:O	1:E:295:LYS:HG2	2.20	0.42
1:H:195:PRO:O	1:H:221:VAL:HA	2.19	0.42
1:C:277:LYS:HD3	1:C:281:ASP:HB3	2.01	0.42
1:H:61:GLU:OE2	1:H:67:GLY:HA3	2.20	0.42
1:H:163:ALA:HB3	1:H:214:ARG:HB2	2.02	0.42
1:A:151:TRP:HB2	1:A:223:ILE:HD11	2.01	0.42
1:D:58:HIS:CE1	1:D:95:LYS:HA	2.54	0.42
1:D:355:GLU:OE2	1:D:359:ARG:NE	2.53	0.42
1:G:63:TYR:CD2	1:G:114:LEU:HD12	2.55	0.42
1:F:208:ILE:CG2	1:F:211:SER:HB3	2.50	0.42
1:B:113:TYR:CE1	1:B:191:HIS:HE1	2.37	0.42
1:B:301:GLN:OE1	1:C:305:VAL:HG21	2.19	0.42
1:C:71:LEU:HA	1:C:307:ALA:HB1	2.01	0.42
1:E:286:GLN:HB3	1:H:379:ALA:CB	2.50	0.42
1:H:142:THR:HA	1:H:154:ASN:O	2.20	0.42
1:A:65:GLY:HA2	1:A:118:ALA:HB1	2.01	0.42
1:D:28:ILE:HD13	1:D:80:ILE:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:ASP:HA	1:D:177:PRO:HD2	1.88	0.42
1:G:14:GLU:O	1:G:18:GLU:HG3	2.20	0.42
1:G:70:ALA:CB	1:G:311:GLU:HG2	2.49	0.42
1:G:86:SER:HA	1:G:208:ILE:HG13	2.02	0.42
1:G:126:TYR:O	1:G:160:ILE:HD12	2.19	0.42
1:F:122:ALA:HB2	1:F:167:LYS:HD2	2.02	0.42
1:F:171:VAL:HG21	1:F:218:PHE:CZ	2.54	0.42
1:F:306:ALA:O	1:F:309:LYS:HB2	2.20	0.42
1:B:101:LEU:HD11	1:B:109:VAL:HG22	2.01	0.42
1:C:261:ALA:HA	1:C:357:MET:CE	2.50	0.42
1:A:104:SER:HB3	1:A:241:ARG:NH1	2.35	0.42
1:A:203:GLU:OE1	1:G:349:THR:HG21	2.20	0.42
1:B:21:ARG:NH2	1:B:82:ARG:NH1	2.68	0.42
1:B:45:ALA:O	1:B:49:LEU:HG	2.19	0.42
1:C:55:HIS:CD2	1:C:56:ALA:N	2.87	0.42
1:C:63:TYR:CD2	1:C:115:PRO:HD3	2.54	0.42
1:H:31:HIS:O	1:H:35:VAL:CG2	2.54	0.42
1:H:316:ASP:N	1:H:316:ASP:OD1	2.53	0.42
1:A:93:VAL:HG11	1:A:162:ASN:HB3	2.02	0.41
1:D:55:HIS:O	1:D:94:ASN:ND2	2.53	0.41
1:F:244:ASP:HB3	1:F:317:LEU:CD2	2.44	0.41
1:B:277:LYS:HG2	1:B:281:ASP:HB2	2.02	0.41
1:A:153:LEU:HD23	1:A:153:LEU:HA	1.81	0.41
1:A:236:LEU:HD12	1:A:236:LEU:HA	1.64	0.41
1:A:265:ALA:HB1	1:A:342:LEU:CD1	2.50	0.41
1:G:96:LEU:HG	1:G:126:TYR:CB	2.51	0.41
1:G:305:VAL:HG21	1:F:301:GLN:OE1	2.20	0.41
1:B:71:LEU:HD22	1:B:75:ILE:HD11	2.02	0.41
1:B:156:GLN:HA	1:B:216:LEU:O	2.21	0.41
1:B:206:LEU:HB2	1:E:355:GLU:HG3	2.02	0.41
1:C:20:ILE:HG21	1:C:76:VAL:HA	2.02	0.41
1:C:31:HIS:O	1:C:35:VAL:HG23	2.20	0.41
1:C:157:LYS:HD3	1:C:157:LYS:HA	1.83	0.41
1:H:89:LEU:HD21	1:H:367:TYR:OH	2.20	0.41
1:H:196:GLY:HA3	1:H:219:ASP:O	2.20	0.41
1:D:269:VAL:CG2	1:D:280:ALA:HB2	2.51	0.41
1:G:208:ILE:O	1:G:208:ILE:HG23	2.21	0.41
1:B:355:GLU:HG3	1:E:206:LEU:HB2	2.02	0.41
1:C:372:GLN:OE1	1:C:372:GLN:N	2.52	0.41
1:A:89:LEU:HA	1:A:92:ALA:HB3	2.02	0.41
1:A:128:LEU:HD22	1:A:239:ALA:HB1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:16:LEU:O	1:D:20:ILE:HG22	2.20	0.41
1:D:161:THR:HG22	1:D:211:SER:OG	2.21	0.41
1:D:288:MET:HE2	1:D:288:MET:HB2	1.71	0.41
1:F:13:HIS:O	1:F:16:LEU:HB3	2.21	0.41
1:E:298:ALA:HB2	1:H:302:MET:HE2	2.01	0.41
1:E:345:GLY:O	1:E:349:THR:HG23	2.21	0.41
1:H:70:ALA:N	1:H:311:GLU:OE1	2.48	0.41
1:H:266:LEU:O	1:H:270:LYS:HG3	2.20	0.41
1:A:326:CYS:SG	1:A:371:ASN:HB3	2.60	0.41
1:D:89:LEU:O	1:D:93:VAL:HG23	2.20	0.41
1:G:93:VAL:HG11	1:G:162:ASN:HB2	2.03	0.41
1:F:208:ILE:HG12	1:F:363:ILE:HG12	2.01	0.41
1:E:269:VAL:HG23	1:E:280:ALA:HB2	2.03	0.41
1:H:32:ALA:HB2	1:H:84:CYS:HB2	2.01	0.41
1:H:35:VAL:HG13	1:H:42:PRO:CA	2.51	0.41
1:H:191:HIS:CD2	1:H:227:ARG:HH12	2.39	0.41
1:D:157:LYS:HG3	1:D:171:VAL:HG23	2.01	0.41
1:G:58:HIS:CE1	1:G:95:LYS:HA	2.55	0.41
1:F:264:TYR:CZ	1:F:353:PRO:HG3	2.56	0.41
1:B:97:GLY:HA2	1:B:126:TYR:HB2	2.02	0.41
1:B:353:PRO:O	1:B:357:MET:HG3	2.21	0.41
1:C:367:TYR:HB2	2:H:401:875:C1'	2.50	0.41
1:E:9:PRO:HD3	1:H:7:TYR:OH	2.20	0.41
1:H:89:LEU:HB3	1:H:93:VAL:HG23	2.01	0.41
1:H:197:PHE:HB2	1:H:221:VAL:HG21	2.03	0.41
1:A:234:GLU:HA	1:A:237:ARG:CD	2.50	0.41
1:A:287:PHE:HE1	1:D:376:VAL:HG23	1.86	0.41
1:B:191:HIS:CD2	1:B:227:ARG:CZ	3.04	0.41
1:B:244:ASP:HB3	1:B:317:LEU:HD23	2.02	0.41
1:C:59:VAL:HG11	1:C:117:LEU:HD23	2.02	0.41
1:C:208:ILE:HD12	1:C:208:ILE:HA	1.86	0.41
1:E:7:TYR:HE2	1:H:71:LEU:HD11	1.86	0.41
1:E:160:ILE:HD13	1:E:160:ILE:HA	1.90	0.41
1:E:215:GLU:HG2	1:E:217:ILE:HD13	2.01	0.41
1:H:53:ASP:HB3	1:H:66:VAL:CG2	2.50	0.41
1:A:81:ALA:N	1:A:88:SER:HB3	2.35	0.41
1:A:85:ALA:HA	1:A:88:SER:OG	2.20	0.41
1:A:117:LEU:HD13	1:A:124:PHE:CD1	2.55	0.41
1:A:126:TYR:O	1:A:160:ILE:HD12	2.20	0.41
1:A:292:MET:SD	1:A:342:LEU:HD11	2.60	0.41
1:F:24:ALA:HB1	1:F:83:VAL:CG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:143:ARG:HG2	1:E:174:VAL:HG13	2.01	0.41
1:H:168:TYR:HE1	1:H:191:HIS:CG	2.39	0.41
1:H:199:PHE:CE1	1:H:216:LEU:HD22	2.56	0.41
1:A:59:VAL:HB	1:A:65:GLY:HA3	2.02	0.41
1:D:259:GLN:NE2	1:D:263:ASP:OD1	2.48	0.41
1:D:356:ARG:O	1:D:356:ARG:HG2	2.21	0.41
1:G:17:ARG:NH2	1:G:75:ILE:HD12	2.33	0.41
1:G:17:ARG:NH1	1:G:79:GLU:OE2	2.54	0.41
1:G:82:ARG:HD2	1:G:259:GLN:CG	2.50	0.41
1:G:208:ILE:O	1:G:209:LYS:C	2.59	0.41
1:F:77:ILE:HD13	1:F:249:THR:HB	2.02	0.41
1:B:28:ILE:HD11	1:B:49:LEU:HD21	2.02	0.41
1:B:86:SER:HB3	1:B:211:SER:H	1.85	0.41
1:B:320:TYR:OH	1:C:297:GLU:OE1	2.29	0.41
1:B:363:ILE:HG23	1:E:348:TYR:CE1	2.56	0.41
1:C:58:HIS:NE2	1:C:98:SER:HB2	2.36	0.41
1:C:59:VAL:HG21	1:C:118:ALA:CB	2.50	0.41
1:C:152:ILE:HD13	1:C:222:ARG:HB2	2.02	0.41
1:E:14:GLU:O	1:E:17:ARG:HB3	2.21	0.41
1:E:123:MET:HB2	1:E:166:SER:HA	2.03	0.41
1:E:185:ILE:O	1:E:235:GLY:CA	2.69	0.41
1:E:382:LEU:HD11	1:H:293:ALA:HB2	2.02	0.41
1:H:83:VAL:O	1:H:356:ARG:NH2	2.54	0.41
1:H:275:PHE:HB2	1:H:282:PHE:HZ	1.86	0.41
1:H:356:ARG:HG2	1:H:360:ASP:OD2	2.21	0.41
1:A:99:MET:N	1:A:100:PRO:HD2	2.36	0.41
1:D:284:GLY:HA3	1:G:287:PHE:CZ	2.56	0.41
1:D:373:ILE:HD13	1:D:373:ILE:HA	1.90	0.41
1:G:102:ILE:HG12	1:G:114:LEU:HD11	2.02	0.41
1:G:172:MET:HE3	1:G:239:ALA:HB2	2.03	0.41
1:B:124:PHE:CE1	1:B:168:TYR:HB2	2.56	0.41
1:B:130:GLU:HG3	1:B:157:LYS:HD3	2.04	0.41
1:B:208:ILE:HD12	1:B:208:ILE:HG23	1.72	0.41
1:B:299:ALA:O	1:B:303:VAL:HG23	2.21	0.41
1:B:355:GLU:OE2	1:B:359:ARG:NH2	2.53	0.41
1:C:88:SER:OG	1:C:253:GLN:HG3	2.21	0.41
1:C:171:VAL:HG21	1:C:218:PHE:HZ	1.85	0.41
1:C:282:PHE:HB3	1:E:283:GLN:OE1	2.21	0.41
1:C:354:VAL:HA	1:C:357:MET:HE3	2.02	0.41
1:E:215:GLU:HG2	1:E:217:ILE:CD1	2.50	0.41
1:E:368:GLU:OE1	1:E:368:GLU:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:383:LEU:HD22	1:H:280:ALA:HB1	2.02	0.41
1:H:82:ARG:CZ	1:H:263:ASP:OD2	2.69	0.41
1:H:301:GLN:OE1	1:H:301:GLN:HA	2.20	0.41
1:G:99:MET:HB3	1:G:242:THR:HG23	2.03	0.40
1:G:195:PRO:O	1:G:221:VAL:HA	2.21	0.40
1:B:89:LEU:HA	1:B:89:LEU:HD23	1.93	0.40
1:B:278:ALA:O	1:B:281:ASP:HB2	2.21	0.40
1:E:164:GLY:HA3	1:E:214:ARG:NH2	2.36	0.40
1:A:123:MET:CE	1:A:165:ILE:HG22	2.51	0.40
1:D:108:GLU:O	1:D:112:ARG:HG3	2.22	0.40
1:G:89:LEU:HB3	1:G:93:VAL:CG2	2.50	0.40
1:G:163:ALA:C	1:G:214:ARG:HD2	2.41	0.40
1:G:269:VAL:HG13	1:G:279:ILE:CG1	2.47	0.40
1:B:363:ILE:H	1:B:363:ILE:HG13	1.66	0.40
1:C:206:LEU:HB2	1:H:355:GLU:CG	2.49	0.40
1:C:319:PHE:HD2	1:C:320:TYR:CD1	2.39	0.40
1:C:350:ARG:NH2	1:H:204:ARG:HB3	2.36	0.40
1:E:45:ALA:HB1	1:E:87:SER:HB3	2.03	0.40
1:E:277:LYS:HE2	1:E:282:PHE:CE1	2.56	0.40
1:E:342:LEU:HD23	1:E:342:LEU:HA	1.86	0.40
1:A:59:VAL:HG11	1:A:118:ALA:HB2	2.03	0.40
1:A:68:ALA:HB1	1:A:72:ALA:HB3	2.03	0.40
1:A:139:SER:HA	1:A:181:ARG:HD3	2.02	0.40
1:A:297:GLU:CD	1:A:300:ARG:HH11	2.24	0.40
1:A:308:ALA:O	1:A:312:ARG:HG3	2.21	0.40
1:D:305:VAL:HG12	1:D:309:LYS:HD2	2.03	0.40
1:G:279:ILE:HA	1:G:282:PHE:CD2	2.57	0.40
1:F:96:LEU:HD11	1:F:126:TYR:CD2	2.57	0.40
1:B:266:LEU:CD2	1:B:289:LEU:HD22	2.52	0.40
1:B:338:ASP:O	1:B:341:GLN:HB3	2.21	0.40
1:C:77:ILE:HD13	1:C:249:THR:HB	2.02	0.40
1:E:42:PRO:HB2	1:E:45:ALA:HB3	2.03	0.40
1:E:50:ARG:CZ	1:E:120:GLY:O	2.69	0.40
1:A:183:ARG:HH11	1:A:237:ARG:NH1	2.19	0.40
1:A:346:TYR:O	1:A:349:THR:OG1	2.37	0.40
1:G:56:ALA:O	1:G:59:VAL:HG23	2.20	0.40
1:G:176:ASP:HB3	1:G:179:GLY:CA	2.52	0.40
1:G:181:ARG:NH1	1:C:351:ASP:OD1	2.54	0.40
1:F:88:SER:OG	1:F:253:GLN:NE2	2.54	0.40
1:B:69:ASP:HA	1:B:311:GLU:OE1	2.20	0.40
1:B:197:PHE:CD1	1:B:218:PHE:CE1	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:297:GLU:OE2	1:B:300:ARG:NH1	2.54	0.40
1:C:204:ARG:HB3	1:H:350:ARG:HB2	2.02	0.40
1:C:323:ALA:HA	1:C:378:MET:CE	2.52	0.40
1:E:41:PHE:O	1:E:43:GLN:N	2.53	0.40
1:A:97:GLY:HA2	1:A:126:TYR:HB2	2.01	0.40
1:A:319:PHE:CD1	1:A:378:MET:HG2	2.56	0.40
1:D:73:THR:O	1:D:77:ILE:HD12	2.21	0.40
1:D:342:LEU:HD23	1:D:342:LEU:HA	1.73	0.40
1:G:253:GLN:O	1:G:257:ILE:HG13	2.22	0.40
1:G:280:ALA:HB1	1:F:383:LEU:HD11	2.03	0.40
1:B:132:GLU:OE2	1:B:141:ARG:HG2	2.22	0.40
1:B:197:PHE:CD1	1:B:218:PHE:HE1	2.39	0.40
1:B:359:ARG:HD3	1:E:359:ARG:HD3	2.03	0.40
1:C:363:ILE:CG2	1:C:367:TYR:CD2	3.05	0.40
1:E:131:ARG:HB3	1:E:156:GLN:OE1	2.21	0.40
1:E:168:TYR:HB3	1:E:189:VAL:CG2	2.52	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	366/385 (95%)	349 (95%)	17 (5%)	0	100	100
1	B	378/385 (98%)	357 (94%)	21 (6%)	0	100	100
1	C	378/385 (98%)	353 (93%)	25 (7%)	0	100	100
1	D	372/385 (97%)	350 (94%)	22 (6%)	0	100	100
1	E	380/385 (99%)	361 (95%)	19 (5%)	0	100	100
1	F	377/385 (98%)	357 (95%)	20 (5%)	0	100	100
1	G	377/385 (98%)	352 (93%)	25 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	378/385 (98%)	355 (94%)	23 (6%)	0	100	100
All	All	3006/3080 (98%)	2834 (94%)	172 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	292/304 (96%)	281 (96%)	11 (4%)	33	64
1	B	299/304 (98%)	294 (98%)	5 (2%)	60	82
1	C	298/304 (98%)	293 (98%)	5 (2%)	60	82
1	D	297/304 (98%)	290 (98%)	7 (2%)	49	75
1	E	300/304 (99%)	292 (97%)	8 (3%)	44	72
1	F	297/304 (98%)	289 (97%)	8 (3%)	44	72
1	G	298/304 (98%)	291 (98%)	7 (2%)	50	75
1	H	298/304 (98%)	292 (98%)	6 (2%)	55	79
All	All	2379/2432 (98%)	2322 (98%)	57 (2%)	49	75

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	TYR
1	A	112	ARG
1	A	128	LEU
1	A	129	SER
1	A	131	ARG
1	A	141	ARG
1	A	146	ARG
1	A	181	ARG
1	A	204	ARG
1	A	348	TYR

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Mol	Chain	Res	Type
1	A	367	TYR
1	D	40	ARG
1	D	53	ASP
1	D	143	ARG
1	D	170	THR
1	D	218	PHE
1	D	264	TYR
1	D	367	TYR
1	G	183	ARG
1	G	201	GLU
1	G	208	ILE
1	G	271	GLU
1	G	312	ARG
1	G	316	ASP
1	G	317	LEU
1	F	37	GLU
1	F	86	SER
1	F	87	SER
1	F	141	ARG
1	F	231	LYS
1	F	245	HIS
1	F	272	ARG
1	F	363	ILE
1	B	12	GLU
1	B	71	LEU
1	B	111	GLN
1	B	146	ARG
1	B	363	ILE
1	C	82	ARG
1	C	108	GLU
1	C	174	VAL
1	C	362	LYS
1	C	363	ILE
1	E	4	PHE
1	E	8	ARG
1	E	112	ARG
1	E	234	GLU
1	E	272	ARG
1	E	311	GLU
1	E	367	TYR
1	E	380	ARG
1	H	37	GLU

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Mol	Chain	Res	Type
1	H	69	ASP
1	H	194	ASP
1	H	204	ARG
1	H	294	MET
1	H	363	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	31	HIS
1	D	286	GLN
1	D	374	GLN
1	D	381	GLN
1	G	381	GLN
1	B	162	ASN
1	C	184	ASN
1	C	253	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	875	E	402	-	32,38,38	0.72	0	37,57,57	2.06	8 (21%)
2	875	E	401	-	32,38,38	0.61	0	37,57,57	0.90	2 (5%)
2	875	H	401	-	32,38,38	0.59	0	37,57,57	0.99	2 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	875	E	402	-	-	10/28/48/48	0/3/3/3
2	875	E	401	-	-	6/28/48/48	0/3/3/3
2	875	H	401	-	-	15/28/48/48	0/3/3/3

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	402	875	C5A-C6A-N6A	6.78	130.66	120.35
2	E	402	875	C2A-N1A-C6A	5.19	127.64	118.75
2	E	402	875	N3A-C2A-N1A	-4.75	121.26	128.68
2	H	401	875	O3B-C3B-C2B	-3.85	99.38	111.82
2	E	402	875	O3B-C3B-C2B	-3.21	101.43	111.82
2	E	402	875	O3B-C3B-C4B	-2.91	102.63	111.05
2	E	402	875	C5A-C6A-N1A	-2.83	113.94	120.35
2	E	401	875	C5A-C6A-N6A	2.48	124.12	120.35
2	H	401	875	C5A-C6A-N6A	2.44	124.06	120.35
2	E	402	875	PA-O5B-C5B	-2.39	107.67	121.68
2	E	401	875	P-O3P-PA	-2.34	124.80	132.83
2	E	402	875	C3B-C2B-C1B	2.11	104.16	100.98

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	401	875	C5B-O5B-PA-O2A
2	E	401	875	O4B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
2	E	401	875	C5'-O5'-P-O2P
2	E	402	875	C5B-O5B-PA-O2A
2	E	402	875	N10-C1'-C2'-O2'
2	E	402	875	C3'-C4'-C5'-O5'
2	E	402	875	O4'-C4'-C5'-O5'
2	H	401	875	O4B-C4B-C5B-O5B
2	H	401	875	N10-C1'-C2'-O2'
2	H	401	875	N10-C1'-C2'-C3'
2	H	401	875	C1'-C2'-C3'-O3'
2	H	401	875	C1'-C2'-C3'-C4'
2	H	401	875	O2'-C2'-C3'-O3'
2	H	401	875	O2'-C2'-C3'-C4'
2	H	401	875	C3'-C4'-C5'-O5'
2	E	402	875	O4B-C4B-C5B-O5B
2	E	402	875	C3B-C4B-C5B-O5B
2	H	401	875	C3B-C4B-C5B-O5B
2	H	401	875	O3'-C3'-C4'-C5'
2	H	401	875	C2'-C3'-C4'-C5'
2	H	401	875	C2'-C3'-C4'-O4'
2	H	401	875	O3'-C3'-C4'-O4'
2	E	401	875	C5'-O5'-P-O3P
2	E	402	875	P-O3P-PA-O2A
2	E	401	875	C5'-O5'-P-O1P
2	H	401	875	O4'-C4'-C5'-O5'
2	E	402	875	O3'-C3'-C4'-C5'
2	E	401	875	C5B-O5B-PA-O3P
2	E	402	875	C5B-O5B-PA-O3P
2	E	402	875	N10-C1'-C2'-C3'
2	H	401	875	C5B-O5B-PA-O2A

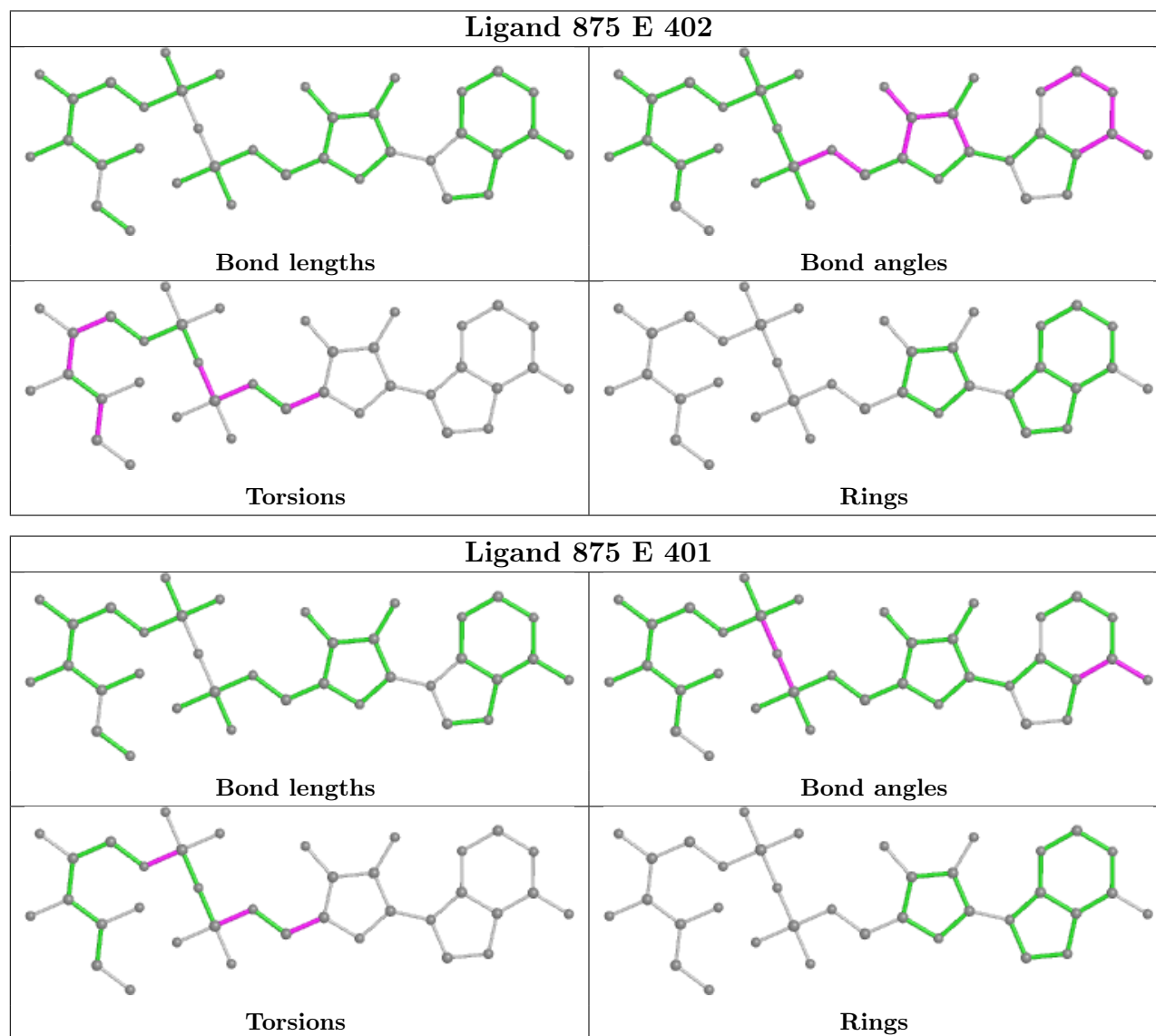
There are no ring outliers.

3 monomers are involved in 8 short contacts:

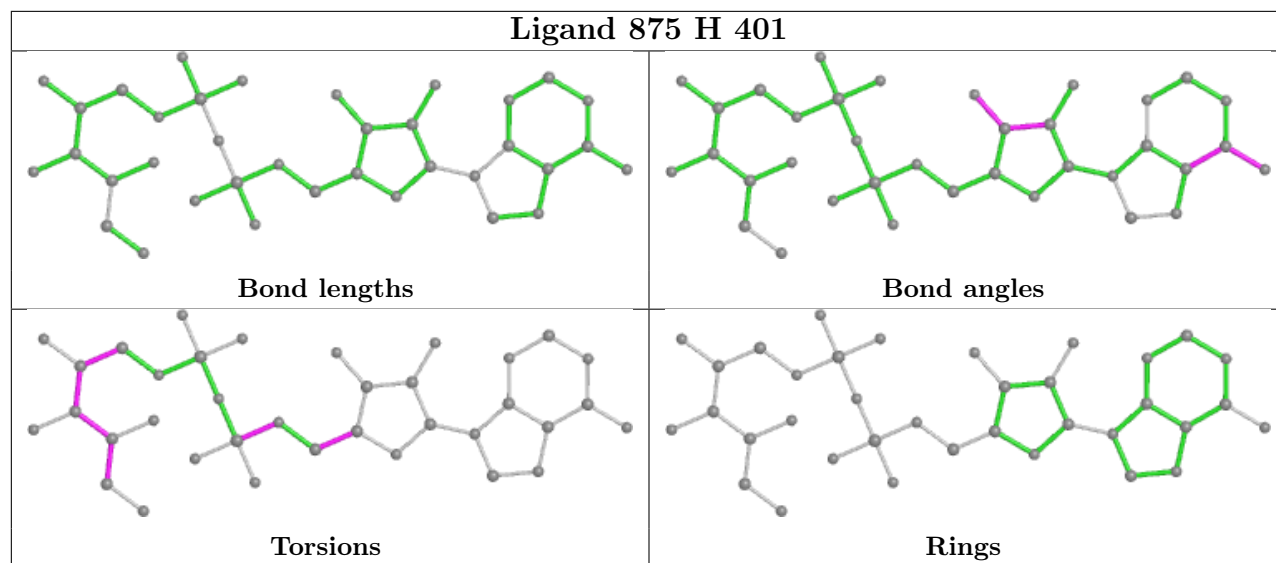
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	402	875	3	0
2	E	401	875	2	0
2	H	401	875	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	370/385 (96%)	-0.02	5 (1%) 75 59	52, 71, 94, 104	0
1	B	380/385 (98%)	-0.11	3 (0%) 86 74	39, 62, 90, 110	0
1	C	380/385 (98%)	-0.12	0 100 100	44, 64, 95, 108	0
1	D	376/385 (97%)	0.06	7 (1%) 66 48	48, 74, 100, 109	0
1	E	382/385 (99%)	-0.13	4 (1%) 82 70	41, 64, 105, 117	0
1	F	379/385 (98%)	-0.14	6 (1%) 72 53	48, 65, 84, 104	0
1	G	379/385 (98%)	-0.06	6 (1%) 72 53	52, 74, 86, 104	0
1	H	380/385 (98%)	-0.20	0 100 100	43, 68, 88, 100	0
All	All	3026/3080 (98%)	-0.09	31 (1%) 82 70	39, 68, 96, 117	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	182	GLY	5.3
1	D	97	GLY	4.5
1	F	181	ARG	3.8
1	F	149	ASP	3.4
1	F	276	GLY	2.8
1	E	141	ARG	2.8
1	F	148	GLY	2.8
1	G	135	SER	2.7
1	D	108	GLU	2.5
1	A	181	ARG	2.5
1	E	143	ARG	2.5
1	B	5	ASP	2.5
1	G	93	VAL	2.4
1	B	181	ARG	2.4
1	D	93	VAL	2.4
1	G	125	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	147	ASP	2.3
1	A	92	ALA	2.3
1	D	148	GLY	2.3
1	D	156	GLN	2.3
1	A	180	PRO	2.2
1	D	118	ALA	2.2
1	E	145	VAL	2.2
1	A	220	ASN	2.2
1	G	134	GLY	2.2
1	E	129	SER	2.2
1	G	92	ALA	2.2
1	F	272	ARG	2.1
1	G	97	GLY	2.0
1	B	180	PRO	2.0
1	D	121	GLU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

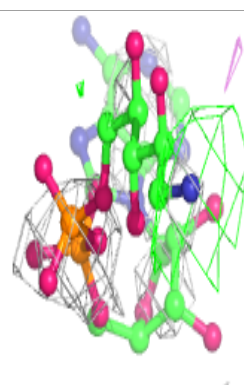
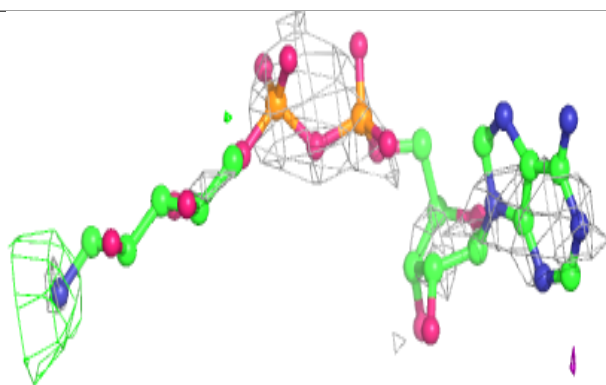
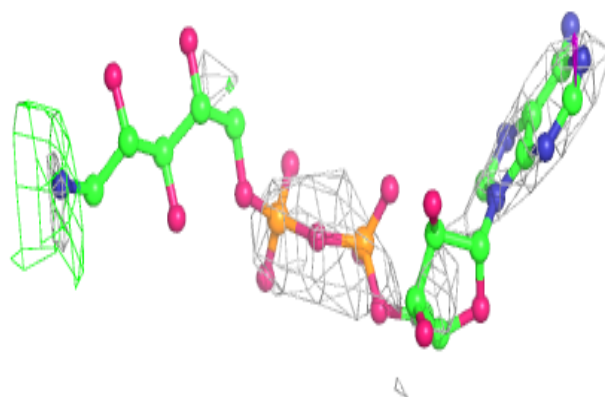
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	875	E	401	36/36	0.61	0.53	56,69,99,106	36
2	875	E	402	36/36	0.71	0.42	64,77,93,103	36
2	875	H	401	36/36	0.72	0.43	67,78,95,108	36

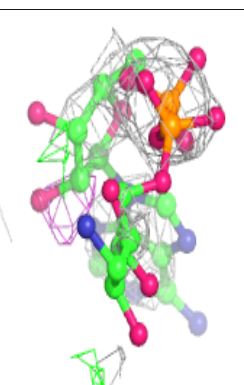
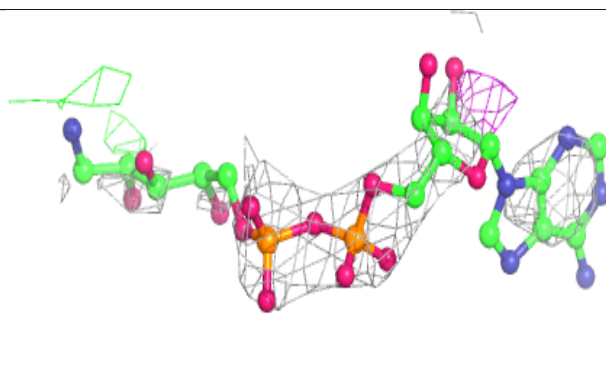
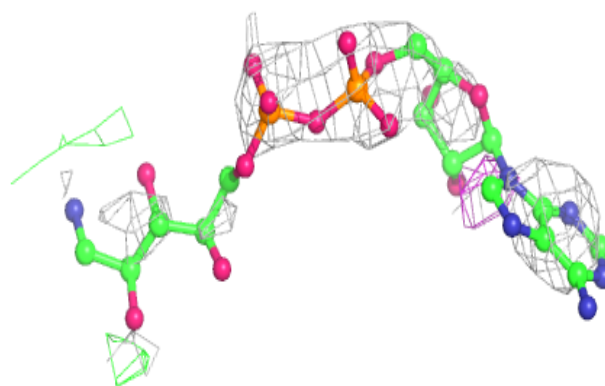
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

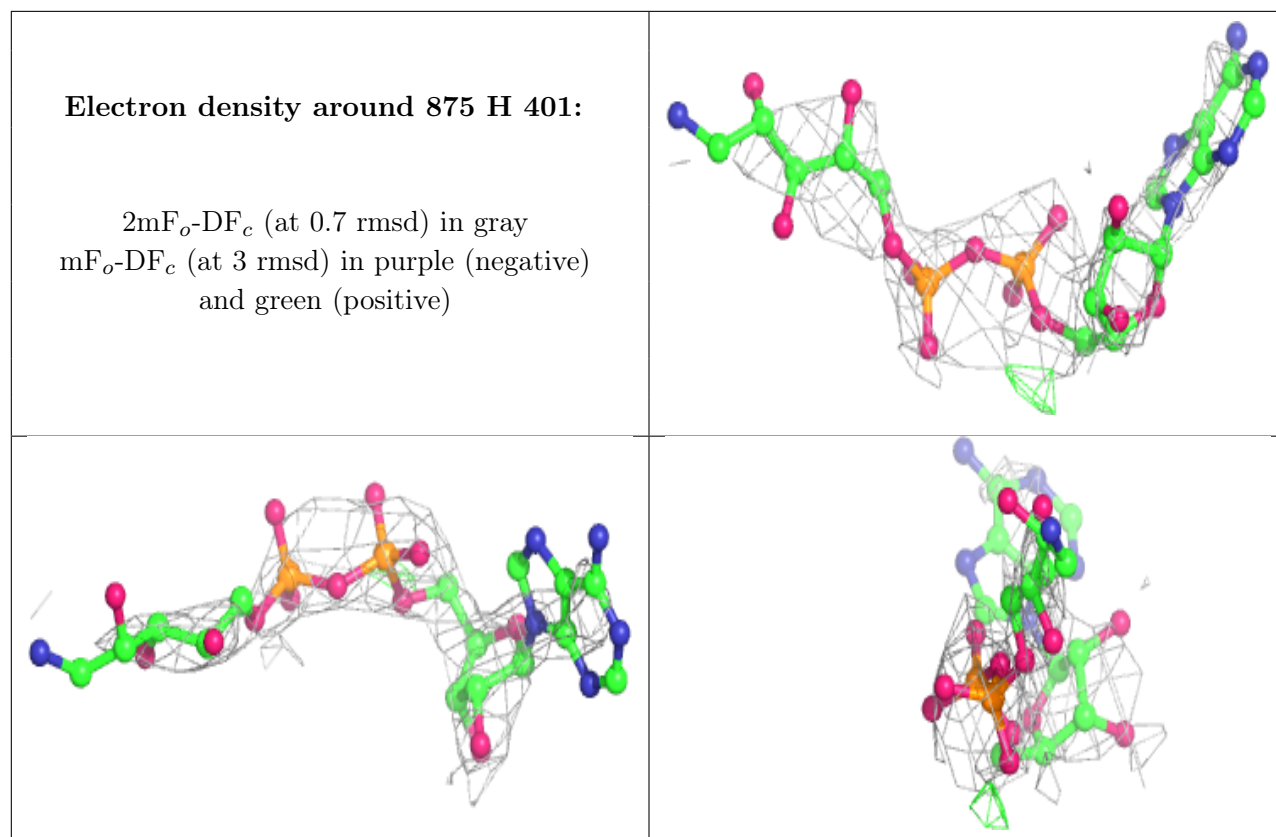
**Electron density around 875 E 401:**

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

**Electron density around 875 E 402:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.