



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:45 am BST

PDB ID : 4I58  
Title : Cyclohexylamine Oxidase from Brevibacterium oxydans IH-35A  
Authors : Mirza, I.A.; Berghuis, A.M.  
Deposited on : 2012-11-28  
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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

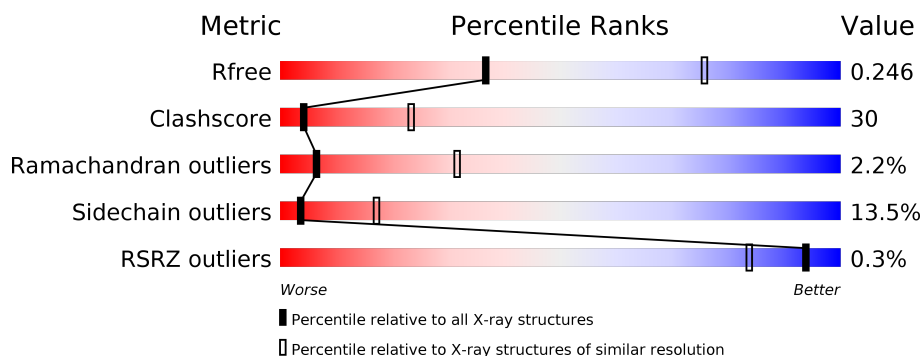
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . 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	471	
1	B	471	
1	C	471	
1	D	471	

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 14032 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 Cyclohexylamine Oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total	C	N	O	S	0	0	0
			3455	2198	589	660	8			
1	B	451	Total	C	N	O	S	0	0	0
			3455	2198	589	660	8			
1	C	451	Total	C	N	O	S	0	0	0
			3455	2198	589	660	8			
1	D	451	Total	C	N	O	S	0	0	0
			3455	2198	589	660	8			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

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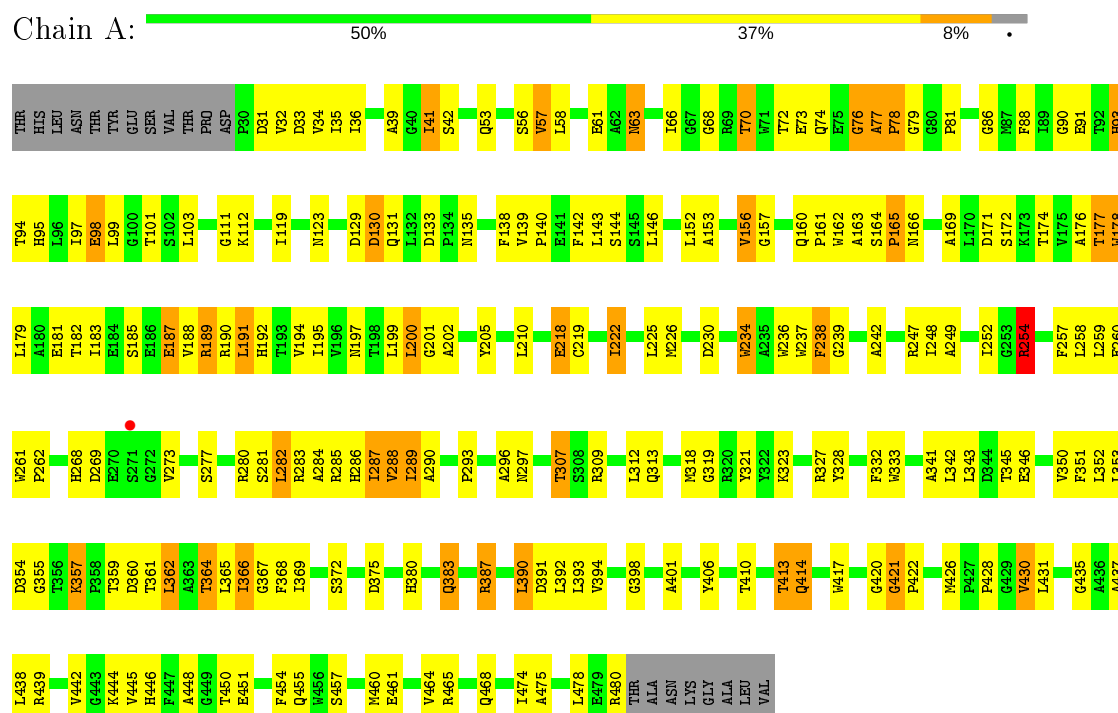
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

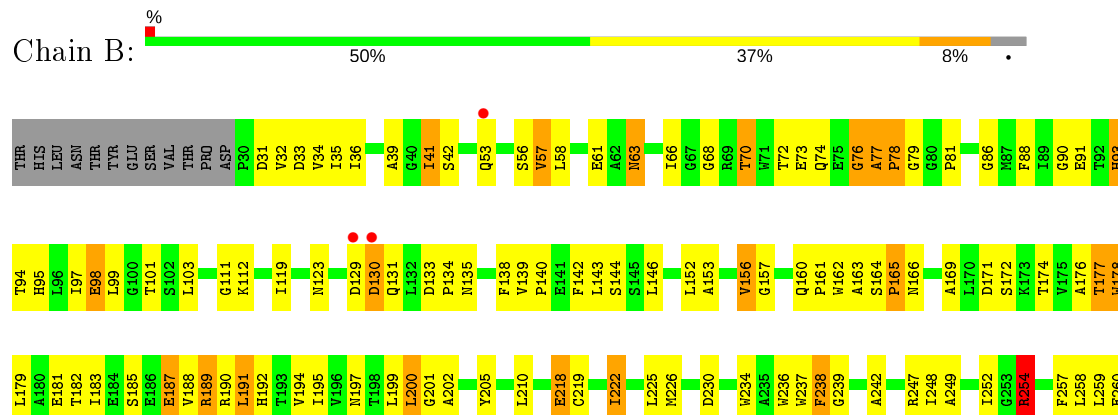
### 3 Residue-property plots

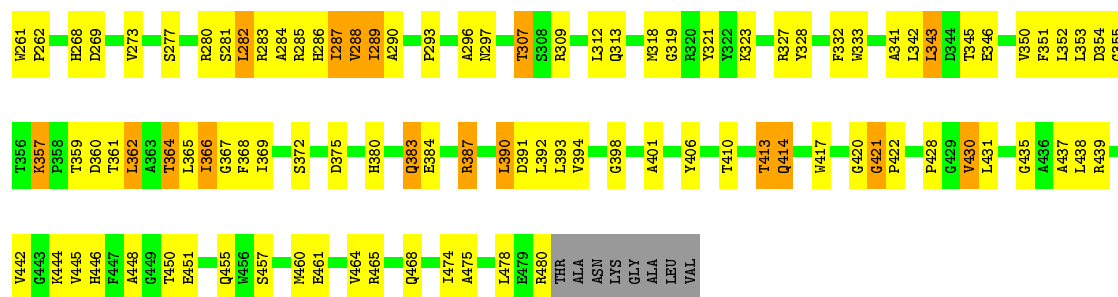
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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



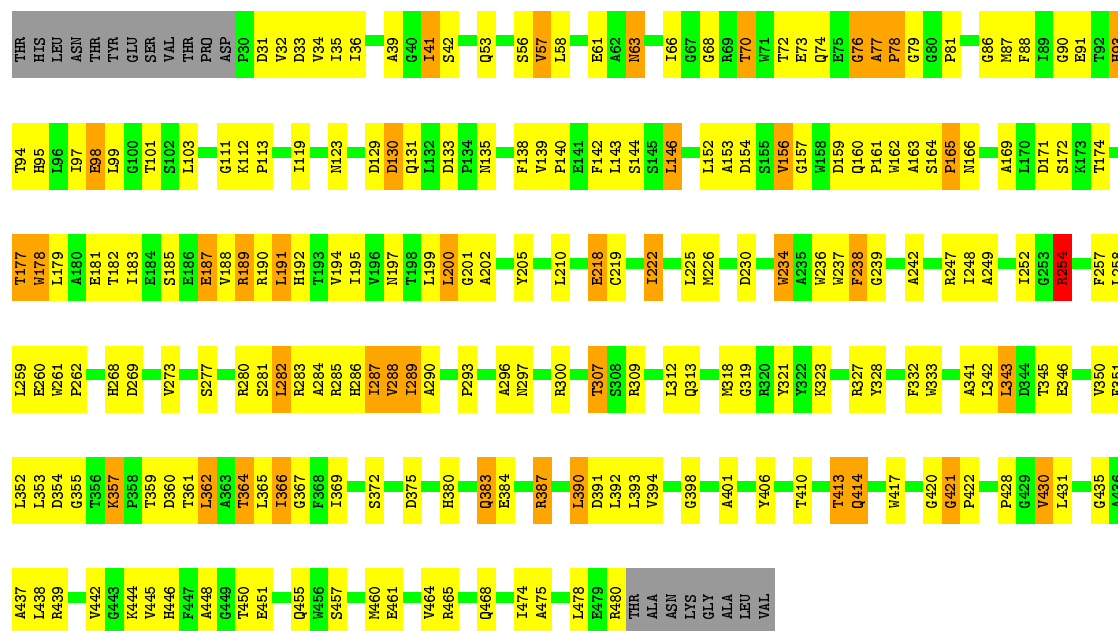
#### • Molecule 1: Cyclohexylamine Oxidase





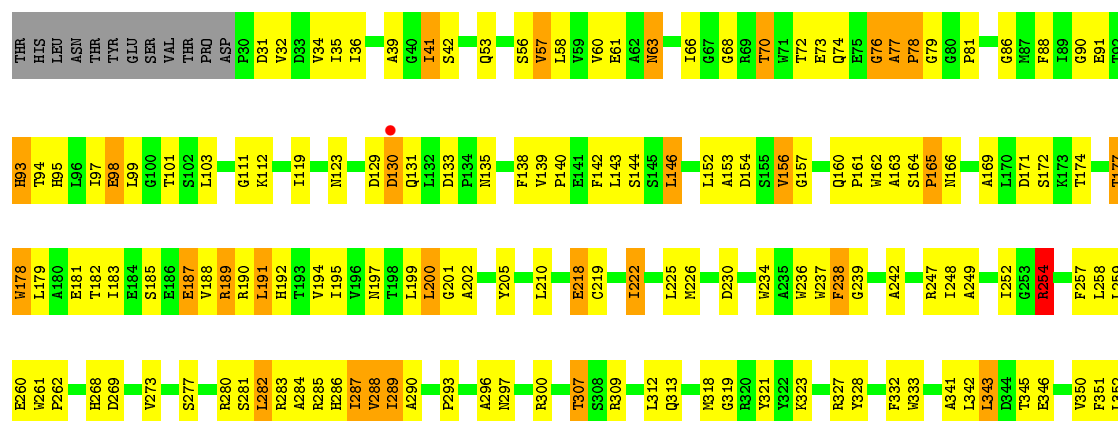
• Molecule 1: Cyclohexylamine Oxidase

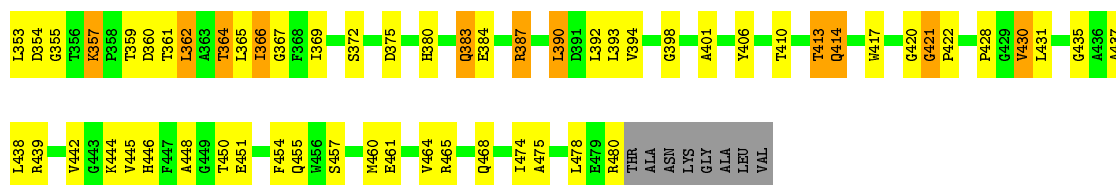
Chain C: 50% 37% 8% •



• Molecule 1: Cyclohexylamine Oxidase

Chain D: 51% 37% 8% •





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	217.72Å 234.59Å 90.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.80 – 3.00 49.37 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.9 (45.80-3.00) 92.0 (49.37-3.00)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.54 (at 3.01Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.237 , 0.251 0.232 , 0.246	Depositor DCC
$R_{free}$ test set	4483 reflections (10.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.9	Xtriage
Anisotropy	0.461	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 33.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	14032	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.41	0/3548	0.70	0/4841
1	B	0.41	0/3548	0.70	0/4841
1	C	0.41	0/3548	0.70	0/4841
1	D	0.41	0/3548	0.70	0/4841
All	All	0.41	0/14192	0.70	0/19364

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	3455	0	3317	205	0
1	B	3455	0	3317	203	0
1	C	3455	0	3317	209	1
1	D	3455	0	3317	204	1
2	A	53	0	31	4	0
2	B	53	0	31	4	0
2	C	53	0	31	4	0
2	D	53	0	31	3	0
All	All	14032	0	13392	810	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 30.

All (810) 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:222:ILE:H	1:D:222:ILE:HD13	1.24	1.01
1:B:387:ARG:HH11	1:B:387:ARG:HB2	1.29	0.98
1:C:222:ILE:HD13	1:C:222:ILE:H	1.24	0.98
1:A:387:ARG:HB2	1:A:387:ARG:HH11	1.28	0.98
1:B:222:ILE:HD13	1:B:222:ILE:H	1.24	0.97
1:A:222:ILE:H	1:A:222:ILE:HD13	1.24	0.97
1:C:387:ARG:HH11	1:C:387:ARG:HB2	1.28	0.96
1:D:387:ARG:HH11	1:D:387:ARG:HB2	1.29	0.94
1:C:321:TYR:H	1:C:413:THR:HG22	1.35	0.92
1:D:293:PRO:HD3	1:D:451:GLU:HG3	1.51	0.92
1:D:321:TYR:H	1:D:413:THR:HG22	1.35	0.91
1:A:321:TYR:H	1:A:413:THR:HG22	1.35	0.91
1:C:293:PRO:HD3	1:C:451:GLU:HG3	1.51	0.90
1:A:293:PRO:HD3	1:A:451:GLU:HG3	1.51	0.90
1:B:321:TYR:H	1:B:413:THR:HG22	1.35	0.89
1:B:248:ILE:O	1:B:252:ILE:HG22	1.73	0.89
1:D:78:PRO:HB2	1:D:327:ARG:HD2	1.54	0.89
1:B:293:PRO:HD3	1:B:451:GLU:HG3	1.51	0.88
1:D:248:ILE:O	1:D:252:ILE:HG22	1.73	0.88
1:A:248:ILE:O	1:A:252:ILE:HG22	1.73	0.88
1:B:78:PRO:HB2	1:B:327:ARG:HD2	1.54	0.88
1:A:78:PRO:HB2	1:A:327:ARG:HD2	1.54	0.87
1:C:248:ILE:O	1:C:252:ILE:HG22	1.73	0.87
1:C:78:PRO:HB2	1:C:327:ARG:HD2	1.54	0.86
1:C:222:ILE:CD1	1:C:222:ILE:H	1.89	0.85
1:A:222:ILE:N	1:A:222:ILE:HD13	1.92	0.84
1:A:222:ILE:H	1:A:222:ILE:CD1	1.89	0.84
1:B:222:ILE:H	1:B:222:ILE:CD1	1.89	0.84
1:D:222:ILE:HD13	1:D:222:ILE:N	1.92	0.84
1:D:222:ILE:H	1:D:222:ILE:CD1	1.89	0.84
1:C:391:ASP:OD1	1:D:95:HIS:HE1	1.61	0.83
1:B:112:LYS:HE3	1:B:354:ASP:OD2	1.79	0.82
1:B:222:ILE:N	1:B:222:ILE:HD13	1.92	0.82
1:C:112:LYS:HE3	1:C:354:ASP:OD2	1.79	0.82
1:D:79:GLY:H	1:D:362:LEU:HD21	1.43	0.82
1:A:79:GLY:H	1:A:362:LEU:HD21	1.43	0.82
1:A:112:LYS:HE3	1:A:354:ASP:OD2	1.79	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:GLY:H	1:B:362:LEU:HD21	1.43	0.81
1:C:222:ILE:HD13	1:C:222:ILE:N	1.92	0.81
1:C:79:GLY:H	1:C:362:LEU:HD21	1.43	0.81
1:D:112:LYS:HE3	1:D:354:ASP:OD2	1.79	0.81
1:B:442:VAL:O	1:B:445:VAL:HG22	1.82	0.79
1:C:442:VAL:O	1:C:445:VAL:HG22	1.82	0.79
1:D:442:VAL:O	1:D:445:VAL:HG22	1.82	0.79
1:A:442:VAL:O	1:A:445:VAL:HG22	1.82	0.78
1:A:76:GLY:C	1:A:78:PRO:HD2	2.05	0.77
1:A:387:ARG:HB2	1:A:387:ARG:NH1	2.00	0.77
1:C:76:GLY:C	1:C:78:PRO:HD2	2.05	0.77
1:D:76:GLY:C	1:D:78:PRO:HD2	2.05	0.77
1:A:327:ARG:HG2	1:A:364:THR:HB	1.68	0.76
1:B:327:ARG:HG2	1:B:364:THR:HB	1.68	0.76
1:D:387:ARG:HB2	1:D:387:ARG:NH1	2.00	0.76
1:B:387:ARG:HB2	1:B:387:ARG:NH1	2.00	0.76
1:B:76:GLY:C	1:B:78:PRO:HD2	2.05	0.75
1:C:327:ARG:HG2	1:C:364:THR:HB	1.68	0.75
1:C:387:ARG:NH1	1:C:387:ARG:HB2	2.00	0.75
1:C:68:GLY:C	1:C:70:THR:H	1.91	0.74
1:D:327:ARG:HG2	1:D:364:THR:HB	1.68	0.74
1:A:95:HIS:HE1	1:B:391:ASP:OD1	1.70	0.74
1:B:68:GLY:C	1:B:70:THR:H	1.91	0.74
1:A:68:GLY:C	1:A:70:THR:H	1.91	0.74
1:C:78:PRO:CB	1:C:327:ARG:HD2	2.18	0.73
1:D:78:PRO:CB	1:D:327:ARG:HD2	2.18	0.73
1:A:78:PRO:CB	1:A:327:ARG:HD2	2.18	0.72
1:B:160:GLN:HB3	1:B:163:ALA:HB3	1.71	0.72
1:B:78:PRO:CB	1:B:327:ARG:HD2	2.18	0.72
1:C:98:GLU:O	1:C:101:THR:HG22	1.90	0.72
1:D:201:GLY:HA3	1:D:319:GLY:HA3	1.72	0.72
1:A:160:GLN:HB3	1:A:163:ALA:HB3	1.71	0.72
1:C:201:GLY:HA3	1:C:319:GLY:HA3	1.72	0.71
1:C:178:TRP:O	1:C:182:THR:HG22	1.89	0.71
1:D:178:TRP:O	1:D:182:THR:HG22	1.90	0.71
1:D:68:GLY:C	1:D:70:THR:H	1.91	0.71
1:A:178:TRP:O	1:A:182:THR:HG22	1.90	0.71
1:A:98:GLU:O	1:A:101:THR:HG22	1.90	0.71
1:D:160:GLN:HB3	1:D:163:ALA:HB3	1.71	0.71
1:D:98:GLU:O	1:D:101:THR:HG22	1.90	0.71
1:A:201:GLY:HA3	1:A:319:GLY:HA3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:GLY:HA3	1:B:319:GLY:HA3	1.72	0.70
1:B:178:TRP:O	1:B:182:THR:HG22	1.90	0.70
1:D:99:LEU:O	1:D:103:LEU:HD23	1.92	0.70
1:C:99:LEU:O	1:C:103:LEU:HD23	1.92	0.70
1:C:160:GLN:HB3	1:C:163:ALA:HB3	1.71	0.70
1:A:99:LEU:O	1:A:103:LEU:HD23	1.92	0.70
1:B:98:GLU:O	1:B:101:THR:HG22	1.90	0.70
1:A:91:GLU:OE2	1:A:230:ASP:HB2	1.91	0.69
1:C:91:GLU:OE2	1:C:230:ASP:HB2	1.91	0.69
1:D:91:GLU:OE2	1:D:230:ASP:HB2	1.91	0.69
1:B:99:LEU:O	1:B:103:LEU:HD23	1.92	0.69
1:D:70:THR:CG2	1:D:242:ALA:HA	2.23	0.69
1:B:70:THR:CG2	1:B:242:ALA:HA	2.23	0.69
1:B:63:ASN:HD22	1:B:63:ASN:H	1.41	0.69
1:B:91:GLU:OE2	1:B:230:ASP:HB2	1.91	0.69
1:D:63:ASN:HD22	1:D:63:ASN:H	1.41	0.68
1:C:70:THR:CG2	1:C:242:ALA:HA	2.23	0.68
1:A:70:THR:CG2	1:A:242:ALA:HA	2.23	0.68
1:A:63:ASN:H	1:A:63:ASN:HD22	1.41	0.68
1:B:79:GLY:HA3	1:B:362:LEU:HD22	1.75	0.68
1:A:79:GLY:HA3	1:A:362:LEU:HD22	1.76	0.68
1:C:63:ASN:H	1:C:63:ASN:HD22	1.41	0.68
1:B:35:ILE:HG13	1:B:284:ALA:HB2	1.76	0.67
1:B:41:ILE:HD12	1:B:42:SER:H	1.59	0.67
1:B:185:SER:OG	1:B:187:GLU:HG2	1.94	0.67
1:A:185:SER:OG	1:A:187:GLU:HG2	1.94	0.67
1:C:79:GLY:HA3	1:C:362:LEU:HD22	1.76	0.67
1:D:41:ILE:HD12	1:D:42:SER:H	1.59	0.67
1:A:35:ILE:HG13	1:A:284:ALA:HB2	1.76	0.66
1:D:185:SER:OG	1:D:187:GLU:HG2	1.94	0.66
1:A:41:ILE:HD12	1:A:42:SER:H	1.59	0.66
1:D:189:ARG:HH11	1:D:189:ARG:HG2	1.61	0.66
1:D:35:ILE:HG13	1:D:284:ALA:HB2	1.76	0.66
1:C:185:SER:OG	1:C:187:GLU:HG2	1.94	0.66
1:C:189:ARG:HG2	1:C:189:ARG:HH11	1.61	0.66
1:D:79:GLY:HA3	1:D:362:LEU:HD22	1.76	0.66
1:B:189:ARG:HH11	1:B:189:ARG:HG2	1.61	0.66
1:A:189:ARG:HH11	1:A:189:ARG:HG2	1.61	0.66
1:C:35:ILE:HG13	1:C:284:ALA:HB2	1.76	0.65
1:C:41:ILE:HD12	1:C:42:SER:H	1.59	0.65
1:B:323:LYS:HE3	1:B:366:ILE:CD1	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:119:ILE:HD12	1:D:392:LEU:HD11	1.79	0.64
1:A:323:LYS:HE3	1:A:366:ILE:CD1	2.27	0.64
1:C:119:ILE:HD12	1:C:392:LEU:HD11	1.79	0.64
1:D:323:LYS:HE3	1:D:366:ILE:CD1	2.27	0.63
1:A:70:THR:O	1:A:70:THR:HG22	1.98	0.63
1:C:323:LYS:HE3	1:C:366:ILE:CD1	2.27	0.63
1:D:70:THR:HG22	1:D:70:THR:O	1.98	0.63
1:D:94:THR:HG23	1:D:95:HIS:N	2.14	0.63
1:D:57:VAL:HG11	1:D:252:ILE:HD11	1.81	0.63
1:A:78:PRO:HG2	1:A:327:ARG:NH1	2.14	0.63
1:A:119:ILE:HD12	1:A:392:LEU:HD11	1.79	0.63
1:C:78:PRO:HG2	1:C:327:ARG:NH1	2.14	0.63
1:A:94:THR:HG23	1:A:95:HIS:N	2.14	0.62
1:B:70:THR:O	1:B:70:THR:HG22	1.98	0.62
1:B:94:THR:HG23	1:B:95:HIS:N	2.14	0.62
1:C:57:VAL:HG11	1:C:252:ILE:HD11	1.81	0.62
1:D:139:VAL:N	1:D:140:PRO:HD2	2.14	0.62
1:B:177:THR:O	1:B:181:GLU:HG3	2.00	0.62
1:C:139:VAL:N	1:C:140:PRO:HD2	2.14	0.62
1:C:70:THR:O	1:C:70:THR:HG22	1.98	0.62
1:B:119:ILE:HD12	1:B:392:LEU:HD11	1.79	0.62
1:B:78:PRO:HG2	1:B:327:ARG:NH1	2.14	0.62
1:C:177:THR:O	1:C:181:GLU:HG3	1.99	0.62
1:A:139:VAL:N	1:A:140:PRO:HD2	2.14	0.62
1:C:94:THR:HG23	1:C:95:HIS:N	2.14	0.62
1:A:390:LEU:O	1:A:394:VAL:HG23	2.00	0.62
1:C:390:LEU:O	1:C:394:VAL:HG23	2.00	0.62
1:D:390:LEU:O	1:D:394:VAL:HG23	2.00	0.62
1:D:285:ARG:O	1:D:444:LYS:HG2	2.00	0.62
1:C:199:LEU:HD21	1:C:225:LEU:HG	1.82	0.62
1:D:177:THR:O	1:D:181:GLU:HG3	2.00	0.62
1:D:199:LEU:HD21	1:D:225:LEU:HG	1.82	0.62
1:A:199:LEU:HD21	1:A:225:LEU:HG	1.82	0.61
1:A:57:VAL:HG11	1:A:252:ILE:HD11	1.81	0.61
1:D:78:PRO:HG2	1:D:327:ARG:NH1	2.14	0.61
1:A:177:THR:O	1:A:181:GLU:HG3	1.99	0.61
1:A:321:TYR:HB2	1:A:421:GLY:HA2	1.82	0.61
1:B:182:THR:HG23	1:B:183:ILE:HG13	1.82	0.61
1:C:321:TYR:HB2	1:C:421:GLY:HA2	1.82	0.61
1:B:139:VAL:N	1:B:140:PRO:HD2	2.14	0.61
1:B:390:LEU:O	1:B:394:VAL:HG23	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:TYR:HB2	1:B:421:GLY:HA2	1.82	0.61
1:D:182:THR:HG23	1:D:183:ILE:HG13	1.82	0.61
1:B:57:VAL:HG11	1:B:252:ILE:HD11	1.81	0.61
1:C:182:THR:HG23	1:C:183:ILE:HG13	1.82	0.61
1:A:285:ARG:O	1:A:444:LYS:HG2	2.00	0.61
1:A:289:ILE:HD11	1:A:296:ALA:HB1	1.83	0.61
1:C:285:ARG:O	1:C:444:LYS:HG2	2.00	0.61
1:D:289:ILE:HD11	1:D:296:ALA:HB1	1.83	0.61
1:D:321:TYR:HB2	1:D:421:GLY:HA2	1.82	0.61
1:B:199:LEU:HD21	1:B:225:LEU:HG	1.82	0.61
1:B:285:ARG:O	1:B:444:LYS:HG2	2.00	0.61
1:B:287:ILE:HD13	1:B:445:VAL:HA	1.83	0.61
1:B:414:GLN:C	1:B:414:GLN:CD	2.59	0.61
1:A:182:THR:HG23	1:A:183:ILE:HG13	1.82	0.60
1:D:36:ILE:HG12	1:D:288:VAL:CG1	2.31	0.60
1:D:197:ASN:HA	1:D:202:ALA:O	2.02	0.60
1:D:323:LYS:HE3	1:D:366:ILE:HD11	1.84	0.60
1:A:287:ILE:HD13	1:A:445:VAL:HA	1.84	0.60
1:B:289:ILE:HD11	1:B:296:ALA:HB1	1.83	0.60
1:A:414:GLN:CD	1:A:414:GLN:C	2.59	0.60
1:C:249:ALA:HA	1:C:257:PHE:CE1	2.37	0.60
1:C:289:ILE:HD11	1:C:296:ALA:HB1	1.83	0.60
1:D:414:GLN:CD	1:D:414:GLN:C	2.59	0.60
1:A:323:LYS:HE3	1:A:366:ILE:HD11	1.84	0.60
1:B:53:GLN:NE2	1:B:475:ALA:HB1	2.17	0.60
1:B:36:ILE:HG12	1:B:288:VAL:CG1	2.31	0.60
1:C:414:GLN:CD	1:C:414:GLN:C	2.59	0.60
1:B:197:ASN:HA	1:B:202:ALA:O	2.02	0.59
1:C:197:ASN:HA	1:C:202:ALA:O	2.02	0.59
1:C:36:ILE:HG12	1:C:288:VAL:CG1	2.31	0.59
1:D:53:GLN:NE2	1:D:475:ALA:HB1	2.17	0.59
1:A:53:GLN:NE2	1:A:475:ALA:HB1	2.17	0.59
1:C:287:ILE:HD13	1:C:445:VAL:HA	1.84	0.59
1:A:197:ASN:HA	1:A:202:ALA:O	2.02	0.59
1:A:36:ILE:HG12	1:A:288:VAL:CG1	2.31	0.59
1:A:41:ILE:HD12	1:A:42:SER:N	2.18	0.59
1:B:249:ALA:HA	1:B:257:PHE:CE1	2.37	0.59
1:C:53:GLN:NE2	1:C:475:ALA:HB1	2.17	0.59
1:D:249:ALA:HA	1:D:257:PHE:CE1	2.37	0.59
1:D:41:ILE:HD12	1:D:42:SER:N	2.18	0.59
1:A:249:ALA:HA	1:A:257:PHE:CE1	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:LYS:HE3	1:B:366:ILE:HD11	1.84	0.58
1:B:190:ARG:HD3	1:B:346:GLU:OE1	2.04	0.58
1:C:323:LYS:HE3	1:C:366:ILE:HD11	1.84	0.58
1:D:287:ILE:HD13	1:D:445:VAL:HA	1.84	0.58
1:A:190:ARG:HD3	1:A:346:GLU:OE1	2.04	0.58
1:C:41:ILE:HD12	1:C:42:SER:N	2.18	0.58
1:B:129:ASP:C	1:B:130:ASP:OD1	2.42	0.58
1:C:129:ASP:C	1:C:130:ASP:OD1	2.42	0.58
1:C:190:ARG:HD3	1:C:346:GLU:OE1	2.04	0.58
1:C:219:CYS:HB3	1:C:225:LEU:HD13	1.86	0.58
1:C:357:LYS:HG2	1:C:360:ASP:CG	2.24	0.58
1:D:222:ILE:O	1:D:226:MET:N	2.35	0.58
1:A:129:ASP:C	1:A:130:ASP:OD1	2.42	0.58
1:B:34:VAL:HG22	1:B:286:HIS:HB2	1.86	0.58
1:A:219:CYS:HB3	1:A:225:LEU:HD13	1.86	0.58
1:B:318:MET:HB3	1:B:420:GLY:HA3	1.86	0.58
1:B:41:ILE:HD12	1:B:42:SER:N	2.18	0.58
1:C:321:TYR:N	1:C:413:THR:HG22	2.15	0.58
1:C:53:GLN:HE21	1:C:475:ALA:HB1	1.69	0.58
1:D:219:CYS:HB3	1:D:225:LEU:HD13	1.86	0.58
1:D:357:LYS:HG2	1:D:360:ASP:CG	2.24	0.58
1:A:53:GLN:HE21	1:A:475:ALA:HB1	1.69	0.58
1:D:79:GLY:HA3	1:D:361:THR:OG1	2.03	0.58
1:A:297:ASN:HD22	1:A:313:GLN:HE21	1.52	0.57
1:B:321:TYR:N	1:B:413:THR:HG22	2.15	0.57
1:C:297:ASN:HD22	1:C:313:GLN:HE21	1.52	0.57
1:C:318:MET:HB3	1:C:420:GLY:HA3	1.86	0.57
1:A:357:LYS:HG2	1:A:360:ASP:CG	2.24	0.57
1:A:79:GLY:HA3	1:A:361:THR:OG1	2.03	0.57
1:B:53:GLN:HE21	1:B:475:ALA:HB1	1.69	0.57
1:D:129:ASP:C	1:D:130:ASP:OD1	2.42	0.57
1:D:190:ARG:HD3	1:D:346:GLU:OE1	2.04	0.57
1:A:318:MET:HB3	1:A:420:GLY:HA3	1.86	0.57
1:A:34:VAL:HG22	1:A:286:HIS:HB2	1.86	0.57
1:C:79:GLY:HA3	1:C:361:THR:OG1	2.03	0.57
1:D:53:GLN:HE21	1:D:475:ALA:HB1	1.69	0.57
1:C:268:HIS:CG	1:C:268:HIS:O	2.57	0.57
1:B:297:ASN:HD22	1:B:313:GLN:HE21	1.52	0.57
1:B:357:LYS:HG2	1:B:360:ASP:CG	2.24	0.57
1:B:328:TYR:O	1:B:362:LEU:HB2	2.05	0.57
1:C:63:ASN:N	1:C:63:ASN:HD22	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:297:ASN:HD22	1:D:313:GLN:HE21	1.52	0.57
1:B:139:VAL:O	1:B:143:LEU:HD23	2.05	0.57
1:B:79:GLY:HA3	1:B:361:THR:OG1	2.03	0.57
1:C:328:TYR:O	1:C:362:LEU:HB2	2.05	0.57
1:C:451:GLU:HA	1:C:457:SER:OG	2.05	0.57
1:A:451:GLU:HA	1:A:457:SER:OG	2.05	0.57
1:B:451:GLU:HA	1:B:457:SER:OG	2.05	0.57
1:C:273:VAL:O	1:C:283:ARG:HG3	2.05	0.57
1:D:318:MET:HB3	1:D:420:GLY:HA3	1.86	0.57
1:D:312:LEU:HD21	1:D:438:LEU:HG	1.86	0.57
1:A:90:GLY:H	1:A:93:HIS:CD2	2.23	0.57
1:B:219:CYS:HB3	1:B:225:LEU:HD13	1.86	0.57
1:C:139:VAL:O	1:C:143:LEU:HD23	2.05	0.57
1:D:451:GLU:HA	1:D:457:SER:OG	2.05	0.57
1:A:153:ALA:O	1:A:156:VAL:O	2.24	0.56
1:A:273:VAL:O	1:A:283:ARG:HG3	2.05	0.56
1:A:312:LEU:HD21	1:A:438:LEU:HG	1.86	0.56
1:B:153:ALA:O	1:B:156:VAL:O	2.23	0.56
1:B:90:GLY:H	1:B:93:HIS:CD2	2.23	0.56
1:D:273:VAL:O	1:D:283:ARG:HG3	2.05	0.56
1:B:268:HIS:CG	1:B:268:HIS:O	2.57	0.56
1:C:153:ALA:O	1:C:156:VAL:O	2.24	0.56
1:D:139:VAL:O	1:D:143:LEU:HD23	2.05	0.56
1:D:34:VAL:HG21	1:D:474:ILE:HG21	1.88	0.56
1:D:39:ALA:O	1:D:66:ILE:O	2.23	0.56
1:A:268:HIS:CG	1:A:268:HIS:O	2.57	0.56
1:B:312:LEU:HD21	1:B:438:LEU:HG	1.86	0.56
1:C:90:GLY:H	1:C:93:HIS:CD2	2.23	0.56
1:D:153:ALA:O	1:D:156:VAL:O	2.24	0.56
1:D:369:ILE:N	1:D:369:ILE:HD12	2.21	0.56
1:C:312:LEU:HD21	1:C:438:LEU:HG	1.86	0.56
1:A:328:TYR:O	1:A:362:LEU:HB2	2.05	0.56
1:A:139:VAL:O	1:A:143:LEU:HD23	2.05	0.56
1:B:254:ARG:HG3	1:B:254:ARG:HH11	1.69	0.56
1:B:93:HIS:HA	1:B:461:GLU:HG3	1.88	0.56
1:D:328:TYR:O	1:D:362:LEU:HB2	2.05	0.56
1:A:369:ILE:N	1:A:369:ILE:HD12	2.21	0.56
1:A:321:TYR:N	1:A:413:THR:HG22	2.15	0.56
1:B:273:VAL:O	1:B:283:ARG:HG3	2.05	0.56
1:B:39:ALA:O	1:B:66:ILE:O	2.23	0.56
1:C:34:VAL:HG22	1:C:286:HIS:HB2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:ALA:O	1:C:66:ILE:O	2.23	0.56
1:D:34:VAL:HG22	1:D:286:HIS:HB2	1.86	0.56
1:D:268:HIS:CG	1:D:268:HIS:O	2.57	0.56
1:A:93:HIS:HA	1:A:461:GLU:HG3	1.88	0.56
1:A:34:VAL:HG21	1:A:474:ILE:HG21	1.88	0.56
1:C:380:HIS:HD2	1:D:454:PHE:CZ	2.24	0.56
1:D:254:ARG:HG3	1:D:254:ARG:HH11	1.69	0.56
1:A:435:GLY:O	1:A:438:LEU:HB2	2.06	0.55
1:D:90:GLY:H	1:D:93:HIS:CD2	2.23	0.55
1:A:254:ARG:HH11	1:A:254:ARG:HG3	1.69	0.55
1:B:222:ILE:O	1:B:226:MET:N	2.35	0.55
1:C:254:ARG:HG3	1:C:254:ARG:HH11	1.69	0.55
1:A:39:ALA:O	1:A:66:ILE:O	2.23	0.55
1:B:369:ILE:HD12	1:B:369:ILE:N	2.21	0.55
1:C:369:ILE:N	1:C:369:ILE:HD12	2.21	0.55
1:B:435:GLY:O	1:B:438:LEU:HB2	2.06	0.55
1:D:435:GLY:O	1:D:438:LEU:HB2	2.06	0.55
1:A:86:GLY:HA2	2:A:501:FAD:N5	2.22	0.55
1:D:93:HIS:HA	1:D:461:GLU:HG3	1.88	0.55
1:C:93:HIS:HA	1:C:461:GLU:HG3	1.88	0.54
1:C:435:GLY:O	1:C:438:LEU:HB2	2.06	0.54
1:C:34:VAL:HG21	1:C:474:ILE:HG21	1.88	0.54
1:C:86:GLY:HA2	2:C:501:FAD:N5	2.22	0.54
1:B:194:VAL:HG21	1:B:345:THR:HA	1.89	0.54
1:B:57:VAL:CG1	1:B:252:ILE:HD11	2.37	0.54
1:D:260:GLU:C	1:D:262:PRO:HD3	2.28	0.54
1:B:34:VAL:HG21	1:B:474:ILE:HG21	1.88	0.54
1:C:260:GLU:C	1:C:262:PRO:HD3	2.28	0.54
1:C:391:ASP:OD1	1:D:95:HIS:CE1	2.51	0.54
1:C:380:HIS:CD2	1:D:454:PHE:CZ	2.95	0.54
1:C:191:LEU:O	1:C:195:ILE:HG13	2.08	0.54
1:A:191:LEU:O	1:A:195:ILE:HG13	2.07	0.54
1:B:191:LEU:O	1:B:195:ILE:HG13	2.07	0.54
1:D:194:VAL:HG21	1:D:345:THR:HA	1.89	0.54
1:C:194:VAL:HG21	1:C:345:THR:HA	1.89	0.54
1:D:57:VAL:CG1	1:D:252:ILE:HD11	2.37	0.54
1:D:68:GLY:C	1:D:70:THR:N	2.61	0.54
1:A:222:ILE:O	1:A:226:MET:N	2.35	0.54
1:A:94:THR:HG23	1:A:95:HIS:H	1.73	0.54
1:A:260:GLU:C	1:A:262:PRO:HD3	2.28	0.54
1:B:86:GLY:HA2	2:B:501:FAD:N5	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:86:GLY:HA2	2:D:501:FAD:N5	2.22	0.54
1:D:191:LEU:O	1:D:195:ILE:HG13	2.07	0.53
1:B:187:GLU:O	1:B:191:LEU:HG	2.09	0.53
1:A:194:VAL:HG21	1:A:345:THR:HA	1.89	0.53
1:D:187:GLU:O	1:D:191:LEU:HG	2.09	0.53
1:A:57:VAL:CG1	1:A:252:ILE:HD11	2.38	0.53
1:B:260:GLU:C	1:B:262:PRO:HD3	2.28	0.53
1:C:57:VAL:CG1	1:C:252:ILE:HD11	2.37	0.53
1:A:161:PRO:HG2	1:A:162:TRP:CE3	2.43	0.53
1:D:161:PRO:HG2	1:D:162:TRP:CE3	2.44	0.53
1:A:187:GLU:O	1:A:191:LEU:HG	2.09	0.53
1:C:187:GLU:O	1:C:191:LEU:HG	2.09	0.53
1:B:68:GLY:C	1:B:70:THR:N	2.61	0.53
1:C:222:ILE:CD1	1:C:222:ILE:N	2.60	0.53
1:B:161:PRO:HG2	1:B:162:TRP:CE3	2.43	0.53
1:B:94:THR:HG23	1:B:95:HIS:H	1.73	0.52
1:C:197:ASN:O	1:C:200:LEU:O	2.27	0.52
1:C:161:PRO:HG2	1:C:162:TRP:CE3	2.44	0.52
1:D:94:THR:HG23	1:D:95:HIS:H	1.73	0.52
1:C:352:LEU:O	1:C:353:LEU:HD12	2.09	0.52
1:A:197:ASN:O	1:A:200:LEU:O	2.27	0.52
1:C:383:GLN:H	1:C:383:GLN:NE2	2.08	0.52
1:D:352:LEU:O	1:D:353:LEU:HD12	2.09	0.52
1:D:383:GLN:H	1:D:383:GLN:NE2	2.08	0.52
1:C:281:SER:O	1:C:282:LEU:HD13	2.10	0.52
1:B:352:LEU:O	1:B:353:LEU:HD12	2.10	0.52
1:D:63:ASN:N	1:D:63:ASN:HD22	2.02	0.52
1:C:78:PRO:CG	1:C:327:ARG:NH1	2.73	0.52
1:D:197:ASN:O	1:D:200:LEU:O	2.27	0.52
1:A:383:GLN:NE2	1:A:383:GLN:H	2.08	0.52
1:B:281:SER:O	1:B:282:LEU:HD13	2.10	0.52
1:D:341:ALA:HA	1:D:352:LEU:O	2.10	0.52
1:A:78:PRO:CG	1:A:327:ARG:NH1	2.73	0.52
1:C:222:ILE:O	1:C:226:MET:N	2.35	0.52
1:C:464:VAL:O	1:C:468:GLN:HG3	2.10	0.52
1:A:352:LEU:O	1:A:353:LEU:HD12	2.09	0.51
1:B:341:ALA:HA	1:B:352:LEU:O	2.10	0.51
1:C:68:GLY:C	1:C:70:THR:N	2.61	0.51
1:C:94:THR:HG23	1:C:95:HIS:H	1.73	0.51
1:D:156:VAL:HG23	1:D:161:PRO:HA	1.92	0.51
1:D:78:PRO:CG	1:D:327:ARG:NH1	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:321:TYR:CG	1:C:422:PRO:HD3	2.46	0.51
1:B:156:VAL:HG23	1:B:161:PRO:HA	1.92	0.51
1:B:383:GLN:H	1:B:383:GLN:NE2	2.08	0.51
1:D:249:ALA:HB1	1:D:254:ARG:HD2	1.92	0.51
1:A:341:ALA:HA	1:A:352:LEU:O	2.10	0.51
1:C:156:VAL:HG23	1:C:161:PRO:HA	1.92	0.51
1:A:321:TYR:CG	1:A:422:PRO:HD3	2.46	0.51
1:A:464:VAL:O	1:A:468:GLN:HG3	2.11	0.51
1:B:197:ASN:O	1:B:200:LEU:O	2.27	0.51
1:B:464:VAL:O	1:B:468:GLN:HG3	2.10	0.51
1:D:464:VAL:O	1:D:468:GLN:HG3	2.10	0.51
1:A:199:LEU:HD22	1:A:226:MET:CE	2.41	0.51
1:A:258:LEU:HD12	1:A:258:LEU:N	2.25	0.51
1:A:281:SER:O	1:A:282:LEU:HD13	2.10	0.51
1:A:79:GLY:H	1:A:362:LEU:CD2	2.18	0.51
1:B:321:TYR:CG	1:B:422:PRO:HD3	2.46	0.51
1:B:79:GLY:H	1:B:362:LEU:CD2	2.18	0.51
1:C:341:ALA:HA	1:C:352:LEU:O	2.10	0.51
1:A:70:THR:HG23	1:A:242:ALA:HA	1.93	0.51
1:B:70:THR:HG23	1:B:242:ALA:HA	1.93	0.51
1:C:480:ARG:NE	1:C:480:ARG:HA	2.26	0.51
1:D:321:TYR:CG	1:D:422:PRO:HD3	2.46	0.51
1:B:78:PRO:CG	1:B:327:ARG:NH1	2.73	0.51
1:B:480:ARG:NE	1:B:480:ARG:HA	2.26	0.51
1:C:70:THR:HG23	1:C:242:ALA:HA	1.93	0.51
1:D:77:ALA:HB3	1:D:406:TYR:CE1	2.46	0.51
1:A:190:ARG:O	1:A:194:VAL:HG23	2.12	0.50
1:A:249:ALA:HB1	1:A:254:ARG:HD2	1.92	0.50
1:B:199:LEU:HD22	1:B:226:MET:CE	2.41	0.50
1:B:32:VAL:HG23	1:B:56:SER:HB2	1.94	0.50
1:C:258:LEU:HD12	1:C:258:LEU:N	2.25	0.50
1:D:281:SER:O	1:D:282:LEU:HD13	2.10	0.50
1:A:156:VAL:HG23	1:A:161:PRO:HA	1.92	0.50
1:B:77:ALA:HB3	1:B:406:TYR:CE1	2.46	0.50
1:C:190:ARG:O	1:C:194:VAL:HG23	2.12	0.50
1:C:199:LEU:HD22	1:C:226:MET:CE	2.41	0.50
1:C:323:LYS:HE3	1:C:366:ILE:HD12	1.93	0.50
1:D:258:LEU:HD12	1:D:258:LEU:N	2.26	0.50
1:A:480:ARG:NE	1:A:480:ARG:HA	2.26	0.50
1:A:32:VAL:HG23	1:A:56:SER:HB2	1.94	0.50
1:B:34:VAL:HA	1:B:286:HIS:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:SER:HB2	1:D:165:PRO:HD2	1.94	0.50
1:A:34:VAL:HA	1:A:286:HIS:O	2.12	0.50
1:C:32:VAL:HG23	1:C:56:SER:HB2	1.93	0.50
1:D:323:LYS:HE3	1:D:366:ILE:HD12	1.94	0.50
1:D:32:VAL:HG23	1:D:56:SER:HB2	1.93	0.50
1:C:164:SER:HB2	1:C:165:PRO:HD2	1.94	0.50
1:C:249:ALA:HB1	1:C:254:ARG:HD2	1.92	0.50
1:D:199:LEU:HD22	1:D:226:MET:CE	2.41	0.50
1:C:77:ALA:HB3	1:C:406:TYR:CE1	2.46	0.50
1:A:77:ALA:HB3	1:A:406:TYR:CE1	2.46	0.50
1:B:237:TRP:O	1:B:239:GLY:N	2.45	0.50
1:B:420:GLY:O	1:B:421:GLY:O	2.30	0.50
1:D:70:THR:HG23	1:D:242:ALA:HA	1.93	0.50
1:A:164:SER:HB2	1:A:165:PRO:HD2	1.94	0.50
1:B:190:ARG:O	1:B:194:VAL:HG23	2.12	0.50
1:D:190:ARG:O	1:D:194:VAL:HG23	2.12	0.50
1:A:237:TRP:O	1:A:239:GLY:N	2.45	0.49
1:A:420:GLY:O	1:A:421:GLY:O	2.30	0.49
1:B:249:ALA:HB1	1:B:254:ARG:HD2	1.92	0.49
1:B:258:LEU:HD12	1:B:258:LEU:N	2.25	0.49
1:C:79:GLY:H	1:C:362:LEU:CD2	2.18	0.49
1:A:194:VAL:HG21	1:A:345:THR:HG22	1.94	0.49
1:B:63:ASN:HD22	1:B:63:ASN:N	2.02	0.49
1:D:237:TRP:O	1:D:239:GLY:N	2.45	0.49
1:D:321:TYR:N	1:D:413:THR:HG22	2.15	0.49
1:C:194:VAL:HG21	1:C:345:THR:HG22	1.95	0.49
1:C:34:VAL:HA	1:C:286:HIS:O	2.11	0.49
1:C:420:GLY:O	1:C:421:GLY:O	2.30	0.49
1:D:34:VAL:HA	1:D:286:HIS:O	2.12	0.49
1:D:480:ARG:NE	1:D:480:ARG:HA	2.26	0.49
1:A:323:LYS:HE3	1:A:366:ILE:HD12	1.93	0.49
1:B:164:SER:HB2	1:B:165:PRO:HD2	1.94	0.49
1:B:327:ARG:HB2	1:B:406:TYR:HB3	1.95	0.49
1:D:194:VAL:HG21	1:D:345:THR:HG22	1.94	0.49
1:B:194:VAL:HG21	1:B:345:THR:HG22	1.94	0.49
1:B:61:GLU:OE1	1:B:61:GLU:HA	2.13	0.49
1:A:61:GLU:OE1	1:A:61:GLU:HA	2.13	0.49
1:B:323:LYS:HE3	1:B:366:ILE:HD12	1.94	0.49
1:C:237:TRP:O	1:C:239:GLY:N	2.45	0.49
1:A:68:GLY:C	1:A:70:THR:N	2.61	0.49
1:A:76:GLY:C	1:A:78:PRO:CD	2.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:61:GLU:HA	1:C:61:GLU:OE1	2.13	0.49
1:D:442:VAL:HB	1:D:445:VAL:HG22	1.95	0.49
1:C:442:VAL:HB	1:C:445:VAL:HG22	1.95	0.49
1:C:76:GLY:C	1:C:78:PRO:CD	2.78	0.48
1:D:420:GLY:O	1:D:421:GLY:O	2.30	0.48
1:A:442:VAL:HB	1:A:445:VAL:HG22	1.95	0.48
1:B:442:VAL:HB	1:B:445:VAL:CG2	2.43	0.48
1:D:61:GLU:HA	1:D:61:GLU:OE1	2.13	0.48
1:B:76:GLY:C	1:B:78:PRO:CD	2.78	0.48
1:A:327:ARG:HB2	1:A:406:TYR:HB3	1.95	0.48
1:A:442:VAL:HB	1:A:445:VAL:CG2	2.44	0.48
1:B:442:VAL:HB	1:B:445:VAL:HG22	1.95	0.48
1:B:93:HIS:HA	1:B:461:GLU:CG	2.44	0.48
1:C:286:HIS:HD2	1:C:446:HIS:CE1	2.32	0.48
1:A:142:PHE:CE1	1:A:191:LEU:HD13	2.49	0.48
1:C:142:PHE:CE1	1:C:191:LEU:HD13	2.49	0.48
1:C:442:VAL:HB	1:C:445:VAL:CG2	2.43	0.48
1:A:103:LEU:HD12	1:A:247:ARG:CG	2.44	0.48
1:A:190:ARG:HH22	1:C:154:ASP:HB3	1.78	0.48
1:A:93:HIS:HA	1:A:461:GLU:CG	2.44	0.48
1:D:76:GLY:C	1:D:78:PRO:CD	2.78	0.48
1:C:103:LEU:HD12	1:C:247:ARG:CG	2.44	0.48
1:C:93:HIS:HA	1:C:461:GLU:CG	2.44	0.48
1:C:93:HIS:CB	1:C:461:GLU:HG2	2.44	0.48
1:A:129:ASP:C	1:A:131:GLN:H	2.18	0.48
1:A:93:HIS:CB	1:A:461:GLU:HG2	2.44	0.48
1:D:93:HIS:HA	1:D:461:GLU:CG	2.44	0.48
1:A:286:HIS:HD2	1:A:446:HIS:CE1	2.32	0.48
1:B:98:GLU:HA	1:B:101:THR:HG22	1.96	0.48
1:B:142:PHE:CE1	1:B:191:LEU:HD13	2.49	0.48
1:B:103:LEU:HD12	1:B:247:ARG:CG	2.44	0.48
1:C:327:ARG:HB2	1:C:406:TYR:HB3	1.95	0.48
1:D:286:HIS:HD2	1:D:446:HIS:CE1	2.32	0.48
1:B:286:HIS:HD2	1:B:446:HIS:CE1	2.32	0.47
1:D:103:LEU:HD12	1:D:247:ARG:CG	2.44	0.47
1:D:327:ARG:HB2	1:D:406:TYR:HB3	1.95	0.47
1:D:442:VAL:HB	1:D:445:VAL:CG2	2.44	0.47
1:D:142:PHE:CE1	1:D:191:LEU:HD13	2.49	0.47
1:A:98:GLU:HA	1:A:101:THR:HG22	1.96	0.47
1:B:350:VAL:HG22	1:B:351:PHE:N	2.30	0.47
1:D:93:HIS:CB	1:D:461:GLU:HG2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:ASP:C	1:B:131:GLN:H	2.18	0.47
1:D:98:GLU:HA	1:D:101:THR:HG22	1.96	0.47
1:B:61:GLU:HB3	1:B:259:LEU:HA	1.97	0.47
1:B:93:HIS:CB	1:B:461:GLU:HG2	2.44	0.47
1:C:129:ASP:C	1:C:131:GLN:H	2.18	0.47
1:C:350:VAL:HG22	1:C:351:PHE:N	2.30	0.47
1:C:41:ILE:HD11	2:C:501:FAD:O5'	2.15	0.47
1:D:129:ASP:C	1:D:131:GLN:H	2.18	0.47
1:A:169:ALA:O	1:A:172:SER:HB3	2.15	0.47
1:A:218:GLU:OE1	1:A:457:SER:HB3	2.15	0.47
1:B:218:GLU:OE1	1:B:457:SER:HB3	2.15	0.47
1:D:79:GLY:H	1:D:362:LEU:CD2	2.18	0.47
1:D:90:GLY:O	1:D:93:HIS:HB2	2.15	0.47
1:A:61:GLU:HB3	1:A:259:LEU:HA	1.97	0.47
1:A:350:VAL:HG22	1:A:351:PHE:N	2.30	0.47
1:B:90:GLY:O	1:B:93:HIS:HB2	2.15	0.47
1:B:372:SER:O	1:B:375:ASP:HB2	2.15	0.46
1:C:61:GLU:HB3	1:C:259:LEU:HA	1.97	0.46
1:C:90:GLY:O	1:C:93:HIS:HB2	2.15	0.46
1:D:290:ALA:HB2	1:D:448:ALA:HB3	1.98	0.46
1:D:41:ILE:HD11	2:D:501:FAD:O5'	2.15	0.46
1:A:372:SER:O	1:A:375:ASP:HB2	2.15	0.46
1:A:90:GLY:O	1:A:93:HIS:HB2	2.15	0.46
1:C:218:GLU:OE1	1:C:457:SER:HB3	2.15	0.46
1:C:372:SER:O	1:C:375:ASP:HB2	2.15	0.46
1:C:98:GLU:HA	1:C:101:THR:HG22	1.96	0.46
1:B:333:TRP:CE2	1:B:365:LEU:HD13	2.51	0.46
1:C:365:LEU:HD12	1:C:365:LEU:HA	1.85	0.46
1:D:350:VAL:HG22	1:D:351:PHE:N	2.30	0.46
1:B:103:LEU:HD12	1:B:247:ARG:HB3	1.97	0.46
1:B:41:ILE:HD11	2:B:501:FAD:O5'	2.15	0.46
1:C:103:LEU:HD12	1:C:247:ARG:HB3	1.97	0.46
1:C:290:ALA:HB2	1:C:448:ALA:HB3	1.98	0.46
1:A:63:ASN:N	1:A:63:ASN:HD22	2.02	0.46
1:C:190:ARG:HH22	1:D:154:ASP:HB3	1.81	0.46
1:D:169:ALA:O	1:D:172:SER:HB3	2.15	0.46
1:D:61:GLU:HB3	1:D:259:LEU:HA	1.97	0.46
1:A:290:ALA:HB2	1:A:448:ALA:HB3	1.98	0.46
1:C:79:GLY:CA	1:C:362:LEU:HD22	2.45	0.46
1:C:93:HIS:CG	1:C:461:GLU:HG2	2.51	0.46
1:D:333:TRP:CE2	1:D:365:LEU:HD13	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ILE:HD11	2:A:501:FAD:O5'	2.15	0.45
1:C:174:THR:H	1:C:177:THR:HG23	1.81	0.45
1:D:174:THR:H	1:D:177:THR:HG23	1.81	0.45
1:D:268:HIS:ND1	1:D:268:HIS:O	2.49	0.45
1:D:372:SER:O	1:D:375:ASP:HB2	2.15	0.45
1:A:328:TYR:CE1	1:A:401:ALA:HA	2.51	0.45
1:A:357:LYS:HG2	1:A:360:ASP:OD2	2.17	0.45
1:B:169:ALA:O	1:B:172:SER:HB3	2.15	0.45
1:B:93:HIS:CG	1:B:461:GLU:HG2	2.51	0.45
1:D:328:TYR:CE1	1:D:401:ALA:HA	2.52	0.45
1:D:218:GLU:OE1	1:D:457:SER:HB3	2.15	0.45
1:B:78:PRO:CG	1:B:327:ARG:CZ	2.95	0.45
1:C:169:ALA:O	1:C:172:SER:HB3	2.15	0.45
1:C:273:VAL:HB	1:C:287:ILE:CG2	2.47	0.45
1:C:328:TYR:CD1	1:C:332:PHE:HE2	2.35	0.45
1:C:333:TRP:CE2	1:C:365:LEU:HD13	2.51	0.45
1:B:133:ASP:OD1	1:B:135:ASN:HB2	2.17	0.45
1:B:268:HIS:O	1:B:268:HIS:ND1	2.49	0.45
1:B:328:TYR:CE1	1:B:401:ALA:HA	2.51	0.45
1:B:78:PRO:HG3	1:B:327:ARG:CZ	2.47	0.45
1:A:78:PRO:CG	1:A:327:ARG:CZ	2.95	0.45
1:A:78:PRO:HG3	1:A:327:ARG:CZ	2.46	0.45
1:C:328:TYR:CE1	1:C:401:ALA:HA	2.51	0.45
1:D:103:LEU:HD12	1:D:247:ARG:HB3	1.97	0.45
1:D:78:PRO:CG	1:D:327:ARG:CZ	2.95	0.45
1:A:289:ILE:HD11	1:A:296:ALA:CB	2.46	0.45
1:A:328:TYR:CD1	1:A:332:PHE:HE2	2.35	0.45
1:A:333:TRP:CE2	1:A:365:LEU:HD13	2.51	0.45
1:B:290:ALA:HB2	1:B:448:ALA:HB3	1.97	0.45
1:C:94:THR:HG22	1:C:465:ARG:HH21	1.82	0.45
1:A:174:THR:H	1:A:177:THR:HG23	1.81	0.45
1:B:273:VAL:HB	1:B:287:ILE:CG2	2.47	0.45
1:B:357:LYS:HG2	1:B:360:ASP:OD2	2.17	0.45
1:D:94:THR:HG22	1:D:465:ARG:HH21	1.82	0.45
1:A:268:HIS:ND1	1:A:268:HIS:O	2.49	0.45
1:B:174:THR:H	1:B:177:THR:HG23	1.81	0.45
1:D:133:ASP:OD1	1:D:135:ASN:HB2	2.17	0.45
1:D:289:ILE:HD11	1:D:296:ALA:CB	2.46	0.45
1:B:171:ASP:HB2	1:B:210:LEU:CD2	2.47	0.45
1:B:188:VAL:HA	1:B:191:LEU:HD11	1.99	0.45
1:C:133:ASP:OD1	1:C:135:ASN:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:188:VAL:HA	1:C:191:LEU:HD11	1.99	0.45
1:D:273:VAL:HB	1:D:287:ILE:CG2	2.47	0.45
1:A:119:ILE:HA	1:A:123:ASN:O	2.16	0.45
1:A:273:VAL:HB	1:A:287:ILE:CG2	2.47	0.45
1:B:261:TRP:CE3	1:B:277:SER:HB2	2.52	0.45
1:B:328:TYR:CD1	1:B:332:PHE:HE2	2.35	0.45
1:C:78:PRO:HG3	1:C:327:ARG:CZ	2.47	0.45
1:A:103:LEU:HD12	1:A:247:ARG:HB3	1.97	0.44
1:A:391:ASP:OD1	1:C:95:HIS:HE1	1.99	0.44
1:C:119:ILE:HA	1:C:123:ASN:O	2.16	0.44
1:C:78:PRO:CG	1:C:327:ARG:CZ	2.95	0.44
1:D:93:HIS:CG	1:D:461:GLU:HG2	2.51	0.44
1:A:88:PHE:CZ	1:A:353:LEU:HD23	2.53	0.44
1:C:268:HIS:ND1	1:C:268:HIS:O	2.49	0.44
1:C:289:ILE:HD11	1:C:296:ALA:CB	2.46	0.44
1:D:450:THR:O	1:D:457:SER:HA	2.17	0.44
1:A:179:LEU:HD22	1:A:183:ILE:HD12	2.00	0.44
1:A:93:HIS:CG	1:A:461:GLU:HG2	2.51	0.44
1:B:179:LEU:HD22	1:B:183:ILE:HD12	2.00	0.44
1:C:357:LYS:HG2	1:C:360:ASP:OD2	2.17	0.44
1:D:171:ASP:HB2	1:D:210:LEU:CD2	2.47	0.44
1:D:321:TYR:CD1	1:D:422:PRO:HD3	2.53	0.44
1:D:328:TYR:CD1	1:D:332:PHE:HE2	2.35	0.44
1:D:88:PHE:CZ	1:D:353:LEU:HD23	2.53	0.44
1:A:188:VAL:HA	1:A:191:LEU:HD11	1.99	0.44
1:B:33:ASP:N	1:B:56:SER:OG	2.47	0.44
1:A:94:THR:HG22	1:A:465:ARG:HH21	1.82	0.44
1:C:321:TYR:CD1	1:C:422:PRO:HD3	2.53	0.44
1:D:179:LEU:HD22	1:D:183:ILE:HD12	2.00	0.44
1:D:293:PRO:O	1:D:313:GLN:HB2	2.18	0.44
1:D:357:LYS:HG2	1:D:360:ASP:OD2	2.17	0.44
1:D:78:PRO:HG3	1:D:327:ARG:CZ	2.46	0.44
1:A:133:ASP:OD1	1:A:135:ASN:HB2	2.17	0.44
1:A:380:HIS:CE1	1:C:159:ASP:OD2	2.71	0.44
1:C:171:ASP:HB2	1:C:210:LEU:CD2	2.48	0.44
1:C:179:LEU:HD22	1:C:183:ILE:HD12	2.00	0.44
1:C:450:THR:O	1:C:457:SER:HA	2.17	0.44
1:D:119:ILE:HA	1:D:123:ASN:O	2.16	0.44
1:A:450:THR:O	1:A:457:SER:HA	2.17	0.44
1:A:70:THR:O	1:A:70:THR:CG2	2.65	0.44
1:A:93:HIS:O	1:A:97:ILE:HG13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:ILE:HA	1:B:123:ASN:O	2.16	0.44
1:B:88:PHE:CZ	1:B:353:LEU:HD23	2.53	0.44
1:C:199:LEU:HD12	1:C:199:LEU:HA	1.76	0.44
1:C:261:TRP:CE3	1:C:277:SER:HB2	2.52	0.44
1:A:171:ASP:HB2	1:A:210:LEU:CD2	2.48	0.43
1:A:261:TRP:CE3	1:A:277:SER:HB2	2.53	0.43
1:B:70:THR:CG2	1:B:70:THR:O	2.65	0.43
1:C:93:HIS:O	1:C:97:ILE:HG13	2.18	0.43
1:D:188:VAL:HA	1:D:191:LEU:HD11	1.99	0.43
1:D:261:TRP:CE3	1:D:277:SER:HB2	2.53	0.43
1:B:94:THR:HG22	1:B:465:ARG:HH21	1.82	0.43
1:B:93:HIS:O	1:B:97:ILE:HG13	2.18	0.43
1:C:88:PHE:CZ	1:C:353:LEU:HD23	2.53	0.43
1:D:95:HIS:HD2	1:D:468:GLN:OE1	2.01	0.43
1:A:321:TYR:CD1	1:A:422:PRO:HD3	2.53	0.43
1:B:293:PRO:O	1:B:313:GLN:HB2	2.18	0.43
1:C:95:HIS:HD2	1:C:468:GLN:OE1	2.01	0.43
1:A:160:GLN:O	1:A:161:PRO:C	2.57	0.43
1:A:33:ASP:N	1:A:56:SER:OG	2.47	0.43
1:B:450:THR:O	1:B:457:SER:HA	2.17	0.43
1:D:93:HIS:O	1:D:97:ILE:HG13	2.18	0.43
1:A:293:PRO:O	1:A:313:GLN:HB2	2.18	0.43
1:A:79:GLY:CA	1:A:362:LEU:HD22	2.45	0.43
1:A:454:PHE:CZ	1:B:380:HIS:HD2	2.36	0.43
1:A:95:HIS:HD2	1:A:468:GLN:OE1	2.01	0.43
1:A:94:THR:CG2	1:A:95:HIS:N	2.81	0.43
1:B:199:LEU:HD22	1:B:226:MET:HE2	1.99	0.43
1:C:160:GLN:O	1:C:161:PRO:C	2.57	0.43
1:C:174:THR:HG22	1:C:428:PRO:HG2	2.01	0.43
1:C:293:PRO:O	1:C:313:GLN:HB2	2.18	0.43
1:D:94:THR:CG2	1:D:95:HIS:N	2.81	0.43
1:B:289:ILE:HD11	1:B:296:ALA:CB	2.46	0.43
1:B:321:TYR:CD1	1:B:422:PRO:HD3	2.53	0.43
1:D:393:LEU:HB3	1:D:401:ALA:HB1	2.00	0.43
1:A:309:ARG:HA	1:A:437:ALA:HB1	2.01	0.43
1:C:430:VAL:CG2	1:C:431:LEU:N	2.82	0.43
1:B:174:THR:HG22	1:B:428:PRO:HG2	2.01	0.43
1:B:393:LEU:HB3	1:B:401:ALA:HB1	2.00	0.43
1:C:87:MET:HE2	1:C:236:TRP:NE1	2.34	0.43
1:A:166:ASN:ND2	1:A:169:ALA:HB3	2.34	0.43
1:B:309:ARG:HA	1:B:437:ALA:HB1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:ASN:ND2	1:C:169:ALA:HB3	2.34	0.43
1:D:318:MET:CB	1:D:420:GLY:HA3	2.49	0.43
1:A:297:ASN:HD22	1:A:313:GLN:HG3	1.84	0.42
1:B:430:VAL:CG2	1:B:431:LEU:N	2.82	0.42
1:C:138:PHE:C	1:C:140:PRO:HD2	2.40	0.42
1:C:189:ARG:CG	1:C:189:ARG:HH11	2.31	0.42
1:C:297:ASN:HD22	1:C:313:GLN:HG3	1.84	0.42
1:D:160:GLN:O	1:D:161:PRO:C	2.57	0.42
1:D:365:LEU:HA	1:D:365:LEU:HD12	1.85	0.42
1:A:138:PHE:C	1:A:140:PRO:HD2	2.40	0.42
1:A:185:SER:HG	1:A:187:GLU:HG2	1.81	0.42
1:B:189:ARG:CG	1:B:189:ARG:HH11	2.31	0.42
1:C:309:ARG:HA	1:C:437:ALA:HB1	2.01	0.42
1:A:430:VAL:CG2	1:A:431:LEU:N	2.82	0.42
1:B:95:HIS:HD2	1:B:468:GLN:OE1	2.01	0.42
1:D:353:LEU:O	1:D:366:ILE:HG23	2.19	0.42
1:D:394:VAL:HA	1:D:398:GLY:O	2.20	0.42
1:B:79:GLY:CA	1:B:362:LEU:HD22	2.45	0.42
1:B:72:THR:HG22	1:B:73:GLU:N	2.35	0.42
1:C:94:THR:CG2	1:C:95:HIS:N	2.81	0.42
1:B:297:ASN:HD22	1:B:313:GLN:HG3	1.84	0.42
1:C:353:LEU:O	1:C:366:ILE:HG23	2.19	0.42
1:D:138:PHE:C	1:D:140:PRO:HD2	2.40	0.42
1:D:88:PHE:HB2	2:D:501:FAD:O4	2.20	0.42
1:A:88:PHE:CE2	1:A:353:LEU:HD23	2.55	0.42
1:A:394:VAL:HA	1:A:398:GLY:O	2.20	0.42
1:A:393:LEU:HB3	1:A:401:ALA:HB1	2.00	0.42
1:A:318:MET:CB	1:A:420:GLY:HA3	2.49	0.42
1:A:454:PHE:CZ	1:B:380:HIS:CD2	3.08	0.42
1:B:166:ASN:ND2	1:B:169:ALA:HB3	2.34	0.42
1:B:178:TRP:CD1	1:B:179:LEU:N	2.88	0.42
1:B:94:THR:CG2	1:B:95:HIS:N	2.81	0.42
1:C:393:LEU:HB3	1:C:401:ALA:HB1	2.00	0.42
1:D:430:VAL:CG2	1:D:431:LEU:N	2.82	0.42
1:A:199:LEU:HD22	1:A:226:MET:HE3	2.02	0.42
1:B:353:LEU:O	1:B:366:ILE:HG23	2.19	0.42
1:B:88:PHE:CE2	1:B:353:LEU:HD23	2.55	0.42
1:D:309:ARG:HA	1:D:437:ALA:HB1	2.01	0.42
1:A:174:THR:HG22	1:A:428:PRO:HG2	2.01	0.42
1:A:353:LEU:O	1:A:366:ILE:HG23	2.19	0.42
1:B:138:PHE:C	1:B:140:PRO:HD2	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:178:TRP:CD1	1:C:179:LEU:N	2.88	0.42
1:C:88:PHE:CE2	1:C:353:LEU:HD23	2.55	0.42
1:C:103:LEU:HD12	1:C:247:ARG:HG3	2.02	0.42
1:D:178:TRP:CD1	1:D:179:LEU:N	2.88	0.42
1:A:178:TRP:CD1	1:A:179:LEU:N	2.88	0.42
1:B:460:MET:O	1:B:461:GLU:C	2.58	0.42
1:B:63:ASN:HB3	1:B:417:TRP:NE1	2.35	0.42
1:C:352:LEU:HD12	1:C:367:GLY:CA	2.50	0.42
1:C:380:HIS:HB3	1:C:384:GLU:OE2	2.20	0.42
1:D:166:ASN:ND2	1:D:169:ALA:HB3	2.34	0.42
1:D:297:ASN:HD22	1:D:313:GLN:HG3	1.84	0.42
1:D:88:PHE:CE2	1:D:353:LEU:HD23	2.55	0.42
1:A:103:LEU:HD12	1:A:247:ARG:HG3	2.02	0.41
1:A:72:THR:HG22	1:A:73:GLU:N	2.35	0.41
1:B:160:GLN:O	1:B:161:PRO:C	2.57	0.41
1:B:362:LEU:HD23	1:B:362:LEU:H	1.85	0.41
1:D:480:ARG:CA	1:D:480:ARG:NE	2.83	0.41
1:D:77:ALA:N	1:D:78:PRO:CD	2.83	0.41
1:A:362:LEU:HD23	1:A:362:LEU:H	1.85	0.41
1:A:63:ASN:HB3	1:A:417:TRP:NE1	2.35	0.41
1:A:460:MET:O	1:A:461:GLU:C	2.58	0.41
1:A:480:ARG:NE	1:A:480:ARG:CA	2.83	0.41
1:C:261:TRP:CZ3	1:C:277:SER:HB2	2.55	0.41
1:C:394:VAL:HA	1:C:398:GLY:O	2.20	0.41
1:C:318:MET:CB	1:C:420:GLY:HA3	2.49	0.41
1:D:103:LEU:HD12	1:D:247:ARG:HG3	2.02	0.41
1:D:199:LEU:HD22	1:D:226:MET:HE2	2.02	0.41
1:D:261:TRP:CZ3	1:D:277:SER:HB2	2.55	0.41
1:D:362:LEU:HD23	1:D:362:LEU:O	2.20	0.41
1:B:394:VAL:HA	1:B:398:GLY:O	2.20	0.41
1:B:77:ALA:N	1:B:78:PRO:CD	2.83	0.41
1:C:112:LYS:HA	1:C:113:PRO:HD3	1.86	0.41
1:C:74:GLN:HA	1:C:81:PRO:HA	2.03	0.41
1:D:174:THR:HG22	1:D:428:PRO:HG2	2.01	0.41
1:A:74:GLN:HA	1:A:81:PRO:HA	2.03	0.41
1:C:362:LEU:O	1:C:362:LEU:HD23	2.20	0.41
1:D:236:TRP:CH2	1:D:355:GLY:HA2	2.56	0.41
1:D:362:LEU:HD23	1:D:362:LEU:H	1.85	0.41
1:A:352:LEU:HD12	1:A:367:GLY:CA	2.50	0.41
1:A:88:PHE:HB2	2:A:501:FAD:O4	2.20	0.41
1:B:261:TRP:CZ3	1:B:277:SER:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:362:LEU:HD23	1:B:362:LEU:O	2.20	0.41
1:C:362:LEU:H	1:C:362:LEU:HD23	1.85	0.41
1:D:352:LEU:HD12	1:D:367:GLY:CA	2.50	0.41
1:B:380:HIS:HB3	1:B:384:GLU:OE2	2.20	0.41
1:B:74:GLN:HA	1:B:81:PRO:HA	2.02	0.41
1:C:63:ASN:HB3	1:C:417:TRP:NE1	2.35	0.41
1:C:88:PHE:HB2	2:C:501:FAD:O4	2.20	0.41
1:C:77:ALA:N	1:C:78:PRO:CD	2.83	0.41
1:D:342:LEU:HB3	1:D:352:LEU:CB	2.51	0.41
1:A:261:TRP:CZ3	1:A:277:SER:HB2	2.55	0.41
1:B:236:TRP:CH2	1:B:355:GLY:HA2	2.56	0.41
1:B:352:LEU:HD12	1:B:367:GLY:CA	2.50	0.41
1:C:33:ASP:N	1:C:56:SER:OG	2.47	0.41
1:D:72:THR:HG22	1:D:73:GLU:N	2.35	0.41
1:D:74:GLN:HA	1:D:81:PRO:HA	2.02	0.41
1:B:103:LEU:HD12	1:B:247:ARG:HG3	2.02	0.41
1:C:199:LEU:HD22	1:C:226:MET:HE3	2.02	0.41
1:D:380:HIS:HB3	1:D:384:GLU:OE2	2.20	0.41
1:A:77:ALA:N	1:A:78:PRO:CD	2.83	0.41
1:B:133:ASP:HA	1:B:134:PRO:HD3	1.93	0.41
1:B:35:ILE:HA	1:B:58:LEU:O	2.21	0.41
1:B:88:PHE:HB2	2:B:501:FAD:O4	2.20	0.41
1:A:365:LEU:HD12	1:A:365:LEU:HA	1.85	0.41
1:B:350:VAL:HG23	1:B:368:PHE:O	2.21	0.41
1:B:350:VAL:CG2	1:B:351:PHE:N	2.84	0.41
1:D:460:MET:O	1:D:461:GLU:C	2.58	0.41
1:B:174:THR:C	1:B:176:ALA:N	2.75	0.41
1:B:289:ILE:O	1:B:289:ILE:HG12	2.21	0.41
1:C:236:TRP:CH2	1:C:355:GLY:HA2	2.56	0.41
1:C:35:ILE:HA	1:C:58:LEU:O	2.21	0.41
1:C:72:THR:HG22	1:C:73:GLU:N	2.35	0.41
1:D:146:LEU:HA	1:D:146:LEU:HD12	1.81	0.41
1:D:152:LEU:HD22	1:D:178:TRP:CZ3	2.56	0.41
1:D:199:LEU:HD12	1:D:199:LEU:HA	1.76	0.41
1:D:289:ILE:HG12	1:D:289:ILE:O	2.21	0.41
1:D:35:ILE:HA	1:D:58:LEU:O	2.21	0.41
1:B:152:LEU:HD22	1:B:178:TRP:CZ3	2.56	0.40
1:B:422:PRO:HA	2:B:501:FAD:C8M	2.52	0.40
1:C:70:THR:O	1:C:70:THR:CG2	2.65	0.40
1:C:91:GLU:HB3	1:C:234:TRP:CD2	2.56	0.40
1:A:199:LEU:HD12	1:A:199:LEU:HA	1.76	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:VAL:HG23	1:A:368:PHE:O	2.21	0.40
1:A:362:LEU:HD23	1:A:362:LEU:O	2.20	0.40
1:B:249:ALA:HA	1:B:257:PHE:HE1	1.84	0.40
1:B:41:ILE:HD12	1:B:41:ILE:N	2.37	0.40
1:C:152:LEU:HD22	1:C:178:TRP:CZ3	2.57	0.40
1:C:342:LEU:HD23	1:C:343:LEU:N	2.37	0.40
1:D:79:GLY:CA	1:D:362:LEU:HD22	2.45	0.40
1:A:152:LEU:HD22	1:A:178:TRP:CZ3	2.56	0.40
1:A:236:TRP:CH2	1:A:355:GLY:HA2	2.56	0.40
1:A:86:GLY:HA2	2:A:501:FAD:C5X	2.51	0.40
1:A:91:GLU:HB3	1:A:234:TRP:CD2	2.57	0.40
1:B:318:MET:CB	1:B:420:GLY:HA3	2.49	0.40
1:B:93:HIS:HB3	1:B:461:GLU:HG2	2.03	0.40
1:C:41:ILE:HD12	1:C:41:ILE:N	2.37	0.40
1:C:460:MET:O	1:C:461:GLU:C	2.58	0.40
1:D:103:LEU:HD12	1:D:247:ARG:CB	2.51	0.40
1:D:350:VAL:CG2	1:D:351:PHE:N	2.84	0.40
1:A:174:THR:C	1:A:176:ALA:N	2.75	0.40
1:A:342:LEU:HB3	1:A:352:LEU:CB	2.51	0.40
1:A:35:ILE:HA	1:A:58:LEU:O	2.21	0.40
1:B:103:LEU:HD12	1:B:247:ARG:CB	2.51	0.40
1:B:342:LEU:HD23	1:B:343:LEU:N	2.37	0.40
1:C:146:LEU:HD12	1:C:146:LEU:HA	1.81	0.40
1:C:289:ILE:O	1:C:289:ILE:HG12	2.21	0.40
1:C:342:LEU:HB3	1:C:352:LEU:CB	2.51	0.40
1:D:319:GLY:O	1:D:421:GLY:N	2.34	0.40
1:D:63:ASN:HB3	1:D:417:TRP:NE1	2.35	0.40
1:A:199:LEU:HD22	1:A:226:MET:HE2	2.04	0.40
1:A:289:ILE:HG12	1:A:289:ILE:O	2.21	0.40
1:A:426:MET:SD	1:A:430:VAL:CG2	3.10	0.40
1:C:86:GLY:HA2	2:C:501:FAD:C5X	2.51	0.40
1:D:171:ASP:HB2	1:D:210:LEU:HD23	2.03	0.40
1:D:199:LEU:HD22	1:D:226:MET:HE3	2.03	0.40
1:D:60:VAL:HG13	1:D:261:TRP:HB3	2.03	0.40
1:D:342:LEU:HD23	1:D:343:LEU:N	2.37	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:C:300:ARG:NH1	1:D:300:ARG:NH1[4_559]	2.17	0.03

## 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	449/471 (95%)	406 (90%)	33 (7%)	10 (2%)	6	31
1	B	449/471 (95%)	406 (90%)	33 (7%)	10 (2%)	6	31
1	C	449/471 (95%)	406 (90%)	33 (7%)	10 (2%)	6	31
1	D	449/471 (95%)	406 (90%)	33 (7%)	10 (2%)	6	31
All	All	1796/1884 (95%)	1624 (90%)	132 (7%)	40 (2%)	6	31

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	421	GLY
1	B	421	GLY
1	C	421	GLY
1	D	421	GLY
1	A	238	PHE
1	A	254	ARG
1	B	238	PHE
1	B	254	ARG
1	C	238	PHE
1	C	254	ARG
1	D	238	PHE
1	D	254	ARG
1	A	77	ALA
1	A	78	PRO
1	A	307	THR
1	B	77	ALA
1	B	78	PRO
1	B	307	THR
1	C	77	ALA
1	C	78	PRO
1	C	307	THR
1	D	77	ALA

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Mol	Chain	Res	Type
1	D	78	PRO
1	D	307	THR
1	A	76	GLY
1	B	76	GLY
1	C	76	GLY
1	D	76	GLY
1	A	165	PRO
1	B	165	PRO
1	C	165	PRO
1	D	165	PRO
1	A	111	GLY
1	B	111	GLY
1	C	111	GLY
1	D	111	GLY
1	A	157	GLY
1	B	157	GLY
1	C	157	GLY
1	D	157	GLY

### 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	348/367 (95%)	301 (86%)	47 (14%)	4	17
1	B	348/367 (95%)	301 (86%)	47 (14%)	4	17
1	C	348/367 (95%)	301 (86%)	47 (14%)	4	17
1	D	348/367 (95%)	301 (86%)	47 (14%)	4	17
All	All	1392/1468 (95%)	1204 (86%)	188 (14%)	4	17

All (188) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ASP
1	A	41	ILE
1	A	57	VAL

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Mol	Chain	Res	Type
1	A	63	ASN
1	A	70	THR
1	A	93	HIS
1	A	98	GLU
1	A	130	ASP
1	A	144	SER
1	A	146	LEU
1	A	156	VAL
1	A	177	THR
1	A	178	TRP
1	A	187	GLU
1	A	189	ARG
1	A	191	LEU
1	A	192	HIS
1	A	200	LEU
1	A	205	TYR
1	A	218	GLU
1	A	222	ILE
1	A	234	TRP
1	A	238	PHE
1	A	254	ARG
1	A	269	ASP
1	A	280	ARG
1	A	282	LEU
1	A	287	ILE
1	A	288	VAL
1	A	289	ILE
1	A	307	THR
1	A	343	LEU
1	A	357	LYS
1	A	359	THR
1	A	362	LEU
1	A	364	THR
1	A	366	ILE
1	A	383	GLN
1	A	387	ARG
1	A	390	LEU
1	A	410	THR
1	A	413	THR
1	A	414	GLN
1	A	430	VAL
1	A	439	ARG

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Mol	Chain	Res	Type
1	A	455	GLN
1	A	478	LEU
1	B	31	ASP
1	B	41	ILE
1	B	57	VAL
1	B	63	ASN
1	B	70	THR
1	B	93	HIS
1	B	98	GLU
1	B	130	ASP
1	B	144	SER
1	B	146	LEU
1	B	156	VAL
1	B	177	THR
1	B	178	TRP
1	B	187	GLU
1	B	189	ARG
1	B	191	LEU
1	B	192	HIS
1	B	200	LEU
1	B	205	TYR
1	B	218	GLU
1	B	222	ILE
1	B	234	TRP
1	B	238	PHE
1	B	254	ARG
1	B	269	ASP
1	B	280	ARG
1	B	282	LEU
1	B	287	ILE
1	B	288	VAL
1	B	289	ILE
1	B	307	THR
1	B	343	LEU
1	B	357	LYS
1	B	359	THR
1	B	362	LEU
1	B	364	THR
1	B	366	ILE
1	B	383	GLN
1	B	387	ARG
1	B	390	LEU

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Mol	Chain	Res	Type
1	B	410	THR
1	B	413	THR
1	B	414	GLN
1	B	430	VAL
1	B	439	ARG
1	B	455	GLN
1	B	478	LEU
1	C	31	ASP
1	C	41	ILE
1	C	57	VAL
1	C	63	ASN
1	C	70	THR
1	C	93	HIS
1	C	98	GLU
1	C	130	ASP
1	C	144	SER
1	C	146	LEU
1	C	156	VAL
1	C	177	THR
1	C	178	TRP
1	C	187	GLU
1	C	189	ARG
1	C	191	LEU
1	C	192	HIS
1	C	200	LEU
1	C	205	TYR
1	C	218	GLU
1	C	222	ILE
1	C	234	TRP
1	C	238	PHE
1	C	254	ARG
1	C	269	ASP
1	C	280	ARG
1	C	282	LEU
1	C	287	ILE
1	C	288	VAL
1	C	289	ILE
1	C	307	THR
1	C	343	LEU
1	C	357	LYS
1	C	359	THR
1	C	362	LEU

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Mol	Chain	Res	Type
1	C	364	THR
1	C	366	ILE
1	C	383	GLN
1	C	387	ARG
1	C	390	LEU
1	C	410	THR
1	C	413	THR
1	C	414	GLN
1	C	430	VAL
1	C	439	ARG
1	C	455	GLN
1	C	478	LEU
1	D	31	ASP
1	D	41	ILE
1	D	57	VAL
1	D	63	ASN
1	D	70	THR
1	D	93	HIS
1	D	98	GLU
1	D	130	ASP
1	D	144	SER
1	D	146	LEU
1	D	156	VAL
1	D	177	THR
1	D	178	TRP
1	D	187	GLU
1	D	189	ARG
1	D	191	LEU
1	D	192	HIS
1	D	200	LEU
1	D	205	TYR
1	D	218	GLU
1	D	222	ILE
1	D	234	TRP
1	D	238	PHE
1	D	254	ARG
1	D	269	ASP
1	D	280	ARG
1	D	282	LEU
1	D	287	ILE
1	D	288	VAL
1	D	289	ILE

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Mol	Chain	Res	Type
1	D	307	THR
1	D	343	LEU
1	D	357	LYS
1	D	359	THR
1	D	362	LEU
1	D	364	THR
1	D	366	ILE
1	D	383	GLN
1	D	387	ARG
1	D	390	LEU
1	D	410	THR
1	D	413	THR
1	D	414	GLN
1	D	430	VAL
1	D	439	ARG
1	D	455	GLN
1	D	478	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	74	GLN
1	A	93	HIS
1	A	95	HIS
1	A	166	ASN
1	A	192	HIS
1	A	233	GLN
1	A	279	GLN
1	A	286	HIS
1	A	297	ASN
1	A	298	GLN
1	A	336	GLN
1	A	373	ASN
1	A	380	HIS
1	A	383	GLN
1	A	400	GLN
1	B	63	ASN
1	B	74	GLN
1	B	93	HIS
1	B	95	HIS
1	B	166	ASN

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Mol	Chain	Res	Type
1	B	192	HIS
1	B	233	GLN
1	B	279	GLN
1	B	286	HIS
1	B	297	ASN
1	B	298	GLN
1	B	336	GLN
1	B	373	ASN
1	B	380	HIS
1	B	383	GLN
1	B	400	GLN
1	C	63	ASN
1	C	74	GLN
1	C	93	HIS
1	C	95	HIS
1	C	166	ASN
1	C	192	HIS
1	C	233	GLN
1	C	279	GLN
1	C	286	HIS
1	C	297	ASN
1	C	298	GLN
1	C	336	GLN
1	C	373	ASN
1	C	380	HIS
1	C	383	GLN
1	C	400	GLN
1	D	63	ASN
1	D	74	GLN
1	D	93	HIS
1	D	95	HIS
1	D	166	ASN
1	D	192	HIS
1	D	233	GLN
1	D	279	GLN
1	D	286	HIS
1	D	297	ASN
1	D	298	GLN
1	D	336	GLN
1	D	373	ASN
1	D	383	GLN
1	D	400	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

4 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	FAD	A	501	-	51,58,58	1.76	8 (15%)	60,89,89	2.08	10 (16%)
2	FAD	D	501	-	51,58,58	1.77	8 (15%)	60,89,89	2.07	10 (16%)
2	FAD	B	501	-	51,58,58	1.76	8 (15%)	60,89,89	2.08	10 (16%)
2	FAD	C	501	-	51,58,58	1.76	8 (15%)	60,89,89	2.08	10 (16%)

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	FAD	A	501	-	-	1/30/50/50	0/6/6/6
2	FAD	D	501	-	-	1/30/50/50	0/6/6/6
2	FAD	B	501	-	-	1/30/50/50	0/6/6/6
2	FAD	C	501	-	-	1/30/50/50	0/6/6/6

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	FAD	C4X-C10	5.27	1.44	1.38
2	A	501	FAD	C4X-C10	5.26	1.44	1.38
2	D	501	FAD	C4X-C10	5.26	1.44	1.38
2	C	501	FAD	C4X-C10	5.23	1.44	1.38
2	A	501	FAD	C9A-N10	4.75	1.44	1.38
2	B	501	FAD	C9A-N10	4.73	1.44	1.38
2	C	501	FAD	C9A-N10	4.71	1.44	1.38
2	D	501	FAD	C9A-N10	4.71	1.44	1.38
2	A	501	FAD	C4X-N5	4.52	1.39	1.33
2	B	501	FAD	C4X-N5	4.52	1.39	1.33
2	D	501	FAD	C4X-N5	4.51	1.39	1.33
2	C	501	FAD	C4X-N5	4.47	1.39	1.33
2	D	501	FAD	C1'-N10	4.16	1.52	1.48
2	C	501	FAD	C1'-N10	4.11	1.52	1.48
2	A	501	FAD	C1'-N10	4.11	1.52	1.48
2	B	501	FAD	C1'-N10	4.09	1.52	1.48
2	A	501	FAD	C10-N1	3.88	1.38	1.33
2	D	501	FAD	C10-N1	3.87	1.38	1.33
2	C	501	FAD	C10-N1	3.85	1.38	1.33
2	B	501	FAD	C10-N1	3.84	1.38	1.33
2	B	501	FAD	C4-N3	3.56	1.39	1.33
2	D	501	FAD	C4-N3	3.55	1.39	1.33
2	A	501	FAD	C4-N3	3.53	1.39	1.33
2	C	501	FAD	C4-N3	3.52	1.39	1.33
2	C	501	FAD	C2A-N1A	2.33	1.38	1.33
2	B	501	FAD	C2A-N1A	2.33	1.38	1.33
2	D	501	FAD	C2A-N1A	2.32	1.38	1.33
2	A	501	FAD	C2A-N1A	2.31	1.38	1.33
2	D	501	FAD	C2A-N3A	2.29	1.35	1.32
2	B	501	FAD	C2A-N3A	2.28	1.35	1.32
2	A	501	FAD	C2A-N3A	2.27	1.35	1.32
2	C	501	FAD	C2A-N3A	2.25	1.35	1.32

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	FAD	C4-N3-C2	10.95	124.39	115.14
2	C	501	FAD	C4-N3-C2	10.94	124.38	115.14
2	B	501	FAD	C4-N3-C2	10.93	124.37	115.14
2	D	501	FAD	C4-N3-C2	10.88	124.33	115.14
2	C	501	FAD	C1'-N10-C9A	4.94	122.18	118.29
2	D	501	FAD	C1'-N10-C9A	4.90	122.15	118.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	FAD	C1'-N10-C9A	4.89	122.14	118.29
2	B	501	FAD	C1'-N10-C9A	4.86	122.12	118.29
2	B	501	FAD	C4X-C4-N3	-4.71	116.99	123.43
2	A	501	FAD	C4X-C4-N3	-4.70	117.01	123.43
2	C	501	FAD	C4X-C4-N3	-4.68	117.03	123.43
2	D	501	FAD	C4X-C4-N3	-4.68	117.03	123.43
2	B	501	FAD	C4X-N5-C5X	4.23	121.00	116.77
2	C	501	FAD	C4X-N5-C5X	4.22	120.99	116.77
2	D	501	FAD	C4X-N5-C5X	4.19	120.96	116.77
2	A	501	FAD	C4X-N5-C5X	4.18	120.95	116.77
2	A	501	FAD	O4B-C1B-C2B	-2.47	103.31	106.93
2	B	501	FAD	O4B-C1B-C2B	-2.46	103.32	106.93
2	D	501	FAD	O4B-C1B-C2B	-2.46	103.33	106.93
2	C	501	FAD	O4B-C1B-C2B	-2.45	103.34	106.93
2	A	501	FAD	O3'-C3'-C4'	-2.30	103.25	108.81
2	C	501	FAD	O3'-C3'-C4'	-2.30	103.25	108.81
2	D	501	FAD	O3'-C3'-C4'	-2.30	103.27	108.81
2	B	501	FAD	O3'-C3'-C4'	-2.30	103.27	108.81
2	C	501	FAD	C4-C4X-C10	-2.29	118.44	119.95
2	C	501	FAD	C5A-C6A-N6A	2.26	123.78	120.35
2	D	501	FAD	C4-C4X-C10	-2.26	118.46	119.95
2	D	501	FAD	C5A-C6A-N6A	2.26	123.78	120.35
2	A	501	FAD	C5A-C6A-N6A	2.25	123.76	120.35
2	B	501	FAD	C5A-C6A-N6A	2.24	123.76	120.35
2	A	501	FAD	C4-C4X-C10	-2.22	118.48	119.95
2	B	501	FAD	C4-C4X-C10	-2.20	118.49	119.95
2	C	501	FAD	N3A-C2A-N1A	-2.11	125.38	128.68
2	A	501	FAD	N3A-C2A-N1A	-2.10	125.40	128.68
2	B	501	FAD	N3A-C2A-N1A	-2.10	125.40	128.68
2	D	501	FAD	N3A-C2A-N1A	-2.09	125.42	128.68
2	C	501	FAD	C5X-C9A-N10	2.07	119.22	117.72
2	D	501	FAD	C5X-C9A-N10	2.04	119.19	117.72
2	B	501	FAD	C5X-C9A-N10	2.04	119.19	117.72
2	A	501	FAD	C5X-C9A-N10	2.03	119.19	117.72

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	FAD	O4B-C4B-C5B-O5B
2	D	501	FAD	O4B-C4B-C5B-O5B
2	B	501	FAD	O4B-C4B-C5B-O5B

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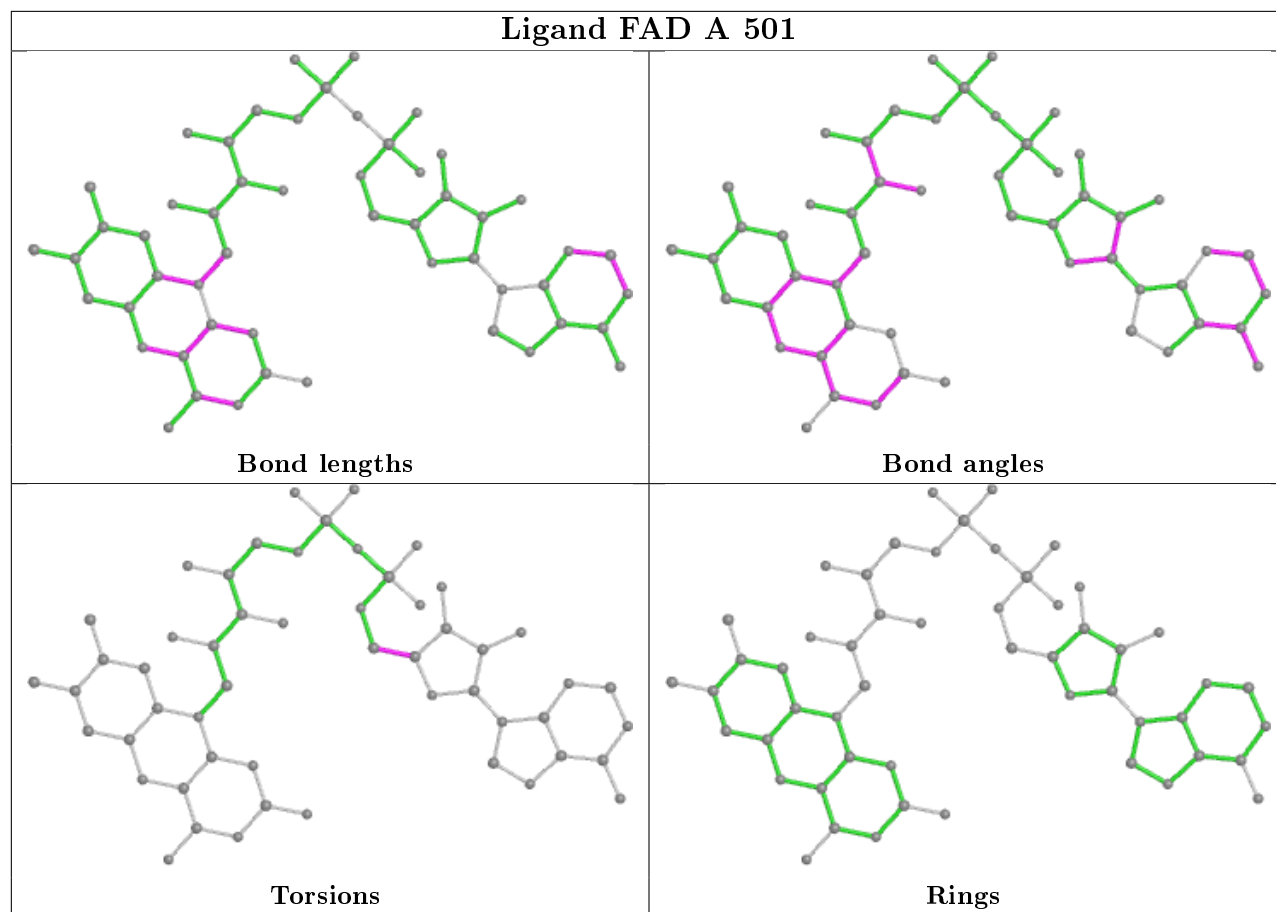
Mol	Chain	Res	Type	Atoms
2	C	501	FAD	O4B-C4B-C5B-O5B

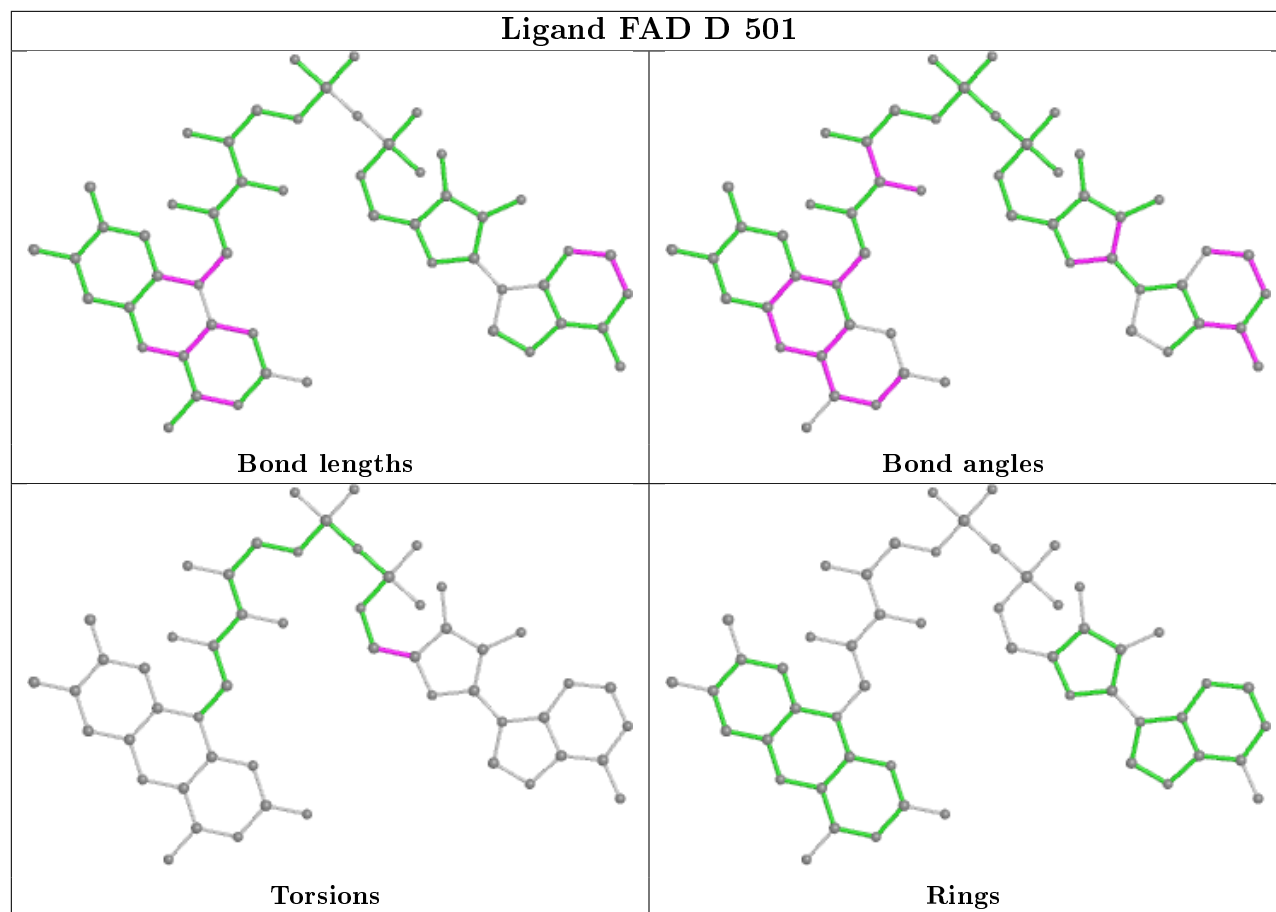
There are no ring outliers.

4 monomers are involved in 15 short contacts:

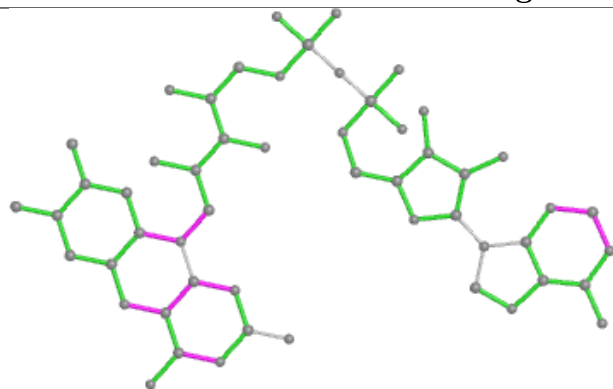
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	FAD	4	0
2	D	501	FAD	3	0
2	B	501	FAD	4	0
2	C	501	FAD	4	0

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

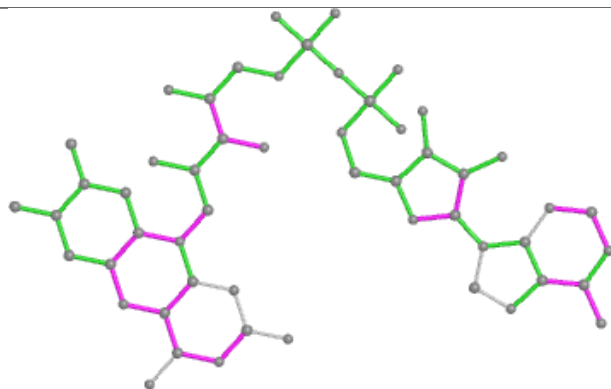




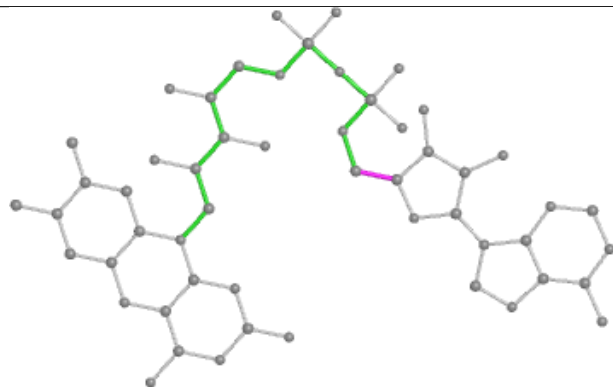
## Ligand FAD B 501



Bond lengths



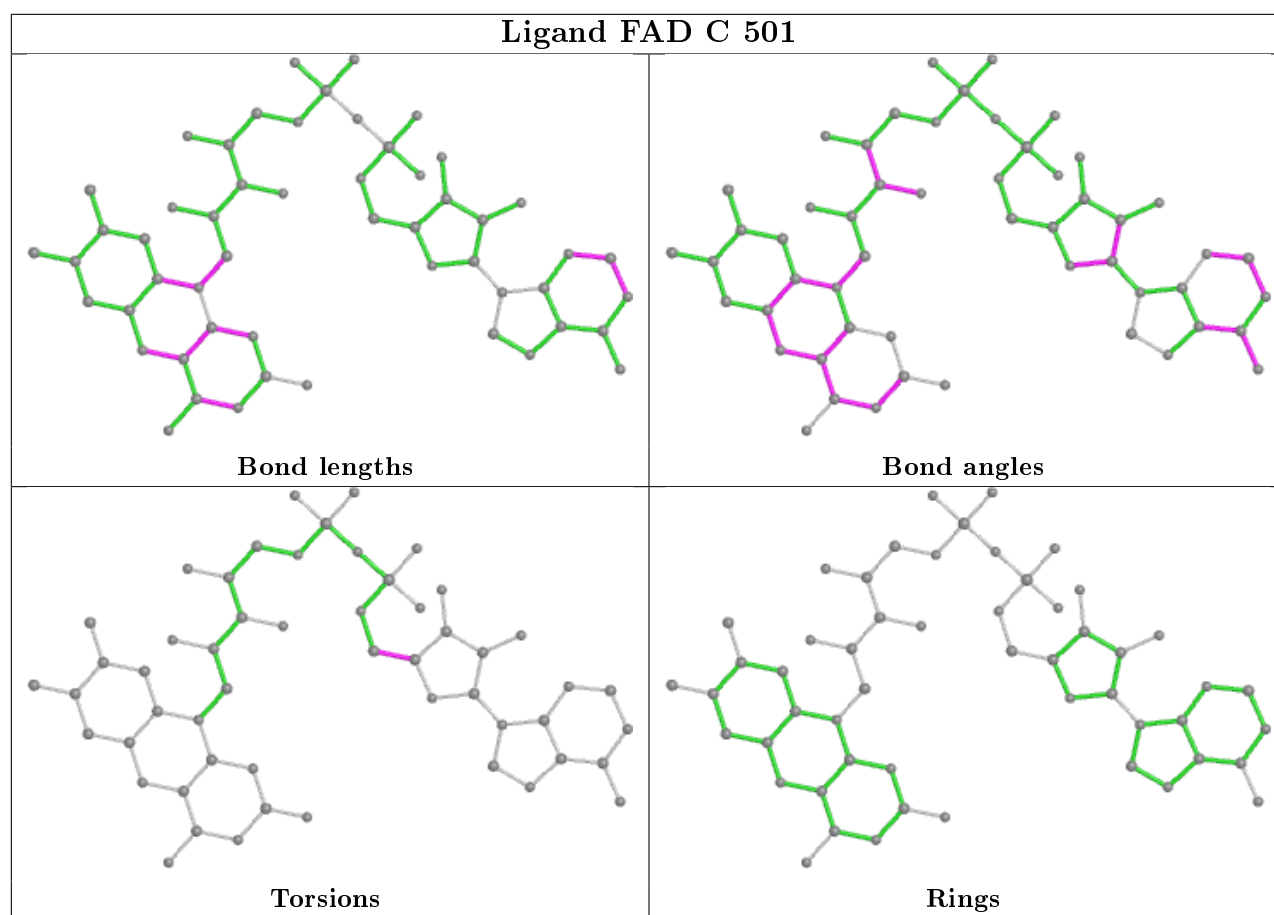
Bond angles



Torsions



Rings



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	451/471 (95%)	-0.25	1 (0%) 95 87	13, 24, 44, 67	0
1	B	451/471 (95%)	-0.28	3 (0%) 87 69	13, 24, 44, 67	0
1	C	451/471 (95%)	-0.27	0 100 100	13, 24, 44, 67	0
1	D	451/471 (95%)	-0.31	1 (0%) 95 87	13, 24, 44, 67	0
All	All	1804/1884 (95%)	-0.28	5 (0%) 94 84	13, 24, 45, 67	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	130	ASP	2.7
1	D	130	ASP	2.5
1	A	271	SER	2.4
1	B	53	GLN	2.2
1	B	129	ASP	2.2

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

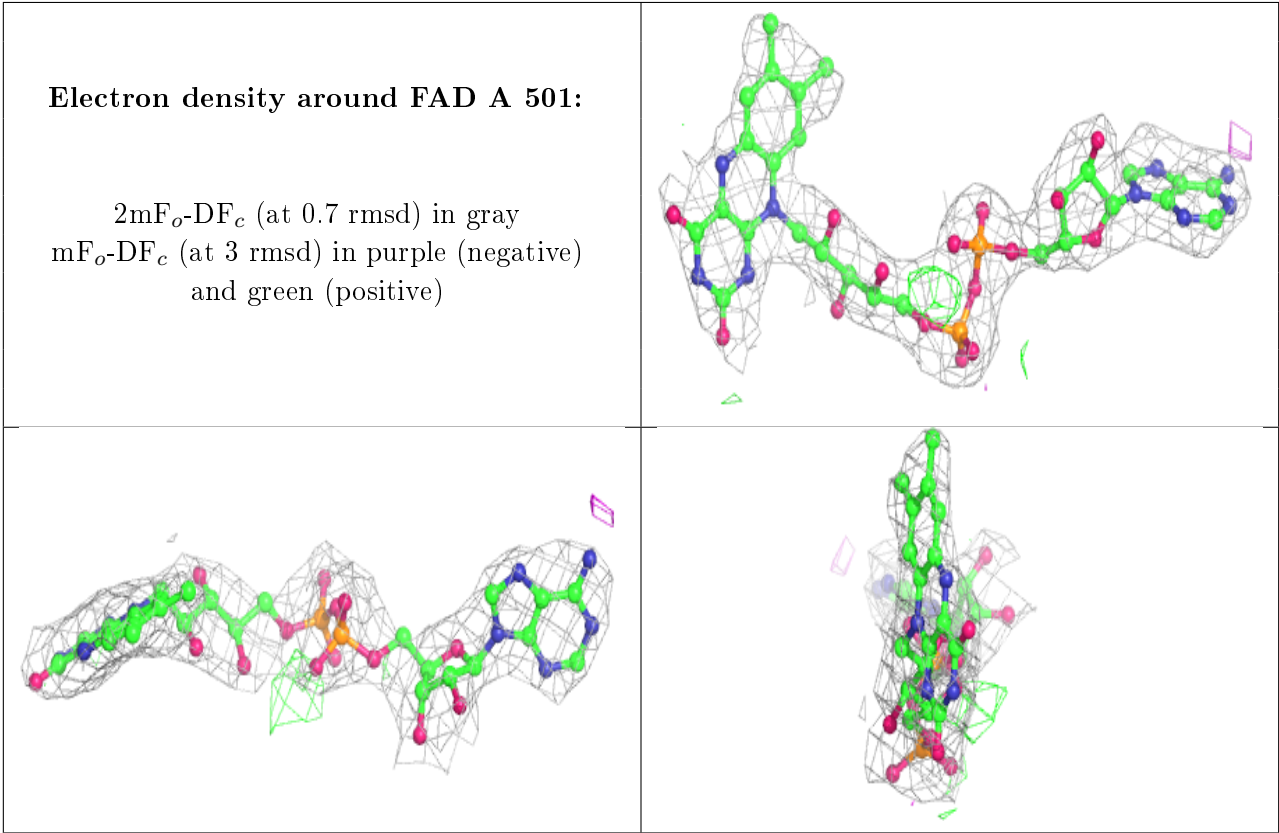
### 6.4 Ligands [i](#)

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.

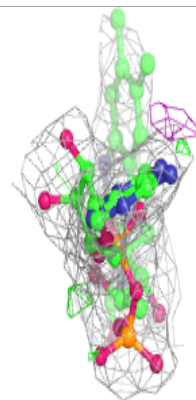
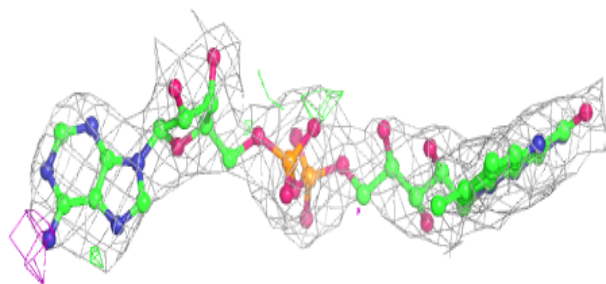
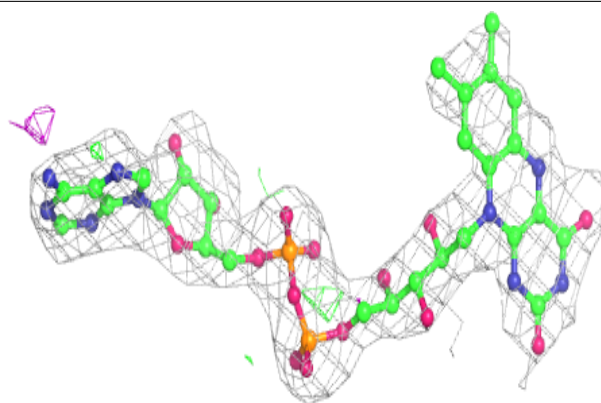
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	FAD	A	501	53/53	0.94	0.20	18,26,35,36	0
2	FAD	C	501	53/53	0.94	0.18	18,26,35,36	0
2	FAD	B	501	53/53	0.95	0.19	18,26,35,36	0
2	FAD	D	501	53/53	0.95	0.17	18,26,35,36	0

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.

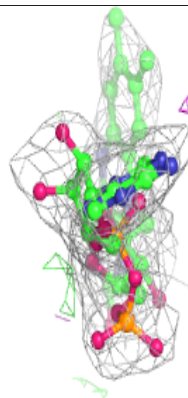
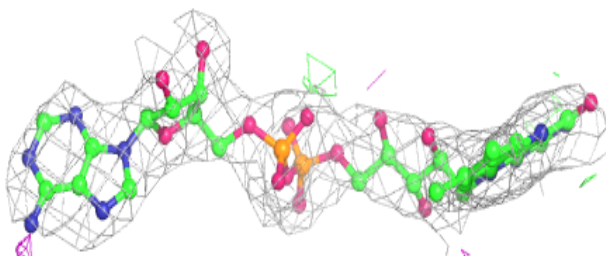
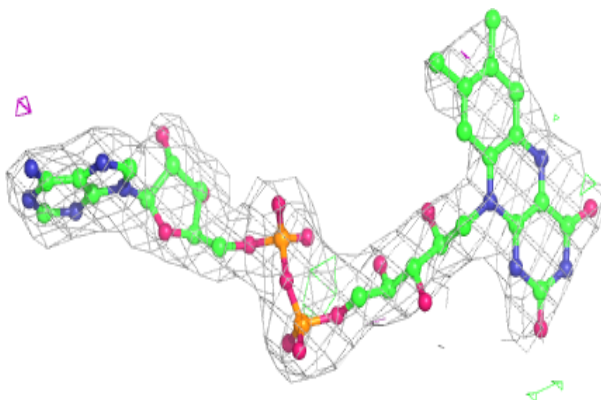


**Electron density around FAD C 501:**

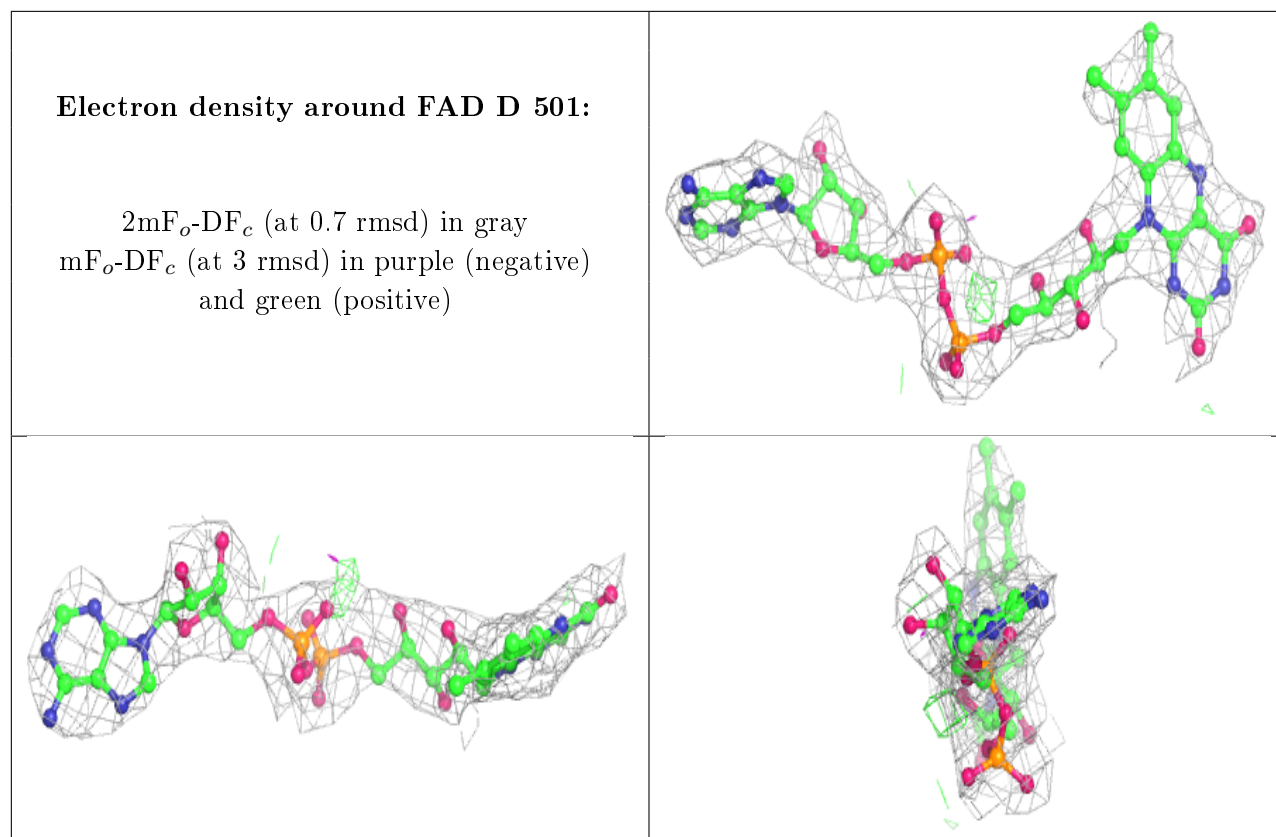
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around FAD B 501:**

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







## 6.5 Other polymers [i](#)

There are no such residues in this entry.