



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 04:10 PM BST

PDB ID : 6VXE  
Title : Crystal structure of hydroxyproline dehydratase (HypD) from *Clostridioides difficile* with substrate trans-4-hydroxy-L-proline bound  
Authors : Backman, L.R.F.; Drennan, C.L.  
Deposited on : 2020-02-21  
Resolution : 2.46 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

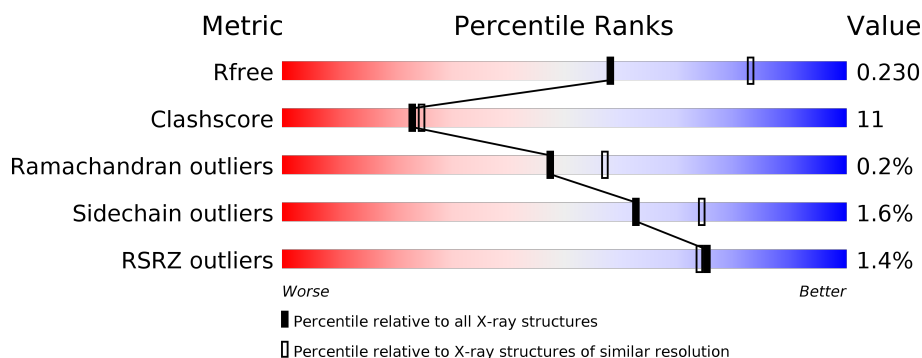
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.46 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . 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	809	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>22%</div> <div>..</div> </div> </div>
1	B	809	<div> <div>%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>..</div> </div> </div>
1	C	809	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>..</div> </div> </div>
1	D	809	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>23%</div> <div>.</div> </div> </div>
1	E	809	<div> <div></div> <div> <div>76%</div> <div>21%</div> <div>..</div> </div> </div>
1	F	809	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>20%</div> <div>..</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	809	
1	H	809	

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	HYP	B	801	-	-	X	-
2	HYP	D	801	-	-	X	-
2	HYP	G	801	-	-	X	-
2	HYP	H	801	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 51664 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 Trans-4-hydroxy-L-proline dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	B	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	C	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	D	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	E	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	F	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	G	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			
1	H	789	Total	C	N	O	S	0	1	0
			6267	3953	1061	1211	42			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A031WDE4
A	-18	GLY	-	expression tag	UNP A0A031WDE4
A	-17	SER	-	expression tag	UNP A0A031WDE4
A	-16	SER	-	expression tag	UNP A0A031WDE4
A	-15	HIS	-	expression tag	UNP A0A031WDE4
A	-14	HIS	-	expression tag	UNP A0A031WDE4
A	-13	HIS	-	expression tag	UNP A0A031WDE4
A	-12	HIS	-	expression tag	UNP A0A031WDE4
A	-11	HIS	-	expression tag	UNP A0A031WDE4
A	-10	HIS	-	expression tag	UNP A0A031WDE4
A	-9	SER	-	expression tag	UNP A0A031WDE4
A	-8	SER	-	expression tag	UNP A0A031WDE4
A	-7	GLY	-	expression tag	UNP A0A031WDE4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP A0A031WDE4
A	-5	VAL	-	expression tag	UNP A0A031WDE4
A	-4	PRO	-	expression tag	UNP A0A031WDE4
A	-3	ARG	-	expression tag	UNP A0A031WDE4
A	-2	GLY	-	expression tag	UNP A0A031WDE4
A	-1	SER	-	expression tag	UNP A0A031WDE4
A	0	HIS	-	expression tag	UNP A0A031WDE4
B	-19	MET	-	initiating methionine	UNP A0A031WDE4
B	-18	GLY	-	expression tag	UNP A0A031WDE4
B	-17	SER	-	expression tag	UNP A0A031WDE4
B	-16	SER	-	expression tag	UNP A0A031WDE4
B	-15	HIS	-	expression tag	UNP A0A031WDE4
B	-14	HIS	-	expression tag	UNP A0A031WDE4
B	-13	HIS	-	expression tag	UNP A0A031WDE4
B	-12	HIS	-	expression tag	UNP A0A031WDE4
B	-11	HIS	-	expression tag	UNP A0A031WDE4
B	-10	HIS	-	expression tag	UNP A0A031WDE4
B	-9	SER	-	expression tag	UNP A0A031WDE4
B	-8	SER	-	expression tag	UNP A0A031WDE4
B	-7	GLY	-	expression tag	UNP A0A031WDE4
B	-6	LEU	-	expression tag	UNP A0A031WDE4
B	-5	VAL	-	expression tag	UNP A0A031WDE4
B	-4	PRO	-	expression tag	UNP A0A031WDE4
B	-3	ARG	-	expression tag	UNP A0A031WDE4
B	-2	GLY	-	expression tag	UNP A0A031WDE4
B	-1	SER	-	expression tag	UNP A0A031WDE4
B	0	HIS	-	expression tag	UNP A0A031WDE4
C	-19	MET	-	initiating methionine	UNP A0A031WDE4
C	-18	GLY	-	expression tag	UNP A0A031WDE4
C	-17	SER	-	expression tag	UNP A0A031WDE4
C	-16	SER	-	expression tag	UNP A0A031WDE4
C	-15	HIS	-	expression tag	UNP A0A031WDE4
C	-14	HIS	-	expression tag	UNP A0A031WDE4
C	-13	HIS	-	expression tag	UNP A0A031WDE4
C	-12	HIS	-	expression tag	UNP A0A031WDE4
C	-11	HIS	-	expression tag	UNP A0A031WDE4
C	-10	HIS	-	expression tag	UNP A0A031WDE4
C	-9	SER	-	expression tag	UNP A0A031WDE4
C	-8	SER	-	expression tag	UNP A0A031WDE4
C	-7	GLY	-	expression tag	UNP A0A031WDE4
C	-6	LEU	-	expression tag	UNP A0A031WDE4
C	-5	VAL	-	expression tag	UNP A0A031WDE4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP A0A031WDE4
C	-3	ARG	-	expression tag	UNP A0A031WDE4
C	-2	GLY	-	expression tag	UNP A0A031WDE4
C	-1	SER	-	expression tag	UNP A0A031WDE4
C	0	HIS	-	expression tag	UNP A0A031WDE4
D	-19	MET	-	initiating methionine	UNP A0A031WDE4
D	-18	GLY	-	expression tag	UNP A0A031WDE4
D	-17	SER	-	expression tag	UNP A0A031WDE4
D	-16	SER	-	expression tag	UNP A0A031WDE4
D	-15	HIS	-	expression tag	UNP A0A031WDE4
D	-14	HIS	-	expression tag	UNP A0A031WDE4
D	-13	HIS	-	expression tag	UNP A0A031WDE4
D	-12	HIS	-	expression tag	UNP A0A031WDE4
D	-11	HIS	-	expression tag	UNP A0A031WDE4
D	-10	HIS	-	expression tag	UNP A0A031WDE4
D	-9	SER	-	expression tag	UNP A0A031WDE4
D	-8	SER	-	expression tag	UNP A0A031WDE4
D	-7	GLY	-	expression tag	UNP A0A031WDE4
D	-6	LEU	-	expression tag	UNP A0A031WDE4
D	-5	VAL	-	expression tag	UNP A0A031WDE4
D	-4	PRO	-	expression tag	UNP A0A031WDE4
D	-3	ARG	-	expression tag	UNP A0A031WDE4
D	-2	GLY	-	expression tag	UNP A0A031WDE4
D	-1	SER	-	expression tag	UNP A0A031WDE4
D	0	HIS	-	expression tag	UNP A0A031WDE4
E	-19	MET	-	initiating methionine	UNP A0A031WDE4
E	-18	GLY	-	expression tag	UNP A0A031WDE4
E	-17	SER	-	expression tag	UNP A0A031WDE4
E	-16	SER	-	expression tag	UNP A0A031WDE4
E	-15	HIS	-	expression tag	UNP A0A031WDE4
E	-14	HIS	-	expression tag	UNP A0A031WDE4
E	-13	HIS	-	expression tag	UNP A0A031WDE4
E	-12	HIS	-	expression tag	UNP A0A031WDE4
E	-11	HIS	-	expression tag	UNP A0A031WDE4
E	-10	HIS	-	expression tag	UNP A0A031WDE4
E	-9	SER	-	expression tag	UNP A0A031WDE4
E	-8	SER	-	expression tag	UNP A0A031WDE4
E	-7	GLY	-	expression tag	UNP A0A031WDE4
E	-6	LEU	-	expression tag	UNP A0A031WDE4
E	-5	VAL	-	expression tag	UNP A0A031WDE4
E	-4	PRO	-	expression tag	UNP A0A031WDE4
E	-3	ARG	-	expression tag	UNP A0A031WDE4

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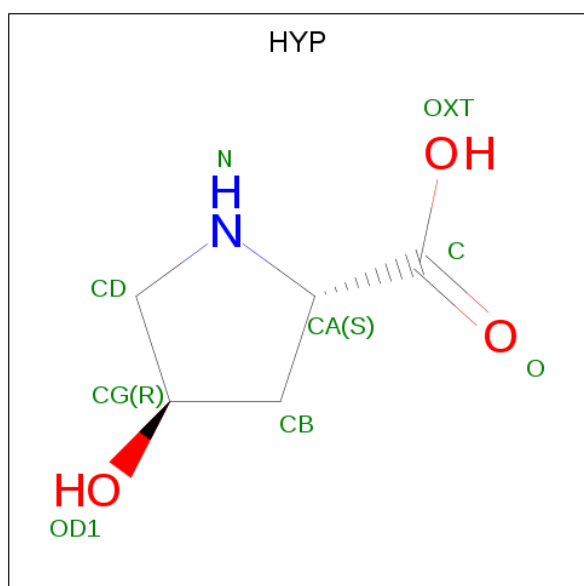
Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP A0A031WDE4
E	-1	SER	-	expression tag	UNP A0A031WDE4
E	0	HIS	-	expression tag	UNP A0A031WDE4
F	-19	MET	-	initiating methionine	UNP A0A031WDE4
F	-18	GLY	-	expression tag	UNP A0A031WDE4
F	-17	SER	-	expression tag	UNP A0A031WDE4
F	-16	SER	-	expression tag	UNP A0A031WDE4
F	-15	HIS	-	expression tag	UNP A0A031WDE4
F	-14	HIS	-	expression tag	UNP A0A031WDE4
F	-13	HIS	-	expression tag	UNP A0A031WDE4
F	-12	HIS	-	expression tag	UNP A0A031WDE4
F	-11	HIS	-	expression tag	UNP A0A031WDE4
F	-10	HIS	-	expression tag	UNP A0A031WDE4
F	-9	SER	-	expression tag	UNP A0A031WDE4
F	-8	SER	-	expression tag	UNP A0A031WDE4
F	-7	GLY	-	expression tag	UNP A0A031WDE4
F	-6	LEU	-	expression tag	UNP A0A031WDE4
F	-5	VAL	-	expression tag	UNP A0A031WDE4
F	-4	PRO	-	expression tag	UNP A0A031WDE4
F	-3	ARG	-	expression tag	UNP A0A031WDE4
F	-2	GLY	-	expression tag	UNP A0A031WDE4
F	-1	SER	-	expression tag	UNP A0A031WDE4
F	0	HIS	-	expression tag	UNP A0A031WDE4
G	-19	MET	-	initiating methionine	UNP A0A031WDE4
G	-18	GLY	-	expression tag	UNP A0A031WDE4
G	-17	SER	-	expression tag	UNP A0A031WDE4
G	-16	SER	-	expression tag	UNP A0A031WDE4
G	-15	HIS	-	expression tag	UNP A0A031WDE4
G	-14	HIS	-	expression tag	UNP A0A031WDE4
G	-13	HIS	-	expression tag	UNP A0A031WDE4
G	-12	HIS	-	expression tag	UNP A0A031WDE4
G	-11	HIS	-	expression tag	UNP A0A031WDE4
G	-10	HIS	-	expression tag	UNP A0A031WDE4
G	-9	SER	-	expression tag	UNP A0A031WDE4
G	-8	SER	-	expression tag	UNP A0A031WDE4
G	-7	GLY	-	expression tag	UNP A0A031WDE4
G	-6	LEU	-	expression tag	UNP A0A031WDE4
G	-5	VAL	-	expression tag	UNP A0A031WDE4
G	-4	PRO	-	expression tag	UNP A0A031WDE4
G	-3	ARG	-	expression tag	UNP A0A031WDE4
G	-2	GLY	-	expression tag	UNP A0A031WDE4
G	-1	SER	-	expression tag	UNP A0A031WDE4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP A0A031WDE4
H	-19	MET	-	initiating methionine	UNP A0A031WDE4
H	-18	GLY	-	expression tag	UNP A0A031WDE4
H	-17	SER	-	expression tag	UNP A0A031WDE4
H	-16	SER	-	expression tag	UNP A0A031WDE4
H	-15	HIS	-	expression tag	UNP A0A031WDE4
H	-14	HIS	-	expression tag	UNP A0A031WDE4
H	-13	HIS	-	expression tag	UNP A0A031WDE4
H	-12	HIS	-	expression tag	UNP A0A031WDE4
H	-11	HIS	-	expression tag	UNP A0A031WDE4
H	-10	HIS	-	expression tag	UNP A0A031WDE4
H	-9	SER	-	expression tag	UNP A0A031WDE4
H	-8	SER	-	expression tag	UNP A0A031WDE4
H	-7	GLY	-	expression tag	UNP A0A031WDE4
H	-6	LEU	-	expression tag	UNP A0A031WDE4
H	-5	VAL	-	expression tag	UNP A0A031WDE4
H	-4	PRO	-	expression tag	UNP A0A031WDE4
H	-3	ARG	-	expression tag	UNP A0A031WDE4
H	-2	GLY	-	expression tag	UNP A0A031WDE4
H	-1	SER	-	expression tag	UNP A0A031WDE4
H	0	HIS	-	expression tag	UNP A0A031WDE4

- Molecule 2 is 4-HYDROXYPROLINE (three-letter code: HYP) (formula:  $C_5H_9NO_3$ ) (labeled as "Ligand of Interest" by author).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 9 5 1 3	0	0
2	B	1	Total C N O 9 5 1 3	0	0
2	C	1	Total C N O 9 5 1 3	0	0
2	D	1	Total C N O 9 5 1 3	0	0
2	E	1	Total C N O 9 5 1 3	0	0
2	F	1	Total C N O 9 5 1 3	0	0
2	G	1	Total C N O 9 5 1 3	0	0
2	H	1	Total C N O 9 5 1 3	0	0

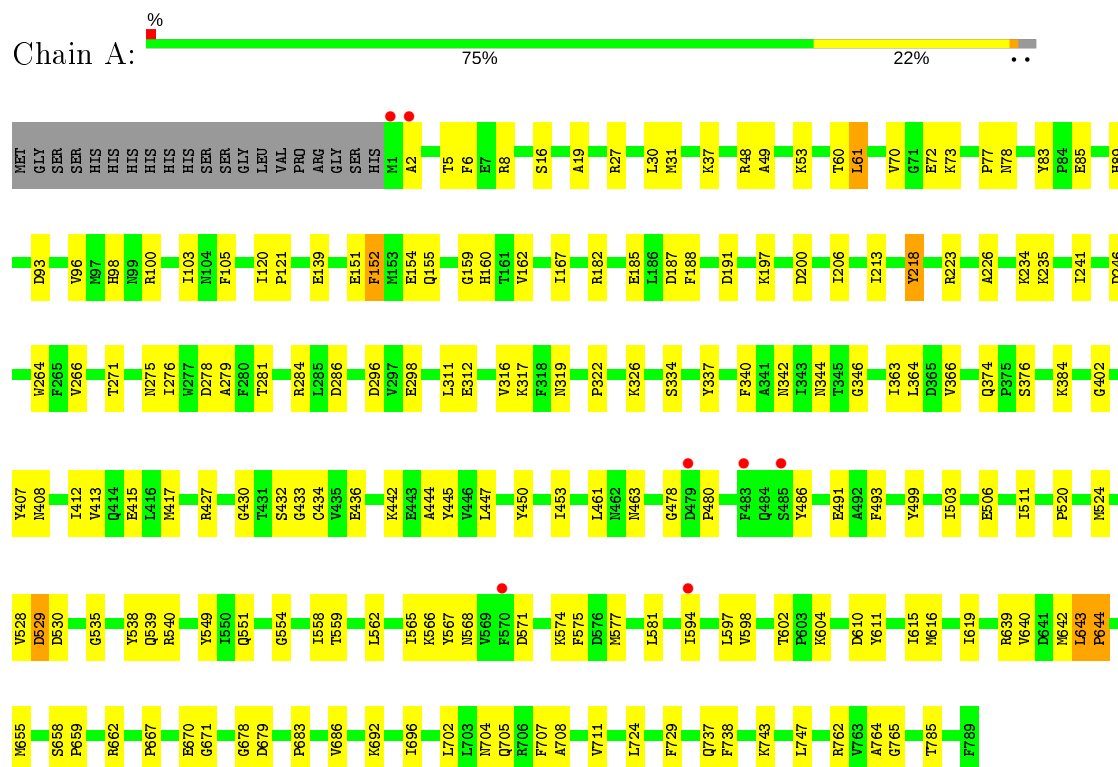
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	192	Total O 192 192	0	0
3	B	183	Total O 183 183	0	0
3	C	132	Total O 132 132	0	0
3	D	205	Total O 205 205	0	0
3	E	171	Total O 171 171	0	0
3	F	216	Total O 216 216	0	0
3	G	221	Total O 221 221	0	0
3	H	136	Total O 136 136	0	0

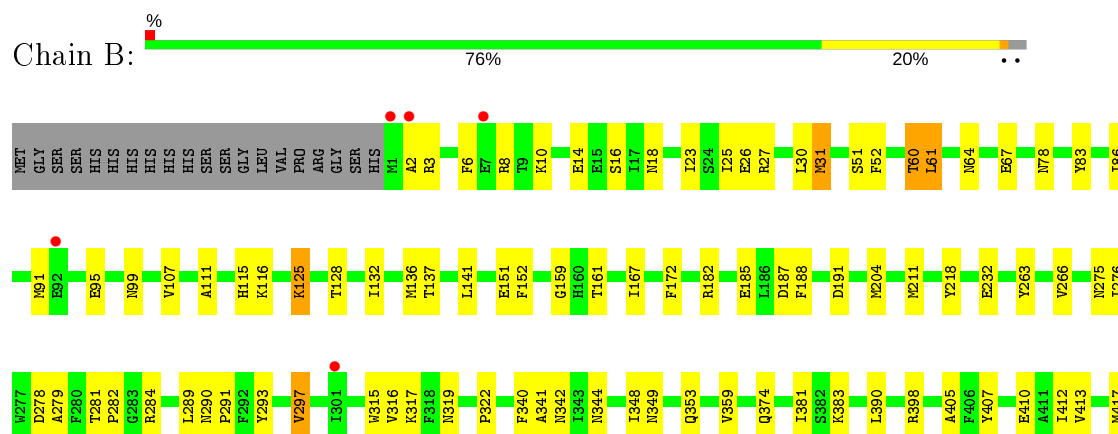
### 3 Residue-property plots [i](#)

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.

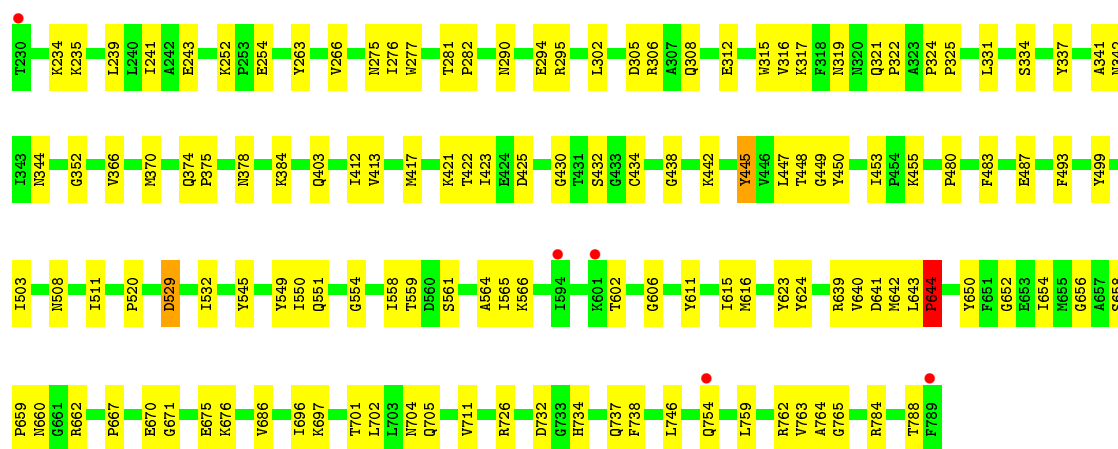
- Molecule 1: Trans-4-hydroxy-L-proline dehydratase



- Molecule 1: Trans-4-hydroxy-L-proline dehydratase

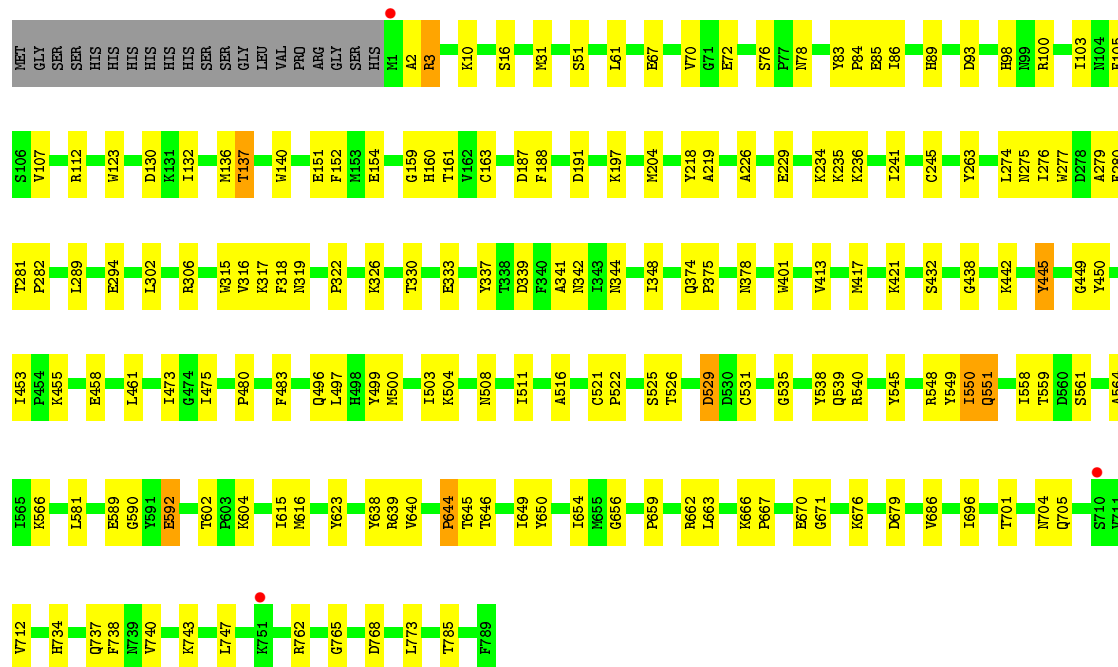






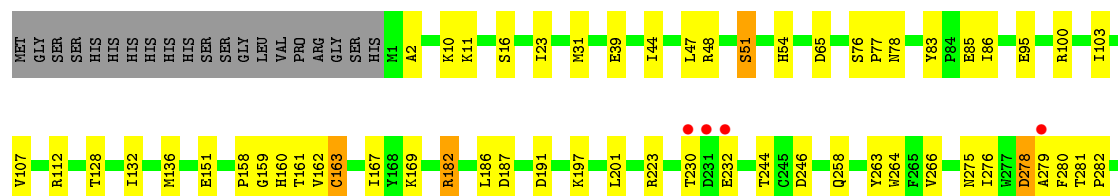
• Molecule 1: Trans-4-hydroxy-L-proline dehydratase

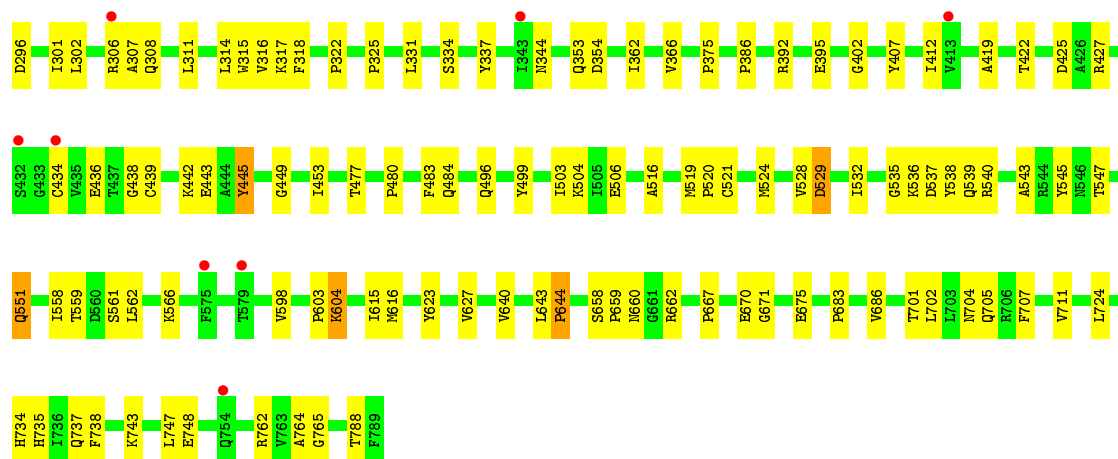
Chain E: 76% 21% ..



• Molecule 1: Trans-4-hydroxy-L-proline dehydratase

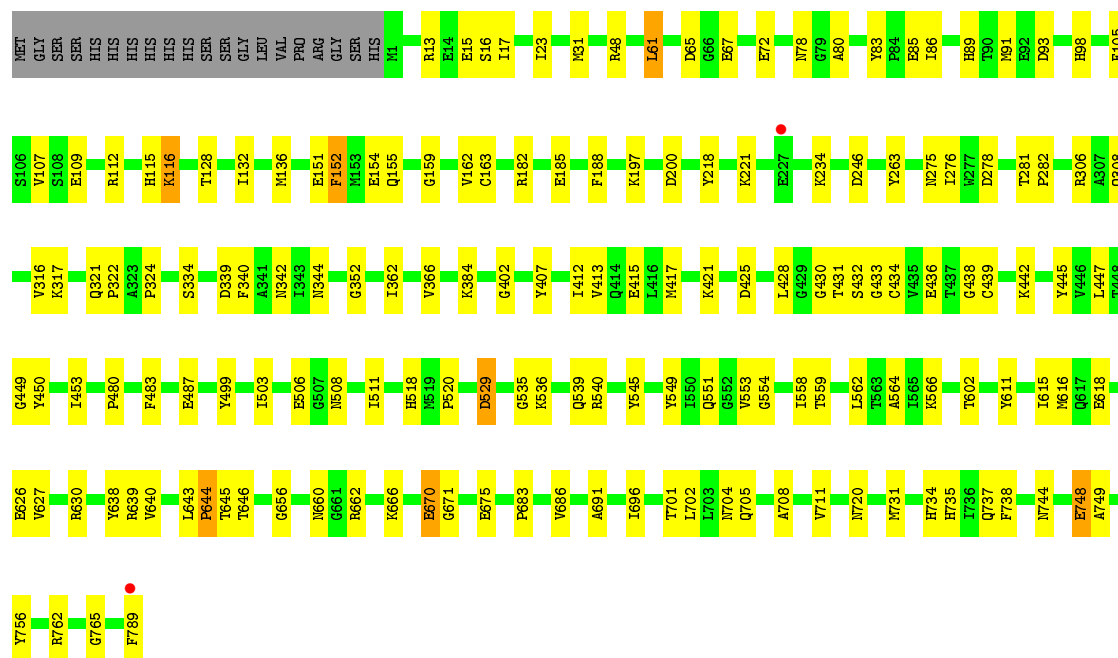
Chain F: 77% 20% ..





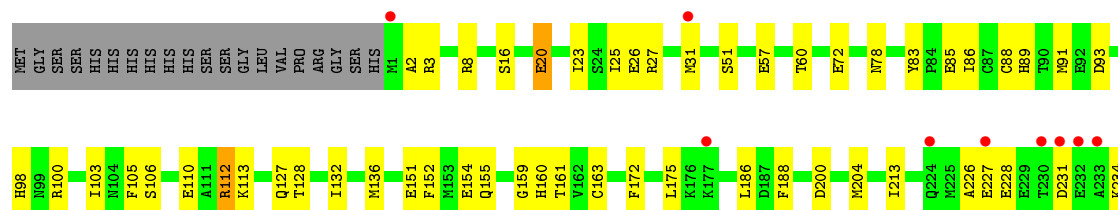
• Molecule 1: Trans-4-hydroxy-L-proline dehydratase

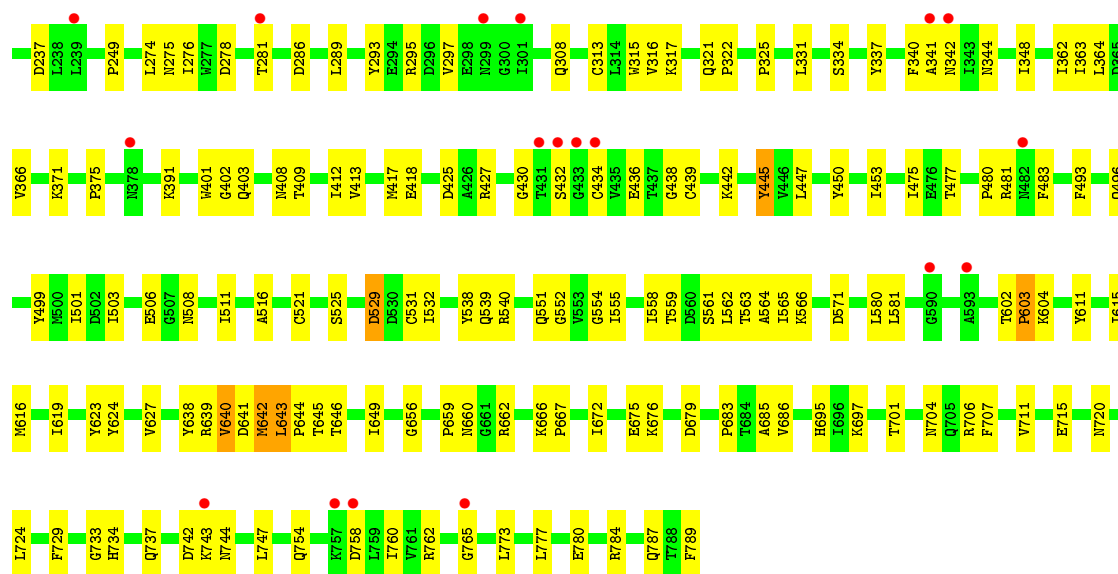
Chain G: 78% 19%



• Molecule 1: Trans-4-hydroxy-L-proline dehydratase

Chain H: 3% 72% 25%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.35Å 341.65Å 122.61Å 90.00° 107.14° 90.00°	Depositor
Resolution (Å)	49.30 – 2.46 49.30 – 2.46	Depositor EDS
% Data completeness (in resolution range)	96.2 (49.30-2.46) 96.2 (49.30-2.46)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.20	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.195 , 0.230 0.194 , 0.230	Depositor DCC
$R_{free}$ test set	13595 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.5	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 23.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	51664	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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: HYP

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	0.61	3/6391 (0.0%)	0.67	7/8629 (0.1%)
1	B	0.63	5/6391 (0.1%)	0.70	8/8629 (0.1%)
1	C	0.62	3/6391 (0.0%)	0.70	8/8629 (0.1%)
1	D	0.52	0/6391	0.63	3/8629 (0.0%)
1	E	0.57	1/6391 (0.0%)	0.72	8/8629 (0.1%)
1	F	0.62	2/6391 (0.0%)	0.68	6/8629 (0.1%)
1	G	0.54	0/6391	0.63	2/8629 (0.0%)
1	H	0.55	3/6391 (0.0%)	0.74	18/8629 (0.2%)
All	All	0.58	17/51128 (0.0%)	0.68	60/69032 (0.1%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	662	ARG	C-N	-19.84	0.88	1.34
1	B	60	THR	C-N	-14.79	1.00	1.34
1	A	60	THR	C-N	-13.35	1.03	1.34
1	H	2	ALA	C-N	-11.62	1.07	1.34
1	F	604	LYS	C-N	-10.47	1.09	1.34
1	A	642	MET	C-N	-8.85	1.13	1.34
1	E	2	ALA	C-N	-8.76	1.14	1.34
1	C	642	MET	C-N	-7.72	1.16	1.34
1	B	61	LEU	C-N	-7.68	1.16	1.34
1	B	30	LEU	C-N	-6.92	1.18	1.34
1	H	604	LYS	C-N	-6.78	1.18	1.34
1	B	31[A]	MET	C-N	-6.53	1.19	1.34
1	B	31[B]	MET	C-N	-6.53	1.19	1.34
1	C	21	PRO	N-CD	-6.49	1.38	1.47
1	A	61	LEU	C-N	-5.83	1.20	1.34
1	H	642	MET	C-N	-5.45	1.21	1.34
1	F	163	CYS	CB-SG	-5.39	1.73	1.81



All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	3	ARG	O-C-N	17.73	153.34	123.20
1	C	643	LEU	O-C-N	-17.28	88.26	121.10
1	E	3	ARG	CA-C-N	-15.30	85.61	116.20
1	H	643	LEU	O-C-N	-15.05	92.51	121.10
1	B	61	LEU	O-C-N	-13.90	100.46	122.70
1	E	2	ALA	O-C-N	-13.15	101.66	122.70
1	H	3	ARG	O-C-N	12.71	144.81	123.20
1	C	643	LEU	CA-C-N	12.18	151.19	117.10
1	H	3	ARG	CA-C-N	-11.93	92.35	116.20
1	A	643	LEU	O-C-N	-11.05	100.10	121.10
1	H	643	LEU	CA-C-N	10.86	147.51	117.10
1	H	603	PRO	O-C-N	-10.62	105.71	122.70
1	F	603	PRO	O-C-N	-10.47	105.95	122.70
1	E	2	ALA	C-N-CA	9.58	145.64	121.70
1	H	603	PRO	C-N-CA	9.54	145.54	121.70
1	E	3	ARG	C-N-CA	-9.40	102.55	122.30
1	B	61	LEU	CA-C-N	9.27	137.60	117.20
1	C	661	GLY	O-C-N	-9.03	108.25	122.70
1	E	2	ALA	CA-C-N	8.89	136.76	117.20
1	H	604	LYS	CA-C-N	-8.57	98.33	117.20
1	H	604	LYS	O-C-N	8.40	136.14	122.70
1	F	603	PRO	C-N-CA	8.22	142.25	121.70
1	H	2	ALA	O-C-N	-7.97	109.95	122.70
1	A	643	LEU	CA-C-N	7.95	139.35	117.10
1	A	61	LEU	O-C-N	-7.72	110.36	122.70
1	H	3	ARG	C-N-CA	-7.42	106.71	122.30
1	B	60	THR	O-C-N	-7.22	111.14	122.70
1	H	604	LYS	C-N-CA	-7.06	104.05	121.70
1	F	603	PRO	CA-C-N	6.94	132.47	117.20
1	C	643	LEU	C-N-CD	-6.73	105.80	120.60
1	B	644	PRO	N-CA-CB	-6.72	95.21	102.60
1	C	661	GLY	CA-C-N	6.18	130.79	117.20
1	F	529	ASP	CA-C-N	-6.15	103.67	117.20
1	F	529	ASP	C-N-CA	6.08	136.91	121.70
1	H	295	ARG	NE-CZ-NH1	-6.06	117.27	120.30
1	B	61	LEU	C-N-CA	6.05	136.83	121.70
1	A	60	THR	O-C-N	-5.99	113.11	122.70
1	H	603	PRO	CA-C-N	5.99	130.37	117.20
1	B	529	ASP	CA-C-N	-5.87	104.30	117.20
1	G	529	ASP	CA-C-N	-5.84	104.35	117.20
1	H	643	LEU	CA-CB-CG	5.78	128.59	115.30
1	E	529	ASP	CA-C-N	-5.77	104.51	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	643	LEU	CA-CB-CG	5.63	128.25	115.30
1	D	529	ASP	CA-C-N	-5.58	104.92	117.20
1	A	529	ASP	CA-C-N	-5.55	104.99	117.20
1	D	529	ASP	C-N-CA	5.52	135.50	121.70
1	C	529	ASP	CA-C-N	-5.46	105.18	117.20
1	A	530	ASP	CB-CA-C	5.42	121.23	110.40
1	H	2	ALA	CA-C-N	5.41	129.11	117.20
1	B	60	THR	C-N-CA	5.39	135.18	121.70
1	H	529	ASP	CA-C-N	-5.36	105.41	117.20
1	G	529	ASP	C-N-CA	5.35	135.08	121.70
1	F	278	ASP	CB-CG-OD2	-5.32	113.51	118.30
1	B	529	ASP	C-N-CA	5.30	134.95	121.70
1	H	643	LEU	C-N-CD	-5.17	109.22	120.60
1	D	644	PRO	N-CA-CB	-5.17	96.92	102.60
1	C	530	ASP	CB-CA-C	5.09	120.57	110.40
1	H	529	ASP	C-N-CA	5.06	134.35	121.70
1	E	529	ASP	C-N-CA	5.05	134.33	121.70
1	A	529	ASP	C-N-CA	5.03	134.28	121.70

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	6267	0	6163	153	0
1	B	6267	0	6164	146	0
1	C	6267	0	6165	181	0
1	D	6267	0	6165	153	0
1	E	6267	0	6165	129	1
1	F	6267	0	6164	110	0
1	G	6267	0	6167	111	0
1	H	6267	0	6163	171	1
2	A	9	0	8	2	0
2	B	9	0	8	8	0
2	C	9	0	8	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	9	0	8	4	0
2	E	9	0	8	3	0
2	F	9	0	8	3	0
2	G	9	0	8	5	0
2	H	9	0	8	5	0
3	A	192	0	0	10	0
3	B	183	0	0	12	0
3	C	132	0	0	15	0
3	D	205	0	0	18	0
3	E	171	0	0	12	0
3	F	216	0	0	12	0
3	G	221	0	0	9	0
3	H	136	0	0	17	0
All	All	51664	0	49380	1138	1

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 11.

All (1138) 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:D:31[B]:MET:CE	1:D:85:GLU:CD	1.78	1.48
1:D:31[B]:MET:CE	1:D:85:GLU:OE1	1.65	1.41
1:A:31[B]:MET:HE1	1:A:85:GLU:CD	1.51	1.30
1:D:31[B]:MET:HE1	1:D:85:GLU:CD	1.34	1.27
1:A:31[B]:MET:CE	1:A:85:GLU:OE2	1.86	1.23
1:A:31[B]:MET:CE	1:A:85:GLU:CD	2.07	1.22
1:B:278:ASP:OD1	2:B:801:HYP:CD	1.86	1.21
1:B:278:ASP:OD1	2:B:801:HYP:HD23	1.35	1.20
1:A:31[B]:MET:HE1	1:A:85:GLU:OE2	1.40	1.19
1:D:31[B]:MET:HE3	1:D:85:GLU:OE2	1.44	1.14
1:C:447:LEU:CG	1:C:551:GLN:NE2	2.11	1.14
1:C:447:LEU:HB3	1:C:551:GLN:HE22	1.09	1.13
1:H:676:LYS:NZ	1:H:780:GLU:O	1.81	1.12
1:C:447:LEU:CG	1:C:551:GLN:HE21	1.64	1.11
1:D:31[B]:MET:HE3	1:D:85:GLU:CD	1.57	1.11
1:C:447:LEU:CD2	1:C:551:GLN:HE21	1.65	1.09
1:E:281:THR:HG21	1:E:342:ASN:N	1.68	1.09
1:C:447:LEU:HG	1:C:551:GLN:NE2	1.68	1.08
1:F:521:CYS:SG	1:F:539:GLN:HG2	1.94	1.07
1:A:271:THR:HB	3:A:901:HOH:O	1.54	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:453:ILE:HG22	1:B:558:ILE:HD13	1.35	1.06
1:D:453:ILE:HG22	1:D:558:ILE:HD13	1.37	1.05
1:A:453:ILE:HG22	1:A:558:ILE:HD13	1.35	1.04
1:B:281:THR:HG21	1:B:342:ASN:N	1.71	1.04
1:C:453:ILE:HG22	1:C:558:ILE:HD13	1.38	1.03
1:H:737:GLN:HE22	1:H:765:GLY:H	1.04	1.01
1:H:27:ARG:NH1	1:H:31[A]:MET:SD	2.35	1.00
1:C:447:LEU:CB	1:C:551:GLN:HE22	1.73	1.00
1:H:334:SER:OG	2:H:801:HYP:O	1.79	0.99
1:F:301:ILE:O	1:F:306:ARG:NH1	1.97	0.98
1:G:656:GLY:O	1:G:662:ARG:NH1	1.97	0.98
1:C:158:PRO:HD2	1:C:539:GLN:HE22	1.28	0.97
1:B:704:ASN:HD21	1:B:737:GLN:HE21	1.12	0.96
1:C:447:LEU:HB3	1:C:551:GLN:NE2	1.80	0.96
1:C:453:ILE:HG22	1:C:558:ILE:CD1	1.94	0.96
1:F:23:ILE:HD11	1:F:325:PRO:HG3	1.47	0.96
1:C:281:THR:HG21	1:C:342:ASN:N	1.80	0.95
1:A:737:GLN:HE22	1:A:765:GLY:H	1.06	0.95
1:D:737:GLN:HE22	1:D:765:GLY:H	1.15	0.95
1:H:281:THR:HG21	1:H:342:ASN:N	1.81	0.94
1:E:737:GLN:HE22	1:E:765:GLY:H	1.11	0.94
1:C:651:PHE:O	1:C:655:MET:HG3	1.67	0.94
1:C:737:GLN:HE22	1:C:765:GLY:H	1.14	0.94
1:E:281:THR:HG21	1:E:342:ASN:H	1.27	0.93
1:G:737:GLN:HE22	1:G:765:GLY:H	1.01	0.93
1:F:279:ALA:O	3:F:901:HOH:O	1.86	0.93
1:B:2:ALA:HB1	3:B:916:HOH:O	1.67	0.92
1:C:136:MET:CE	1:C:507:GLY:HA3	1.98	0.92
1:C:447:LEU:CB	1:C:551:GLN:NE2	2.30	0.92
1:C:334:SER:OG	2:C:801:HYP:O	1.87	0.92
1:C:136:MET:HE1	1:C:507:GLY:HA3	1.52	0.92
1:C:447:LEU:HD23	1:C:551:GLN:HE21	1.32	0.91
1:D:453:ILE:HG22	1:D:558:ILE:CD1	2.01	0.90
1:B:398:ARG:HB2	1:B:712:VAL:CG1	2.02	0.90
1:H:656:GLY:O	1:H:662:ARG:NH1	2.03	0.90
1:B:95:GLU:O	1:B:99:ASN:ND2	2.04	0.89
1:B:278:ASP:CG	2:B:801:HYP:HD23	1.93	0.89
1:F:434:CYS:SG	2:F:801:HYP:HD22	2.13	0.89
1:G:334:SER:OG	2:G:801:HYP:OXT	1.91	0.89
1:A:453:ILE:HG22	1:A:558:ILE:CD1	2.03	0.88
1:B:125:LYS:NZ	3:B:902:HOH:O	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:453:ILE:HG22	1:B:558:ILE:CD1	2.01	0.88
1:B:322:PRO:O	3:B:901:HOH:O	1.91	0.88
1:B:281:THR:HG21	1:B:342:ASN:H	1.31	0.87
1:E:137:THR:HG22	1:E:140:TRP:H	1.40	0.87
1:A:31[B]:MET:HE3	1:A:85:GLU:CD	1.92	0.87
1:A:436:GLU:OE1	1:A:643:LEU:HD22	1.76	0.86
1:A:271:THR:CB	3:A:901:HOH:O	2.16	0.85
1:C:521:CYS:SG	1:C:539:GLN:HG2	2.16	0.85
1:B:737:GLN:HE22	1:B:765:GLY:H	1.21	0.85
1:E:704:ASN:HD21	1:E:737:GLN:HE21	1.20	0.85
1:A:31[B]:MET:HE3	1:A:85:GLU:OE1	1.77	0.84
1:A:2:ALA:HB1	3:A:1053:HOH:O	1.76	0.84
1:B:281:THR:CG2	1:B:341:ALA:HA	2.07	0.83
1:D:31[B]:MET:HE1	1:D:85:GLU:CG	2.07	0.83
1:B:27:ARG:NH2	1:B:31[A]:MET:HE1	1.94	0.83
1:E:281:THR:CG2	1:E:341:ALA:HA	2.08	0.83
1:F:737:GLN:HE22	1:F:765:GLY:H	1.27	0.83
1:B:398:ARG:HB2	1:B:712:VAL:HG11	1.61	0.83
1:D:31[B]:MET:HE1	1:D:85:GLU:OE1	1.44	0.82
1:C:136:MET:HE2	1:C:140:TRP:CD2	2.14	0.82
1:C:374:GLN:HG3	3:C:946:HOH:O	1.79	0.82
1:H:453:ILE:HG22	1:H:558:ILE:HD13	1.62	0.81
1:D:31[B]:MET:HE2	1:D:85:GLU:OE1	1.77	0.81
1:G:453:ILE:HG22	1:G:558:ILE:HD13	1.61	0.81
1:B:3:ARG:HG2	1:B:3:ARG:HH11	1.44	0.81
1:F:566:LYS:HD3	1:F:615:ILE:HD11	1.62	0.81
1:F:334:SER:OG	2:F:801:HYP:O	1.99	0.81
1:B:656:GLY:O	1:B:662:ARG:NH1	2.14	0.80
1:E:656:GLY:O	1:E:662:ARG:NH1	2.14	0.80
1:F:704:ASN:HD21	1:F:737:GLN:HE21	1.26	0.80
1:G:434:CYS:SG	2:G:801:HYP:HD22	2.22	0.80
1:H:662:ARG:NH2	1:H:666:LYS:O	2.16	0.79
1:C:136:MET:HE2	1:C:140:TRP:CG	2.18	0.79
1:D:31[B]:MET:CE	1:D:85:GLU:OE2	2.09	0.79
1:H:281:THR:CG2	1:H:341:ALA:HA	2.12	0.79
1:H:281:THR:HG21	1:H:342:ASN:H	1.46	0.79
1:C:564:ALA:HA	1:C:602:THR:HG21	1.63	0.79
1:C:281:THR:CG2	1:C:341:ALA:HA	2.13	0.78
1:C:429:GLY:O	3:C:901:HOH:O	2.01	0.78
1:C:447:LEU:HD23	1:C:551:GLN:NE2	1.99	0.78
1:C:136:MET:CE	1:C:507:GLY:CA	2.61	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:453:ILE:CG2	1:B:558:ILE:HD13	2.11	0.78
1:A:743:LYS:HE2	1:A:747:LEU:HD11	1.64	0.78
1:H:308:GLN:HG3	1:H:366:VAL:HG12	1.66	0.78
1:C:281:THR:HG21	1:C:342:ASN:H	1.46	0.77
1:H:453:ILE:HG22	1:H:558:ILE:CD1	2.15	0.77
1:C:454:PRO:HB2	1:C:655:MET:CE	2.14	0.77
1:C:136:MET:CE	1:C:140:TRP:CD1	2.68	0.77
1:A:31[B]:MET:HE3	1:A:85:GLU:OE2	1.83	0.76
1:E:100:ARG:NH2	1:E:326:LYS:O	2.18	0.76
1:B:704:ASN:ND2	1:B:737:GLN:HE21	1.83	0.76
1:D:281:THR:HG21	1:D:342:ASN:N	2.00	0.76
1:C:308:GLN:HG3	1:C:366:VAL:HG12	1.67	0.75
1:B:27:ARG:HH22	1:B:31[A]:MET:HE1	1.52	0.75
1:E:281:THR:CG2	1:E:342:ASN:N	2.49	0.75
1:H:436:GLU:OE1	1:H:643:LEU:HD22	1.87	0.74
1:H:704:ASN:ND2	3:H:903:HOH:O	2.19	0.74
1:F:182:ARG:HD3	1:F:532:ILE:O	1.87	0.74
1:A:655:MET:CE	1:A:662:ARG:NH2	2.50	0.74
1:D:334:SER:OG	2:D:801:HYP:O	2.05	0.74
1:B:564:ALA:HA	1:B:602:THR:HG21	1.70	0.73
1:H:743:LYS:HE2	1:H:747:LEU:HD11	1.68	0.73
1:B:281:THR:CG2	1:B:341:ALA:CA	2.67	0.73
1:A:31[B]:MET:CE	1:A:85:GLU:OE1	2.33	0.73
1:A:598:VAL:O	1:A:604:LYS:NZ	2.21	0.73
1:E:281:THR:HG22	1:E:341:ALA:CA	2.19	0.72
1:D:566:LYS:HD3	1:D:615:ILE:HD11	1.70	0.72
1:C:453:ILE:CG2	1:C:558:ILE:HD13	2.17	0.72
1:F:449:GLY:H	1:F:551:GLN:HE22	1.38	0.72
1:G:72:GLU:OE2	1:G:317:LYS:NZ	2.22	0.72
1:H:683:PRO:HG3	1:H:787:GLN:HB3	1.71	0.72
1:D:434:CYS:SG	2:D:801:HYP:HD22	2.29	0.72
1:E:662:ARG:NH2	1:E:666:LYS:O	2.22	0.72
1:C:575:PHE:CD2	1:C:594:ILE:HG12	2.24	0.72
1:B:281:THR:HG22	1:B:341:ALA:CA	2.19	0.72
1:E:281:THR:CG2	1:E:341:ALA:CA	2.67	0.72
1:D:146:ALA:O	1:D:455:LYS:NZ	2.23	0.71
1:H:758:ASP:O	1:H:758:ASP:OD1	2.08	0.71
1:D:15:GLU:OE1	3:D:901:HOH:O	2.07	0.71
1:D:550:ILE:HG22	1:D:623:TYR:OH	1.90	0.71
1:A:453:ILE:CG2	1:A:558:ILE:HD13	2.17	0.71
1:E:704:ASN:ND2	1:E:737:GLN:HE21	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:31[A]:MET:HE3	1:F:85:GLU:HB3	1.71	0.71
1:G:704:ASN:HD21	1:G:737:GLN:HE21	1.39	0.71
1:D:27:ARG:HH12	1:D:31[B]:MET:HE3	1.56	0.70
1:D:453:ILE:CG2	1:D:558:ILE:HD13	2.20	0.70
1:A:298:GLU:O	1:A:298:GLU:HG2	1.91	0.70
1:H:231:ASP:HB3	1:H:234:LYS:HB2	1.74	0.70
1:B:278:ASP:OD1	2:B:801:HYP:HD22	1.89	0.69
1:C:229:GLU:HG2	1:C:234:LYS:HG3	1.75	0.69
1:B:442:LYS:NZ	1:B:529:ASP:OD2	2.25	0.69
1:C:362:ILE:O	1:C:366:VAL:HG13	1.93	0.69
1:C:281:THR:CG2	1:C:341:ALA:CA	2.71	0.69
1:G:339:ASP:OD2	3:G:901:HOH:O	2.10	0.69
1:A:27:ARG:HH12	1:A:31[B]:MET:HE3	1.57	0.69
1:F:296:ASP:OD1	3:F:903:HOH:O	2.10	0.69
1:D:442:LYS:HG2	1:D:529:ASP:HB2	1.73	0.69
1:A:188:PHE:HB2	1:B:506:GLU:HG3	1.75	0.68
1:E:100:ARG:NH1	1:E:103:ILE:O	2.26	0.68
1:C:136:MET:HE2	1:C:140:TRP:CE2	2.29	0.68
1:C:136:MET:HE3	1:C:507:GLY:HA3	1.75	0.68
1:C:136:MET:HE3	1:C:507:GLY:CA	2.23	0.68
1:C:655:MET:SD	1:C:668:VAL:CG1	2.83	0.67
1:H:281:THR:CG2	1:H:341:ALA:CA	2.71	0.67
1:D:644:PRO:HG3	1:D:671:GLY:H	1.58	0.67
1:E:604:LYS:HE2	3:E:956:HOH:O	1.93	0.67
1:A:683:PRO:HA	1:A:686:VAL:HG13	1.75	0.67
1:C:72:GLU:OE2	1:C:317:LYS:NZ	2.27	0.67
1:D:656:GLY:O	1:D:662:ARG:NH2	2.27	0.67
1:H:566:LYS:HD3	1:H:615:ILE:HD11	1.76	0.67
1:B:566:LYS:HD3	1:B:615:ILE:HD11	1.77	0.67
1:C:380:GLN:OE1	3:C:903:HOH:O	2.13	0.67
1:B:281:THR:CG2	1:B:342:ASN:N	2.55	0.66
1:A:480:PRO:HB2	1:A:577:MET:HG2	1.77	0.66
1:B:116:LYS:O	3:B:904:HOH:O	2.12	0.66
1:E:70:VAL:HG12	1:E:218:TYR:CE1	2.31	0.66
1:H:281:THR:HG22	1:H:341:ALA:CA	2.25	0.66
1:H:91:MET:HE1	1:H:112:ARG:HG2	1.78	0.66
1:B:27:ARG:NH2	1:B:31[A]:MET:CE	2.59	0.66
1:C:704:ASN:HD21	1:C:737:GLN:HE21	1.43	0.66
1:A:453:ILE:O	1:A:558:ILE:HD12	1.96	0.65
1:G:278:ASP:N	3:G:902:HOH:O	2.12	0.65
1:C:200:ASP:OD1	3:C:902:HOH:O	2.13	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:453:ILE:O	1:G:558:ILE:HD12	1.96	0.65
1:H:151:GLU:OE2	3:H:902:HOH:O	2.14	0.65
1:E:453:ILE:HG22	1:E:558:ILE:HD13	1.78	0.65
1:A:655:MET:CE	1:A:662:ARG:HH21	2.09	0.65
1:H:31[B]:MET:SD	1:H:51:SER:HB3	2.37	0.65
1:B:398:ARG:HB2	1:B:712:VAL:HG12	1.79	0.65
1:F:39:GLU:OE2	3:F:904:HOH:O	2.15	0.65
1:E:737:GLN:NE2	1:E:765:GLY:H	1.89	0.65
1:G:564:ALA:HA	1:G:602:THR:HG21	1.79	0.65
1:B:461:LEU:HB3	1:B:581:LEU:HD21	1.79	0.64
1:E:504:LYS:HG2	1:E:550:ILE:HD13	1.78	0.64
1:G:704:ASN:ND2	1:G:737:GLN:HE21	1.95	0.64
1:A:78:ASN:HA	1:A:322:PRO:HD3	1.78	0.64
1:C:349:ASN:HD21	1:C:353:GLN:HE21	1.43	0.64
1:A:655:MET:HE2	1:A:662:ARG:NH2	2.13	0.64
1:B:554:GLY:O	1:B:558:ILE:HG22	1.96	0.64
1:C:136:MET:HE2	1:C:140:TRP:CD1	2.31	0.64
1:A:658:SER:OG	1:A:662:ARG:HB3	1.97	0.64
1:D:107:VAL:HG12	1:D:112:ARG:HG3	1.80	0.64
1:H:436:GLU:HG3	1:H:643:LEU:CD2	2.28	0.64
1:D:737:GLN:NE2	1:D:765:GLY:H	1.91	0.63
1:G:306:ARG:NH1	3:G:910:HOH:O	2.27	0.63
1:C:403:GLN:HG2	3:C:905:HOH:O	1.99	0.63
1:C:742:ASP:HB3	1:C:745:VAL:HG23	1.79	0.63
1:G:308:GLN:HG3	1:G:366:VAL:HG12	1.80	0.63
1:D:726:ARG:NH1	3:D:902:HOH:O	2.15	0.63
1:C:281:THR:HG22	1:C:341:ALA:CA	2.29	0.63
1:G:65:ASP:OD1	1:G:234:LYS:NZ	2.26	0.63
1:B:159:GLY:HA3	1:B:276:ILE:HB	1.81	0.63
1:D:83:TYR:CG	1:D:275:ASN:HB2	2.34	0.62
1:D:704:ASN:ND2	3:D:905:HOH:O	2.18	0.62
1:D:342:ASN:HB3	1:D:432:SER:HA	1.80	0.62
1:B:349:ASN:HD21	1:B:353:GLN:HG3	1.63	0.62
1:D:623:TYR:CE2	1:D:642:MET:HE1	2.35	0.62
1:A:162:VAL:HG13	1:A:281:THR:HG23	1.82	0.62
1:C:442:LYS:HG2	1:C:529:ASP:HB2	1.81	0.62
1:A:37:LYS:O	1:B:125:LYS:HE3	1.99	0.62
1:C:23:ILE:HD11	1:C:107:VAL:HG13	1.81	0.62
1:D:159:GLY:HA3	1:D:276:ILE:HB	1.82	0.62
1:D:493:PHE:CE1	1:D:558:ILE:HD11	2.35	0.62
1:F:704:ASN:ND2	1:F:737:GLN:HE21	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:348:ILE:HG12	3:E:907:HOH:O	2.00	0.61
1:D:281:THR:CG2	1:D:341:ALA:HA	2.30	0.61
1:G:566:LYS:HD3	1:G:611:TYR:OH	2.00	0.61
1:C:454:PRO:HB2	1:C:655:MET:HE1	1.81	0.61
1:C:660:ASN:ND2	1:C:675:GLU:HG2	2.15	0.61
1:G:737:GLN:NE2	1:G:765:GLY:H	1.86	0.61
1:E:644:PRO:HG3	1:E:671:GLY:H	1.65	0.61
1:G:48:ARG:HG3	1:G:520:PRO:HD2	1.82	0.61
1:H:403:GLN:HG2	3:H:969:HOH:O	1.99	0.61
1:B:413:VAL:O	1:B:417:MET:HG3	2.01	0.61
1:C:132:ILE:O	1:C:136:MET:HG2	2.01	0.61
1:E:70:VAL:CG1	1:E:218:TYR:CE1	2.84	0.61
1:F:521:CYS:SG	1:F:539:GLN:CG	2.81	0.61
1:A:450:TYR:CD1	1:A:551:GLN:HG3	2.36	0.61
1:E:326:LYS:NZ	3:E:901:HOH:O	2.18	0.61
1:E:401:TRP:N	3:E:910:HOH:O	2.28	0.61
1:H:391:LYS:NZ	1:H:715:GLU:OE2	2.28	0.61
1:F:519:MET:O	1:F:539:GLN:HG3	2.01	0.60
1:A:493:PHE:CE1	1:A:558:ILE:HD11	2.37	0.60
1:C:447:LEU:HG	1:C:551:GLN:HE21	1.35	0.60
1:F:442:LYS:HG2	1:F:529:ASP:HB2	1.82	0.60
1:F:11:LYS:NZ	1:F:65:ASP:OD2	2.21	0.60
1:C:31[B]:MET:HE3	1:C:123:TRP:CZ2	2.37	0.60
1:B:662:ARG:NH2	1:B:666:LYS:O	2.31	0.60
1:E:31[A]:MET:CE	1:E:51:SER:OG	2.50	0.60
1:B:737:GLN:NE2	1:B:765:GLY:H	1.96	0.60
1:E:281:THR:CG2	1:E:341:ALA:C	2.70	0.60
1:H:737:GLN:NE2	1:H:765:GLY:H	1.87	0.60
1:C:231:ASP:HB3	1:C:234:LYS:HB3	1.82	0.60
1:H:72:GLU:OE2	1:H:317:LYS:NZ	2.34	0.60
1:D:453:ILE:O	1:D:558:ILE:HD12	2.01	0.59
1:E:159:GLY:HA3	1:E:276:ILE:HB	1.83	0.59
1:A:334:SER:OG	2:A:801:HYP:OXT	2.20	0.59
1:A:442:LYS:NZ	1:A:529:ASP:OD2	2.34	0.59
1:F:159:GLY:HA3	1:F:276:ILE:HB	1.84	0.59
1:D:239:LEU:O	1:D:243:GLU:HG2	2.02	0.59
1:F:77:PRO:HD3	3:F:957:HOH:O	2.01	0.59
1:H:27:ARG:CZ	1:H:31[A]:MET:SD	2.91	0.59
1:H:551:GLN:HG3	1:H:641:ASP:OD1	2.02	0.59
1:C:277:TRP:O	1:C:278:ASP:HB2	2.02	0.59
1:D:31[B]:MET:HE3	1:D:85:GLU:OE1	1.63	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:624:TYR:CZ	1:B:697:LYS:HD2	2.38	0.59
1:H:434:CYS:HB3	1:H:765:GLY:HA3	1.85	0.59
1:B:2:ALA:HB3	1:B:10:LYS:HG2	1.83	0.59
1:C:158:PRO:HD2	1:C:539:GLN:NE2	2.10	0.59
1:H:660:ASN:ND2	1:H:675:GLU:HG2	2.17	0.59
1:C:73:LYS:HE3	1:C:271:THR:HB	1.85	0.58
1:G:744:ASN:O	1:G:748:GLU:HB2	2.04	0.58
1:H:564:ALA:HA	1:H:602:THR:HG21	1.83	0.58
1:D:352:GLY:O	1:D:384:LYS:NZ	2.31	0.58
1:F:169:LYS:NZ	3:F:928:HOH:O	2.36	0.58
1:G:683:PRO:HA	1:G:686:VAL:HG13	1.83	0.58
1:H:453:ILE:CG2	1:H:558:ILE:HD13	2.31	0.58
1:B:637:GLU:OE2	1:B:639:ARG:NH2	2.36	0.58
1:G:342:ASN:HB3	1:G:432:SER:HA	1.85	0.58
1:D:70:VAL:HG21	1:D:241:ILE:HG21	1.84	0.58
1:A:159:GLY:HA3	1:A:276:ILE:HB	1.85	0.58
1:B:16:SER:HB2	1:B:316:VAL:HG13	1.86	0.58
1:B:281:THR:HG22	1:B:341:ALA:HB1	1.86	0.58
1:G:109:GLU:OE2	1:G:112:ARG:NH2	2.36	0.58
1:D:423:ILE:HG13	1:D:423:ILE:O	2.04	0.58
1:A:554:GLY:O	1:A:558:ILE:HG22	2.03	0.58
1:H:683:PRO:HA	1:H:686:VAL:HG13	1.86	0.58
1:C:281:THR:HG22	1:C:341:ALA:HB1	1.85	0.57
1:H:554:GLY:O	1:H:558:ILE:HG22	2.04	0.57
1:B:91:MET:CE	1:B:115:HIS:HD2	2.17	0.57
1:B:436:GLU:OE2	2:B:801:HYP:HG	2.04	0.57
1:C:704:ASN:ND2	3:C:925:HOH:O	2.37	0.57
1:H:281:THR:CG2	1:H:342:ASN:N	2.62	0.57
1:H:737:GLN:OE1	1:H:762:ARG:NH1	2.32	0.57
1:A:223:ARG:NH2	1:A:246:ASP:OD2	2.32	0.57
1:A:450:TYR:CE1	1:A:551:GLN:HG3	2.40	0.57
1:B:64:ASN:ND2	1:B:67:GLU:OE2	2.37	0.57
1:C:651:PHE:O	1:C:655:MET:CG	2.47	0.57
1:H:278:ASP:N	3:H:901:HOH:O	2.01	0.57
1:B:281:THR:CG2	1:B:341:ALA:C	2.73	0.57
1:D:662:ARG:HD2	1:D:667:PRO:O	2.05	0.57
1:G:499:TYR:CZ	1:G:503:ILE:HD11	2.40	0.57
1:G:566:LYS:HD3	1:G:611:TYR:CZ	2.40	0.57
1:C:498:HIS:ND1	1:C:626:GLU:OE2	2.35	0.57
1:G:159:GLY:HA3	1:G:276:ILE:HB	1.87	0.57
1:D:53:LYS:HD2	1:D:206:ILE:HG23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:281:THR:CG2	1:C:342:ASN:N	2.64	0.57
1:D:70:VAL:HG21	1:D:241:ILE:CG2	2.35	0.56
1:A:568:ASN:OD1	1:A:602:THR:HG21	2.04	0.56
1:C:453:ILE:HG22	1:C:558:ILE:HD12	1.85	0.56
1:G:438:GLY:HA3	1:G:445:TYR:CZ	2.41	0.56
1:H:720:ASN:HB3	1:H:789:PHE:CD1	2.40	0.56
1:D:378:ASN:OD1	3:D:904:HOH:O	2.17	0.56
1:D:83:TYR:CD1	1:D:275:ASN:HB2	2.41	0.56
1:H:342:ASN:HB3	1:H:432:SER:HA	1.87	0.56
1:B:438:GLY:HA3	1:B:445:TYR:CZ	2.41	0.56
1:E:31[A]:MET:HE1	1:E:51:SER:HB3	1.87	0.56
1:H:281:THR:CG2	1:H:341:ALA:C	2.74	0.56
1:A:655:MET:HE1	1:A:662:ARG:HH21	1.70	0.56
1:H:91:MET:CE	1:H:112:ARG:HG2	2.35	0.56
1:C:342:ASN:HB3	1:C:432:SER:HA	1.87	0.56
1:B:317:LYS:HE2	1:B:317:LYS:HA	1.88	0.56
1:B:524:MET:O	1:B:528:VAL:HG23	2.05	0.56
1:G:644:PRO:HG3	1:G:671:GLY:H	1.69	0.56
1:G:436:GLU:HG2	1:G:447:LEU:HD21	1.88	0.56
1:B:293:TYR:O	1:B:297:VAL:HG13	2.06	0.56
1:B:707:PHE:HZ	1:B:724:LEU:HD22	1.71	0.56
1:C:56:ILE:HG21	1:C:210:ALA:O	2.06	0.56
1:C:519:MET:O	1:C:539:GLN:HG3	2.06	0.56
1:E:83:TYR:CG	1:E:275:ASN:HB2	2.41	0.56
1:C:83:TYR:CD1	1:C:275:ASN:HB2	2.41	0.55
1:D:641:ASP:OD2	3:D:906:HOH:O	2.18	0.55
1:B:61:LEU:HD22	1:B:218:TYR:CE2	2.41	0.55
1:D:221:LYS:O	1:D:225:MET:HG2	2.07	0.55
1:D:499:TYR:CZ	1:D:503:ILE:HD11	2.41	0.55
1:D:704:ASN:HD21	1:D:737:GLN:HE21	1.53	0.55
1:D:737:GLN:CD	1:D:762:ARG:HE	2.09	0.55
1:E:277:TRP:CZ3	2:E:801:HYP:HA	2.41	0.55
1:H:204:MET:HE2	1:H:532:ILE:HG12	1.89	0.55
1:B:83:TYR:CG	1:B:275:ASN:HB2	2.42	0.55
1:D:306:ARG:NH1	3:D:929:HOH:O	2.35	0.55
1:C:655:MET:SD	1:C:668:VAL:HG11	2.47	0.55
1:F:54:HIS:ND1	3:F:902:HOH:O	2.05	0.55
1:A:70:VAL:CG1	1:A:218:TYR:CE1	2.90	0.55
1:B:284:ARG:NH2	1:B:348:ILE:O	2.37	0.55
1:F:434:CYS:HB3	1:F:765:GLY:HA3	1.89	0.55
1:H:20:GLU:OE1	1:H:106:SER:OG	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:480:PRO:HA	1:D:483:PHE:CD2	2.42	0.55
1:C:671:GLY:N	3:C:906:HOH:O	2.40	0.55
1:B:447:LEU:HD22	2:B:801:HYP:OD1	2.07	0.55
1:C:575:PHE:CE2	1:C:594:ILE:HG12	2.42	0.55
1:D:737:GLN:HE22	1:D:765:GLY:N	1.96	0.55
1:G:182:ARG:HD2	1:G:185:GLU:OE2	2.06	0.55
1:A:415:GLU:HG3	1:A:696:ILE:HA	1.90	0.54
1:A:73:LYS:HE3	1:A:271:THR:HG23	1.89	0.54
1:G:163:CYS:HB3	3:G:970:HOH:O	2.06	0.54
1:D:449:GLY:H	1:D:551:GLN:HE22	1.54	0.54
1:H:701:THR:H	1:H:734:HIS:CD2	2.25	0.54
1:B:27:ARG:CZ	1:B:31[A]:MET:HE3	2.37	0.54
1:E:107:VAL:HG12	1:E:112:ARG:HG3	1.89	0.54
1:C:83:TYR:CG	1:C:275:ASN:HB2	2.43	0.54
1:G:91:MET:HE3	1:G:116:LYS:HA	1.90	0.54
1:C:447:LEU:CD2	1:C:551:GLN:NE2	2.44	0.54
1:D:48:ARG:HG3	1:D:520:PRO:HD2	1.90	0.54
1:H:551:GLN:HG2	1:H:643:LEU:HD11	1.90	0.54
1:D:281:THR:HG21	1:D:342:ASN:H	1.71	0.54
1:E:31[A]:MET:HE3	1:E:51:SER:OG	2.07	0.54
1:E:442:LYS:HG2	1:E:529:ASP:HB2	1.90	0.54
1:E:737:GLN:HE22	1:E:765:GLY:N	1.93	0.54
1:G:442:LYS:NZ	1:G:529:ASP:OD2	2.40	0.54
1:H:645:THR:HG22	1:H:646:THR:N	2.23	0.54
1:H:743:LYS:HG2	1:H:747:LEU:CD1	2.38	0.54
1:A:408:ASN:HB2	1:A:729:PHE:CD1	2.43	0.54
1:A:597:LEU:O	1:A:602:THR:HG23	2.08	0.54
1:A:8:ARG:HH21	1:A:8:ARG:HG3	1.73	0.54
1:C:281:THR:CG2	1:C:341:ALA:C	2.76	0.54
1:H:362:ILE:O	1:H:366:VAL:HG13	2.08	0.54
1:H:704:ASN:HD21	1:H:737:GLN:HE21	1.55	0.54
1:A:447:LEU:N	3:A:915:HOH:O	2.41	0.53
1:C:136:MET:HE1	1:C:507:GLY:CA	2.27	0.53
1:C:339:ASP:N	1:C:374:GLN:OE1	2.33	0.53
1:C:676:LYS:HE2	1:C:780:GLU:O	2.09	0.53
1:G:61:LEU:O	1:G:221:LYS:HE3	2.08	0.53
1:H:274:LEU:HD12	1:H:521:CYS:HB3	1.89	0.53
1:C:562:LEU:HD12	1:C:619:ILE:HD11	1.90	0.53
1:G:23:ILE:HD11	1:G:107:VAL:HG13	1.90	0.53
1:F:660:ASN:ND2	1:F:675:GLU:HG2	2.23	0.53
1:B:26:GLU:OE2	1:B:60:THR:HG23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:132:ILE:O	1:G:136:MET:HG2	2.08	0.53
1:E:417:MET:HE1	1:H:418:GLU:HB2	1.90	0.53
1:C:454:PRO:HB2	1:C:655:MET:HE3	1.88	0.53
1:D:107:VAL:HG12	1:D:112:ARG:CG	2.38	0.53
3:A:1042:HOH:O	1:D:422:THR:HB	2.09	0.53
1:H:737:GLN:HE22	1:H:765:GLY:N	1.88	0.53
1:A:737:GLN:NE2	1:A:765:GLY:H	1.90	0.53
1:B:568:ASN:HB3	1:B:575:PHE:CE1	2.43	0.53
1:C:662:ARG:NH1	1:C:666:LYS:O	2.42	0.53
1:A:342:ASN:HB3	1:A:432:SER:HA	1.89	0.53
1:A:644:PRO:HG3	1:A:671:GLY:H	1.74	0.53
1:H:501:ILE:HD13	1:H:627:VAL:HG23	1.90	0.53
1:A:312:GLU:HG3	1:A:366:VAL:HG22	1.90	0.53
1:B:31[B]:MET:SD	1:B:51:SER:HB3	2.49	0.53
1:B:91:MET:HE2	1:B:115:HIS:HD2	1.74	0.53
1:H:226:ALA:C	1:H:228:GLU:H	2.12	0.53
1:H:281:THR:HG22	1:H:341:ALA:HB1	1.91	0.53
1:C:340:PHE:HB3	1:C:433:GLY:HA2	1.90	0.53
1:F:107:VAL:HG12	1:F:112:ARG:HG3	1.91	0.53
1:G:487:GLU:CD	1:G:487:GLU:H	2.12	0.53
1:C:136:MET:CE	1:C:140:TRP:NE1	2.71	0.52
1:D:754:GLN:HB2	3:D:977:HOH:O	2.09	0.52
1:F:107:VAL:CG1	1:F:112:ARG:HG3	2.39	0.52
1:F:499:TYR:CZ	1:F:503:ILE:HD11	2.44	0.52
1:F:707:PHE:HZ	1:F:724:LEU:HD22	1.73	0.52
1:B:559:THR:HG21	1:B:616:MET:HB2	1.90	0.52
1:D:624:TYR:CE1	1:D:697:LYS:HB3	2.44	0.52
1:E:743:LYS:HG2	1:E:747:LEU:HD11	1.91	0.52
1:A:340:PHE:HB3	1:A:433:GLY:HA2	1.91	0.52
1:C:222:ALA:HB3	1:C:242:ALA:HB2	1.89	0.52
1:D:281:THR:CG2	1:D:341:ALA:CA	2.87	0.52
1:H:16:SER:HB2	1:H:316:VAL:HG13	1.90	0.52
1:H:711:VAL:O	3:H:905:HOH:O	2.19	0.52
1:E:450:TYR:OH	2:E:801:HYP:HB3	2.09	0.52
1:A:70:VAL:HG12	1:A:218:TYR:CE1	2.45	0.52
1:A:407:TYR:OH	1:A:434:CYS:O	2.22	0.52
1:C:480:PRO:HA	1:C:483:PHE:CD2	2.45	0.52
1:C:493:PHE:CE1	1:C:558:ILE:HD11	2.45	0.52
1:E:679:ASP:OD1	1:E:785:THR:OG1	2.27	0.52
1:G:566:LYS:HD2	1:G:615:ILE:HD11	1.91	0.52
1:H:161:THR:HB	1:H:538:TYR:OH	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:281:THR:HG21	1:C:341:ALA:C	2.31	0.52
1:D:108:SER:O	1:D:112:ARG:HG3	2.10	0.52
1:E:281:THR:HG22	1:E:341:ALA:C	2.30	0.52
1:E:705:GLN:O	1:E:738:PHE:HA	2.10	0.52
1:B:383:LYS:NZ	3:B:905:HOH:O	2.17	0.52
1:B:683:PRO:HA	1:B:686:VAL:HG13	1.92	0.52
1:C:136:MET:CE	1:C:140:TRP:CG	2.92	0.52
1:F:683:PRO:HA	1:F:686:VAL:HG13	1.91	0.52
1:B:281:THR:HG22	1:B:341:ALA:CB	2.39	0.51
1:D:412:ILE:HG21	1:D:430:GLY:HA2	1.90	0.51
1:H:501:ILE:HD13	1:H:627:VAL:CG2	2.40	0.51
1:F:362:ILE:O	1:F:366:VAL:HG13	2.10	0.51
1:G:449:GLY:H	1:G:551:GLN:HE22	1.58	0.51
1:D:281:THR:HG22	1:D:341:ALA:HB1	1.92	0.51
1:G:618:GLU:OE1	3:G:904:HOH:O	2.19	0.51
1:A:376:SER:CB	3:A:907:HOH:O	2.58	0.51
1:F:419:ALA:O	3:F:905:HOH:O	2.19	0.51
1:H:278:ASP:HA	3:H:901:HOH:O	2.11	0.51
1:D:100:ARG:NH1	1:D:331:LEU:HD22	2.26	0.51
1:F:561:SER:HB3	1:F:659:PRO:HD2	1.92	0.51
1:F:737:GLN:NE2	1:F:765:GLY:H	2.03	0.51
1:G:480:PRO:HA	1:G:483:PHE:CD2	2.46	0.51
1:H:286:ASP:HB3	1:H:363:ILE:HD12	1.93	0.51
1:H:561:SER:HB3	1:H:659:PRO:HD2	1.92	0.51
1:G:362:ILE:O	1:G:366:VAL:HG13	2.09	0.51
1:B:25:ILE:HG12	1:B:111:ALA:HA	1.93	0.51
1:H:151:GLU:OE1	3:H:904:HOH:O	2.19	0.51
1:H:172:PHE:HD2	1:H:249:PRO:HB2	1.76	0.51
1:H:89:HIS:HB3	1:H:93:ASP:HB2	1.92	0.51
1:A:461:LEU:HB3	1:A:581:LEU:HD21	1.93	0.51
1:A:704:ASN:HD21	1:A:737:GLN:HE21	1.59	0.51
1:B:281:THR:HG23	1:B:341:ALA:HA	1.92	0.51
1:E:450:TYR:HA	1:E:551:GLN:HB2	1.92	0.51
1:G:660:ASN:ND2	1:G:675:GLU:HG2	2.25	0.51
1:H:436:GLU:HG2	1:H:447:LEU:HD21	1.93	0.51
1:C:679:ASP:OD1	1:C:785:THR:OG1	2.29	0.51
1:E:103:ILE:HA	1:E:337:TYR:CZ	2.46	0.51
1:H:516:ALA:HB1	1:H:540:ARG:HB3	1.92	0.51
1:A:447:LEU:HB3	1:A:551:GLN:HE22	1.76	0.51
1:A:704:ASN:ND2	1:A:737:GLN:HE21	2.08	0.51
1:B:3:ARG:HG2	1:B:3:ARG:NH1	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:64:ASN:ND2	1:D:67:GLU:OE2	2.37	0.51
1:E:70:VAL:HG21	1:E:241:ILE:HG21	1.93	0.51
1:F:167:ILE:HG21	1:F:266:VAL:HG21	1.93	0.51
1:G:61:LEU:HG	1:G:218:TYR:CZ	2.46	0.51
1:C:704:ASN:ND2	1:C:737:GLN:HE21	2.06	0.50
1:E:281:THR:HG22	1:E:341:ALA:HB1	1.93	0.50
1:E:564:ALA:HA	1:E:602:THR:HG21	1.93	0.50
1:H:402:GLY:HA3	1:H:762:ARG:HD3	1.92	0.50
1:B:508:ASN:HB3	1:B:638:TYR:OH	2.11	0.50
1:B:519:MET:O	1:B:539:GLN:HG2	2.11	0.50
1:E:85:GLU:HG2	1:E:86:ILE:HG13	1.92	0.50
1:E:342:ASN:HB3	1:E:432:SER:HA	1.93	0.50
1:G:83:TYR:CG	1:G:275:ASN:HB2	2.46	0.50
1:H:660:ASN:HD22	1:H:675:GLU:HG2	1.76	0.50
1:A:567:TYR:O	1:A:571:ASP:HB2	2.11	0.50
1:C:422:THR:HB	3:C:995:HOH:O	2.11	0.50
1:E:315:TRP:CD1	1:E:375:PRO:HD2	2.46	0.50
1:E:67:GLU:HG2	3:E:992:HOH:O	2.12	0.50
1:F:103:ILE:HA	1:F:337:TYR:CZ	2.47	0.50
1:A:284:ARG:NH2	1:A:346:GLY:O	2.44	0.50
1:C:348:ILE:HG23	1:C:409:THR:HG21	1.93	0.50
1:E:461:LEU:HB3	1:E:581:LEU:HD21	1.93	0.50
1:G:197:LYS:HA	1:G:535:GLY:O	2.12	0.50
1:C:3:ARG:HD3	1:C:369:GLU:O	2.11	0.50
1:E:31[B]:MET:SD	1:E:85:GLU:OE1	2.69	0.50
1:A:450:TYR:HA	1:A:551:GLN:HG2	1.94	0.50
1:B:480:PRO:HA	1:B:483:PHE:CD2	2.46	0.50
1:B:278:ASP:OD2	2:B:801:HYP:HD23	2.12	0.50
1:C:136:MET:CE	1:C:140:TRP:CE2	2.94	0.50
1:D:564:ALA:HA	1:D:602:THR:HG21	1.94	0.50
1:H:450:TYR:HE1	1:H:643:LEU:HD12	1.77	0.50
1:D:306:ARG:HG2	3:D:929:HOH:O	2.11	0.50
1:E:413:VAL:O	1:E:417:MET:HG3	2.12	0.50
1:H:8:ARG:NH1	1:H:237:ASP:OD2	2.37	0.50
1:H:442:LYS:HG2	1:H:529:ASP:HB2	1.93	0.50
1:B:182:ARG:HD2	1:B:185:GLU:OE2	2.12	0.50
1:C:554:GLY:O	1:C:558:ILE:HG22	2.12	0.50
1:F:263:TYR:CZ	1:F:282:PRO:HD3	2.47	0.50
1:G:453:ILE:HG22	1:G:558:ILE:CD1	2.35	0.50
1:B:281:THR:HG21	1:B:341:ALA:C	2.28	0.49
1:C:333:GLU:OE2	3:C:907:HOH:O	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:204:MET:HB3	1:E:526:THR:HG22	1.92	0.49
1:H:493:PHE:CE1	1:H:558:ILE:HD11	2.47	0.49
1:A:103:ILE:HA	1:A:337:TYR:CZ	2.47	0.49
1:A:707:PHE:HZ	1:A:724:LEU:HD22	1.77	0.49
1:F:302:LEU:HD21	1:F:307:ALA:HB2	1.94	0.49
1:G:508:ASN:HB3	1:G:638:TYR:OH	2.12	0.49
1:F:662:ARG:HD2	1:F:667:PRO:O	2.12	0.49
1:H:737:GLN:CD	1:H:762:ARG:HE	2.16	0.49
1:B:279:ALA:HA	3:B:976:HOH:O	2.12	0.49
1:B:412:ILE:HG23	1:B:437:THR:HG23	1.94	0.49
1:B:571:ASP:OD1	3:B:906:HOH:O	2.19	0.49
1:C:644:PRO:HG3	1:C:671:GLY:H	1.77	0.49
1:H:645:THR:HG22	1:H:646:THR:H	1.77	0.49
1:A:737:GLN:CD	1:A:762:ARG:HE	2.16	0.49
1:E:31[B]:MET:HE3	1:E:123:TRP:CZ2	2.47	0.49
1:A:16:SER:HB2	1:A:316:VAL:HG13	1.94	0.49
1:B:23:ILE:HD11	1:B:107:VAL:HG13	1.95	0.49
1:F:162:VAL:HG13	1:F:281:THR:HG23	1.95	0.49
1:H:375:PRO:HA	3:H:1010:HOH:O	2.12	0.49
1:H:477:THR:HG21	1:H:496:GLN:HG2	1.93	0.49
1:C:530:ASP:OD2	1:C:544:ARG:HB2	2.12	0.49
1:E:187:ASP:O	1:E:191:ASP:HB3	2.12	0.49
1:F:539:GLN:NE2	3:F:908:HOH:O	2.21	0.49
1:F:623:TYR:CE2	1:F:640:VAL:HG22	2.46	0.49
1:B:574:LYS:HE2	1:G:246:ASP:OD2	2.13	0.49
1:G:670:GLU:OE1	1:G:704:ASN:HB2	2.11	0.49
1:H:31[A]:MET:HE3	1:H:85:GLU:OE1	2.12	0.49
1:H:720:ASN:HB3	1:H:789:PHE:CG	2.48	0.49
1:C:26:GLU:OE2	1:C:60:THR:HG23	2.13	0.49
1:F:438:GLY:HA3	1:F:445:TYR:CZ	2.48	0.49
1:F:702:LEU:HD11	1:F:765:GLY:N	2.28	0.49
1:H:200:ASP:O	1:H:204:MET:HG3	2.12	0.49
1:H:78:ASN:HA	1:H:322:PRO:HD3	1.95	0.49
1:C:477:THR:HG21	1:C:496:GLN:HG2	1.94	0.49
1:C:136:MET:CE	1:C:507:GLY:HA2	2.41	0.49
1:D:425:ASP:OD2	1:D:545:TYR:OH	2.22	0.49
1:D:660:ASN:HD22	1:D:675:GLU:HG2	1.78	0.49
1:E:160:HIS:ND1	1:E:160:HIS:O	2.45	0.49
1:G:352:GLY:O	1:G:384:LYS:NZ	2.33	0.49
1:B:132:ILE:O	1:B:136:MET:HG2	2.12	0.49
1:B:167:ILE:HG21	1:B:266:VAL:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:LEU:HD23	1:B:736:ILE:HD12	1.95	0.49
1:D:763:VAL:O	1:D:784:ARG:NH2	2.41	0.49
1:F:427:ARG:HH11	1:G:696:ILE:HD12	1.77	0.49
1:H:86:ILE:HA	1:H:128:THR:OG1	2.13	0.49
1:A:31[B]:MET:HE1	1:A:85:GLU:CG	2.38	0.48
1:B:624:TYR:CE1	1:B:697:LYS:HB3	2.48	0.48
1:F:16:SER:HB2	1:F:316:VAL:HG13	1.94	0.48
1:G:98:HIS:HA	1:G:105:PHE:O	2.12	0.48
1:H:453:ILE:HG22	1:H:558:ILE:HD12	1.94	0.48
1:A:152:PHE:HE1	1:A:450:TYR:CE2	2.31	0.48
1:B:187:ASP:O	1:B:191:ASP:HB3	2.13	0.48
1:B:278:ASP:OD1	2:B:801:HYP:N	2.45	0.48
1:B:421:LYS:HA	1:B:545:TYR:CE1	2.49	0.48
1:E:566:LYS:HD3	1:E:615:ILE:HD11	1.96	0.48
1:E:549:TYR:CE2	1:E:639:ARG:HB2	2.48	0.48
1:E:663:LEU:HB2	1:E:666:LYS:HD3	1.94	0.48
1:F:434:CYS:SG	2:F:801:HYP:CD	2.94	0.48
1:F:86:ILE:HA	1:F:128:THR:OG1	2.14	0.48
1:H:562:LEU:HD12	1:H:619:ILE:HD11	1.95	0.48
1:A:412:ILE:HG21	1:A:430:GLY:HA2	1.94	0.48
1:B:746:LEU:CD2	1:B:759:LEU:HD21	2.44	0.48
1:D:2:ALA:O	1:D:10:LYS:NZ	2.42	0.48
1:F:315:TRP:CD1	1:F:375:PRO:HD2	2.48	0.48
1:C:281:THR:HG23	1:C:341:ALA:HA	1.92	0.48
1:E:281:THR:HG23	1:E:341:ALA:HA	1.91	0.48
1:H:442:LYS:NZ	1:H:529:ASP:OD2	2.39	0.48
1:D:549:TYR:CE2	1:D:639:ARG:HB2	2.48	0.48
1:E:302:LEU:HD12	1:E:306:ARG:HB3	1.96	0.48
1:E:72:GLU:HB3	3:E:937:HOH:O	2.12	0.48
1:E:76:SER:HA	3:E:906:HOH:O	2.12	0.48
1:H:103:ILE:HA	1:H:337:TYR:CZ	2.49	0.48
1:A:83:TYR:CG	1:A:275:ASN:HB2	2.49	0.48
1:A:565:ILE:HD11	1:A:659:PRO:HG2	1.95	0.48
1:B:340:PHE:HB3	1:B:433:GLY:HA2	1.95	0.48
1:B:52:PHE:CZ	1:B:523:LEU:HD22	2.49	0.48
1:B:644:PRO:HG3	1:B:671:GLY:H	1.79	0.48
1:D:711:VAL:HG21	1:D:788:THR:HA	1.94	0.48
1:F:160:HIS:NE2	1:F:436:GLU:OE2	2.44	0.48
1:G:765:GLY:O	3:G:905:HOH:O	2.20	0.48
1:G:89:HIS:HB3	1:G:93:ASP:HB2	1.95	0.48
1:A:326:LYS:HE3	3:A:926:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:ARG:HH11	1:D:696:ILE:HD12	1.77	0.48
1:B:78:ASN:HA	1:B:322:PRO:HD3	1.95	0.48
1:E:163:CYS:HB2	1:E:280:PHE:CE2	2.49	0.48
1:E:480:PRO:HA	1:E:483:PHE:CD2	2.49	0.48
1:C:281:THR:HG22	1:C:341:ALA:CB	2.43	0.48
1:D:565:ILE:HD11	1:D:659:PRO:HG2	1.96	0.48
1:F:354:ASP:OD2	3:F:906:HOH:O	2.20	0.48
1:H:281:THR:HG22	1:H:341:ALA:C	2.34	0.48
1:A:223:ARG:HH22	1:A:246:ASP:CG	2.16	0.48
1:C:669:SER:O	3:C:906:HOH:O	2.20	0.48
1:D:80:ALA:HB1	1:D:324:PRO:HA	1.95	0.48
1:D:746:LEU:CD2	1:D:759:LEU:HD21	2.44	0.48
1:E:132:ILE:O	1:E:136:MET:HG2	2.13	0.48
1:E:16:SER:HB2	1:E:316:VAL:HG13	1.96	0.48
1:E:281:THR:HG22	1:E:341:ALA:CB	2.44	0.48
1:F:524:MET:O	1:F:528:VAL:HG23	2.14	0.48
1:F:644:PRO:HG3	1:F:671:GLY:H	1.78	0.48
1:H:436:GLU:HG3	1:H:643:LEU:HD21	1.96	0.48
1:A:705:GLN:O	1:A:738:PHE:HA	2.13	0.48
1:B:702:LEU:HD11	1:B:765:GLY:N	2.28	0.48
1:C:159:GLY:HA3	1:C:276:ILE:HB	1.96	0.48
1:C:167:ILE:HG21	1:C:266:VAL:HG21	1.96	0.48
1:C:436:GLU:HG2	1:C:447:LEU:HD21	1.96	0.48
1:D:702:LEU:HD11	1:D:764:ALA:C	2.34	0.48
1:E:508:ASN:HB3	1:E:638:TYR:OH	2.14	0.48
1:A:151:GLU:CD	1:A:511:ILE:HD13	2.35	0.47
1:B:86:ILE:HA	1:B:128:THR:OG1	2.14	0.47
1:C:707:PHE:HZ	1:C:724:LEU:HD22	1.79	0.47
1:D:200:ASP:O	1:D:204:MET:HG3	2.14	0.47
1:D:554:GLY:O	1:D:558:ILE:HG22	2.14	0.47
1:E:421:LYS:HA	1:E:545:TYR:CE1	2.49	0.47
1:F:392:ARG:O	1:F:395:GLU:HB2	2.14	0.47
1:F:705:GLN:O	1:F:738:PHE:HA	2.13	0.47
1:H:340:PHE:CD2	2:H:801:HYP:HD22	2.49	0.47
1:B:480:PRO:HB2	1:B:577:MET:HG2	1.95	0.47
1:C:525:SER:O	1:C:531:CYS:HB2	2.14	0.47
1:D:448:THR:HB	1:D:508:ASN:ND2	2.29	0.47
1:E:449:GLY:H	1:E:551:GLN:HE22	1.61	0.47
1:E:277:TRP:CE3	2:E:801:HYP:HA	2.49	0.47
1:F:223:ARG:NH2	1:F:246:ASP:OD2	2.32	0.47
1:G:559:THR:HG21	1:G:616:MET:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:GLU:OE2	1:A:317:LYS:NZ	2.46	0.47
1:A:702:LEU:HD11	1:A:765:GLY:N	2.30	0.47
1:G:152:PHE:CE2	2:G:801:HYP:HB2	2.49	0.47
1:G:188:PHE:HB2	1:H:506:GLU:HG3	1.95	0.47
1:G:16:SER:HB2	1:G:316:VAL:HG13	1.96	0.47
1:H:412:ILE:HG21	1:H:430:GLY:HA2	1.96	0.47
1:H:645:THR:HG1	2:H:801:HYP:HB3	1.79	0.47
1:B:204:MET:HB3	1:B:526:THR:HG22	1.97	0.47
1:A:162:VAL:HG21	1:A:432:SER:HB3	1.96	0.47
1:D:670:GLU:OE1	3:D:908:HOH:O	2.20	0.47
1:E:263:TYR:CZ	1:E:282:PRO:HD3	2.50	0.47
1:F:158:PRO:HG2	1:F:539:GLN:OE1	2.15	0.47
1:F:559:THR:HG21	1:F:616:MET:HB2	1.97	0.47
1:A:559:THR:HG21	1:A:616:MET:HB2	1.97	0.47
1:D:156:ARG:HD3	1:D:277:TRP:CE2	2.49	0.47
1:D:499:TYR:CE2	1:D:503:ILE:HD11	2.49	0.47
1:D:765:GLY:O	3:D:907:HOH:O	2.20	0.47
1:H:281:THR:HG23	1:H:341:ALA:HA	1.93	0.47
1:A:48:ARG:NH1	1:A:85:GLU:OE2	2.46	0.47
1:C:522:PRO:O	1:C:526:THR:HG23	2.15	0.47
1:C:701:THR:H	1:C:734:HIS:CD2	2.32	0.47
1:F:244:THR:HG23	1:F:258:GLN:HG2	1.96	0.47
1:H:83:TYR:CG	1:H:275:ASN:HB2	2.50	0.47
1:H:408:ASN:HB2	1:H:729:PHE:CD1	2.49	0.47
1:E:130:ASP:OD1	3:E:902:HOH:O	2.20	0.47
1:C:136:MET:HE3	1:C:507:GLY:HA2	1.94	0.47
1:D:34:ALA:HB1	1:D:51:SER:HA	1.97	0.47
1:D:702:LEU:HD11	1:D:765:GLY:N	2.29	0.47
1:E:701:THR:H	1:E:734:HIS:CD2	2.32	0.47
1:F:78:ASN:HA	1:F:322:PRO:HD3	1.97	0.47
1:H:23:ILE:HG22	1:H:325:PRO:HG3	1.97	0.47
1:C:559:THR:HG21	1:C:616:MET:HB2	1.97	0.47
1:C:705:GLN:O	1:C:738:PHE:HA	2.15	0.47
1:C:737:GLN:NE2	1:C:765:GLY:H	1.97	0.47
1:D:204:MET:CE	1:D:532:ILE:HG12	2.45	0.47
1:D:70:VAL:HG12	1:D:218:TYR:CE1	2.49	0.47
1:E:475:ILE:O	1:E:496:GLN:NE2	2.48	0.47
1:A:182:ARG:HD2	1:A:185:GLU:OE2	2.15	0.46
1:A:413:VAL:O	1:A:417:MET:HG3	2.16	0.46
1:B:746:LEU:HD22	1:B:759:LEU:HD21	1.96	0.46
1:G:645:THR:HG22	1:G:646:THR:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:LEU:HD22	1:A:218:TYR:CE2	2.50	0.46
1:A:96:VAL:O	1:A:100:ARG:HG2	2.14	0.46
1:B:584:LEU:HD11	1:B:659:PRO:HG3	1.98	0.46
1:C:623:TYR:CE2	1:C:640:VAL:HG22	2.49	0.46
1:G:428:LEU:HD12	1:G:442:LYS:HE2	1.97	0.46
1:A:463:ASN:OD1	1:A:478:GLY:N	2.40	0.46
1:A:278:ASP:OD2	2:A:801:HYP:OD1	2.34	0.46
1:F:425:ASP:HB3	1:F:439:CYS:SG	2.56	0.46
1:C:103:ILE:HA	1:C:337:TYR:CZ	2.50	0.46
1:F:480:PRO:HA	1:F:483:PHE:CD2	2.50	0.46
1:H:315:TRP:CD1	1:H:375:PRO:HD2	2.51	0.46
1:A:567:TYR:CD2	1:A:602:THR:HG22	2.51	0.46
1:C:25:ILE:HD12	1:C:25:ILE:C	2.36	0.46
1:C:670:GLU:C	3:C:906:HOH:O	2.53	0.46
1:G:737:GLN:HE22	1:G:765:GLY:N	1.86	0.46
1:H:413:VAL:O	1:H:417:MET:HG3	2.16	0.46
1:A:27:ARG:NH1	1:A:31[B]:MET:HE3	2.28	0.46
1:D:366:VAL:O	1:D:370:MET:HG2	2.15	0.46
1:E:98:HIS:HA	1:E:105:PHE:O	2.16	0.46
1:E:61:LEU:HD22	1:E:218:TYR:CE2	2.51	0.46
1:F:407:TYR:HB3	1:F:412:ILE:HD11	1.98	0.46
1:F:551:GLN:H	1:F:551:GLN:NE2	2.14	0.46
1:A:286:ASP:HB3	1:A:363:ILE:HD12	1.96	0.46
1:A:319:ASN:HA	1:A:374:GLN:HB2	1.97	0.46
1:A:5:THR:HB	1:A:6:PHE:CE1	2.51	0.46
1:A:679:ASP:OD1	1:A:785:THR:OG1	2.34	0.46
1:D:658:SER:OG	1:D:662:ARG:HB3	2.15	0.46
1:H:340:PHE:O	3:H:906:HOH:O	2.20	0.46
1:B:704:ASN:ND2	3:B:932:HOH:O	2.37	0.46
1:C:136:MET:HE1	1:C:140:TRP:NE1	2.30	0.46
1:E:590:GLY:N	1:E:592:GLU:OE1	2.45	0.46
1:F:660:ASN:HD22	1:F:675:GLU:HG2	1.79	0.46
1:G:162:VAL:HG13	1:G:281:THR:HG23	1.97	0.46
1:H:281:THR:HG22	1:H:341:ALA:CB	2.45	0.46
1:H:743:LYS:HG2	1:H:747:LEU:HD11	1.98	0.46
1:H:679:ASP:OD2	1:H:787:GLN:NE2	2.49	0.46
1:A:506:GLU:HG3	1:B:188:PHE:HB2	1.98	0.46
1:C:508:ASN:HB3	1:C:638:TYR:OH	2.16	0.46
1:A:226:ALA:O	1:A:235:LYS:NZ	2.45	0.46
1:A:31[B]:MET:CE	1:A:48:ARG:HH12	2.29	0.46
1:D:103:ILE:HA	1:D:337:TYR:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:450:TYR:OH	2:D:801:HYP:HB3	2.16	0.46
1:F:453:ILE:HG22	1:F:558:ILE:HD12	1.97	0.46
1:G:78:ASN:HA	1:G:322:PRO:HD3	1.97	0.46
1:H:480:PRO:HA	1:H:483:PHE:CD2	2.51	0.46
1:H:642:MET:HE2	1:H:642:MET:HA	1.98	0.46
1:A:200:ASP:OD2	1:A:540:ARG:NE	2.46	0.45
1:C:475:ILE:O	1:C:496:GLN:NE2	2.48	0.45
1:D:151:GLU:CD	1:D:511:ILE:HD13	2.37	0.45
1:D:225:MET:HA	1:D:228:GLU:HG2	1.98	0.45
1:F:308:GLN:HG3	1:F:366:VAL:HG12	1.99	0.45
1:H:565:ILE:HD11	1:H:659:PRO:HG2	1.97	0.45
1:H:707:PHE:HZ	1:H:724:LEU:HD22	1.80	0.45
1:C:742:ASP:HB3	1:C:745:VAL:CG2	2.45	0.45
1:F:160:HIS:O	1:F:160:HIS:ND1	2.49	0.45
1:F:516:ALA:HB1	1:F:540:ARG:HB3	1.97	0.45
1:B:172:PHE:CZ	1:B:211:MET:HG3	2.51	0.45
1:C:349:ASN:HD21	1:C:353:GLN:NE2	2.14	0.45
1:C:448:THR:O	1:C:504:LYS:NZ	2.40	0.45
1:E:644:PRO:HD2	3:E:924:HOH:O	2.15	0.45
1:H:100:ARG:CZ	1:H:331:LEU:HD22	2.46	0.45
1:H:475:ILE:O	1:H:496:GLN:NE2	2.49	0.45
1:A:31[B]:MET:HE1	1:A:48:ARG:HH22	1.81	0.45
1:A:499:TYR:CZ	1:A:503:ILE:HD11	2.51	0.45
1:B:27:ARG:CZ	1:B:31[A]:MET:CE	2.92	0.45
1:C:13:ARG:HG2	1:C:17:ILE:HD13	1.98	0.45
1:C:443:GLU:HG2	1:C:445:TYR:HD1	1.80	0.45
1:E:188:PHE:HB2	1:F:506:GLU:HG3	1.97	0.45
1:E:455:LYS:HG3	1:E:458:GLU:OE1	2.17	0.45
1:D:421:LYS:HA	1:D:545:TYR:CE1	2.52	0.45
1:E:438:GLY:HA3	1:E:445:TYR:CZ	2.52	0.45
1:E:499:TYR:CZ	1:E:503:ILE:HD11	2.51	0.45
1:H:676:LYS:HZ2	1:H:780:GLU:HA	1.82	0.45
1:H:85:GLU:HG2	1:H:86:ILE:HG13	1.98	0.45
1:C:438:GLY:HA3	1:C:445:TYR:CZ	2.52	0.45
1:D:23:ILE:HG22	1:D:325:PRO:HG3	1.99	0.45
1:E:197:LYS:HA	1:E:535:GLY:O	2.16	0.45
1:F:44:ILE:O	1:F:48:ARG:HG2	2.16	0.45
1:H:580:LEU:HD21	1:H:659:PRO:HB3	1.98	0.45
1:A:708:ALA:O	1:A:711:VAL:HG22	2.17	0.45
1:B:281:THR:HG22	1:B:341:ALA:C	2.36	0.45
1:B:463:ASN:OD1	1:B:476:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:278:ASP:HB3	3:C:971:HOH:O	2.16	0.45
1:C:341:ALA:HB3	3:C:946:HOH:O	2.16	0.45
1:D:290:ASN:ND2	1:D:294:GLU:OE2	2.48	0.45
1:E:497:LEU:HD21	1:E:623:TYR:HA	1.98	0.45
1:G:407:TYR:OH	1:G:434:CYS:O	2.22	0.45
1:G:91:MET:HE2	1:G:115:HIS:HD2	1.82	0.45
1:H:98:HIS:HA	1:H:105:PHE:O	2.17	0.45
1:A:402:GLY:O	3:A:902:HOH:O	2.21	0.45
1:D:85:GLU:HG2	1:D:86:ILE:HG13	1.99	0.45
1:E:78:ASN:HA	1:E:322:PRO:HD3	1.97	0.45
1:F:422:THR:HB	3:F:1032:HOH:O	2.17	0.45
1:F:521:CYS:HG	1:F:539:GLN:HG2	1.78	0.45
1:A:234:LYS:HB2	1:A:234:LYS:HE3	1.77	0.45
1:A:655:MET:HE2	1:A:662:ARG:HH22	1.82	0.45
1:C:103:ILE:HA	1:C:337:TYR:CE2	2.51	0.45
1:D:26:GLU:OE1	1:D:60:THR:HG23	2.17	0.45
1:D:152:PHE:HZ	2:D:801:HYP:HB2	1.82	0.45
1:E:504:LYS:HE3	1:E:508:ASN:HD21	1.82	0.45
1:A:658:SER:HG	1:A:662:ARG:HB3	1.82	0.45
1:C:342:ASN:HA	1:C:376:SER:HB3	1.99	0.45
1:C:521:CYS:SG	1:C:539:GLN:CG	2.98	0.45
1:D:252:LYS:HE3	1:D:254:GLU:OE2	2.17	0.45
1:D:156:ARG:HD3	1:D:277:TRP:CD2	2.52	0.45
1:D:281:THR:HG22	1:D:341:ALA:CA	2.47	0.45
1:A:417:MET:HE2	1:D:417:MET:HB2	1.98	0.45
1:E:330:THR:HA	1:E:333:GLU:HG2	1.98	0.45
1:G:749:ALA:HA	1:G:756:TYR:CD1	2.51	0.45
1:H:499:TYR:CZ	1:H:503:ILE:HD11	2.52	0.45
1:A:187:ASP:O	1:A:191:ASP:HB3	2.18	0.44
1:A:444:ALA:HB2	1:A:538:TYR:CE1	2.53	0.44
1:A:655:MET:SD	1:A:662:ARG:NH2	2.90	0.44
1:C:551:GLN:HG3	1:C:641:ASP:OD1	2.18	0.44
1:C:561:SER:HB3	1:C:659:PRO:HD2	1.98	0.44
1:C:676:LYS:NZ	1:C:783:GLY:HA3	2.32	0.44
1:G:317:LYS:O	1:G:321:GLN:HG2	2.18	0.44
1:H:425:ASP:HB3	1:H:439:CYS:SG	2.57	0.44
1:H:525:SER:O	1:H:531:CYS:HB2	2.17	0.44
1:C:35:TYR:HB3	1:C:122:PHE:CZ	2.53	0.44
1:C:31[B]:MET:HB3	1:C:31[B]:MET:HE3	1.87	0.44
1:D:167:ILE:HG21	1:D:266:VAL:HG21	1.99	0.44
1:D:295:ARG:NE	3:D:947:HOH:O	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:559:THR:HG21	1:E:616:MET:HB2	2.00	0.44
1:E:663:LEU:O	1:E:666:LYS:HB2	2.16	0.44
1:F:182:ARG:O	1:F:186:LEU:HG	2.17	0.44
1:H:160:HIS:CD2	1:H:447:LEU:HD13	2.52	0.44
1:A:436:GLU:OE1	1:A:643:LEU:CD2	2.59	0.44
1:D:676:LYS:HD3	1:D:676:LYS:HA	1.79	0.44
1:G:425:ASP:HB3	1:G:439:CYS:SG	2.57	0.44
1:H:685:ALA:HB3	3:H:932:HOH:O	2.18	0.44
1:C:660:ASN:HD22	1:C:675:GLU:HG2	1.79	0.44
1:E:3:ARG:O	1:E:10:LYS:HA	2.16	0.44
1:G:402:GLY:HA3	1:G:762:ARG:HD3	1.99	0.44
1:B:405:ALA:HB2	1:B:762:ARG:NH1	2.33	0.44
1:C:334:SER:OG	2:C:801:HYP:C	2.61	0.44
1:D:701:THR:H	1:D:734:HIS:CD2	2.36	0.44
1:G:701:THR:H	1:G:734:HIS:CD2	2.35	0.44
1:A:662:ARG:HD2	1:A:667:PRO:O	2.17	0.44
1:B:737:GLN:HE22	1:B:765:GLY:N	2.01	0.44
1:E:274:LEU:HD12	1:E:521:CYS:HB3	1.99	0.44
1:G:450:TYR:OH	2:G:801:HYP:HB3	2.18	0.44
1:H:278:ASP:CA	3:H:901:HOH:O	2.55	0.44
1:H:559:THR:HG21	1:H:616:MET:HB2	1.98	0.44
1:A:434:CYS:HB3	1:A:765:GLY:HA3	2.00	0.44
1:B:742:ASP:HB3	1:B:745:VAL:HG23	2.00	0.44
1:E:229:GLU:HG2	1:E:234:LYS:HB2	2.00	0.44
1:H:402:GLY:CA	1:H:762:ARG:HD3	2.48	0.44
1:A:89:HIS:HB3	1:A:93:ASP:HB2	2.00	0.44
1:C:264:TRP:CE2	1:C:317:LYS:HB3	2.52	0.44
1:C:648:HIS:CD2	1:C:670:GLU:HB3	2.53	0.44
1:G:549:TYR:CE2	1:G:639:ARG:HB2	2.52	0.44
1:H:278:ASP:HB3	3:H:906:HOH:O	2.17	0.44
1:H:480:PRO:HG2	1:H:581:LEU:HD11	2.00	0.44
1:B:581:LEU:HA	1:B:581:LEU:HD23	1.82	0.44
1:E:548:ARG:HB3	1:E:638:TYR:CE2	2.53	0.44
1:E:737:GLN:CD	1:E:762:ARG:HE	2.21	0.44
1:H:163:CYS:HB3	3:H:956:HOH:O	2.18	0.44
1:H:552:GLY:HA3	1:H:642:MET:HE1	2.00	0.44
1:D:623:TYR:CE2	1:D:640:VAL:HG22	2.53	0.43
1:G:86:ILE:HA	1:G:128:THR:OG1	2.18	0.43
1:A:197:LYS:HA	1:A:535:GLY:O	2.17	0.43
1:A:566:LYS:HD3	1:A:615:ILE:HD11	1.99	0.43
1:D:139:GLU:H	1:D:139:GLU:CD	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:160:HIS:NE2	1:D:447:LEU:HD13	2.33	0.43
1:D:235:LYS:HG2	1:D:239:LEU:HD23	1.99	0.43
1:D:319:ASN:HA	1:D:374:GLN:HB2	2.00	0.43
1:E:31[B]:MET:HE3	1:E:31[B]:MET:HB3	1.57	0.43
1:F:701:THR:H	1:F:734:HIS:CD2	2.37	0.43
1:A:562:LEU:HD12	1:A:619:ILE:HD11	2.00	0.43
1:A:702:LEU:HD11	1:A:764:ALA:C	2.37	0.43
1:B:562:LEU:HD12	1:B:619:ILE:HD11	2.00	0.43
1:C:91:MET:HE1	1:C:112:ARG:HG2	1.99	0.43
1:E:743:LYS:HG2	1:E:747:LEU:CD1	2.48	0.43
1:G:708:ALA:O	1:G:711:VAL:HG22	2.18	0.43
1:H:697:LYS:O	3:H:907:HOH:O	2.21	0.43
1:H:704:ASN:ND2	1:H:737:GLN:HG3	2.33	0.43
1:A:70:VAL:HG21	1:A:241:ILE:HG21	1.99	0.43
1:C:197:LYS:HA	1:C:535:GLY:O	2.18	0.43
1:D:98:HIS:HA	1:D:105:PHE:O	2.17	0.43
1:D:652:GLY:HA3	1:D:667:PRO:HA	2.00	0.43
1:D:704:ASN:ND2	1:D:737:GLN:HE21	2.15	0.43
1:E:84:PRO:HB2	1:E:123:TRP:CB	2.48	0.43
1:F:47:LEU:O	1:F:51:SER:OG	2.34	0.43
1:G:720:ASN:HB3	1:G:789:PHE:CD1	2.54	0.43
1:H:563:THR:HG21	1:H:603:PRO:O	2.18	0.43
1:H:704:ASN:ND2	1:H:737:GLN:HE21	2.16	0.43
1:H:754:GLN:H	1:H:754:GLN:HG2	1.60	0.43
1:A:610:ASP:OD1	1:A:692:LYS:NZ	2.36	0.43
1:B:151:GLU:OE1	1:B:504:LYS:NZ	2.51	0.43
1:B:652:GLY:HA3	1:B:667:PRO:HA	2.00	0.43
1:C:318:PHE:HB2	1:C:375:PRO:HD3	2.00	0.43
1:C:421:LYS:HA	1:C:545:TYR:CE1	2.54	0.43
1:E:219:ALA:HB2	1:E:245:CYS:HB2	2.00	0.43
1:E:768:ASP:HB3	1:E:773:LEU:HD21	2.01	0.43
1:F:151:GLU:OE2	1:F:504:LYS:NZ	2.52	0.43
1:F:197:LYS:HA	1:F:535:GLY:O	2.19	0.43
1:G:412:ILE:HD13	1:G:430:GLY:HA2	2.00	0.43
1:G:748:GLU:HG3	1:G:756:TYR:OH	2.18	0.43
1:H:481:ARG:NH2	3:H:949:HOH:O	2.51	0.43
1:H:26:GLU:OE1	1:H:60:THR:HG23	2.18	0.43
1:A:139:GLU:H	1:A:139:GLU:CD	2.22	0.43
1:A:19:ALA:HB2	1:A:77:PRO:HB2	2.00	0.43
1:A:279:ALA:HA	3:A:956:HOH:O	2.18	0.43
1:A:27:ARG:HH22	1:A:31[B]:MET:CE	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:263:TYR:C	1:C:263:TYR:CD2	2.91	0.43
1:D:403:GLN:NE2	3:D:920:HOH:O	2.30	0.43
1:F:477:THR:HG21	1:F:496:GLN:HG2	1.99	0.43
1:G:562:LEU:HD23	1:G:562:LEU:HA	1.85	0.43
1:C:236:LYS:HE3	1:C:236:LYS:HB2	1.85	0.43
1:C:412:ILE:HG21	1:C:430:GLY:HA2	2.01	0.43
1:F:2:ALA:O	1:F:10:LYS:NZ	2.49	0.43
1:H:289:LEU:HA	1:H:289:LEU:HD23	1.74	0.43
1:A:549:TYR:CE2	1:A:639:ARG:HB2	2.54	0.43
1:B:410:GLU:HG2	3:B:905:HOH:O	2.18	0.43
1:D:317:LYS:O	1:D:321:GLN:HG2	2.18	0.43
1:D:561:SER:HB3	1:D:659:PRO:HD2	2.00	0.43
1:D:559:THR:HG21	1:D:616:MET:HB2	2.01	0.43
1:F:278:ASP:N	3:F:927:HOH:O	2.42	0.43
1:B:349:ASN:HD21	1:B:353:GLN:CG	2.28	0.43
1:B:319:ASN:HA	1:B:374:GLN:HB2	2.01	0.43
1:B:671:GLY:HA2	3:B:1044:HOH:O	2.19	0.43
1:B:671:GLY:N	3:B:958:HOH:O	2.52	0.43
1:G:413:VAL:O	1:G:417:MET:HG3	2.19	0.43
1:B:453:ILE:O	1:B:558:ILE:HD12	2.19	0.43
1:C:25:ILE:HG12	1:C:111:ALA:HA	2.00	0.43
1:C:332:LYS:HD3	1:C:650:TYR:CD1	2.54	0.43
1:D:6:PHE:CZ	1:D:305:ASP:HB3	2.54	0.43
1:E:163:CYS:HB3	3:E:944:HOH:O	2.19	0.43
1:F:354:ASP:OD1	1:F:386:PRO:HD3	2.19	0.43
1:F:747:LEU:HA	1:F:747:LEU:HD23	1.75	0.43
1:G:660:ASN:HD22	1:G:675:GLU:HG2	1.83	0.43
1:H:88:CYS:N	1:H:127:GLN:OE1	2.36	0.43
1:H:639:ARG:NH1	3:H:928:HOH:O	2.43	0.43
1:C:349:ASN:HD21	1:C:353:GLN:HG2	1.84	0.42
1:F:31[A]:MET:HE1	1:F:85:GLU:OE2	2.19	0.42
1:G:412:ILE:HG21	1:G:430:GLY:HA2	2.01	0.42
1:G:438:GLY:HA3	1:G:445:TYR:CE1	2.54	0.42
1:H:293:TYR:O	1:H:297:VAL:HG13	2.19	0.42
1:H:566:LYS:HG2	1:H:611:TYR:OH	2.19	0.42
1:B:412:ILE:HG21	1:B:430:GLY:HA2	2.01	0.42
1:C:289:LEU:CD1	1:C:311:LEU:HD21	2.49	0.42
1:D:25:ILE:HA	1:D:25:ILE:HD12	1.84	0.42
1:D:263:TYR:CZ	1:D:282:PRO:HD3	2.54	0.42
1:E:154:GLU:OE1	3:E:904:HOH:O	2.21	0.42
1:E:161:THR:HB	1:E:538:TYR:OH	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:13:ARG:O	1:G:17:ILE:HG23	2.18	0.42
1:G:421:LYS:HA	1:G:545:TYR:CE1	2.53	0.42
1:G:67:GLU:HG2	3:G:1053:HOH:O	2.20	0.42
1:H:154:GLU:HG3	1:H:155:GLN:N	2.34	0.42
1:G:506:GLU:HG3	1:H:188:PHE:HB2	2.01	0.42
1:D:102:ILE:HG12	3:D:1035:HOH:O	2.18	0.42
1:E:650:TYR:O	1:E:654:ILE:HG13	2.19	0.42
1:F:76:SER:HA	3:F:957:HOH:O	2.19	0.42
1:F:711:VAL:HG21	1:F:788:THR:HA	2.02	0.42
1:G:162:VAL:HG21	1:G:432:SER:HB3	2.01	0.42
1:H:160:HIS:NE2	1:H:447:LEU:HD13	2.35	0.42
1:H:623:TYR:CE2	1:H:640:VAL:HG22	2.54	0.42
1:A:407:TYR:HB3	1:A:412:ILE:HD11	2.01	0.42
1:A:568:ASN:HD22	1:A:574:LYS:HD2	1.84	0.42
1:B:436:GLU:HG2	1:B:447:LEU:HD11	2.01	0.42
1:B:442:LYS:HG2	1:B:529:ASP:HB2	2.01	0.42
1:C:358:GLU:O	1:C:362:ILE:HG13	2.20	0.42
1:C:367:MET:HG3	1:C:368:ASP:N	2.34	0.42
1:D:160:HIS:O	1:D:160:HIS:ND1	2.53	0.42
1:D:23:ILE:HD11	1:D:107:VAL:HG13	2.01	0.42
1:D:566:LYS:HG2	1:D:611:TYR:OH	2.20	0.42
1:D:705:GLN:O	1:D:738:PHE:HA	2.20	0.42
1:G:80:ALA:HB1	1:G:324:PRO:HA	2.02	0.42
1:A:486:TYR:CD2	1:A:566:LYS:HD2	2.55	0.42
1:B:83:TYR:CD1	1:B:275:ASN:HB2	2.54	0.42
1:B:537:ASP:OD2	1:B:539:GLN:HB2	2.20	0.42
1:D:16:SER:HB2	1:D:316:VAL:HG13	2.02	0.42
1:D:204:MET:HE2	1:D:532:ILE:HG12	2.00	0.42
1:D:65:ASP:OD1	1:D:234:LYS:HE3	2.20	0.42
1:A:8:ARG:NH2	1:A:8:ARG:HG3	2.35	0.42
1:C:633:VAL:HA	1:D:192:LEU:HD22	2.02	0.42
1:F:402:GLY:HA3	1:F:762:ARG:HD3	2.01	0.42
1:G:154:GLU:HG3	1:G:155:GLN:N	2.34	0.42
1:H:57:GLU:HG3	1:H:213:ILE:HG21	2.01	0.42
1:A:296:ASP:OD1	3:A:903:HOH:O	2.22	0.42
1:A:48:ARG:HG3	1:A:520:PRO:HG2	2.00	0.42
1:B:349:ASN:ND2	1:B:353:GLN:HG3	2.33	0.42
1:C:349:ASN:ND2	1:C:353:GLN:HG2	2.35	0.42
1:C:449:GLY:O	1:C:551:GLN:OE1	2.38	0.42
1:E:561:SER:HB3	1:E:659:PRO:HD2	2.00	0.42
1:F:562:LEU:HD23	1:F:562:LEU:HA	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:626:GLU:OE2	1:G:630:ARG:NH2	2.44	0.42
1:A:188:PHE:CB	1:B:506:GLU:HG3	2.47	0.42
1:C:163:CYS:HB3	3:C:958:HOH:O	2.20	0.42
1:C:85:GLU:HG2	1:C:86:ILE:HG13	2.02	0.42
1:E:522:PRO:O	1:E:526:THR:HG23	2.20	0.42
1:G:15:GLU:OE2	3:G:906:HOH:O	2.21	0.42
1:H:159:GLY:HA3	1:H:276:ILE:HB	2.01	0.42
1:H:624:TYR:CE1	1:H:697:LYS:HB3	2.55	0.42
1:B:137:THR:O	1:B:141:LEU:HD22	2.20	0.42
1:C:315:TRP:CD1	1:C:375:PRO:HD2	2.55	0.42
1:C:264:TRP:CZ2	1:C:317:LYS:HB3	2.54	0.42
1:E:226:ALA:O	1:E:235:LYS:HE2	2.20	0.42
1:E:319:ASN:HA	1:E:374:GLN:HB2	2.01	0.42
1:A:53:LYS:HD2	1:A:206:ILE:HG23	2.01	0.42
1:A:31[B]:MET:CE	1:A:48:ARG:HH22	2.33	0.42
1:D:34:ALA:CB	1:D:51:SER:HA	2.50	0.42
1:D:78:ASN:HA	1:D:322:PRO:HD3	2.01	0.42
1:E:289:LEU:HA	1:E:289:LEU:HD23	1.76	0.42
1:E:516:ALA:HB1	1:E:540:ARG:HB3	2.02	0.42
1:H:508:ASN:HB3	1:H:638:TYR:OH	2.20	0.42
1:A:151:GLU:O	1:A:154:GLU:HG2	2.20	0.41
1:A:264:TRP:CE2	1:A:317:LYS:HB3	2.54	0.41
1:A:575:PHE:CD1	1:A:594:ILE:HD12	2.55	0.41
1:B:434:CYS:HB3	1:B:765:GLY:HA3	2.02	0.41
1:B:549:TYR:CE2	1:B:699:GLY:HA3	2.55	0.41
1:C:274:LEU:HD12	1:C:521:CYS:HB3	2.02	0.41
1:D:163:CYS:HB3	3:D:967:HOH:O	2.19	0.41
1:E:696:ILE:HD12	1:H:427:ARG:HH11	1.85	0.41
1:F:132:ILE:O	1:F:136:MET:HG2	2.20	0.41
1:F:264:TRP:CE2	1:F:317:LYS:HB3	2.55	0.41
1:F:402:GLY:CA	1:F:762:ARG:HD3	2.50	0.41
1:G:415:GLU:HG3	1:G:696:ILE:HA	2.02	0.41
1:G:450:TYR:HB3	1:G:553:VAL:HG21	2.02	0.41
1:G:627:VAL:HB	1:G:640:VAL:HG23	2.02	0.41
1:H:695:HIS:CD2	1:H:733:GLY:HA2	2.55	0.41
1:H:773:LEU:HB3	1:H:777:LEU:HD23	2.02	0.41
1:A:162:VAL:HG22	1:A:281:THR:CG2	2.50	0.41
1:C:100:ARG:CZ	1:C:331:LEU:HD22	2.50	0.41
1:C:516:ALA:HB1	1:C:540:ARG:HB3	2.02	0.41
1:D:640:VAL:N	3:D:926:HOH:O	2.51	0.41
1:D:641:ASP:O	1:D:642:MET:HE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:445:TYR:HA	1:F:547:THR:O	2.20	0.41
1:G:431:THR:HA	1:G:436:GLU:O	2.19	0.41
1:G:554:GLY:O	1:G:558:ILE:HG22	2.20	0.41
1:G:645:THR:HG22	1:G:646:THR:H	1.85	0.41
1:H:364:LEU:HA	1:H:364:LEU:HD23	1.78	0.41
1:A:154:GLU:HG3	1:A:155:GLN:N	2.35	0.41
1:B:263:TYR:CZ	1:B:282:PRO:HD3	2.55	0.41
1:B:381:ILE:HG13	1:B:390:LEU:HD13	2.01	0.41
1:C:78:ASN:HA	1:C:322:PRO:HD3	2.01	0.41
1:C:624:TYR:CE1	1:C:697:LYS:HB3	2.56	0.41
1:D:438:GLY:HA3	1:D:445:TYR:CZ	2.55	0.41
1:D:606:GLY:N	3:D:933:HOH:O	2.52	0.41
1:E:151:GLU:CD	1:E:511:ILE:HD13	2.40	0.41
1:F:187:ASP:O	1:F:191:ASP:HB3	2.19	0.41
1:F:701:THR:O	1:F:735:HIS:HB3	2.20	0.41
1:F:737:GLN:CD	1:F:762:ARG:HE	2.24	0.41
1:G:705:GLN:O	1:G:738:PHE:HA	2.20	0.41
1:H:317:LYS:O	1:H:321:GLN:HG2	2.20	0.41
1:H:348:ILE:HG23	1:H:409:THR:HG21	2.02	0.41
1:C:188:PHE:CZ	1:C:198:LYS:HD2	2.56	0.41
1:B:417:MET:HE1	1:C:418:GLU:HB2	2.01	0.41
1:C:480:PRO:HA	1:C:483:PHE:CE2	2.55	0.41
1:E:442:LYS:NZ	1:E:529:ASP:OD2	2.53	0.41
1:G:152:PHE:CZ	2:G:801:HYP:HB2	2.55	0.41
1:G:518:HIS:C	1:G:520:PRO:HD3	2.40	0.41
1:G:85:GLU:HG2	1:G:86:ILE:HG13	2.02	0.41
1:H:154:GLU:HG3	1:H:155:GLN:HG3	2.02	0.41
1:H:186:LEU:HA	1:H:186:LEU:HD23	1.81	0.41
1:H:313:CYS:O	1:H:317:LYS:HG2	2.21	0.41
1:H:401:TRP:N	3:H:946:HOH:O	2.49	0.41
1:H:555:ILE:CG2	1:H:672:ILE:HA	2.50	0.41
1:B:14:GLU:O	1:B:18:ASN:ND2	2.54	0.41
1:B:654:ILE:H	1:B:654:ILE:HG13	1.69	0.41
1:C:151:GLU:CD	1:C:511:ILE:HD13	2.40	0.41
1:C:645:THR:HG22	1:C:646:THR:N	2.36	0.41
1:F:161:THR:HB	1:F:538:TYR:OH	2.21	0.41
1:C:450:TYR:HA	1:C:551:GLN:HB2	2.01	0.41
1:D:110:GLU:HB2	3:D:1067:HOH:O	2.19	0.41
1:D:144:TYR:OH	1:D:154:GLU:OE1	2.29	0.41
1:D:302:LEU:HD12	1:D:306:ARG:HG3	2.01	0.41
1:G:340:PHE:HB3	1:G:433:GLY:HA2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ILE:N	1:A:121:PRO:HD2	2.36	0.41
1:A:364:LEU:HD23	1:A:364:LEU:HA	1.84	0.41
1:B:737:GLN:CD	1:B:762:ARG:HE	2.24	0.41
1:D:487:GLU:HB2	3:D:1020:HOH:O	2.21	0.41
1:E:473:ILE:HG22	1:E:500:MET:HE1	2.02	0.41
1:E:453:ILE:HD11	1:E:623:TYR:CE1	2.56	0.41
1:E:654:ILE:HG13	1:E:654:ILE:H	1.74	0.41
1:F:186:LEU:HD11	1:F:201:LEU:HD12	2.03	0.41
1:F:311:LEU:HD23	1:F:311:LEU:HA	1.84	0.41
1:F:702:LEU:HD11	1:F:764:ALA:C	2.41	0.41
1:G:421:LYS:HG3	1:G:545:TYR:CE2	2.56	0.41
1:A:160:HIS:NE2	1:A:436:GLU:OE2	2.47	0.41
1:C:576:ASP:OD1	1:C:579:THR:OG1	2.24	0.41
1:C:748:GLU:OE2	1:C:752:ASN:ND2	2.53	0.41
1:C:95:GLU:O	1:C:99:ASN:ND2	2.53	0.41
1:D:650:TYR:O	1:D:654:ILE:HG13	2.20	0.41
1:G:704:ASN:ND2	3:G:963:HOH:O	2.50	0.41
1:H:371:LYS:HE3	1:H:760:ILE:HD12	2.02	0.41
1:H:436:GLU:CG	1:H:643:LEU:HD21	2.50	0.41
1:H:450:TYR:OH	2:H:801:HYP:OXT	2.36	0.41
1:A:167:ILE:HG21	1:A:266:VAL:HG21	2.02	0.41
1:A:30:LEU:HD23	1:A:30:LEU:HA	1.93	0.41
1:A:524:MET:O	1:A:528:VAL:HG23	2.19	0.41
1:A:566:LYS:HG2	1:A:611:TYR:OH	2.21	0.41
1:B:695:HIS:CE1	1:B:701:THR:HG1	2.37	0.41
1:C:281:THR:HG22	1:C:341:ALA:C	2.41	0.41
1:C:289:LEU:HA	1:C:289:LEU:HD23	1.88	0.41
1:C:640:VAL:N	3:C:937:HOH:O	2.42	0.41
1:D:660:ASN:ND2	1:D:675:GLU:HG2	2.36	0.41
1:E:378:ASN:OD1	3:E:903:HOH:O	2.21	0.41
1:E:649:ILE:HD13	1:E:667:PRO:HB3	2.03	0.41
1:F:100:ARG:NH1	1:F:331:LEU:HD22	2.36	0.41
1:G:691:ALA:HB1	1:G:731:MET:HB3	2.01	0.41
1:H:172:PHE:CD1	1:H:175:LEU:HD12	2.56	0.41
1:A:6:PHE:CD1	1:A:6:PHE:N	2.87	0.41
1:E:72:GLU:OE2	1:E:317:LYS:NZ	2.52	0.41
1:E:712:VAL:HG21	1:E:740:VAL:HG11	2.03	0.41
1:F:536:LYS:NZ	1:F:536:LYS:HB2	2.36	0.41
1:G:151:GLU:CD	1:G:511:ILE:HD13	2.41	0.41
1:G:702:LEU:HD11	1:G:765:GLY:N	2.36	0.41
1:A:311:LEU:HA	1:A:311:LEU:HD23	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:TYR:CD1	1:A:275:ASN:HB2	2.55	0.41
1:B:6:PHE:CD1	1:B:6:PHE:N	2.89	0.41
1:E:151:GLU:O	1:E:154:GLU:HG2	2.20	0.41
1:E:89:HIS:HB3	1:E:93:ASP:HB2	2.03	0.41
1:G:263:TYR:CZ	1:G:282:PRO:HD3	2.55	0.41
1:H:649:ILE:HD13	1:H:667:PRO:HB3	2.02	0.41
1:H:742:ASP:OD2	1:H:744:ASN:HB2	2.21	0.41
1:B:289:LEU:HB2	1:B:359:VAL:HG11	2.02	0.40
1:B:8:ARG:HG3	1:B:8:ARG:HH21	1.85	0.40
1:E:279:ALA:HB2	1:E:339:ASP:HB3	2.03	0.40
1:E:31[B]:MET:HG2	1:E:51:SER:OG	2.21	0.40
1:E:645:THR:HG22	1:E:646:THR:N	2.36	0.40
1:F:537:ASP:OD2	1:F:539:GLN:HB2	2.22	0.40
1:A:49:ALA:HB1	1:A:206:ILE:HB	2.03	0.40
1:B:407:TYR:HB3	1:B:412:ILE:HD11	2.03	0.40
1:B:161:THR:HB	1:B:538:TYR:OH	2.22	0.40
1:B:623:TYR:CE2	1:B:640:VAL:HG22	2.57	0.40
1:C:348:ILE:HD12	1:C:352:GLY:HA2	2.02	0.40
1:E:525:SER:O	1:E:531:CYS:HB2	2.21	0.40
1:F:314:LEU:HG	1:F:318:PHE:CE2	2.56	0.40
1:F:48:ARG:HG3	1:F:520:PRO:HG2	2.03	0.40
1:F:529:ASP:O	1:F:543:ALA:HA	2.21	0.40
1:H:25:ILE:HA	1:H:25:ILE:HD12	1.93	0.40
1:B:151:GLU:CD	1:B:511:ILE:HD13	2.41	0.40
1:A:384:LYS:NZ	1:D:732:ASP:OD2	2.39	0.40
1:E:318:PHE:HB2	1:E:375:PRO:HD3	2.02	0.40
1:G:31[B]:MET:HB3	1:G:31[B]:MET:HE3	1.94	0.40
1:G:61:LEU:HG	1:G:218:TYR:CE2	2.57	0.40
1:H:450:TYR:OH	2:H:801:HYP:HB3	2.20	0.40
1:H:551:GLN:HG2	1:H:643:LEU:CD1	2.51	0.40
1:H:706:ARG:NH1	1:H:784:ARG:O	2.54	0.40
1:A:604:LYS:HG2	1:A:678:GLY:HA2	2.03	0.40
1:A:98:HIS:HA	1:A:105:PHE:O	2.21	0.40
1:B:290:ASN:HB3	1:B:291:PRO:HD3	2.03	0.40
1:B:348:ILE:HG12	3:B:983:HOH:O	2.22	0.40
1:D:263:TYR:CD2	1:D:263:TYR:C	2.94	0.40
1:D:312:GLU:HG2	1:D:366:VAL:HG13	2.03	0.40
1:F:83:TYR:CG	1:F:275:ASN:HB2	2.56	0.40
1:F:163:CYS:HB2	1:F:280:PHE:CE2	2.56	0.40
1:F:443:GLU:HA	1:F:545:TYR:O	2.21	0.40
1:F:627:VAL:HB	1:F:640:VAL:HG23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:GLU:HG3	1:A:643:LEU:CD2	2.51	0.40
1:B:463:ASN:CG	1:B:476:GLU:HG3	2.42	0.40
1:D:315:TRP:CD1	1:D:375:PRO:HD2	2.56	0.40
1:D:308:GLN:HG3	1:D:366:VAL:HG22	2.03	0.40
1:D:413:VAL:O	1:D:417:MET:HG3	2.20	0.40
1:E:676:LYS:HD3	1:E:676:LYS:HA	1.84	0.40
1:F:598:VAL:O	1:F:604:LYS:NZ	2.51	0.40
1:G:200:ASP:OD2	1:G:540:ARG:NE	2.48	0.40
1:H:132:ILE:O	1:H:136:MET:HG2	2.21	0.40
1:H:151:GLU:CD	1:H:511:ILE:HD13	2.42	0.40
1:H:438:GLY:HA3	1:H:445:TYR:CZ	2.57	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:236:LYS:NZ	1:H:57:GLU:OE2[1_655]	2.19	0.01

## 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	788/809 (97%)	770 (98%)	17 (2%)	1 (0%)	51 64
1	B	788/809 (97%)	771 (98%)	15 (2%)	2 (0%)	41 49
1	C	788/809 (97%)	763 (97%)	22 (3%)	3 (0%)	34 41
1	D	788/809 (97%)	772 (98%)	15 (2%)	1 (0%)	51 64
1	E	788/809 (97%)	770 (98%)	17 (2%)	1 (0%)	51 64
1	F	788/809 (97%)	771 (98%)	15 (2%)	2 (0%)	41 49
1	G	788/809 (97%)	771 (98%)	16 (2%)	1 (0%)	51 64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	788/809 (97%)	766 (97%)	20 (2%)	2 (0%)	41	49
All	All	6304/6472 (97%)	6154 (98%)	137 (2%)	13 (0%)	47	57

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	644	PRO
1	E	644	PRO
1	F	644	PRO
1	G	644	PRO
1	H	644	PRO
1	A	644	PRO
1	C	231	ASP
1	F	232	GLU
1	B	232	GLU
1	B	644	PRO
1	C	232	GLU
1	D	644	PRO
1	H	227	GLU

### 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	678/694 (98%)	669 (99%)	9 (1%)	69	79
1	B	678/694 (98%)	666 (98%)	12 (2%)	59	71
1	C	678/694 (98%)	669 (99%)	9 (1%)	69	79
1	D	678/694 (98%)	672 (99%)	6 (1%)	78	86
1	E	678/694 (98%)	665 (98%)	13 (2%)	57	69
1	F	678/694 (98%)	664 (98%)	14 (2%)	53	66
1	G	678/694 (98%)	667 (98%)	11 (2%)	62	74
1	H	678/694 (98%)	668 (98%)	10 (2%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	5424/5552 (98%)	5340 (98%)	84 (2%)	62	76

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	PHE
1	A	213	ILE
1	A	218	TYR
1	A	344	ASN
1	A	445	TYR
1	A	491	GLU
1	A	539	GLN
1	A	640	VAL
1	A	670	GLU
1	B	125	LYS
1	B	152	PHE
1	B	297	VAL
1	B	315	TRP
1	B	344	ASN
1	B	539	GLN
1	B	551	GLN
1	B	643	LEU
1	B	644	PRO
1	B	670	GLU
1	B	686	VAL
1	B	697	LYS
1	C	104	ASN
1	C	113	LYS
1	C	152	PHE
1	C	239	LEU
1	C	344	ASN
1	C	445	TYR
1	C	640	VAL
1	C	670	GLU
1	C	716	LYS
1	D	20	GLU
1	D	344	ASN
1	D	445	TYR
1	D	643	LEU
1	D	644	PRO
1	D	686	VAL
1	E	137	THR

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Mol	Chain	Res	Type
1	E	152	PHE
1	E	294	GLU
1	E	344	ASN
1	E	445	TYR
1	E	539	GLN
1	E	550	ILE
1	E	551	GLN
1	E	589	GLU
1	E	592	GLU
1	E	640	VAL
1	E	670	GLU
1	E	686	VAL
1	F	51	SER
1	F	95	GLU
1	F	182	ARG
1	F	230	THR
1	F	344	ASN
1	F	353	GLN
1	F	445	TYR
1	F	484	GLN
1	F	551	GLN
1	F	643	LEU
1	F	658	SER
1	F	670	GLU
1	F	743	LYS
1	F	748	GLU
1	G	61	LEU
1	G	116	LYS
1	G	152	PHE
1	G	344	ASN
1	G	536	LYS
1	G	539	GLN
1	G	643	LEU
1	G	666	LYS
1	G	670	GLU
1	G	735	HIS
1	G	748	GLU
1	H	20	GLU
1	H	110	GLU
1	H	112	ARG
1	H	113	LYS
1	H	152	PHE

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Mol	Chain	Res	Type
1	H	344	ASN
1	H	445	TYR
1	H	539	GLN
1	H	571	ASP
1	H	640	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	539	GLN
1	A	704	ASN
1	B	546	ASN
1	B	704	ASN
1	C	353	GLN
1	C	539	GLN
1	C	551	GLN
1	C	704	ASN
1	D	539	GLN
1	D	551	GLN
1	D	704	ASN
1	E	513	ASN
1	E	551	GLN
1	E	704	ASN
1	F	353	GLN
1	F	551	GLN
1	F	704	ASN
1	G	551	GLN
1	G	704	ASN
1	H	704	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

8 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	HYP	B	801	-	6,9,9	0.59	0	5,12,12	3.06	3 (60%)
2	HYP	A	801	-	6,9,9	1.79	2 (33%)	5,12,12	2.47	1 (20%)
2	HYP	G	801	-	6,9,9	2.10	3 (50%)	5,12,12	2.10	2 (40%)
2	HYP	F	801	-	6,9,9	1.23	0	5,12,12	1.79	2 (40%)
2	HYP	E	801	-	6,9,9	1.11	0	5,12,12	1.80	1 (20%)
2	HYP	D	801	-	6,9,9	2.17	4 (66%)	5,12,12	2.30	3 (60%)
2	HYP	H	801	-	6,9,9	1.79	2 (33%)	5,12,12	1.80	2 (40%)
2	HYP	C	801	-	6,9,9	1.67	1 (16%)	5,12,12	2.59	4 (80%)

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	HYP	B	801	-	-	0/0/13/13	0/1/1/1
2	HYP	A	801	-	-	0/0/13/13	0/1/1/1
2	HYP	G	801	-	-	0/0/13/13	0/1/1/1
2	HYP	F	801	-	-	0/0/13/13	0/1/1/1
2	HYP	E	801	-	-	0/0/13/13	0/1/1/1
2	HYP	D	801	-	-	0/0/13/13	0/1/1/1
2	HYP	H	801	-	-	0/0/13/13	0/1/1/1
2	HYP	C	801	-	-	0/0/13/13	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	801	HYP	CB-CG	-2.66	1.47	1.52
2	G	801	HYP	CD-CG	-2.59	1.47	1.53
2	A	801	HYP	CD-CG	-2.59	1.47	1.53
2	G	801	HYP	CA-N	-2.57	1.38	1.50
2	D	801	HYP	CD-CG	-2.56	1.47	1.53
2	G	801	HYP	CB-CA	-2.44	1.49	1.54
2	H	801	HYP	CA-N	-2.40	1.39	1.50
2	D	801	HYP	CA-N	-2.32	1.40	1.50
2	A	801	HYP	CA-N	-2.30	1.40	1.50
2	D	801	HYP	CB-CA	-2.26	1.49	1.54
2	H	801	HYP	CD-CG	-2.11	1.48	1.53
2	C	801	HYP	CA-N	-2.06	1.41	1.50

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HYP	OD1-CG-CD	-4.86	99.72	110.35
2	B	801	HYP	CG-CB-CA	-4.44	98.36	103.96
2	C	801	HYP	OD1-CG-CD	-4.41	100.71	110.35
2	B	801	HYP	OD1-CG-CD	-4.41	100.71	110.35
2	G	801	HYP	OD1-CG-CD	-3.34	103.05	110.35
2	E	801	HYP	CG-CB-CA	3.27	108.09	103.96
2	D	801	HYP	OD1-CG-CB	-3.15	102.25	110.03
2	H	801	HYP	OD1-CG-CD	-2.92	103.95	110.35
2	G	801	HYP	CG-CB-CA	2.92	107.64	103.96
2	D	801	HYP	OD1-CG-CD	-2.81	104.21	110.35
2	B	801	HYP	CB-CG-CD	-2.74	99.91	103.27
2	D	801	HYP	CB-CA-N	-2.52	101.31	106.22
2	F	801	HYP	OD1-CG-CD	-2.46	104.98	110.35
2	H	801	HYP	OD1-CG-CB	-2.35	104.23	110.03
2	F	801	HYP	CG-CB-CA	2.20	106.73	103.96
2	C	801	HYP	CG-CB-CA	-2.17	101.22	103.96
2	C	801	HYP	CB-CA-N	-2.16	102.02	106.22
2	C	801	HYP	OD1-CG-CB	-2.06	104.93	110.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 32 short contacts:

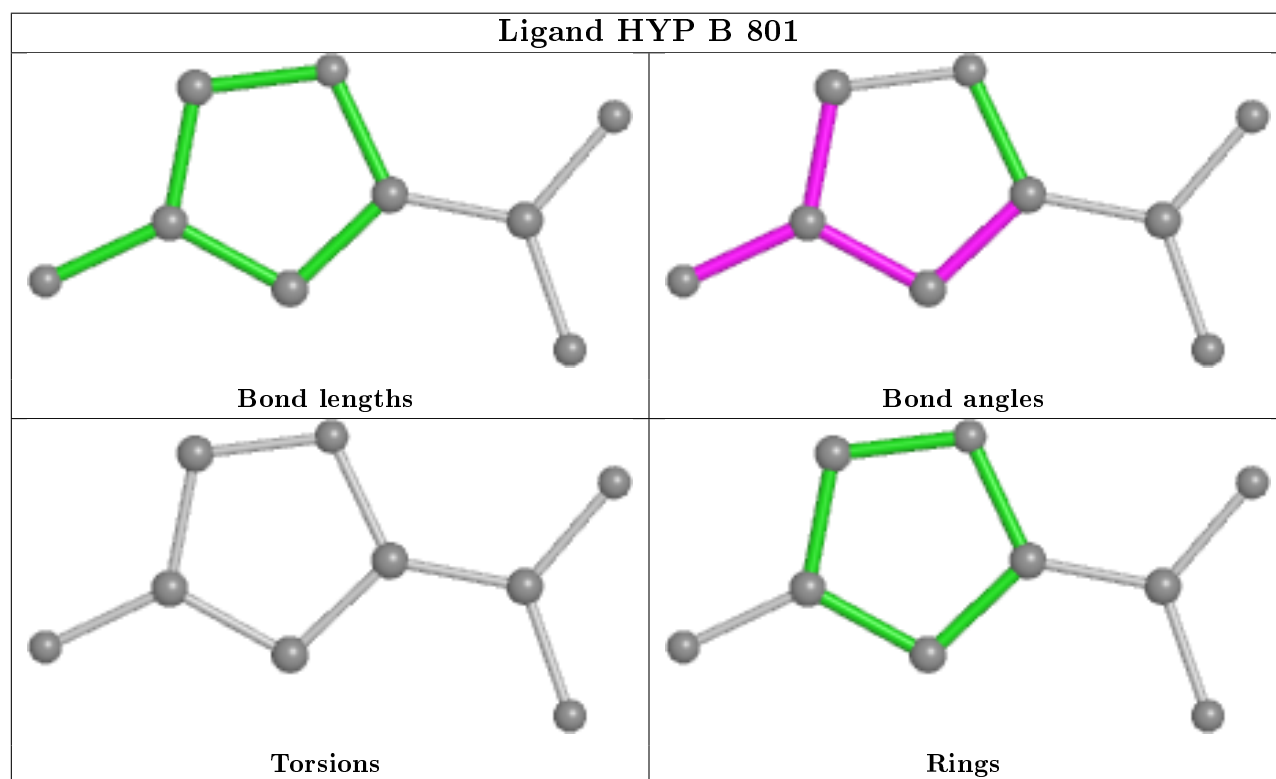
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	HYP	8	0

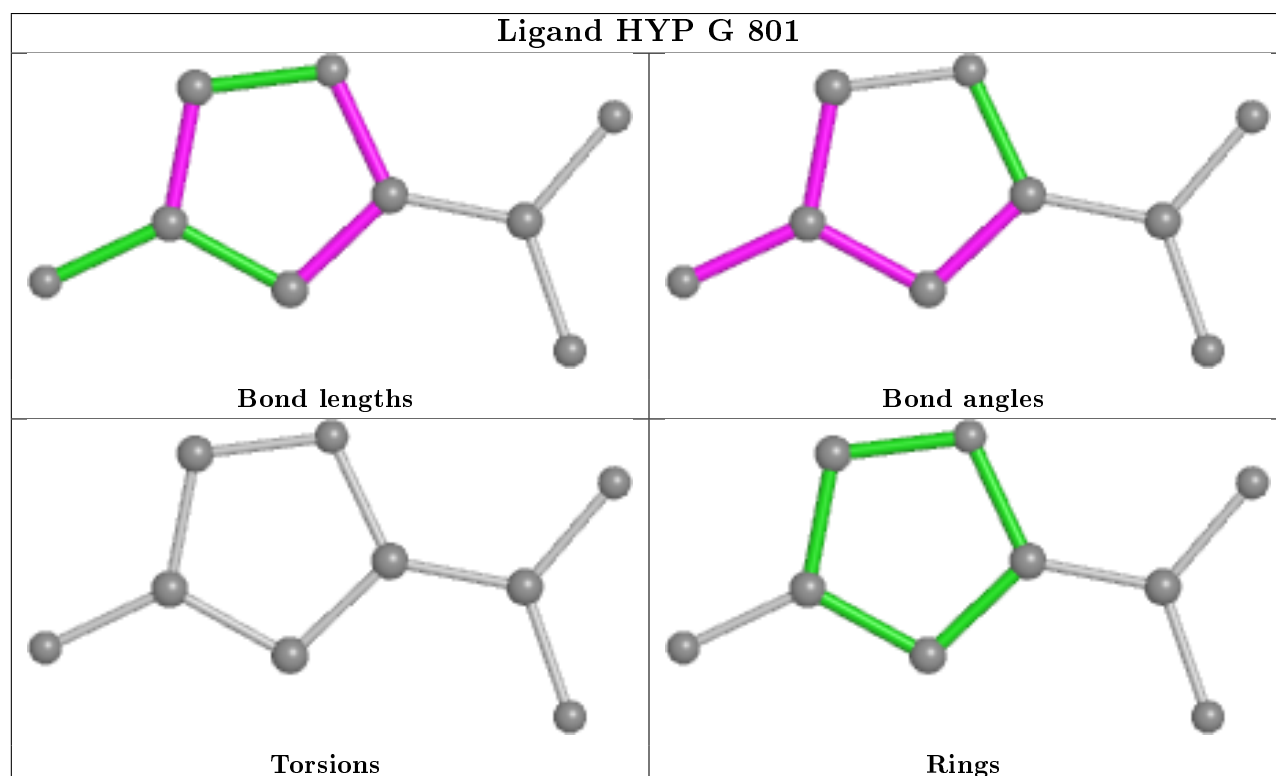
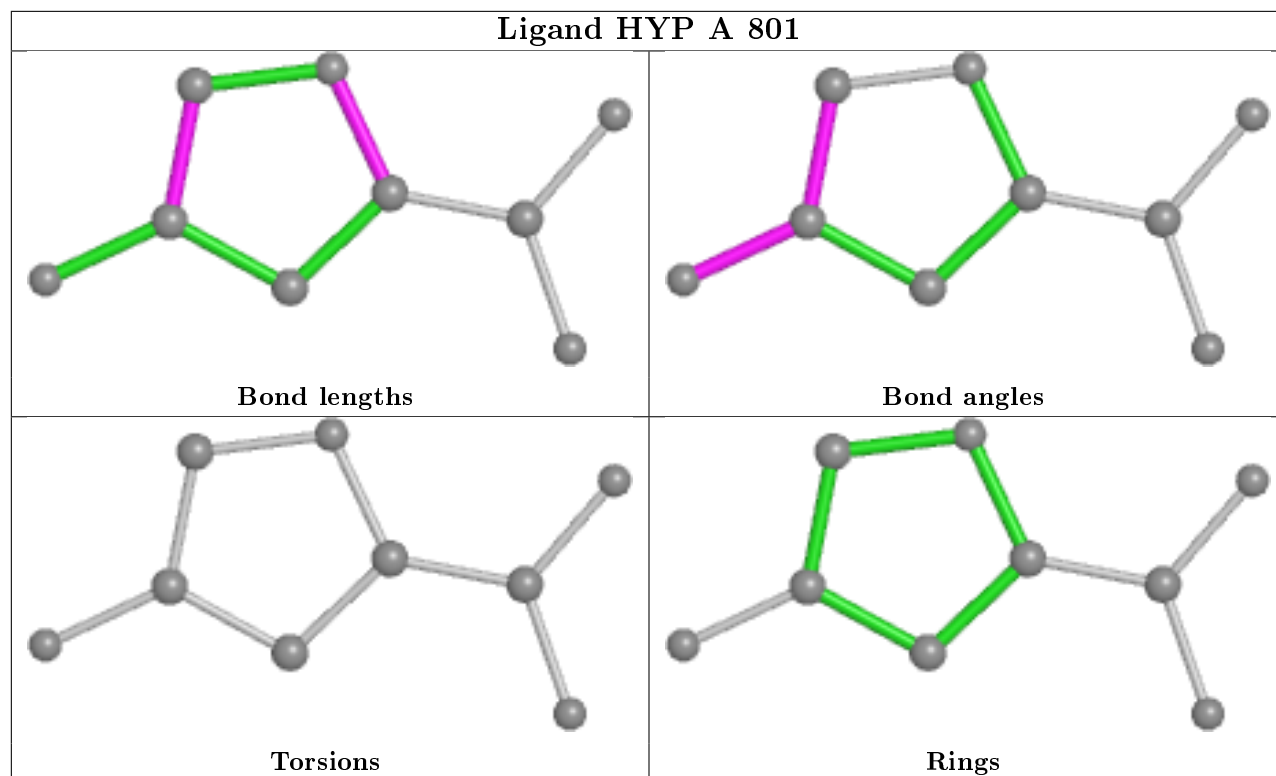
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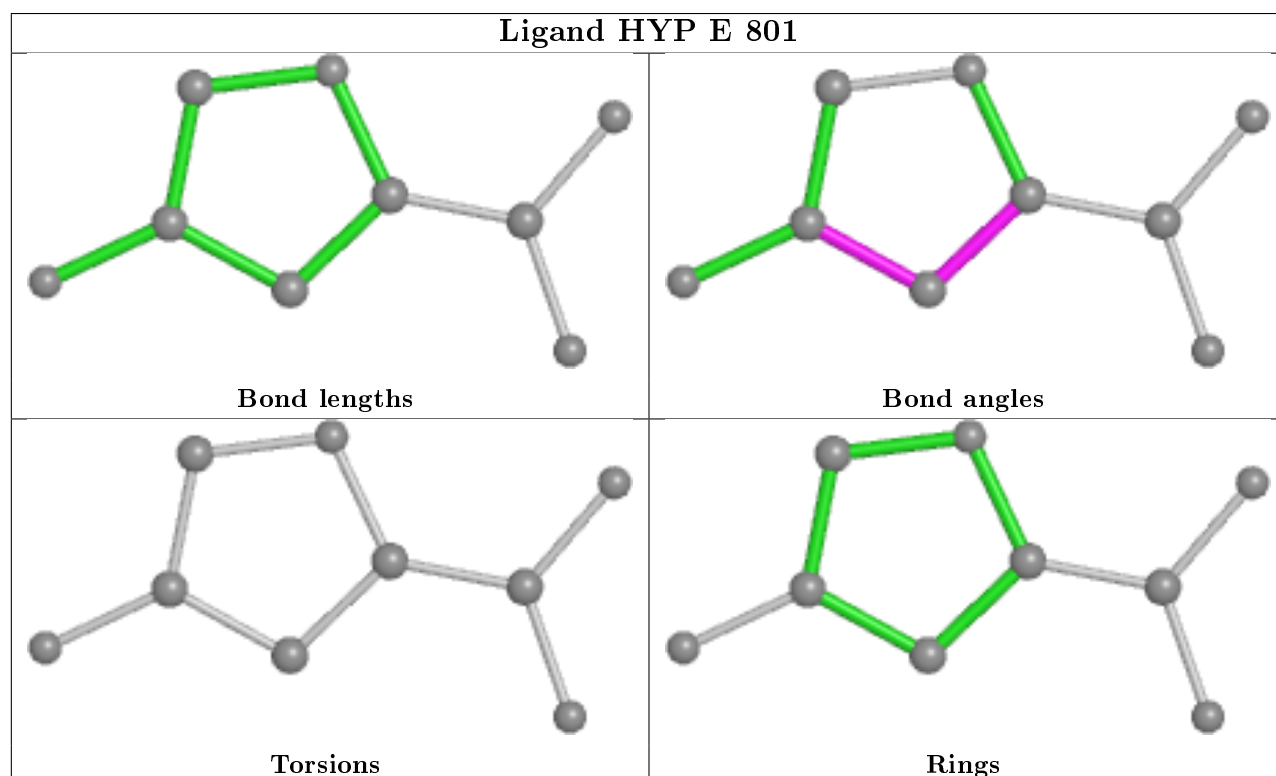
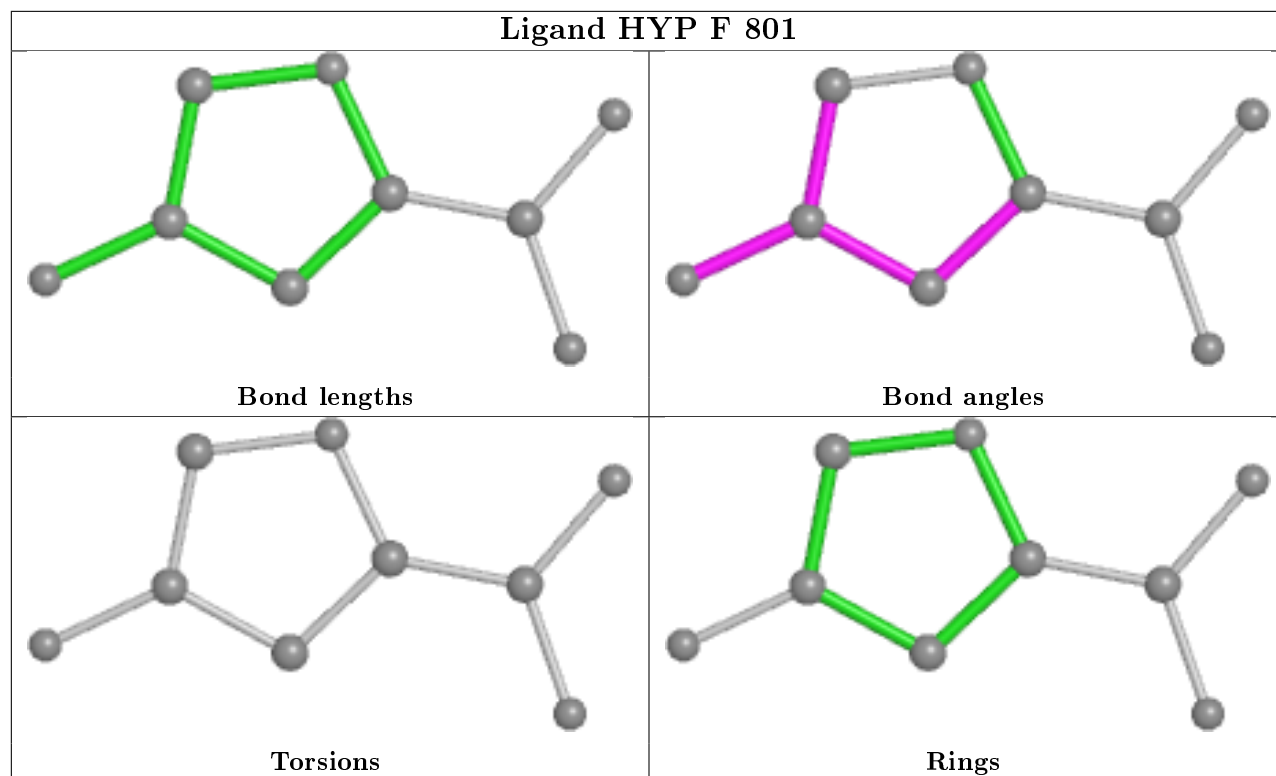
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HYP	2	0
2	G	801	HYP	5	0
2	F	801	HYP	3	0
2	E	801	HYP	3	0
2	D	801	HYP	4	0
2	H	801	HYP	5	0
2	C	801	HYP	2	0

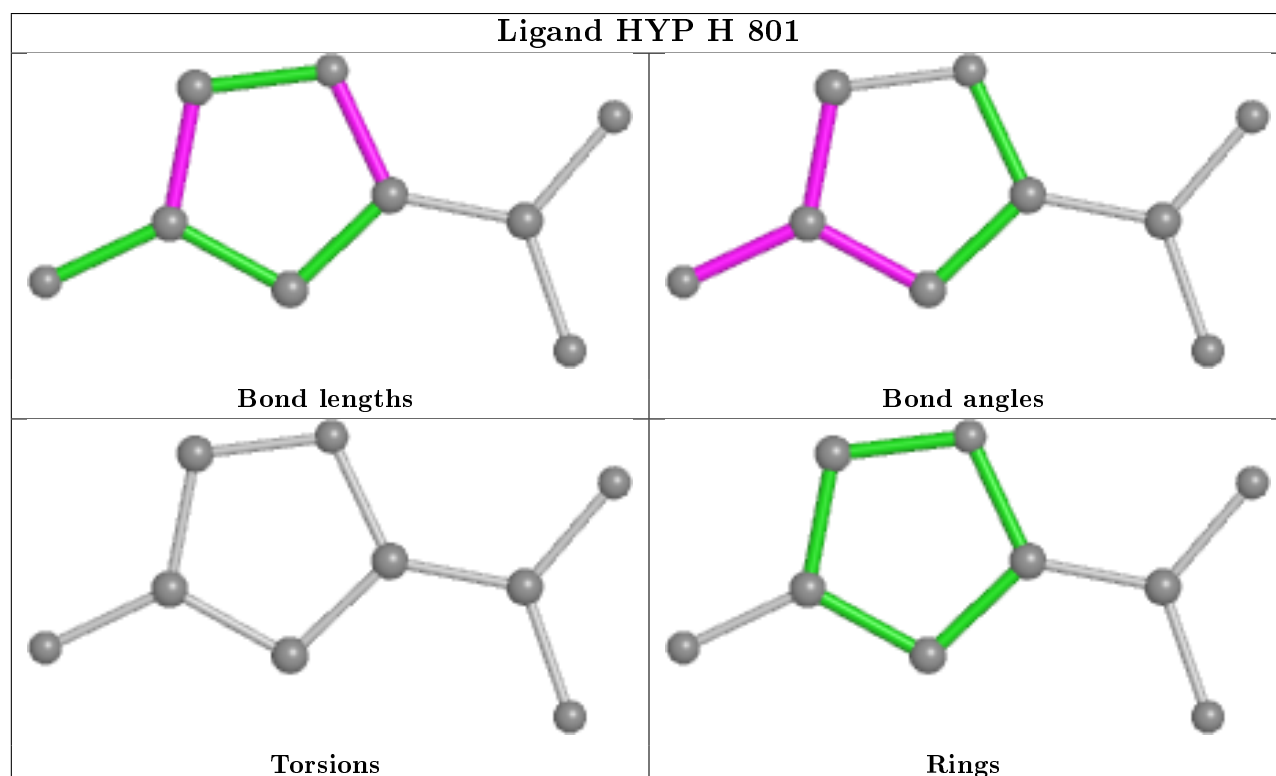
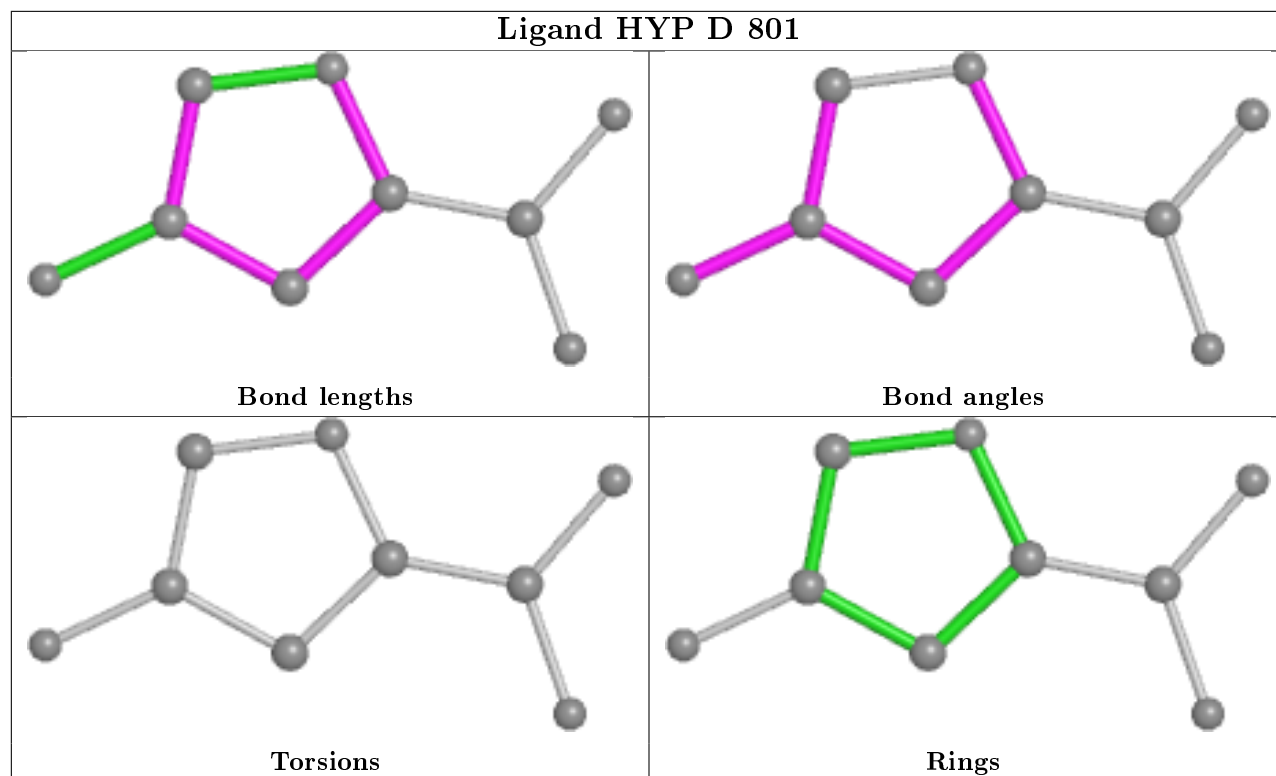
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

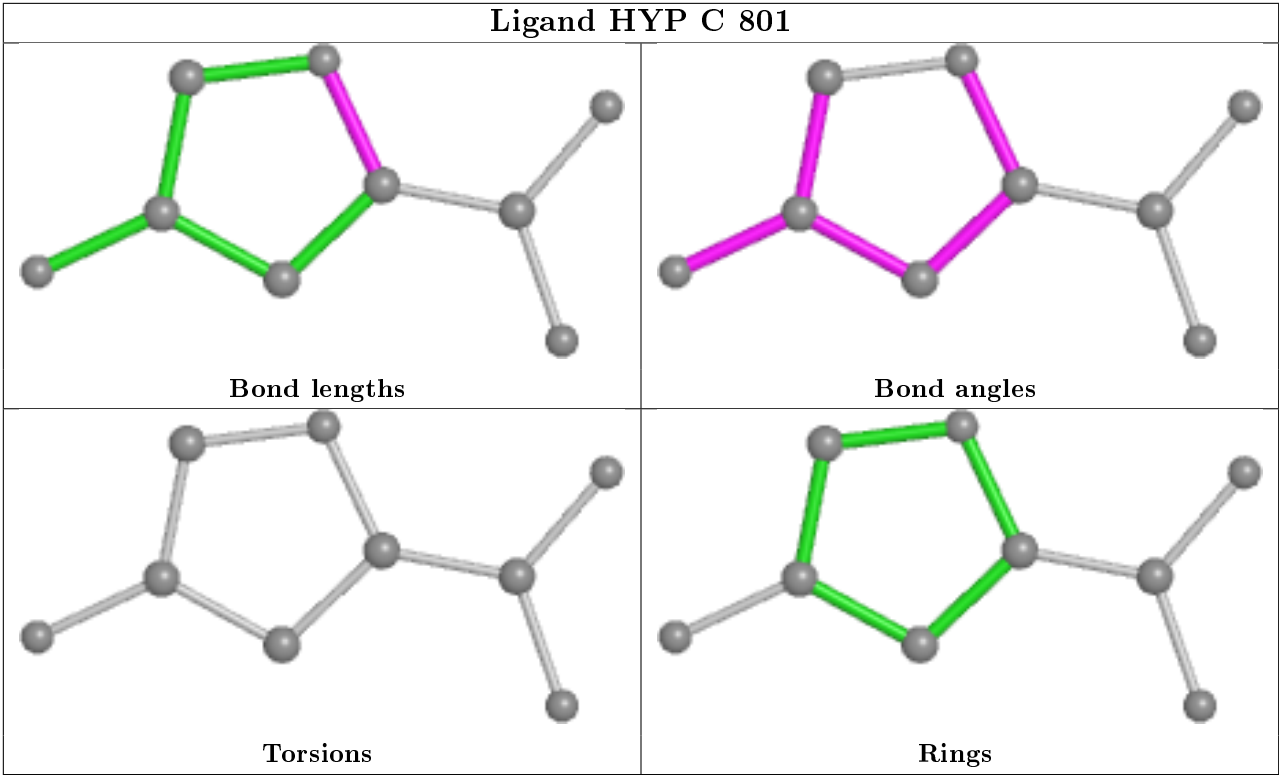












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	4
1	H	2
1	C	2
1	A	2
1	E	1
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	31[A]:MET	C	32:THR	N	1.19
1	B	30:LEU	C	31[A]:MET	N	1.18
1	H	604:LYS	C	605:TYR	N	1.18
1	B	61:LEU	C	62:SER	N	1.16

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	642:MET	C	643:LEU	N	1.16
1	A	642:MET	C	643:LEU	N	1.13
1	E	2:ALA	C	3:ARG	N	1.13
1	F	604:LYS	C	605:TYR	N	1.10
1	H	2:ALA	C	3:ARG	N	1.07
1	A	60:THR	C	61:LEU	N	1.03
1	B	60:THR	C	61:LEU	N	1.00
1	C	662:ARG	C	663:LEU	N	0.88

## 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	789/809 (97%)	0.01	7 (0%) 84 85	22, 34, 47, 67	0
1	B	789/809 (97%)	-0.07	8 (1%) 82 83	26, 34, 45, 59	0
1	C	789/809 (97%)	0.18	22 (2%) 53 49	26, 40, 57, 69	0
1	D	789/809 (97%)	-0.01	8 (1%) 82 83	22, 33, 47, 67	0
1	E	789/809 (97%)	-0.10	3 (0%) 92 93	26, 35, 46, 57	0
1	F	789/809 (97%)	0.01	12 (1%) 73 71	23, 31, 46, 64	0
1	G	789/809 (97%)	-0.20	2 (0%) 94 94	24, 31, 43, 57	0
1	H	789/809 (97%)	0.14	27 (3%) 45 41	24, 39, 55, 70	0
All	All	6312/6472 (97%)	-0.00	89 (1%) 75 74	22, 34, 50, 70	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	1	MET	7.3
1	C	233	ALA	6.1
1	E	1	MET	6.0
1	C	1	MET	5.8
1	A	1	MET	5.7
1	C	230	THR	4.4
1	B	1	MET	4.4
1	H	239	LEU	3.8
1	C	655	MET	3.8
1	B	2	ALA	3.7
1	F	432	SER	3.5
1	A	2	ALA	3.5
1	H	230	THR	3.4
1	C	756	TYR	3.4
1	D	754	GLN	3.2
1	G	789	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	230	THR	3.1
1	H	757	LYS	3.1
1	H	31[A]	MET	2.9
1	H	590	GLY	2.8
1	H	432	SER	2.7
1	D	601	LYS	2.7
1	C	594	ILE	2.6
1	A	485	SER	2.5
1	H	431	THR	2.5
1	A	483	PHE	2.5
1	C	232	GLU	2.5
1	C	2	ALA	2.5
1	D	224	GLN	2.5
1	C	748	GLU	2.5
1	H	227	GLU	2.5
1	H	232	GLU	2.5
1	H	299	ASN	2.5
1	F	232	GLU	2.4
1	H	233	ALA	2.4
1	G	227	GLU	2.4
1	B	7	GLU	2.4
1	C	227	GLU	2.4
1	H	482	ASN	2.4
1	H	743	LYS	2.3
1	C	483	PHE	2.3
1	H	177	LYS	2.3
1	F	231	ASP	2.3
1	C	432	SER	2.3
1	E	710	SER	2.3
1	B	432	SER	2.3
1	H	758	ASP	2.3
1	F	306	ARG	2.2
1	C	278	ASP	2.2
1	H	341	ALA	2.2
1	C	601	LYS	2.2
1	H	231	ASP	2.2
1	B	92	GLU	2.2
1	C	234	LYS	2.2
1	F	413	VAL	2.2
1	H	301	ILE	2.2
1	C	434	CYS	2.2
1	H	342	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	279	ALA	2.2
1	A	479	ASP	2.2
1	B	484	GLN	2.1
1	C	231	ASP	2.1
1	F	230	THR	2.1
1	F	434	CYS	2.1
1	D	1	MET	2.1
1	B	301	ILE	2.1
1	C	306	ARG	2.1
1	A	594	ILE	2.1
1	F	343	ILE	2.1
1	H	378	ASN	2.1
1	H	433	GLY	2.1
1	F	754	GLN	2.1
1	C	277	TRP	2.1
1	F	575	PHE	2.1
1	F	579	THR	2.1
1	C	757	LYS	2.1
1	A	570	PHE	2.1
1	C	224	GLN	2.1
1	H	224	GLN	2.1
1	H	281	THR	2.1
1	D	594	ILE	2.1
1	D	789	PHE	2.1
1	B	744	ASN	2.1
1	D	227	GLU	2.1
1	E	751	LYS	2.1
1	H	593	ALA	2.0
1	H	434	CYS	2.0
1	C	484	GLN	2.0
1	H	765	GLY	2.0

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

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

## 6.3 Carbohydrates ⓘ

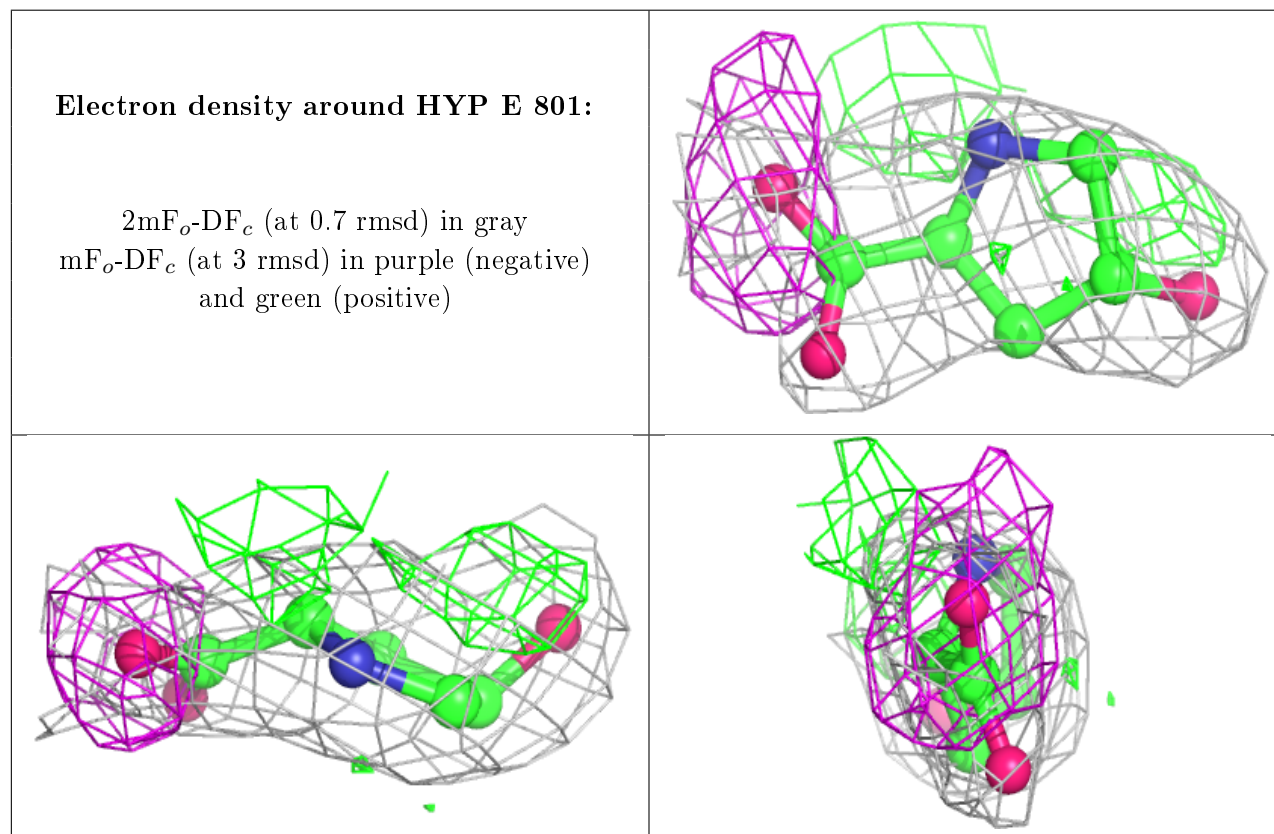
There are no monosaccharides in this entry.

## 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.

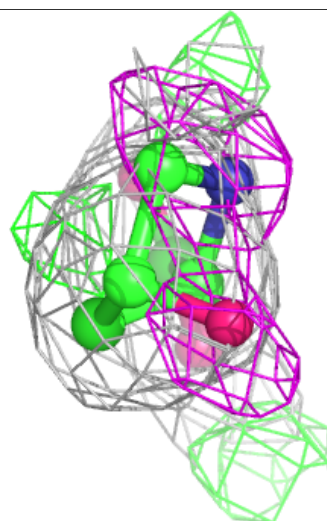
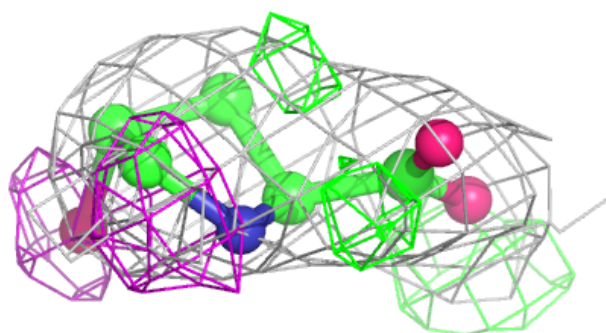
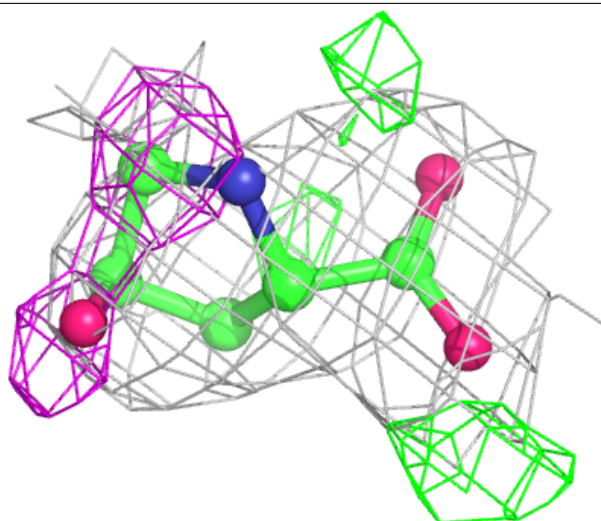
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	HYP	E	801	9/9	0.75	0.37	30,30,30,30	9
2	HYP	B	801	9/9	0.85	0.26	30,30,30,30	0
2	HYP	F	801	9/9	0.86	0.33	30,30,30,30	9
2	HYP	H	801	9/9	0.89	0.28	30,30,30,30	9
2	HYP	A	801	9/9	0.91	0.17	20,20,20,20	0
2	HYP	D	801	9/9	0.93	0.27	30,30,30,30	9
2	HYP	G	801	9/9	0.93	0.19	30,30,30,30	0
2	HYP	C	801	9/9	0.93	0.17	30,30,30,30	0

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



**Electron density around HYP B 801:**

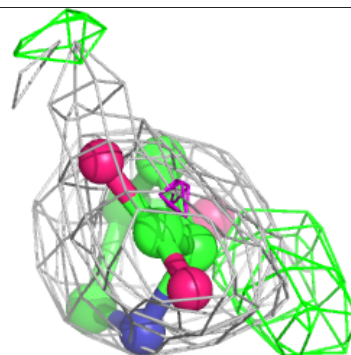
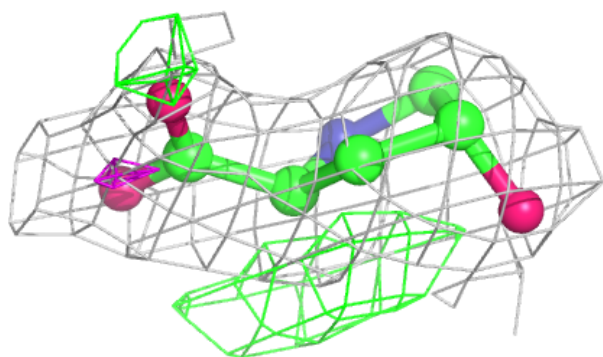
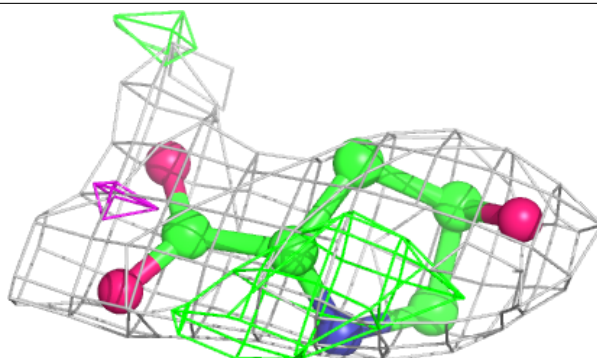
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





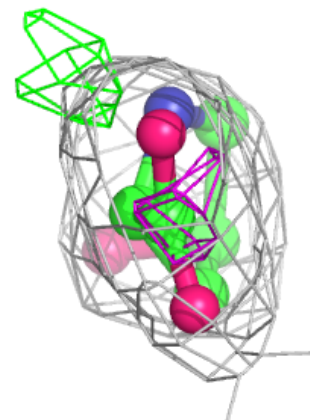
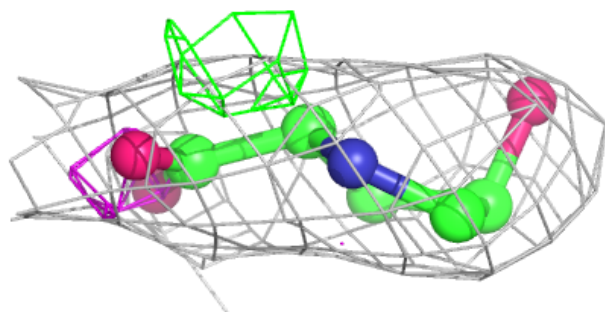
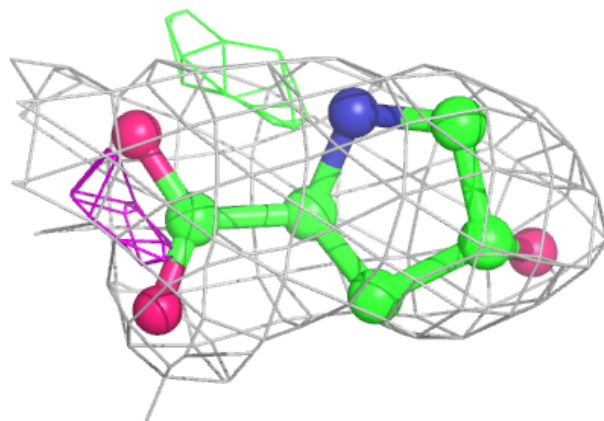
**Electron density around HYP F 801:**

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



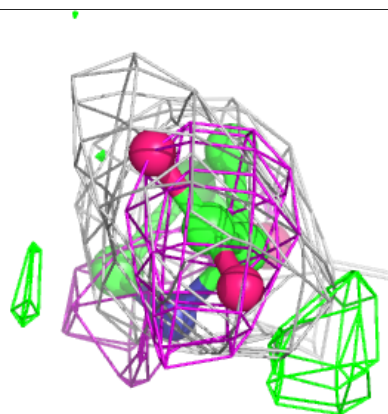
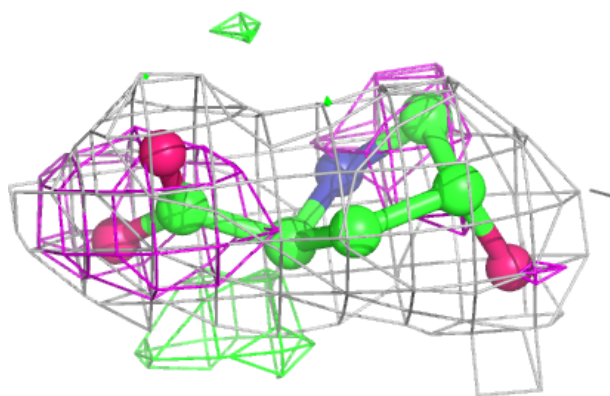
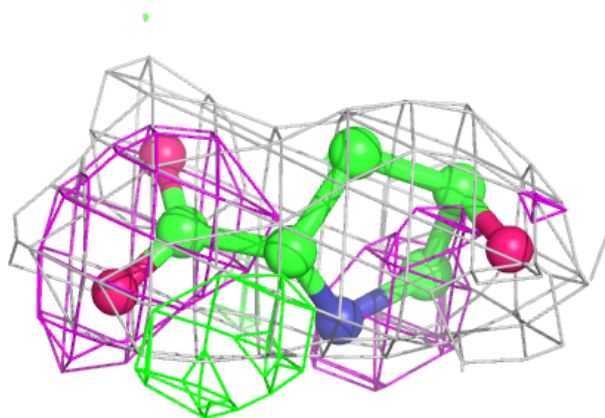
**Electron density around HYP H 801:**

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



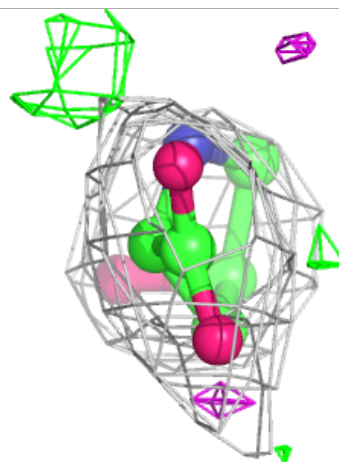
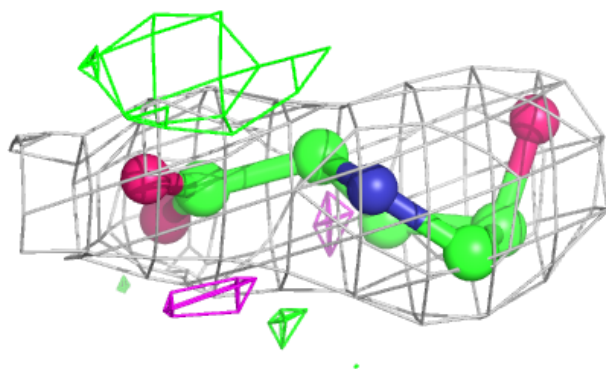
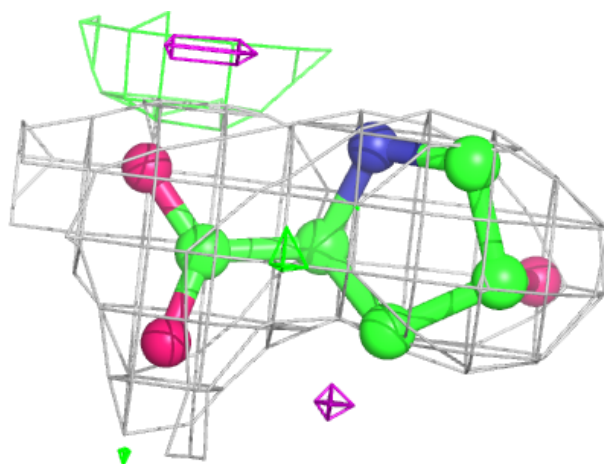
**Electron density around HYP A 801:**

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



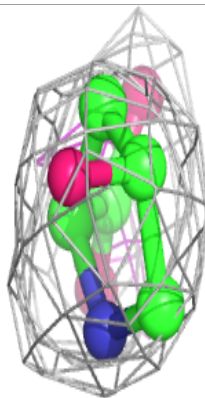
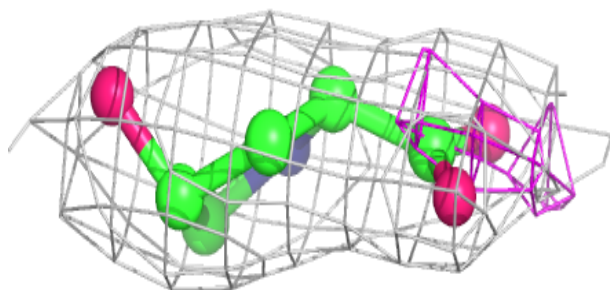
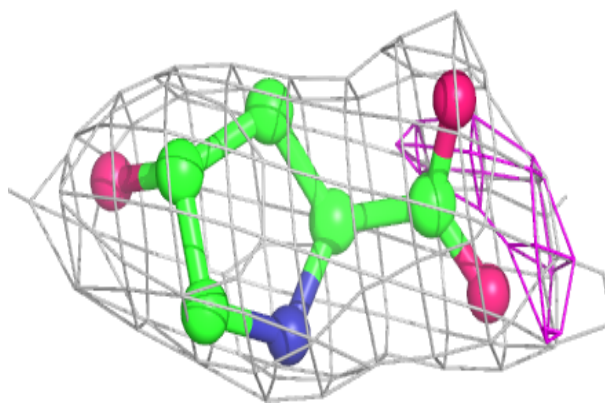
**Electron density around HYP D 801:**

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

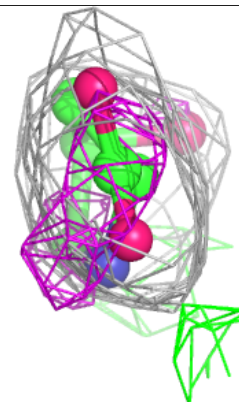
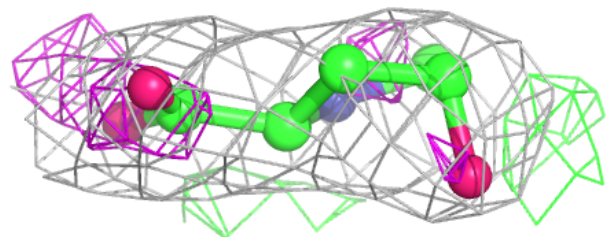
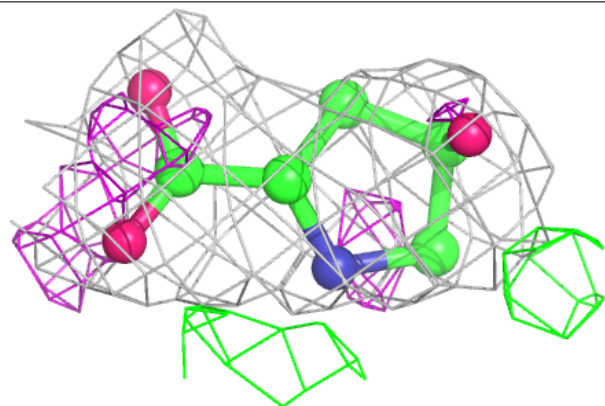


**Electron density around HYP G 801:**

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

**Electron density around HYP C 801:**

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



## 6.5 Other polymers

There are no such residues in this entry.